TRISPECIFIC AND/OR TRIVALENT BINDING PROTEINS FOR PREVENTION OR TREATMENT OF HIV INFECTION

CROSS REFERENCES TO RELATED APPLICATIONS

[0001] This application claims the priority benefit of U.S. Provisional Application Serial No. 62/246,113, filed October 25, 2015, EP Application No. EP16305211.1, filed February 24, 2016, U.S. Provisional Application Serial No. 62/322,029, filed April 13, 2016, and U.S. Provisional Application Serial No. 62/331,169, filed May 03, 2016, which are incorporated herein by reference in their entirety.

[0002] This invention was created in the performance of a Cooperative Research and Development Agreement (NIAID #2014-0038) with the National Institutes of Health, an agency of the Department of Health and Human Services. The Government of the United States has certain rights in this invention.

SUBMISSION OF SEQUENCE LISTING ON ASCII TEXT FILE

[0003] 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: 183952027041SEQLIST.txt, date recorded: October 19, 2016, size: 1,064 KB).

FIELD OF THE INVENTION

[0004] 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 and wherein a second pair of polypeptides forming the binding protein possess a single variable domain. 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

[0005] One of the challenges in treating HIV/AIDS with neutralizing antibodies is potential breakthrough infection due to the high mutation rate of HIV-1 viruses. Additionally, virological events in the early weeks following HIV-1 transmission set the

stage for lifelong chronic infection that remains incurable with currently available combination antiretroviral therapy (cART). This is due, at least in part, to the early establishment of viral reservoirs, including latently infected cells, which persist despite cART, leading to recrudescent infection when treatment is interrupted. Newly discovered anti-HIV-1 neutralizing antibodies with improved breadth and potency may provide more options for HIV/AIDS treatment and prevention; however, breakthrough infection remains a major issue in the field.

BRIEF SUMMARY

[0006] In one embodiment, the disclosure provides 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:

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

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

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

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

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

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; 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.

[0007] In some embodiments, the second polypeptide chain further comprises 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, the third polypeptide chain further comprises 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, 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 first Fc region comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 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 C_{H1}, the second Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} 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 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 C_{H1}, the first Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} 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 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 C_{H1}, the second Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} 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 according to EU Index, wherein the amino acid substitutions are S354C and T366W. 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, and 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 comprise amino acid substitutions at

positions corresponding to positions 428 and 434 of human IgG1 according to EU Index, wherein the amino acid substitutions are M428L and N434S.

[0008] In one embodiment, the disclosure provides 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:

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

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.

[0009] In some embodiments, the C_{H3} domain of the second polypeptide chain comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 according to EU Index, wherein the amino acid substitutions are S354C and T366W; and wherein the 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

according to EU Index, wherein the amino acid substitutions are Y349C, T366S, L368A, and Y407V. In some embodiments, the 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 according to EU Index, wherein the amino acid substitutions are Y349C, T366S, L368A, and Y407V; and wherein the C_{H3} domain of the third polypeptide chain comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 according to EU Index, wherein the amino acid substitutions are S354C and T366W. In some embodiments, the C_{H3} domains of the second and the third polypeptide chains both comprise amino acid substitutions at positions corresponding to positions 428 and 434 of human IgG1 according to EU Index, wherein the amino acid substitutions are M428L and N434S.

[0010] In some embodiments, the one or more HIV target protein is selected from the group consisting of glycoprotein 120, glycoprotein 41 and glycoprotein 160. In some embodiments, the binding protein is trispecific and capable of specifically binding three different epitopes on a single HIV target protein. In some embodiments, the binding protein is trispecific and capable of specifically binding two different epitopes on a first HIV target protein, and one epitope on a second HIV target protein, wherein the first and second HIV target proteins are different. In some embodiments, the binding protein is trispecific and capable of specifically binding three different antigen targets. In some embodiments, the binding protein is capable of inhibiting the function of one or more HIV target proteins. In some embodiments, V_{L1} comprises a CDR-L1, CDR-L2, and CDR-L3 comprising a sequence as set forth in SEQ ID NOs: 266, 267, and 268, respectively; a sequence as set forth in SEQ ID NOs: 269, 270, and 271, respectively; a sequence as set forth in SEQ ID NOs: 500, 501, and 274, respectively; a sequence as set forth in SEQ ID NOs: 275, 276, and 277, respectively; a sequence as set forth in SEQ ID NOs: 281, 282, and 283, respectively; or a sequence as set forth in SEQ ID NOs: 278, 279, and 280, respectively. In some embodiments, V_{L1} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, and 521. In some embodiments, V_{L1} comprises a light chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, and 521. In some embodiments, V_{L2} comprises a CDR-L1, CDR-L2, and CDR-L3 comprising a sequence as set forth in SEQ ID NOs: 266, 267, and 268, respectively; a sequence as set forth in SEQ

ID NOs: 269, 270, and 271, respectively; a sequence as set forth in SEQ ID NOs: 500, 501, and 274, respectively; a sequence as set forth in SEQ ID NOs: 275, 276, and 277, respectively; a sequence as set forth in SEQ ID NOs: 281, 282, and 283, respectively; or a sequence as set forth in SEQ ID NOs: 278, 279, and 280, respectively. In some embodiments, V_{L2} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, and 521. In some embodiments, V_{L2} comprises a light chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, and 521. In some embodiments, V_{L3} comprises a CDR-L1, CDR-L2, and CDR-L3 comprising a sequence as set forth in SEQ ID NOs: 266, 267, and 268, respectively; a sequence as set forth in SEQ ID NOs: 269, 270, and 271, respectively; a sequence as set forth in SEQ ID NOs: 500, 501, and 274, respectively; a sequence as set forth in SEQ ID NOs: 275, 276, and 277, respectively; a sequence as set forth in SEQ ID NOs: 281, 282, and 283, respectively; or a sequence as set forth in SEQ ID NOs: 278, 279, and 280, respectively. In some embodiments, V_{L3} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, and 521. In some embodiments, V_{L3} comprises a light chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, and 521. In some embodiments, V_{H1} comprises a CDR-H1, CDR-H2, and CDR-H3 comprising a sequence as set forth in SEQ ID NOs: 248, 497, and 250, respectively; a sequence as set forth in SEQ ID NOs: 251, 252, and 253, respectively; a sequence as set forth in SEQ ID NOs: 254, 255, and 256, respectively; a sequence as set forth in SEQ ID NOs: 254, 255, and 498, respectively; a sequence as set forth in SEQ ID NOs: 257, 258, and 259, respectively; a sequence as set forth in SEQ ID NOs: 263, 264, and 265, respectively; or a sequence as set forth in SEQ ID NOs: 499, 261, and 262, respectively. In some embodiments, V_{H1} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 502, 503, 504, 505, 506, 507, and 508. In some embodiments, V_{H1} comprises a heavy chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 502, 503, 504, 505, 506, 507, and 508. In some embodiments, V_{H2} comprises a CDR-H1, CDR-H2, and CDR-H3 comprising a sequence as set forth in SEQ ID NOs: 248, 497, and 250, respectively; a sequence as set forth in SEQ

ID NOs: 251, 252, and 253, respectively; a sequence as set forth in SEQ ID NOs: 254, 255, and 256, respectively; a sequence as set forth in SEQ ID NOs: 254, 255, and 498, respectively; a sequence as set forth in SEQ ID NOs: 257, 258, and 259, respectively; a sequence as set forth in SEQ ID NOs: 263, 264, and 265, respectively; or a sequence as set forth in SEQ ID NOs: 499, 261, and 262, respectively. In some embodiments, V_{H2} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 502, 503, 504, 505, 506, 507, and 508. In some embodiments, V_{H2} comprises a heavy chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 502, 503, 504, 505, 506, 507, and 508. In some embodiments, V_{H3} comprises a CDR-H1, CDR-H2, and CDR-H3 comprising a sequence as set forth in SEQ ID NOs: 248, 497, and 250, respectively; a sequence as set forth in SEQ ID NOs: 251, 252, and 253, respectively; a sequence as set forth in SEQ ID NOs: 254, 255, and 256, respectively; a sequence as set forth in SEQ ID NOs: 254, 255, and 498, respectively; a sequence as set forth in SEQ ID NOs: 257, 258, and 259, respectively; a sequence as set forth in SEQ ID NOs: 263, 264, and 265, respectively; or a sequence as set forth in SEQ ID NOs: 499, 261, and 262, respectively. In some embodiments, V_{H3} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 502, 503, 504, 505, 506, 507, and 508. In some embodiments, V_{H3} comprises a heavy chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 502, 503, 504, 505, 506, 507, and 508. In some embodiments, V_{L1} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 500, a CDR-L2 comprising the sequence of SEQ ID NO: 501, and a CDR-L3 comprising the sequence of SEQ ID NO: 274; V_{L2} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 275, a CDR-L2 comprising the sequence of SEQ ID NO: 276, and a CDR-L3 comprising the sequence of SEQ ID NO: 277; V_{L3} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 266, a CDR-L2 comprising the sequence of SEQ ID NO: 267, and a CDR-L3 comprising the sequence of SEQ ID NO: 268; V_{H1} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 254, a CDR-H2 comprising the sequence of SEQ ID NO: 255, and a CDR-H3 comprising the sequence of SEQ ID NO: 256; V_{H2} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 257, a CDR-H2 comprising the sequence of SEQ ID NO: 258, and a CDR-H3 comprising the sequence of SEQ ID NO: 259; and V_{H3} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 248, a CDR-H2 comprising

the sequence of SEQ ID NO: 497, and a CDR-H3 comprising the sequence of SEQ ID NO: 250. In some embodiments, V_{L1} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 518; V_{L2} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 519; V_{L3} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 512; V_{H1} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 504; V_{H2} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 506; and V_{H3} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 502. In some embodiments, V_{L1} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 518; V_{L2} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 519; V_{L3} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 512; V_{H1} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 504; V_{H2} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 506; and V_{H3} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 502. In some embodiments, V_{L1} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 500, a CDR-L2 comprising the sequence of SEQ ID NO: 501, and a CDR-L3 comprising the sequence of SEQ ID NO: 274; V_{L2} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 275, a CDR-L2 comprising the sequence of SEQ ID NO: 276, and a CDR-L3 comprising the sequence of SEQ ID NO: 277; V_{L3} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 269, a CDR-L2 comprising the sequence of SEQ ID NO: 270, and a CDR-L3 comprising the sequence of SEQ ID NO: 271; V_{H1} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 254, a CDR-H2 comprising the sequence of SEQ ID NO: 255, and a CDR-H3 comprising the sequence of SEQ ID NO: 256; V_{H2} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 257, a CDR-H2 comprising the sequence of SEQ ID NO: 258, and a CDR-H3 comprising the sequence of SEQ ID NO: 259; and V_{H3} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 251, a CDR-H2 comprising the sequence of SEQ ID NO: 252, and a CDR-H3 comprising the sequence of SEQ ID NO: 253. In some embodiments, V_{L1} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable

domain comprising the light chain variable domain sequence of SEQ ID NO: 518; V_{L2} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 519; V_{L3} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 513; V_{H1} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 504; V_{H2} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 506; and V_{H3} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 503. In some embodiments, V_{L1} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 518; V_{L2} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 519; V_{L3} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 513; V_{H1} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 504; V_{H2} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 506; and V_{H3} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 503. In some embodiments, V_{L1} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 275, a CDR-L2 comprising the sequence of SEQ ID NO: 276, and a CDR-L3 comprising the sequence of SEQ ID NO: 277; V_{L2} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 500, a CDR-L2 comprising the sequence of SEQ ID NO: 501, and a CDR-L3 comprising the sequence of SEQ ID NO: 274; V_{L3} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 269, a CDR-L2 comprising the sequence of SEQ ID NO: 270, and a CDR-L3 comprising the sequence of SEQ ID NO: 271; V_{H1} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 257, a CDR-H2 comprising the sequence of SEQ ID NO: 258, and a CDR-H3 comprising the sequence of SEQ ID NO: 259; V_{H2} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 254, a CDR-H2 comprising the sequence of SEQ ID NO: 255, and a CDR-H3 comprising the sequence of SEQ ID NO: 256; and V_{H3} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 251, a CDR-H2 comprising the sequence of SEQ ID NO: 252, and a CDR-H3 comprising the sequence of SEQ ID NO: 253. In some embodiments, V_{L1} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 519; V_{L2} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable

domain sequence of SEQ ID NO: 518; V_{L3} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 513; V_{H1} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 506; V_{H2} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 504; and V_{H3} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 503. In some embodiments, V_{L1} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 519; V_{L2} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 518; V_{L3} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 513; V_{H1} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 506; V_{H2} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 504; and V_{H3} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 503. In some embodiments, 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, or L_4 are each independently at least one amino acid in length. In some embodiments, L_1 comprises Asp-Lys-Thr-His-Thr (SEQ ID NO: 525).

[0011] In one embodiment, the disclosure provides a binding protein comprising four polypeptide chains that form three antigen binding sites, 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:

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

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

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

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 the immunoglobulin C_{H1} heavy chain constant domain; 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:

(a) V_{L1}, V_{L2} and V_{L3} are each independently a variable domain derived from an amino acid sequence as set forth in any one of SEQ ID NOs: 2, 4, 10, 12, 18, 20, 26, 28, 34, 36, 42, 44, 50, 52, 58, 60, 66, 68, 74, 76, 82, 84, 90, 92, 98, 100, 106, 108, 114, 116, 122, 124, 130, 132, 138, 140, 146, 148, 154, 156, 162, 164, 170, 172, 178, 180, 186, 188, 194, 196, 202, 204, 210,212, 218, 220, 226, 228, 233, 235, 241, 243; or

(b) V_{L1}, V_{L2} and V_{L3} each independently comprise light chain complementarity determining regions of a variable domain comprising an amino acid sequence as set forth in any one of SEQ ID NOs:266-283; and

wherein:

(a) V_{H1}, V_{H2}, and V_{H3} are each independently a variable domain derived from an amino acid sequence as set forth in any one of SEQ ID NOs: 1, 3, 9, 11, 17, 10, 25, 27, 33, 35, 41, 43, 49, 51, 57, 59, 65, 67, 73, 75, 81, 83, 89, 91, 97, 99, 105, 107, 113, 115, 121, 123, 129, 131, 137, 139, 145, 147, 153, 155, 161, 163, 169, 171, 177, 179, 185, 187, 193, 195, 201, 203, 209, 211, 217, 219, 225, 227, 232, 234, 240, 242; or

(b) V_{H1}, V_{H2}, and V_{H3} each independently comprise heavy chain complementarity determining regions of a variable domain comprising an amino acid sequence as set forth in any one of SEQ ID NOs: 248-265.

[0012] In some embodiments, the second polypeptide chain further comprises 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, the third polypeptide chain further comprises 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, 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 first Fc region

comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 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 C_{H1}, the second Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} 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 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 C_{H1}, the first Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} 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 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 C_{H1}, the second Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} 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 according to EU Index, wherein the amino acid substitutions are S354C and T366W. 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, and 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 comprise amino acid substitutions at positions corresponding to positions 428 and 434 of human IgG1 according to EU Index, wherein the amino acid substitutions are M428L and N434S.

[0013] In one embodiment, the disclosure provides a binding protein comprising four polypeptide chains that form three antigen binding sites, 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 the 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:

(a) V_{L1}, V_{L2} and V_{L3} are each independently a variable domain derived from an amino acid sequence as set forth in any one of SEQ ID NOs: 2, 4, 10, 12, 18, 20, 26, 28, 34, 36, 42, 44, 50, 52, 58, 60, 66, 68, 74, 76, 82, 84, 90, 92, 98, 100, 106, 108, 114, 116, 122, 124, 130, 132, 138, 140, 146, 148, 154, 156, 162, 164, 170, 172, 178, 180, 186, 188, 194, 196, 202, 204, 210,212, 218, 220, 226, 228, 233, 235, 241, 243; or

(b) V_{L1}, V_{L2} and V_{L3} each independently comprise light chain complementarity determining regions of a variable domain comprising an amino acid sequence as set forth in any one of SEQ ID NOs:266-283; and

wherein:

(a) V_{H1}, V_{H2}, and V_{H3} are each independently a variable domain derived from an amino acid sequence as set forth in any one of SEQ ID NOs: 1, 3, 9, 11, 17, 10, 25, 27, 33, 35, 41, 43, 49, 51, 57, 59, 65, 67, 73, 75, 81, 83, 89, 91, 97, 99, 105, 107, 113, 115, 121, 123, 129, 131, 137, 139, 145, 147, 153, 155, 161, 163, 169, 171, 177, 179, 185, 187, 193, 195, 201, 203, 209, 211, 217, 219, 225, 227, 232, 234, 240, 242; or

(b) V_{H1}, V_{H2}, and V_{H3} each independently comprise heavy chain complementarity determining regions of a variable domain comprising an amino acid sequence as set forth in any one of SEQ ID NOs: 248-265.

[0014] In some embodiments, the C_{H3} domain of the second polypeptide chain comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 according to EU Index, wherein the amino acid substitutions are S354C and T366W; and wherein the 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 according to EU Index, wherein the amino acid substitutions are Y349C, T366S, L368A, and Y407V. In some embodiments, the 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 according to EU Index, wherein the amino acid substitutions are Y349C, T366S, L368A, and Y407V; and wherein the C_{H3} domain of the third polypeptide chain comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 according to EU Index, wherein the amino acid substitutions are S354C and T366W. In some embodiments, the C_{H3} domains of the second and the third polypeptide chains both comprise amino acid substitutions at positions corresponding to positions 428 and 434 of human IgG1 according to EU Index, wherein the amino acid substitutions are M428L and N434S.

[0015] In some embodiments, 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, or L_4 are each independently at least one amino acid in length. In some embodiments, L_1 comprises Asp-Lys-Thr-His-Thr (SEQ ID NO: 525).

[0016] In one embodiment, the disclosure provides a trispecific and/or trivalent binding protein comprising four polypeptide chains that form three antigen binding sites that specifically bind three different HIV target proteins, 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:

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

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}-C_L [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

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.

[0017] In one embodiment, the disclosure provides a binding protein comprising four polypeptide chains that form three antigen binding sites, wherein a first polypeptide chain has a structure represented by the formula:

V_{L2}-L_1-V_{L1}-L_2-C_L [I]

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

V_{H1}-L_3-V_{H2}-L_4-C_{H1} [II]

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

V_{H3}- C_{H1} [III]

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

V_{L3}- C_L [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

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:

(a) V_{L1}, V_{L2} and V_{L3} are each independently a variable domain derived from an amino acid sequence as set forth in any one of SEQ ID NOs: 2, 4, 10, 12, 18, 20, 26, 28, 34, 36, 42, 44, 50, 52, 58, 60, 66, 68, 74, 76, 82, 84, 90, 92, 98, 100, 106, 108, 114, 116, 122, 124, 130, 132, 138, 140, 146, 148, 154, 156, 162, 164, 170, 172, 178, 180, 186, 188, 194, 196, 202, 204, 210,212, 218, 220, 226, 228, 233, 235, 241, 243; or

(b) $V_{L1,}$ V_{L2} and V_{L3} each independently comprise light chain complementarity determining regions of a variable domain comprising an amino acid sequence as set forth in any one of SEQ ID NOs:266-283; and

wherein:

(a) $V_{H1,}$ $V_{H2,}$ and V_{H3} are each independently a variable domain derived from an amino acid sequence as set forth in any one of SEQ ID NOs: 1, 3, 9, 11, 17, 10, 25, 27, 33, 35, 41, 43, 49, 51, 57, 59, 65, 67, 73, 75, 81, 83, 89, 91, 97, 99, 105, 107, 113, 115, 121, 123, 129, 131, 137, 139, 145, 147, 153, 155, 161, 163, 169, 171, 177, 179, 185, 187, 193, 195, 201, 203, 209, 211, 217, 219, 225, 227, 232, 234, 240, 242; or

(b) $V_{H1,}$ $V_{H2,}$ and V_{H3} each independently comprise heavy chain complementarity determining regions of a variable domain comprising an amino acid sequence as set forth in any one of SEQ ID NOs: 248-265.

[0018] In another embodiment, the disclosure provides a binding protein comprising a first polypeptide chain, a second polypeptide chain, a third polypeptide chain and a fourth polypeptide chain wherein:

(a) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 4 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 4; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 3 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 3; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 1 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 1; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 2 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 2;

(b) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 12 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 12; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 11 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 11; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 9 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 9; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 10 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 10;

(c) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 20 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 20; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 19 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 19; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 17 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 17; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 18 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 18;

(d) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 28 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 28; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 27 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 27; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 25 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 25; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 26 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 26;

(e) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 36 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 36; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 35 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 35; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 33 or an amino acid sequence that is at least 95% identical to the amino acid sequence of

SEQ ID NO: 33; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 34 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 34;

(f) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 44 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 44; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 43 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 43; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 41 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 41; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 42 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 42;

(g) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 52 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 52; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 51 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 51; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 49 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 49; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 50 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 50;

(h) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 60 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 60; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 59 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 59; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 57 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 57; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 58 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 58;

(i) the first 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; the second 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; the third 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; and the fourth 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;

(j) the first 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; the second 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; the third 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; and the fourth 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;

(k) the first 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; the second 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; the third 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; and the fourth 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;

(l) the first 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; the second 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; the third 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; and the fourth 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;

(m) the first 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; the second 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; the third 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; and the fourth 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;

(n) the first polypeptide 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; the second 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; the third 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; and the fourth 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;

(o) the first 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; the second 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; the third 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; and the fourth 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;

(p) the first 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; the second 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; the third 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; and the fourth 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;

(q) the first 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; the second 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; the third 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; and the fourth 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;

(r) the first 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; the second 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; the third 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; and the fourth 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;

(s) the first 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; the second 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; the third 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; and the fourth 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;

(t) the first 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; the second 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; the third 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; and the fourth 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;

(u) the first 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; the second 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; the third 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; and the fourth 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;

(v) the first 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; the second 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; the third 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; and the fourth 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;

(w) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 180 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 180; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 179 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 179; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 177 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 177; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 178 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 178;

(x) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 188 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 188; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 187 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 187; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 185 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 185; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 186 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 186;

(y) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 196 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 196; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 195 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 195; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 193 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 193; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 194 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 194;

(z) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 204 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 204; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 203 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 203; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 201 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 201; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 202 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 202;

(aa) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 212 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 212; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 211 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 211; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 209 or an amino acid sequence that is at least 95% identical to the amino acid

sequence of SEQ ID NO: 209; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 210 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 210;

(bb) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 220 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 220; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 219 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 219; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 217 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 217; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 218 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 218;

(cc) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 228 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 228; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 227 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 227; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 225 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 225; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 226 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 226;

(dd) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 235 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 235; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 234 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 234; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 232 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 232; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 233 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 233; or

(ee) first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 243 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 243; the second polypeptide chain comprises the amino acid sequence of SEQ ID

NO: 242 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 242; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 240 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 240; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 241 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 241.

[0019] In one embodiment, the disclosure provides a binding protein comprising four polypeptide chains that form three antigen binding sites that specifically bind one or more HIV target proteins and one or more T cell target proteins, wherein a first polypeptide chain comprises a structure represented by the formula:

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

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

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

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

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

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 the immunoglobulin C_{H1} heavy chain constant domain; 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.

[0020] In some embodiments, the second polypeptide chain further comprises 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, the third polypeptide chain further comprises 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, 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 first Fc region comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 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 C_{H1}, the second Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} 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 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 C_{H1}, the first Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} 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 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 C_{H1}, the second Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} 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 according to EU Index, wherein the amino acid substitutions are S354C and T366W. 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, and 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 comprise amino acid substitutions at positions corresponding to positions 428 and 434 of human IgG1 according to EU Index, wherein the amino acid substitutions are M428L and N434S.

[0021] In one embodiment, the disclosure provides a binding protein comprising four polypeptide chains that form three antigen binding sites that specifically bind one or more

HIV target proteins and one or more T cell target proteins, wherein a first polypeptide chain comprises a structure represented by the formula:

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

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

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

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 the 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.

[0022] In some embodiments, the C_{H3} domain of the second polypeptide chain comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 according to EU Index, wherein the amino acid substitutions are S354C and T366W; and wherein the 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 according to EU Index, wherein the amino acid substitutions are Y349C, T366S, L368A, and Y407V. In some embodiments, the 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 according to EU Index, wherein the amino acid substitutions are

Y349C, T366S, L368A, and Y407V; and wherein the C_{H3} domain of the third polypeptide chain comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 according to EU Index, wherein the amino acid substitutions are S354C and T366W. In some embodiments, the C_{H3} domains of the second and the third polypeptide chains both comprise amino acid substitutions at positions corresponding to positions 428 and 434 of human IgG1 according to EU Index, wherein the amino acid substitutions are M428L and N434S.

[0023] In some embodiments, the one or more HIV target proteins are selected from the group consisting of glycoprotein 120, glycoprotein 41 and glycoprotein 160. In some embodiments, the one or more T cell target proteins are CD3 or CD28. In some embodiments, the binding protein is trispecific and capable of specifically binding an HIV target protein and two different epitopes on a single T cell target protein. In some embodiments, the binding protein is trispecific and capable of specifically binding an HIV target protein and two different T cell target proteins. In some embodiments, the binding protein is trispecific and capable of specifically binding a T cell target protein and two different epitopes on a single HIV target protein. In some embodiments, the binding protein is trispecific and capable of specifically binding a T cell target protein and two different HIV target proteins. In some embodiments, the first and second polypeptide chains form two antigen binding sites that specifically target two T cell target proteins, and the third and fourth polypeptide chains form an antigen binding site that specifically binds an HIV target protein. In some embodiments, V_{L1} comprises a CDR-L1, CDR-L2, and CDR-L3 comprising a sequence as set forth in SEQ ID NOs: 266, 267, and 268, respectively; a sequence as set forth in SEQ ID NOs: 269, 270, and 271, respectively; a sequence as set forth in SEQ ID NOs: 500, 501, and 274, respectively; a sequence as set forth in SEQ ID NOs: 275, 276, and 277, respectively; a sequence as set forth in SEQ ID NOs: 281, 282, and 283, respectively; a sequence as set forth in SEQ ID NOs: 278, 279, and 280, respectively; a sequence as set forth in SEQ ID NOs: 488, 489, and 490, respectively; a sequence as set forth in SEQ ID NOs: 491, 492, and 493, respectively; or a sequence as set forth in SEQ ID NOs: 494, 495, and 496, respectively. In some embodiments, V_{L1} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, and 524. In some embodiments, V_{L1} comprises a light chain variable domain comprising a sequence selected from the group

consisting of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, and 524. In some embodiments, V_{L2} comprises a CDR-L1, CDR-L2, and CDR-L3 comprising a sequence as set forth in SEQ ID NOs: 266, 267, and 268, respectively; a sequence as set forth in SEQ ID NOs: 269, 270, and 271, respectively; a sequence as set forth in SEQ ID NOs: 500, 501, and 274, respectively; a sequence as set forth in SEQ ID NOs: 275, 276, and 277, respectively; a sequence as set forth in SEQ ID NOs: 281, 282, and 283, respectively; a sequence as set forth in SEQ ID NOs: 278, 279, and 280, respectively; a sequence as set forth in SEQ ID NOs: 488, 489, and 490, respectively; a sequence as set forth in SEQ ID NOs: 491, 492, and 493, respectively; or a sequence as set forth in SEQ ID NOs: 494, 495, and 496, respectively. In some embodiments, V_{L2} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, and 524. In some embodiments, V_{L2} comprises a light chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, and 524. In some embodiments, V_{L3} comprises a CDR-L1, CDR-L2, and CDR-L3 comprising a sequence as set forth in SEQ ID NOs: 266, 267, and 268, respectively; a sequence as set forth in SEQ ID NOs: 269, 270, and 271, respectively; a sequence as set forth in SEQ ID NOs: 500, 501, and 274, respectively; a sequence as set forth in SEQ ID NOs: 275, 276, and 277, respectively; a sequence as set forth in SEQ ID NOs: 281, 282, and 283, respectively; a sequence as set forth in SEQ ID NOs: 278, 279, and 280, respectively; a sequence as set forth in SEQ ID NOs: 488, 489, and 490, respectively; a sequence as set forth in SEQ ID NOs: 491, 492, and 493, respectively; or a sequence as set forth in SEQ ID NOs: 494, 495, and 496, respectively. In some embodiments, V_{L3} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, and 524. In some embodiments, V_{L3} comprises a light chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, and 524. In some embodiments, V_{H1} comprises a CDR-H1, CDR-H2, and CDR-H3 comprising a sequence as set forth in SEQ ID NOs: 248, 497, and 250, respectively; a sequence as set forth in SEQ ID NOs: 251, 252, and 253, respectively; a sequence as set forth in SEQ ID NOs: 254, 255, and 256, respectively; a sequence as set forth in SEQ ID NOs: 254, 255, and 498, respectively; a sequence as set forth in SEQ ID

NOs: 257, 258, and 259, respectively; a sequence as set forth in SEQ ID NOs: 263, 264, and 265, respectively; a sequence as set forth in SEQ ID NOs: 499, 261, and 262, respectively; a sequence as set forth in SEQ ID NOs: 479, 480, and 481, respectively; a sequence as set forth in SEQ ID NOs: 482, 483, and 484, respectively; or a sequence as set forth in SEQ ID NOs: 485, 486, and 487, respectively. In some embodiments, V_{H1} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 502, 503, 504, 505, 506, 507, 508, 509, 510, and 511. In some embodiments, V_{H1} comprises a heavy chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 502, 503, 504, 505, 506, 507, 508, 509, 510, and 511. In some embodiments, V_{H2} comprises a CDR-H1, CDR-H2, and CDR-H3 comprising a sequence as set forth in SEQ ID NOs: 248, 497, and 250, respectively; a sequence as set forth in SEQ ID NOs: 251, 252, and 253, respectively; a sequence as set forth in SEQ ID NOs: 254, 255, and 256, respectively; a sequence as set forth in SEQ ID NOs: 254, 255, and 498, respectively; a sequence as set forth in SEQ ID NOs: 257, 258, and 259, respectively; a sequence as set forth in SEQ ID NOs: 263, 264, and 265, respectively; a sequence as set forth in SEQ ID NOs: 499, 261, and 262, respectively; a sequence as set forth in SEQ ID NOs: 479, 480, and 481, respectively; a sequence as set forth in SEQ ID NOs: 482, 483, and 484, respectively; or a sequence as set forth in SEQ ID NOs: 485, 486, and 487, respectively. In some embodiments, V_{H2} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 502, 503, 504, 505, 506, 507, 508, 509, 510, and 511. In some embodiments, V_{H2} comprises a heavy chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 502, 503, 504, 505, 506, 507, 508, 509, 510, and 511. In some embodiments, V_{H3} comprises a CDR-H1, CDR-H2, and CDR-H3 comprising a sequence as set forth in SEQ ID NOs: 248, 497, and 250, respectively; a sequence as set forth in SEQ ID NOs: 251, 252, and 253, respectively; a sequence as set forth in SEQ ID NOs: 254, 255, and 256, respectively; a sequence as set forth in SEQ ID NOs: 254, 255, and 498, respectively; a sequence as set forth in SEQ ID NOs: 257, 258, and 259, respectively; a sequence as set forth in SEQ ID NOs: 263, 264, and 265, respectively; a sequence as set forth in SEQ ID NOs: 499, 261, and 262, respectively; a sequence as set forth in SEQ ID NOs: 479, 480, and 481, respectively; a sequence as set forth in SEQ ID NOs: 482, 483, and 484, respectively; or a sequence as set forth in SEQ ID NOs: 485, 486, and 487, respectively. In

some embodiments, V_{H3} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 502, 503, 504, 505, 506, 507, 508, 509, 510, and 511. In some embodiments, V_{H3} comprises a heavy chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 502, 503, 504, 505, 506, 507, 508, 509, 510, and 511. In some embodiments, V_{L1} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 488, a CDR-L2 comprising the sequence of SEQ ID NO: 489, and a CDR-L3 comprising the sequence of SEQ ID NO: 490; V_{L2} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 494, a CDR-L2 comprising the sequence of SEQ ID NO: 495, and a CDR-L3 comprising the sequence of SEQ ID NO: 496; V_{L3} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 269, a CDR-L2 comprising the sequence of SEQ ID NO: 270, and a CDR-L3 comprising the sequence of SEQ ID NO: 271; V_{H1} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 479, a CDR-H2 comprising the sequence of SEQ ID NO: 480, and a CDR-H3 comprising the sequence of SEQ ID NO: 481; V_{H2} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 485, a CDR-H2 comprising the sequence of SEQ ID NO: 486, and a CDR-H3 comprising the sequence of SEQ ID NO: 487; and V_{H3} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 251, a CDR-H2 comprising the sequence of SEQ ID NO: 252, and a CDR-H3 comprising the sequence of SEQ ID NO: 253. In some embodiments, V_{L1} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 522; V_{L2} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 524; V_{L3} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 513; V_{H1} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 509; V_{H2} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 511; and V_{H3} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 503. In some embodiments, V_{L1} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 522; V_{L2} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 524; V_{L3} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 513; V_{H1} comprises a heavy chain variable

domain comprising the sequence of SEQ ID NO: 509; V_{H2} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 511; and V_{H3} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 503. In some embodiments, V_{L1} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 494, a CDR-L2 comprising the sequence of SEQ ID NO: 495, and a CDR-L3 comprising the sequence of SEQ ID NO: 496; V_{L2} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 488, a CDR-L2 comprising the sequence of SEQ ID NO: 489, and a CDR-L3 comprising the sequence of SEQ ID NO: 490; V_{L3} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 269, a CDR-L2 comprising the sequence of SEQ ID NO: 270, and a CDR-L3 comprising the sequence of SEQ ID NO: 271; V_{H1} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 485, a CDR-H2 comprising the sequence of SEQ ID NO: 486, and a CDR-H3 comprising the sequence of SEQ ID NO: 487; V_{H2} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 479, a CDR-H2 comprising the sequence of SEQ ID NO: 480, and a CDR-H3 comprising the sequence of SEQ ID NO: 481; and V_{H3} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 251, a CDR-H2 comprising the sequence of SEQ ID NO: 252, and a CDR-H3 comprising the sequence of SEQ ID NO: 253. In some embodiments, V_{L1} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 524; V_{L2} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 522; V_{L3} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 513; V_{H1} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 511; V_{H2} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 509; and V_{H3} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 503. In some embodiments, V_{L1} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 524; V_{L2} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 522; V_{L3} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 513; V_{H1} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 511; V_{H2} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 509; and V_{H3} comprises a heavy

chain variable domain comprising the sequence of SEQ ID NO: 503. In some embodiments, 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, or L_4 are each independently at least one amino acid in length. In some embodiments, L_1 is Gly-Gln-Pro-Lys-Ala-Ala-Pro (SEQ ID NO: 299).

[0024] In one embodiment, the disclosure provides a binding protein comprising four polypeptide chains that form three antigen binding sites, 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:

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

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

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

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 the immunoglobulin C_{H1} heavy chain constant domain; 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:

(a) V_{L1}, V_{L2} and V_{L3} are each independently a variable domain derived from an amino acid sequence as set forth in any one of SEQ ID NOs: 303, 305, 311, 313, 319, 321, 327, 329, 335, 337, 343, 345, 351, 353, 359, 361, 367, 369, 375, 377, 383, 385, 391, 393, 399, 401, 407, 409, 415, 417, 423, 425, 431, 433, 439, 441, 447, 449, 455, 457, 463, 465, 471, 473; or

(b) V_{L1}, V_{L2} and V_{L3} each independently comprise light chain complementarity determining regions of a variable domain comprising an amino acid sequence as set forth in any one of SEQ ID NOs: 266-271, 275-277, 488-496; and

wherein:

(a) V_{H1}, V_{H2}, and V_{H3} are each independently a variable domain derived from an amino acid sequence as set forth in any one of SEQ ID NOs: 302, 304, 310, 312, 318, 320, 326, 328, 334, 336, 342, 344, 350, 352, 358, 360, 366, 368, 374, 376, 382, 384, 390, 392, 398, 400, 406, 408, 414, 416, 422, 424, 430, 432, 438, 440, 446, 448, 454, 456, 462, 464, 470, 472; or

(b) V_{H1}, V_{H2}, and V_{H3} each independently comprise heavy chain complementarity determining regions of a variable domain comprising an amino acid sequence as set forth in any one of SEQ ID NOs: 248-253, 257-259, 479-487.

[0025] In some embodiments, the second polypeptide chain further comprises 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, the third polypeptide chain further comprises 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, 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 first Fc region comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 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 C_{H1}, the second Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} 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 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 C_{H1}, the first Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} 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 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 C_{H1}, the second Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} 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 according to EU Index, wherein the amino acid substitutions are S354C and T366W. 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, and 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 comprise amino acid substitutions at positions corresponding to positions 428 and 434 of human IgG1 according to EU Index, wherein the amino acid substitutions are M428L and N434S.

[0026] In one embodiment, the disclosure provides a binding protein comprising four polypeptide chains that form three antigen binding sites, 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 the 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:

(a) V_{L1}, V_{L2} and V_{L3} are each independently a variable domain derived from an amino acid sequence as set forth in any one of SEQ ID NOs: 303, 305, 311, 313, 319, 321, 327, 329, 335, 337, 343, 345, 351, 353, 359, 361, 367, 369, 375, 377, 383, 385, 391, 393, 399, 401, 407, 409, 415, 417, 423, 425, 431, 433, 439, 441, 447, 449, 455, 457, 463, 465, 471, 473; or

(b) V_{L1}, V_{L2} and V_{L3} each independently comprise light chain complementarity determining regions of a variable domain comprising an amino acid sequence as set forth in any one of SEQ ID NOs: 266-271, 275-277, 488-496; and
wherein:

(a) V_{H1}, V_{H2}, and V_{H3} are each independently a variable domain derived from an amino acid sequence as set forth in any one of SEQ ID NOs: 302, 304, 310, 312, 318, 320, 326, 328, 334, 336, 342, 344, 350, 352, 358, 360, 366, 368, 374, 376, 382, 384, 390, 392, 398, 400, 406, 408, 414, 416, 422, 424, 430, 432, 438, 440, 446, 448, 454, 456, 462, 464, 470, 472; or

(b) V_{H1}, V_{H2}, and V_{H3} each independently comprise heavy chain complementarity determining regions of a variable domain comprising an amino acid sequence as set forth in any one of SEQ ID NOs: 248-253, 257-259, 479-487.

[0027] In some embodiments, the C_{H3} domain of the second polypeptide chain comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 according to EU Index, wherein the amino acid substitutions are S354C and T366W; and wherein the 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 according to EU Index, wherein the amino acid substitutions are Y349C, T366S, L368A, and Y407V. In some embodiments, the 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 according to EU Index, wherein the amino acid substitutions are Y349C, T366S, L368A, and Y407V; and wherein the C_{H3} domain of the third polypeptide

chain comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 according to EU Index, wherein the amino acid substitutions are S354C and T366W. In some embodiments, the C_{H3} domains of the second and the third polypeptide chains both comprise amino acid substitutions at positions corresponding to positions 428 and 434 of human IgG1 according to EU Index, wherein the amino acid substitutions are M428L and N434S.

[0028] In some embodiments, 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, or L_4 are each independently at least one amino acid in length. In some embodiments, L_1 is Gly-Gln-Pro-Lys-Ala-Ala-Pro (SEQ ID NO: 299).

[0029] In one embodiment, the disclosure provides a binding protein comprising four polypeptide chains that form 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:

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

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

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:

(a) V_{L1}, V_{L2} and V_{L3} are each independently a variable domain derived from an amino acid sequence as set forth in any one of SEQ ID NOs: 303, 305, 311, 313, 319, 321, 327, 329, 335, 337, 343, 345, 351, 353, 359, 361, 367, 369, 375, 377, 383, 385, 391, 393, 399, 401, 407, 409, 415, 417, 423, 425, 431, 433, 439, 441, 447, 449, 455, 457, 463, 465, 471, 473; or

(b) $V_{L1,}$ V_{L2} and V_{L3} each independently comprise light chain complementarity determining regions of a variable domain comprising an amino acid sequence as set forth in any one of SEQ ID NOs: 266-271, 275-277, 488-496; and

wherein:

(a) $V_{H1,}$ $V_{H2,}$ and V_{H3} are each independently a variable domain derived from an amino acid sequence as set forth in any one of SEQ ID NOs: 302, 304, 310, 312, 318, 320, 326, 328, 334, 336, 342, 344, 350, 352, 358, 360, 366, 368, 374, 376, 382, 384, 390, 392, 398, 400, 406, 408, 414, 416, 422, 424, 430, 432, 438, 440, 446, 448, 454, 456, 462, 464, 470, 472; or

(b) $V_{H1,}$ $V_{H2,}$ and V_{H3} each independently comprise heavy chain complementarity determining regions of a variable domain comprising an amino acid sequence as set forth in any one of SEQ ID NOs: 248-253, 257-259, 479-487.

[0030] In another embodiment, the disclosure provides a binding protein comprising a first polypeptide chain, a second polypeptide chain, a third polypeptide chain and a fourth polypeptide chain wherein:

(a) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 305 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 305; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 304 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 304; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 302 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 302; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 303 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 303;

(b) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 313 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 313; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 312 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 312; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 310 or an amino acid sequence that is at least 95% identical to the amino acid

sequence of SEQ ID NO: 310; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 311 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 311;

(c) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 321 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 321; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 320 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 320; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 318 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 318; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 319 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 319;

(d) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 329 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 329; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 328 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 328; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 326 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 326; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 327 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 327;

(e) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 337 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 337; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 336 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 336; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 334 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 334; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 335 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 335;

(f) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 345 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 345; the second polypeptide chain comprises the amino acid sequence of SEQ ID

NO: 344 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 344; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 342 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 342; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 343 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 343;

(g) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 353 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 353; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 352 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:352; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 350 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 350; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 351 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 351;

(h) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 361 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 361; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 360 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 360; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 358 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 358; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 359 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 359;

(i) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 369 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 369; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 368 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 368; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 366 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 366; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 367 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 367;

(j) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 377 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 377; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 376 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 376; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 374 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 374; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 375 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 375;

(k) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 385 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 385; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 384 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 384; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 382 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 382; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 383 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 383;

(l) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 393 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 393; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 392 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 392; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 390 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 390; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 391 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 391;

(m) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 401 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 401; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 400 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 400; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 398 or an amino acid sequence that is at least 95% identical to the amino acid

sequence of SEQ ID NO: 398; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 399 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 399;

(n) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 409 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 409; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 408 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 408; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 406 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 406; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 407 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 407;

(p) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 417 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 417; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 416 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 416; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 414 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 414; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 415 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 415;

(q) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 425 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 425; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 424 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 424; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 422 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 422; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 423 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 423;

(r) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 433 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:433; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:

432 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 432; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 430 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 430; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 431 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 431;

(s) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 441 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 441; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 440 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 440; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 438 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 438; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 439 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 439;

(t) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 449 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 449; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 448 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 448; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 446 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 446; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 447 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 447;

(u) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 457 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 457; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 456 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 456; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 454 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 454; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 455 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 455;

(v) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 465 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 465; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 464 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 464; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 462 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 462; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 463 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 463; or

(w) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 473 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 473; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 472 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 472; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 470 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 470; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 471 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 471.

[0031] In one embodiment, the disclosure provides an isolated nucleic acid molecule comprising a nucleotide sequence encoding the binding protein according to any of the above embodiments. In one embodiment, the disclosure provides an expression vector comprising the nucleic acid molecule according to any of the above embodiments. In one embodiment, the disclosure provides an isolated host cell comprising the nucleic acid molecule according to any of the above embodiments. In one embodiment, the disclosure provides an isolated host cell comprising the expression vector according to any of the above embodiments. In some embodiments, the isolated host cell is a mammalian cell or an insect cell. In one embodiment, the disclosure provides a vector system comprising one or more vectors encoding a first, second, third, and fourth polypeptide chain of a binding protein according to any 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. 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 one or more vectors are expression vectors. In one embodiment, the disclosure provides an isolated host cell comprising the vector system according to any of the above embodiments. In some embodiments, the isolated host cell is a mammalian cell or an insect cell. In one embodiment, the disclosure provides a method of producing a binding protein, the method comprising: a) culturing a host cell according to any of the above embodiments under conditions such that the host cell expresses the binding protein; and b) isolating the binding protein from the host cell.

[0032] In one embodiment, the disclosure provides 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 according to any 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 neutralization of one or more HIV virions. 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.

[0033] In one embodiment, the disclosure provides a binding protein according to any of the above embodiments for the prevention or treatment of an HIV infection in a patient. In some embodiments, the binding protein is co-administered with standard anti-retroviral therapy. In some embodiments, the binding protein causes the neutralization of one or more HIV virions in the patient. 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.

[0034] Specific embodiments of the invention will become evident from the following more detailed description of certain embodiments and the claims.

[0035] 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

[0036] **FIGS. 1A-D** show schematic representations of trispecific binding proteins comprising four polypeptide chains that form three antigen binding sites that specifically bind three different epitopes on one or more antigens, wherein a first pair of polypeptides possess dual variable domains having a cross-over orientation forming two antigen binding sites (comprising V_{H1}-V_{L1} and V_{H2}-V_{L2}) and wherein a second pair of polypeptides possess a single antigen binding site (comprising V_{H3}-V_{L3}), in accordance with some embodiments. **FIG. 1A** shows a trispecific binding protein comprising a "knobs-into-holes" modification, wherein the knob is on the first pair of polypeptides. **FIG. 1B** shows a trispecific binding protein comprising a "knobs-into-holes" modification, wherein the knob is on the second pair of polypeptides. **FIG. 1C** shows the orientation of variable domains on the polypeptide chains, and the knob/hole orientation for binding proteins 1-31 shown in Tables 1 and 2. "Heavy chain A" (*e.g.*, a third polypeptide chain of the present disclosure) indicates the variable domain of heavy chain A. "Light chain A" (*e.g.*, a fourth polypeptide chain of the present disclosure) indicates the variable domain of light chain A. "Heavy chain B" (*e.g.*, a second polypeptide chain of the present disclosure) indicates variable domain 1 and variable domain 2 of heavy chain B. "Light chain B" (*e.g.*, a first polypeptide chain of the present disclosure) indicates variable domain 1 and variable domain 2 of light chain B. **FIG. 1D** shows the orientation of variable domains on the polypeptide chains, and the knob/hole orientation for binding proteins 32-53 shown in Tables 1 and 2. "Heavy chain A" (*e.g.*, a third polypeptide chain of the present disclosure) indicates the variable domain of heavy chain A. "Light chain A" (*e.g.*, a fourth polypeptide chain of the present disclosure) indicates the variable domain of light chain A. "Heavy chain B" (*e.g.*, a second polypeptide chain of the present disclosure) indicates variable domain 1 and variable domain 2 of heavy chain B. "Light chain B" (*e.g.*, a first polypeptide chain of the present disclosure) indicates variable domain 1 and variable domain 2 of light chain B.

[0037] **FIGS. 2A-B** show purification of three trispecific binding proteins first using affinity chromatography, and then using preparative size exclusion chromatography. **FIG. 2A** shows the elution profile of the trispecific binding proteins during purification using protein A affinity chromatography. **FIG. 2B** shows purification of monomeric proteins by Superdex200 size exclusion chromatography.

[0038] **FIGS. 3A-B** show purification of the MPER Ab, CD4BS Ab "b", and V1/V2 directed Ab "a" parental antibodies first using affinity chromatography, and then using

preparative size exclusion chromatography. **FIG. 3A** shows the elution profile of the parental antibodies during purification using protein A affinity chromatography. **FIG. 3B** shows purification of monomeric proteins by Superdex200 size exclusion chromatography.

[0039] **FIGS. 4A-B** show the size exclusion chromatography profiles of bispecific and trispecific binding proteins. **FIG. 4A** shows the size exclusion chromatography profiles of the bispecific binding proteins. **FIG. 4B** shows the size exclusion chromatography profiles of the trispecific binding proteins.

[0040] **FIG. 5** shows the Biacore sensograms of the binding kinetics of three trispecific binding proteins and the parental MPER Ab antibody for an HIV gp41-derived peptide (the MPER binding site), as assessed by the standard Biacore-based kinetic assay.

[0041] **FIG. 6** shows the Biacore sensograms of the binding kinetics of three trispecific binding proteins and the parental CD4BS Ab "b" antibody for recombinant HIV gp120, as assessed by the standard Biacore-based kinetic assay.

[0042] **FIG. 7** shows the results of a pharmacokinetic (PK) study of the indicated proteins after intravenous (IV) injection in rhesus macaques.

[0043] **FIGS. 8A-8B** show schematic representations of trispecific T-cell engagers, in accordance with some embodiments. The binding sites are indicated by the dotted circles.

[0044] **FIG. 9** shows binding properties of the trispecific binding proteins "Binding Protein 32" and "CD3 x CD28 / CD4BS Ab 'b'" to CD3 (CD3E represents CD3epsilon protein; CD3D represents CD3delta protein), CD28, and Resurfaced Stabilized Core 3 (RSC3) protein of gp120, as well as a negative control (human IgG).

[0045] **FIG. 10** shows CD8 T-cell activation using the trispecific proteins "Binding Protein 32" and "CD3 x CD28 / CD4BS Ab 'b'" compared to the parental CD4BS IgG4 antibody, as well as a negative control (No mAb).

[0046] **FIG. 11** shows CD4 T-cell activation using the trispecific proteins "Binding Protein 32" and "CD3 x CD28 / CD4BS Ab 'b'" compared to the parental CD4BS IgG4 antibody, as well as a negative control (No mAb).

[0047] **FIG. 12** shows CD3 downregulation after T cell activation by the trispecific proteins "Binding Protein 32" and "CD3 x CD28 / CD4BS Ab 'b'" compared to the parental CD4BS IgG4 antibody, as well as a negative control (No mAb).

[0048] **FIGS. 13A-C** show fluorescence-activated cell sorting (FACS)-based cytotoxicity assay results for trispecific binding proteins against latently infected HIV-1^+ T cells. **FIG. 13A** shows the results for trispecific binding proteins incubated with CEM-BaL

cells. **FIG. 13B** shows the results for trispecific binding proteins incubated with ACH2 cells. **FIG. 13C** shows the results for trispecific binding proteins incubated with J1.1 cells.

DETAILED DESCRIPTION

[0049] 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 forming the binding protein possess a single variable domain.

[0050] 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

[0051] 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.

[0052] 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.

[0053] 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.

[0054] 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).

[0055] 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.

[0056] 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.

[0057] 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.

[0058] 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.

[0059] 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.

[0060] 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.

[0061] 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, and which 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:

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

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

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.

[0062] A "recombinant" molecule is one that has been prepared, expressed, created, or isolated by recombinant means.

[0063] 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).

[0064] 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."

[0065] 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.

[0066] 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.

[0067] The term "AIDS" as used herein means Acquired Immunodeficiency Syndrome. AIDS is caused by HIV.

[0068] 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.

[0069] 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.

[0070] "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.

[0071] 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.

[0072] 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.

[0073] 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.

[0074] 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.

[0075] The term "trimer apex" refers to apex of HIV-1 envelope glycoprotein gp120.

[0076] The term "monospecific binding protein" refers to a binding protein that specifically binds to one antigen target.

[0077] The term "monovalent binding protein" refers to a binding protein that has one antigen binding site.

[0078] The term "bispecific binding protein" refers to a binding protein that specifically binds to two different antigen targets.

[0079] The term "bivalent binding protein" refers to a binding protein that has two binding sites.

[0080] The term "trispecific binding protein" refers to a binding protein that specifically binds to three different antigen targets.

[0081] 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.

[0082] 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.

[0083] 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.

[0084] 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.

[0085] 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.

[0086] 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.

[0087] 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.

[0088] 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.

[0089] 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.

[0090] 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.

[0091] 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.

[0092] 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.

[0093] 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.

[0094] 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.

[0095] 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.

[0096] 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.

[0097] The term "patient" as used herein includes human and animal subjects.

[0098] 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.

[0099] 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.

[0100] 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.

[0101] 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.

[0102] 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.

[0103] 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

[0104] In one embodiment, 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 (e.g., three different) 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:

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

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

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

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; 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.

[0105] In one embodiment, 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 (e.g., three different) 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.

[0106] 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.

[0107] In some embodiments, V_{L1}, V_{L2} and V_{L3} are each independently a variable domain derived from an amino acid sequence as set forth in any one of SEQ ID NOs: 2, 4, 10, 12, 18, 20, 26, 28, 34, 36, 42, 44, 50, 52, 58, 60, 66, 68, 74, 76, 82, 84, 90, 92, 98, 100, 106, 108, 114, 116, 122, 124, 130, 132, 138, 140, 146, 148, 154, 156, 162, 164, 170, 172, 178, 180, 186, 188, 194, 196, 202, 204, 210,212, 218, 220, 226, 228, 233, 235, 241, 243; and $V_{H1,}$ V_{H2} and $V_{H3,}$ are each independently a variable domain derived from an amino acid sequence as set forth in any one of SEQ ID NOs:1, 3, 9, 11, 17, 10, 25, 27, 33, 35, 41, 43, 49, 51, 57, 59, 65, 67, 73, 75, 81, 83, 89, 91, 97, 99, 105, 107, 113, 115, 121, 123, 129, 131, 137, 139, 145, 147, 153, 155, 161, 163, 169, 171, 177, 179, 185, 187, 193, 195, 201, 203, 209, 211, 217, 219, 225, 227, 232, 234, 240, 242. In other embodiments, V_{L1}, V_{L2} and V_{L3} each independently comprise light chain complementarity determining regions of a variable domain comprising an amino acid sequence as set forth in any one of SEQ ID NOs: 266-283; and $V_{H1,}$ V_{H2} and V_{H3} each independently comprise heavy chain complementarity determining regions of a variable domain comprising an amino acid sequence as set forth in any one of SEQ ID NOs: 248-265. In some embodiments, V_{L1}, V_{L2} and V_{L3} are each independently a light chain variable domain comprising a light chain variable domain sequence of antibody CD4BS “a”, CD4BS “b”, MPER, MPER_100W, V1/V2 directed “a”, V1/V2 directed “b”, or V3 directed described herein. In some embodiments, V_{H1}, V_{H2} and V_{H3} are each independently a heavy chain variable domain comprising a heavy chain variable domain sequence of antibody CD4BS “a”, CD4BS “b”, MPER, MPER_100W, V1/V2 directed “a”, V1/V2 directed “b”, or V3 directed described herein. In some embodiments, V_{L1}, V_{L2} and V_{L3} are each independently a light chain variable domain comprising a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain sequence of antibody CD4BS “a”, CD4BS “b”, MPER, MPER_100W, V1/V2 directed “a”, V1/V2 directed “b”, or V3 directed described herein. In some embodiments, V_{H1}, V_{H2} and V_{H3} are each independently a heavy chain variable domain comprising a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain sequence of antibody CD4BS “a”, CD4BS “b”, MPER, MPER_100W, V1/V2 directed “a”, V1/V2 directed “b”, or V3 directed described herein.

[0108] In some embodiments, V_{L1}, V_{L2} and V_{L3} are each independently a variable domain derived from an amino acid sequence as set forth in any one of SEQ ID NOs: 303, 305, 311, 313, 319, 321, 327, 329, 335, 337, 343, 345, 351, 353, 359, 361, 367, 369, 375, 377, 383,

385, 391, 393, 399, 401, 407, 409, 415, 417, 423, 425, 431, 433, 439, 441, 447, 449, 455, 457, 463, 465, 471, 473; and $V_{H1,}$ V_{H2} and $V_{H3,}$ are each independently a variable domain derived from an amino acid sequence as set forth in any one of SEQ ID NOs: 302, 304, 310, 312, 318, 320, 326, 328, 334, 336, 342, 344, 350, 352, 358, 360, 366, 368, 374, 376, 382, 384, 390, 392, 398, 400, 406, 408, 414, 416, 422, 424, 430, 432, 438, 440, 446, 448, 454, 456, 462, 464, 470, 472. In other embodiments, V_{L1}, V_{L2} and V_{L3} each independently comprise light chain complementarity determining regions of a variable domain comprising an amino acid sequence as set forth in any one of SEQ ID NOs: 266-271, 275-277, 488-496; and $V_{H1,}$ V_{H2} and V_{H3} each independently comprise heavy chain complementarity determining regions of a variable domain comprising an amino acid sequence as set forth in any one of SEQ ID NOs: 248-253, 257-259, 479-487.

[0109] In particular embodiments, the order of the 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) are swapped.

[0110] In some embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 4 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 4; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 3 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 3; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 1 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 1; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 2 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 2.

[0111] In some embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 12 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 12; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 11 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 11; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 9 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 9; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 10 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 10.

[0112] In other embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 20 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 20; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 19 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 19; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 17 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 17; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 18 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 18.

[0113] In other embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 28 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 28; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 27 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 27; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 25 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 25; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 26 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 26.

[0114] In other embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 36 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 36; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 35 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 35; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 33 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 33; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 34 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 34.

[0115] In other embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 44 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 44; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 43 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 43; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 41 or an amino acid sequence that is at least 95% identical to

the amino acid sequence of SEQ ID NO: 41; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 42 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 42.

[0116] In other embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 52 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 52; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 51 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 51; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 49 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 49; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 50 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 50.

[0117] In other embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 60 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 60; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 59 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 59; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 57 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 57; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 58 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 58.

[0118] In other embodiments, the first 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; the second 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; the third 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; and the fourth 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.

[0119] In other embodiments, the first 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; the second 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; the third 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; and the fourth 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.

[0120] In other embodiments, the first 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; the second 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; the third 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; and the fourth 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.

[0121] In other embodiments, the first 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; the second 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; the third 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; and the fourth 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.

[0122] In other embodiments, the first 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; the second 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; the third 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; and the fourth 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.

[0123] In other embodiments, the first polypeptide 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; the second 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; the third 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; and the fourth 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.

[0124] In other embodiments, the first 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; the second 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; the third 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; and the fourth 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.

[0125] In other embodiments, the first 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; the second 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; the third 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; and the fourth 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.

[0126] In other embodiments, the first 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; the second 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; the third 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; and the fourth 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.

[0127] In other embodiments, the first 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; the second 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; the third 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; and the fourth 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.

[0128] In other embodiments, the first 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; the second 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; the third 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; and the fourth 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.

[0129] In other embodiments, the first 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; the second 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; the third 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; and the fourth 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.

[0130] In other embodiments, the first 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; the second 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; the third 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; and the fourth 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.

[0131] In other embodiments, the first 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; the second 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; the third 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; and the fourth 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.

[0132] In other embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 180 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 180; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 179 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 179; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 177 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 177; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 178 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 178.

[0133] In other embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 188 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 188; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 187 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 187; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 185 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 185; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 186 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 186.

[0134] In other embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 196 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 196; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 195 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 195; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 193 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 193; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 194 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 194.

[0135] In other embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 204 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 204; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 203 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 203; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 201 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 201; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 202 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 202.

[0136] In other embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 212 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 212; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 211 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 211; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 209 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 209; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 210 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 210.

[0137] In other embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 220 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 220; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 219 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 219; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 217 or an amino acid sequence that is at least 95%

identical to the amino acid sequence of SEQ ID NO: 217; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 218 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 218.

[0138] In other embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 228 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 228; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 227 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 227; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 225 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 225; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 226 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 226.

[0139] In other embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 235 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 235; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 234 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 234; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 232 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 232; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 233 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 233.

[0140] In other embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 243 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 243; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 242 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 242; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 240 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 240; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 241 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 241.

[0141] In another embodiment, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 305 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 305; the second polypeptide chain comprises the amino

acid sequence of SEQ ID NO: 304 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 304; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 302 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 302; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 303 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 303.

[0142] In another embodiment, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 313 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 313; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 312 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 312; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 310 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 310; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 311 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 311.

[0143] In another embodiment, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 321 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 321; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 320 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 320; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 318 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 318; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 319 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 319.

[0144] In another embodiment, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 329 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 329; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 328 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 328; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 326 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 326; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 327 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 327.

[0145] In another embodiment, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 337 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 337; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 336 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 336; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 334 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 334; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 335 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 335.

[0146] In another embodiment, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 345 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 345; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 344 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 344; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 342 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 342; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 343 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 343.

[0147] In another embodiment, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 353 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 353; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 352 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:352; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 350 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 350; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 351 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 351.

[0148] In another embodiment, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 361 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 361; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 360 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 360; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 358 or an amino acid sequence that is at least 95%

identical to the amino acid sequence of SEQ ID NO: 358; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 359 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 359.

[0149] In another embodiment, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 369 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 369; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 368 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 368; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 366 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 366; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 367 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 367.

[0150] In another embodiment, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 377 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 377; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 376 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 376; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 374 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 374; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 375 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 375.

[0151] In another embodiment, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 385 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 385; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 384 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 384; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 382 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 382; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 383 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 383.

[0152] In another embodiment, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 393 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 393; the second polypeptide chain comprises the amino

acid sequence of SEQ ID NO: 392 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 392; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 390 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 390; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 391 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 391.

[0153] In another embodiment, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 401 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 401; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 400 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 400; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 398 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 398; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 399 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 399.

[0154] In another embodiment, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 409 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 409; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 408 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 408; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 406 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 406; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 407 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 407.

[0155] In another embodiment, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 417 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 417; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 416 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 416; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 414 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 414; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 415 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 415.

[0156] In another embodiment, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 425 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 425; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 424 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 424; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 422 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 422; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 423 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 423.

[0157] In another embodiment, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 433 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:433; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 432 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 432; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 430 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 430; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 431 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 431.

[0158] In another embodiment, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 441 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 441; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 440 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 440; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 438 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 438; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 439 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 439.

[0159] In another embodiment, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 449 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 449; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 448 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 448; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 446 or an amino acid sequence that is at least 95%

identical to the amino acid sequence of SEQ ID NO: 446; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 447 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 447.

[0160] In another embodiment, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 457 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 457; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 456 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 456; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 454 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 454; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 455 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 455.

[0161] In another embodiment, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 465 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 465; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 464 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 464; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 462 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 462; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 463 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 463.

[0162] In another embodiment, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 473 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 473; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 472 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 472; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 470 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 470; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 471 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 471.

[0163] In other 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 (e.g., three) HIV target antigens, wherein a first polypeptide chain has a structure represented by the formula:

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

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

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

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

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

and a fourth polypeptide chain has 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 the immunoglobulin C_{H1} heavy chain constant domain; 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.

[0164] In other 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 (e.g., three) HIV target antigens, wherein a first polypeptide chain has a structure represented by the formula:

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

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

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

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

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

and a fourth polypeptide chain has 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 the immunoglobulin C_{H1} heavy chain constant domain; 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.

Additional examples of trispecific binding proteins

[0165] In some embodiments, V_{L1}, V_{L2} and V_{L3} are each independently a variable domain comprising an amino acid sequence as set forth in any one of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, and 521. In some embodiments, V_{L1}, V_{L2} and V_{L3} are each independently a variable domain comprising an amino acid sequence having at least about 80%, at least about 81%, at least about 82%, at least about 83%, at least about 84%, at least about 85%, at least about 86%, at least about 87%, at least about 88%, at least about 89%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% sequence identity to a sequence as set forth in any one of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, and 521.

[0166] In some embodiments, V_{H1}, V_{H2} and V_{H3} are each independently a variable domain comprising an amino acid sequence as set forth in any one of SEQ ID NOs: 502, 503, 504, 505, 506, 507, and 508. In some embodiments, V_{H1}, V_{H2} and V_{H3} are each independently a variable domain comprising an amino acid sequence having at least about 80%, at least about 81%, at least about 82%, at least about 83%, at least about 84%, at least about 85%, at least about 86%, at least about 87%, at least about 88%, at least about 89%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% sequence identity to a sequence as set forth in any one of SEQ ID NOs: 502, 503, 504, 505, 506, 507, and 508.

[0167] In some embodiments, V_{L1}, V_{L2}, and V_{L3} comprise an amino acid sequence as set forth in SEQ ID NOs: 518, 519, and 512, respectively, and V_{H1}, V_{H2}, and V_{H3} comprise an amino acid sequence as set forth in SEQ ID NOs: 504, 506, and 502, respectively. In some embodiments, V_{L1}, V_{L2}, and V_{L3} comprise an amino acid sequence as set forth in SEQ ID NOs: 518, 519, and 513, respectively, and V_{H1}, V_{H2}, and V_{H3} comprises an amino acid sequence as set forth in SEQ ID NOs: 504, 506, and 503, respectively. In some embodiments, V_{L1}, V_{L2}, and V_{L3} comprises an amino acid sequence as set forth in SEQ ID NOs: 519, 518, and 513, respectively, and V_{H1}, V_{H2}, and V_{H3} comprises an amino acid sequence as set forth in SEQ ID NOs: 506, 504, and 503, respectively.

[0168] In some embodiments, V_{L1}, V_{L2} and V_{L3} are each independently a variable domain comprising a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, and 521. In some embodiments, V_{H1}, V_{H2} and V_{H3} are each independently a variable domain comprising a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 502, 503, 504, 505, 506, 507, and 508. In some embodiments, V_{L1}, V_{L2} and V_{L3} are each independently a variable domain comprising a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising a light chain variable domain sequence shown in Table C. In some embodiments, V_{H1}, V_{H2} and V_{H3} are each independently a variable domain comprising a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising a heavy chain variable domain sequence shown in Table C.

[0169] In some embodiments, V_{L1} is a variable domain comprising a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising a sequence of SEQ ID NO: 518, V_{L2} is a variable domain comprising a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising a sequence of SEQ ID NO: 519, V_{L3} is a variable domain comprising a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising a sequence of SEQ ID NO: 512, V_{H1} is a variable domain comprising a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising a sequence of SEQ ID NO: 504, V_{H2} is a variable domain comprising a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising a sequence of SEQ ID NO: 506, and VH_3 is a variable domain comprising a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising a sequence of SEQ ID NO: 502. In some embodiments, V_{L1} is a variable domain comprising a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising a sequence of

SEQ ID NO: 518, V_{L2} is a variable domain comprising a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising a sequence of SEQ ID NO: 519, V_{L3} is a variable domain comprising a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising a sequence of SEQ ID NO: 513, V_{H1} is a variable domain comprising a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising a sequence of SEQ ID NO: 504, V_{H2} is a variable domain comprising a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising a sequence of SEQ ID NO: 506, and VH_3 is a variable domain comprising a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising a sequence of SEQ ID NO: 503. In some embodiments, V_{L1} is a variable domain comprising a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising a sequence of SEQ ID NO: 519, V_{L2} is a variable domain comprising a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising a sequence of SEQ ID NO: 518, V_{L3} is a variable domain comprising a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising a sequence of SEQ ID NO: 513, and V_{H1} is a variable domain comprising a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising a sequence of SEQ ID NO: 506, V_{H2} is a variable domain comprising a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising a sequence of SEQ ID NO: 504, and VH_3 is a variable domain comprising a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising a sequence of SEQ ID NO: 503.

[0170] In some embodiments, V_{L1}, V_{L2} and V_{L3} are each independently a variable domain comprising: (a) a CDR-L1 comprising a sequence selected from the group consisting of SEQ ID NOs: 266, 269, 275, 278, 281, and 500; (b) a CDR-L2 comprising a sequence selected from the group consisting of SEQ ID NOs: 267, 270, 276, 279, 282, and 501; and/or (c) a CDR-L3 comprising a sequence selected from the group consisting of SEQ ID NOs: 268, 271, 274, 277, 280, and 283. In some embodiments, V_{L1}, V_{L2} and V_{L3} are each independently a variable domain comprising a CDR-L1, CDR-L2, and CDR-L3 comprising amino acid sequences as shown in Table B. In some embodiments, V_{L1}, V_{L2} and V_{L3} are each independently a variable domain comprising a CDR-L1, CDR-L2, and CDR-L3 comprising a sequence as set forth in SEQ ID NOs: 266, 267, and 268, respectively; a sequence as set forth in SEQ ID NOs: 269, 270, and 271, respectively; a sequence as set forth in SEQ ID NOs: 500, 501, and 274, respectively; a sequence as set forth in SEQ ID NOs: 275, 276, and 277, respectively; a sequence as set forth in SEQ ID NOs: 281, 282, and 283, respectively; or a sequence as set forth in SEQ ID NOs: 278, 279, and 280, respectively.

[0171] In some embodiments, V_{H1}, V_{H2} and V_{H3} are each independently a variable domain comprising: (a) a CDR-H1 comprising a sequence selected from the group consisting of SEQ ID NOs: 248, 251, 254, 257, 263, and 499; (b) a CDR-H2 comprising a sequence selected from the group consisting of SEQ ID NOs: 252, 255, 258, 261, 264, and 497; and/or (c) a CDR-H3 comprising a sequence selected from the group consisting of SEQ ID NOs: 250, 253, 256, 259, 262, 265, and 498. In some embodiments, V_{H1}, V_{H2} and V_{H3} are each independently a variable domain comprising a CDR-H1, CDR-H2, and CDR-H3 comprising amino acid sequences as shown in Table B. In some embodiments, V_{H1}, V_{H2} and V_{H3} are each independently a variable domain comprising a CDR-H1, CDR-H2, and CDR-H3 comprising a sequence as set forth in SEQ ID NOs: 248, 497, and 250, respectively; a sequence as set forth in SEQ ID NOs: 251, 252, and 253, respectively; a sequence as set forth in SEQ ID NOs: 254, 255, and 256, respectively; a sequence as set forth in SEQ ID NOs: 254, 255, and 498, respectively; a sequence as set forth in SEQ ID NOs: 257, 258, and 259, respectively; a sequence as set forth in SEQ ID NOs: 263, 264, and 265, respectively; or a sequence as set forth in SEQ ID NOs: 499, 261, and 262, respectively.

[0172] In some embodiments, V_{L1} comprises a CDR-L1, CDR-L2, and CDR-L3 comprising the sequence of SEQ ID NOs: 500, 501, and 274, respectively; V_{L2} comprises a CDR-L1, CDR-L2, and CDR-L3 comprising the sequence of SEQ ID NOs: 275, 276, and 277, respectively; V_{L3} comprises a CDR-L1, CDR-L2, and CDR-L3 comprising the sequence of SEQ ID NOs: 266, 267, and 268, respectively; V_{H1} comprises a CDR-H1, CDR-H2, and CDR-H3 comprising the sequence of SEQ ID NOs: 254, 255, and 256, respectively; V_{H2} comprises a CDR-H1, CDR-H2, and CDR-H3 comprising the sequence of SEQ ID NOs: 257, 258, and 259, respectively; and V_{H3} comprises a CDR-H1, CDR-H2, and CDR-H3 comprising the sequence of SEQ ID NOs: 248, 497, and 250, respectively. In some embodiments, V_{L1} comprises a CDR-L1, CDR-L2, and CDR-L3 comprising the sequence of SEQ ID NOs: 500, 501, and 274, respectively; V_{L2} comprises a CDR-L1, CDR-L2, and CDR-L3 comprising the sequence of SEQ ID NOs: 275, 276, and 277, respectively; V_{L3} comprises a CDR-L1, CDR-L2, and CDR-L3 comprising the sequence of SEQ ID NOs: 269, 270, and 271, respectively; V_{H1} comprises a CDR-H1, CDR-H2, and CDR-H3 comprising the sequence of SEQ ID NOs: 254, 255, and 256, respectively; V_{H2} comprises a CDR-H1, CDR-H2, and CDR-H3 comprising the sequence of SEQ ID NOs: 257, 258, and 259, respectively; and V_{H3} comprises a CDR-H1, CDR-H2, and CDR-H3 comprising the sequence of SEQ ID NOs: 251, 252, and 253, respectively. In some embodiments, V_{L1} comprises a CDR-L1,

CDR-L2, and CDR-L3 comprising the sequence of SEQ ID NOs: 275, 276, and 277, respectively; V_{L2} comprises a CDR-L1, CDR-L2, and CDR-L3 comprising the sequence of SEQ ID NOs: 500, 501, and 274, respectively; V_{L3} comprises a CDR-L1, CDR-L2, and CDR-L3 comprising the sequence of SEQ ID NOs: 269, 270, and 271, respectively; V_{H1} comprises a CDR-H1, CDR-H2, and CDR-H3 comprising the sequence of SEQ ID NOs: 257, 258, and 259, respectively; V_{H2} comprises a CDR-H1, CDR-H2, and CDR-H3 comprising the sequence of SEQ ID NOs: 254, 255, and 256, respectively; and V_{H3} comprises a CDR-H1, CDR-H2, and CDR-H3 comprising the sequence of SEQ ID NOs: 251, 252, and 253, respectively.

Additional trispecific binding proteins targeting one or more HIV target proteins and one or more T cell target proteins

[0173] 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 (*e.g.,* one or two) HIV target proteins and one or more (*e.g.,* one or two) T cell target proteins, wherein a first polypeptide chain has a structure represented by the formula:

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

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

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

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

[0174] 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 (*e.g.,* one or two) HIV target proteins and one or more (*e.g.,* one or two) T cell target proteins, wherein a first polypeptide chain has a structure represented by the formula:

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

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

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

a third polypeptide chain has 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 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 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.

[0175] 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.

[0176] In some embodiments, V_{L1}, V_{L2} and V_{L3} are each independently a variable domain comprising an amino acid sequence as set forth in any one of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, and 524. In some embodiments, V_{L1}, V_{L2} and V_{L3} are each independently a variable domain comprising an amino acid sequence having at least about 80%, at least about 81%, at least about 82%, at least about 83%, at least about 84%, at least about 85%, at least about 86%, at least about 87%, at least about 88%, at least about 89%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% sequence identity to a sequence as set forth in any one of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, and 524.

[0177] In some embodiments, V_{H1}, V_{H2} and V_{H3} are each independently a variable domain comprising an amino acid sequence as set forth in any one of SEQ ID NOs: 502, 503, 504, 505, 506, 507, 508, 509, 510, and 511. In some embodiments, V_{H1}, V_{H2} and V_{H3} are each independently a variable domain comprising an amino acid sequence having at least about 80%, at least about 81%, at least about 82%, at least about 83%, at least about 84%, at least about 85%, at least about 86%, at least about 87%, at least about 88%, at least about 89%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% sequence identity to a sequence as set forth in any one of SEQ ID NOs: 502, 503, 504, 505, 506, 507, 508, 509, 510, and 511.

[0178] In some embodiments, V_{L1}, V_{L2}, and V_{L3} comprise an amino acid sequence as set forth in SEQ ID NOs: 522, 524, and 513, respectively, and V_{H1}, V_{H2}, and V_{H3} comprise an amino acid sequence as set forth in SEQ ID NOs: 509, 511, and 503, respectively. In some embodiments, V_{L1}, V_{L2}, and V_{L3} comprise an amino acid sequence as set forth in SEQ ID NOs: 524, 522, and 513, respectively, and V_{H1}, V_{H2}, and V_{H3} comprise an amino acid sequence as set forth in SEQ ID NOs: 511, 509, and 503, respectively.

[0179] In some embodiments, V_{L1}, V_{L2} and V_{L3} are each independently a variable domain comprising a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, and 524.

[0180] In some embodiments, V_{H1}, V_{H2} and V_{H3} are each independently a variable domain comprising a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 502, 503, 504, 505, 506, 507, 508, 509, 510, and 511.

[0181] In some embodiments, V_{L1} is a variable domain comprising a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising a sequence of SEQ ID NO: 522, V_{L2} is a variable domain comprising a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising a sequence of SEQ ID NO: 524, V_{L3} is a variable domain comprising a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising a sequence of SEQ ID NO: 513, V_{H1} is a variable domain comprising a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising a sequence of SEQ ID NO: 509, V_{H2} is a variable domain comprising a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising a sequence of SEQ ID NO: 511, and VH_3 is a variable domain comprising a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising a sequence of SEQ ID NO: 503. In some embodiments, V_{L1} is a variable domain comprising a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising a sequence of SEQ ID NO: 524, V_{L2} is a variable domain comprising a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising a sequence of SEQ ID NO: 522, V_{L3} is a variable domain comprising a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising a light chain variable domain sequence of SEQ ID NO: 513, V_{H1} is a variable domain comprising a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising a sequence of SEQ ID NO: 511, V_{H2} is a variable domain comprising a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising a sequence of SEQ ID NO: 509, and VH_3 is a variable domain comprising a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising a sequence of SEQ ID NO: 503.

[0182] In some embodiments, V_{L1}, V_{L2} and V_{L3} are each independently a variable domain comprising: (a) a CDR-L1 comprising a sequence selected from the group consisting of SEQ ID NOs: 266, 269, 275, 278, 281, 488, 491, 494 and 500; (b) a CDR-L2 comprising a sequence selected from the group consisting of SEQ ID NOs: 267, 270, 276, 279, 282, 489, 492, 495, and 501; and (c) a CDR-L3 comprising a sequence selected from the group consisting of SEQ ID NOs: 268, 271, 274, 277, 280, 283, 490, 493, and 496. In some embodiments, V_{L1}, V_{L2} and V_{L3} are each independently a variable domain comprising a CDR-L1, CDR-L2, and CDR-L3 comprising amino acid sequences as shown in Table B. In some

embodiments, V_{L1}, V_{L2} and V_{L3} are each independently a variable domain comprising a CDR-L1, CDR-L2, and CDR-L3 comprising a sequence as set forth in SEQ ID NOs: 266, 267, and 268, respectively; a sequence as set forth in SEQ ID NOs: 269, 270, and 271, respectively; a sequence as set forth in SEQ ID NOs: 500, 501, and 274, respectively; a sequence as set forth in SEQ ID NOs: 275, 276, and 277, respectively; a sequence as set forth in SEQ ID NOs: 281, 282, and 283, respectively; a sequence as set forth in SEQ ID NOs: 278, 279, and 280, respectively; a sequence as set forth in SEQ ID NOs: 488, 489, and 490, respectively; a sequence as set forth in SEQ ID NOs: 491, 492, and 493, respectively; or a sequence as set forth in SEQ ID NOs: 494, 495, and 496, respectively.

[0183] In some embodiments, V_{H1}, V_{H2} and V_{H3} are each independently a variable domain comprising: (a) a CDR-H1 comprising a sequence selected from the group consisting of SEQ ID NOs: 248, 251, 254, 257, 263, 479, 482, 485, and 499; (b) a CDR-H2 comprising a sequence selected from the group consisting of SEQ ID NOs: 252, 255, 258, 261, 264, 480, 483, 486, and 497; and (c) a CDR-H3 comprising a sequence selected from the group consisting of SEQ ID NOs: 250, 253, 256, 259, 262, 265, 481, 484, 487, and 498. In some embodiments, V_{H1}, V_{H2} and V_{H3} are each independently a variable domain comprising a CDR-H1, CDR-H2, and CDR-H3 comprising amino acid sequences as shown in Table B. In some embodiments, V_{H1}, V_{H2} and V_{H3} are each independently a variable domain comprising a CDR-H1, CDR-H2, and CDR-H3 comprising a sequence as set forth in SEQ ID NOs: 248, 497, and 250, respectively; a sequence as set forth in SEQ ID NOs: 251, 252, and 253, respectively; a sequence as set forth in SEQ ID NOs: 254, 255, and 256, respectively; a sequence as set forth in SEQ ID NOs: 254, 255, and 498, respectively; a sequence as set forth in SEQ ID NOs: 257, 258, and 259, respectively; a sequence as set forth in SEQ ID NOs: 263, 264, and 265, respectively; a sequence as set forth in SEQ ID NOs: 499, 261, and 262, respectively; a sequence as set forth in SEQ ID NOs: 479, 480, and 481, respectively; a sequence as set forth in SEQ ID NOs: 482, 483, and 484, respectively; or a sequence as set forth in SEQ ID NOs: 485, 486, and 487, respectively.

[0184] In some embodiments, V_{L1} comprises a CDR-L1, CDR-L2, and CDR-L3 comprising the sequence of SEQ ID NOs: 488, 489, and 490, respectively; V_{L2} comprises a CDR-L1, CDR-L2, and CDR-L3 comprising the sequence of SEQ ID NOs: 494, 495, and 496, respectively; V_{L3} comprises a CDR-L1, CDR-L2, and CDR-L3 comprising the sequence of SEQ ID NOs: 269, 270, and 271, respectively; V_{H1} comprises a CDR-H1, CDR-H2, and CDR-H3 comprising the sequence of SEQ ID NOs: 479, 480, and 481, respectively; V_{H2}

comprises a CDR-H1, CDR-H2, and CDR-H3 comprising the sequence of SEQ ID NOs: 485, 486, and 487, respectively; and V_{H3} comprises a CDR-H1, CDR-H2, and CDR-H3 comprising the sequence of SEQ ID NOs: 251, 252, and 253, respectively. In some embodiments, V_{L1} comprises a CDR-L1, CDR-L2, and CDR-L3 comprising the sequence of SEQ ID NOs: 494, 495, and 496, respectively; V_{L2} comprises a CDR-L1, CDR-L2, and CDR-L3 comprising the sequence of SEQ ID NOs: 488, 489, and 490, respectively; V_{L3} comprises a CDR-L1, CDR-L2, and CDR-L3 comprising the sequence of SEQ ID NOs: 269, 270, and 271, respectively; V_{H1} comprises a CDR-H1, CDR-H2, and CDR-H3 comprising the sequence of SEQ ID NOs: 485, 486, and 487, respectively; V_{H2} comprises a CDR-H1, CDR-H2, and CDR-H3 comprising the sequence of SEQ ID NOs: 479, 480, and 481, respectively; and V_{H3} comprises a CDR-H1, CDR-H2, and CDR-H3 comprising the sequence of SEQ ID NOs: 251, 252, and 253, respectively.

[0185] In some embodiments, V_{L1} and V_{H1} are light and heavy chain variable domains comprising a light and heavy chain variable sequence of antibody CD28 or CD28_2 described herein, V_{L2} and V_{H2} are light and heavy chain variable domains comprising a light and heavy chain variable sequence of antibody CD3 described herein, and V_{L3} and V_{H3} are light and heavy chain variable domains comprising a light and heavy chain variable sequence of antibody CD4BS “a”, CD4BS “b”, MPER, MPER_100W, V1/V2 directed “a”, V1/V2 directed “b”, or V3 directed described herein. In some embodiments, V_{L1} and V_{H1} are light and heavy chain variable domains comprising the six CDRs of antibody CD28 or CD28_2 described herein, V_{L2} and V_{H2} are light and heavy chain variable domains comprising the six CDRs of antibody CD3 described herein, and V_{L3} and V_{H3} are light and heavy chain variable domains comprising the six CDRs of antibody CD4BS “a”, CD4BS “b”, MPER, MPER_100W, V1/V2 directed “a”, V1/V2 directed “b”, or V3 directed described herein.

[0186] In some embodiments, V_{L1} and V_{H1} are light and heavy chain variable domains comprising a light and heavy chain variable sequence of antibody CD28 or CD28_2 described herein, V_{L2} and V_{H2} are light and heavy chain variable domains comprising a light and heavy chain variable sequence of antibody CD4BS “a”, CD4BS “b”, MPER, MPER_100W, V1/V2 directed “a”, V1/V2 directed “b”, or V3 directed described herein, and V_{L3} and V_{H3} are light and heavy chain variable domains comprising a light and heavy chain variable sequence of antibody CD3 described herein. In some embodiments, V_{L1} and V_{H1} are light and heavy chain variable domains comprising the six CDRs of antibody CD28 or CD28_2 described herein, V_{L2} and V_{H2} are light and heavy chain variable domains

comprising the six CDRs of antibody CD4BS "a", CD4BS "b", MPER, MPER_100W, V1/V2 directed "a", V1/V2 directed "b", or V3 directed described herein, and V_{L3} and V_{H3} are light and heavy chain variable domains comprising the six CDRs of antibody CD3 described herein.

[0187] In some embodiments, V_{L1} and V_{H1} are light and heavy chain variable domains comprising a light and heavy chain variable sequence of antibody CD3 described herein, V_{L2} and V_{H2} are light and heavy chain variable domains comprising a light and heavy chain variable sequence of antibody CD28 or CD28_2 described herein, and V_{L3} and V_{H3} are light and heavy chain variable domains comprising a light and heavy chain variable sequence of antibody CD4BS "a", CD4BS "b", MPER, MPER_100W, V1/V2 directed "a", V1/V2 directed "b", or V3 directed described herein. In some embodiments, V_{L1} and V_{H1} are light and heavy chain variable domains comprising the six CDRs of antibody CD3 described herein, V_{L2} and V_{H2} are light and heavy chain variable domains comprising the six CDRs of antibody CD28 or CD28_2 described herein, and V_{L3} and V_{H3} are light and heavy chain variable domains comprising the six CDRs of antibody CD4BS "a", CD4BS "b", MPER, MPER_100W, V1/V2 directed "a", V1/V2 directed "b", or V3 directed described herein.

[0188] In some embodiments, V_{L1} and V_{H1} are light and heavy chain variable domains comprising a light and heavy chain variable sequence of antibody CD3 described herein, V_{L2} and V_{H2} are light and heavy chain variable domains comprising a light and heavy chain variable sequence of antibody CD4BS "a", CD4BS "b", MPER, MPER_100W, V1/V2 directed "a", V1/V2 directed "b", or V3 directed described herein, and V_{L3} and V_{H3} are light and heavy chain variable domains comprising a light and heavy chain variable sequence of antibody CD28 or CD28_2 described herein. In some embodiments, V_{L1} and V_{H1} are light and heavy chain variable domains comprising the six CDRs of antibody CD3 described herein, V_{L2} and V_{H2} are light and heavy chain variable domains comprising the six CDRs of antibody CD4BS "a", CD4BS "b", MPER, MPER_100W, V1/V2 directed "a", V1/V2 directed "b", or V3 directed described herein, and V_{L3} and V_{H3} are light and heavy chain variable domains comprising the six CDRs of antibody CD28 or CD28_2 described herein.

[0189] In some embodiments, V_{L1} and V_{H1} are light and heavy chain variable domains comprising a light and heavy chain variable sequence of antibody CD4BS "a", CD4BS "b", MPER, MPER_100W, V1/V2 directed "a", V1/V2 directed "b", or V3 directed described herein, V_{L2} and V_{H2} are light and heavy chain variable domains comprising a light and heavy chain variable sequence of antibody CD28 or CD28_2 described herein, and V_{L3} and V_{H3} are

light and heavy chain variable domains comprising a light and heavy chain variable sequence of antibody CD3 described herein. In some embodiments, V_{L1} and V_{H1} are light and heavy chain variable domains comprising the six CDRs of antibody CD4BS "a", CD4BS "b", MPER, MPER_100W, V1/V2 directed "a", V1/V2 directed "b", or V3 directed described herein, V_{L2} and V_{H2} are light and heavy chain variable domains comprising the six CDRs of antibody CD28 or CD28_2 described herein, and V_{L3} and V_{H3} are light and heavy chain variable domains comprising the six CDRs of antibody CD3 described herein.

[0190] In some embodiments, V_{L1} and V_{H1} are light and heavy chain variable domains comprising a light and heavy chain variable sequence of antibody CD4BS "a", CD4BS "b", MPER, MPER_100W, V1/V2 directed "a", V1/V2 directed "b", or V3 directed described herein, V_{L2} and V_{H2} are light and heavy chain variable domains comprising a light and heavy chain variable sequence of antibody CD3 described herein, and V_{L3} and V_{H3} are light and heavy chain variable domains comprising a light and heavy chain variable sequence of antibody CD28 or CD28_2 described herein. In some embodiments, V_{L1} and V_{H1} are light and heavy chain variable domains comprising the six CDRs of antibody CD4BS "a", CD4BS "b", MPER, MPER_100W, V1/V2 directed "a", V1/V2 directed "b", or V3 directed described herein, V_{L2} and V_{H2} are light and heavy chain variable domains comprising the six CDRs of antibody CD3 or CD28_2 described herein, and V_{L3} and V_{H3} are light and heavy chain variable domains comprising the six CDRs of antibody CD28 or CD28_2 described herein.

Target Proteins

[0191] In one embodiment, the binding proteins specifically bind to one or more HIV target proteins. In some embodiments, the binding proteins are trispecific and specifically bind to 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, a trimer apex of the HIV-1 gp120 protein or gp160. In other embodiments, the binding proteins specifically bind to one or more HIV target proteins 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, which are hereby incorporated into this disclosure by reference.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.

[0192] 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. In another embodiment, the binding protein is capable of binding three different HIV antigen targets that are located on the HIV envelope glycoprotein structure composed of gp120 and gp41 subunits. In other embodiments, the binding protein is capable of inhibiting the function of one or more of the antigen targets.

[0193] In some embodiments, a binding protein of the present disclosure binds one or more HIV target proteins. In some embodiments, the binding protein is capable of specifically binding three different epitopes on a single HIV target protein. In some embodiments, the binding protein is capable of binding two different epitopes on a first HIV target protein, and one epitope on a second HIV target protein. In some embodiments, the first and second HIV target proteins are different. In some embodiments, the binding protein is capable of specifically binding three different 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.

[0194] 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 binding protein is capable of specifically binding one T cell target protein and two different epitopes on a single HIV target protein. In some embodiments, the binding protein is capable of specifically binding one T cell target protein and two different HIV target proteins. 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.

Linkers

[0195] 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.

[0196] Examples of suitable linkers include a single glycine (Gly) residue; a diglycine peptide (Gly-Gly); a tripeptide (Gly-Gly-Gly); a peptide with four glycine residues (Gly-Gly-Gly-Gly; SEQ ID NO: 285); a peptide with five glycine residues (Gly-Gly-Gly-Gly-Gly; SEQ ID NO: 286); a peptide with six glycine residues (Gly-Gly-Gly-Gly-Gly-Gly; SEQ ID NO: 287); a peptide with seven glycine residues (Gly-Gly-Gly-Gly-Gly-Gly-Gly; SEQ ID NO: 288); a peptide with eight glycine residues (Gly-Gly-Gly-Gly-Gly-Gly-Gly-Gly; SEQ ID NO: 289). Other combinations of amino acid residues may be used such as the peptide Gly-Gly-Gly-Gly-Ser (SEQ ID NO: 290), the peptide Gly-Gly-Gly-Gly-Ser-Gly-Gly-Gly-Gly-Ser (SEQ ID NO: 291) and the peptide Gly-Gly-Gly-Gly-Ser-Gly-Gly-Gly-Gly-Ser-Gly-Gly-Gly-Gly-Ser (SEQ ID NO: 292). Other suitable linkers include a single Ser, and Val residue; the dipeptide Arg-Thr, Gln-Pro, Ser-Ser, Thr-Lys, and Ser-Leu; Thr-Lys-Gly-Pro-Ser (SEQ ID NO: 293), Thr-Val-Ala-Ala-Pro (SEQ ID NO: 294), Gln-Pro-Lys-Ala-Ala (SEQ ID NO: 295), Gln-Arg-Ile-Glu-Gly (SEQ ID NO: 296); Ala-Ser-Thr-Lys-Gly-Pro-Ser (SEQ ID NO: 297), Arg-Thr-Val-Ala-Ala-Pro-Ser (SEQ ID NO: 298), Gly-Gln-Pro-Lys-Ala-Ala-Pro (SEQ ID NO: 299), and His-Ile-Asp-Ser-Pro-Asn-Lys (SEQ ID NO: 300). 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.

[0197] 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.

[0198] 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.

[0199] In some embodiments, L_1, L_2, L_3, and/or L_4 comprise the sequence Asp-Lys-Thr-His-Thr (SEQ ID NO: 525). In some embodiments, L_1 comprises the sequence Asp-Lys-Thr-His-Thr (SEQ ID NO: 525). In some embodiments, L_3 comprises the sequence Asp-Lys-Thr-His-Thr (SEQ ID NO: 525).

[0200] In some embodiments, L_1, L_2, L_3, and/or L_4 comprise the sequence Gly-Gln-Pro-Lys-Ala-Ala-Pro (SEQ ID NO: 299). In some embodiments, L_1 comprises the sequence Gly-Gln-Pro-Lys-Ala-Ala-Pro (SEQ ID NO: 299). In some embodiments, L_1 comprises the sequence Gly-Gln-Pro-Lys-Ala-Ala-Pro (SEQ ID NO: 299), L_2 comprises the sequence Thr-Lys-Gly-Pro-Ser-Arg (SEQ ID NO: 526), L_3 comprises the sequence Ser, and L_4 comprises the sequence Arg-Thr. In some embodiments, L_3 comprises the sequence Gly-Gln-Pro-Lys-Ala-Ala-Pro (SEQ ID NO: 299). In some embodiments, L_1 comprises the sequence Ser, L_2 comprises the sequence Arg-Thr, L_3 comprises the sequence Gly-Gln-Pro-Lys-Ala-Ala-Pro (SEQ ID NO: 299) and L_4 comprises the sequence Thr-Lys-Gly-Pro-Ser-Arg (SEQ ID NO: 526).

Fc regions and constant domains

[0201] 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.

[0202] To improve the yields of the binding proteins, in some embodiments, the C_{H3} domains can be altered by the "knob-into-holes" technology which is described in detail with several examples in, for example, International Publication No. WO 96/027011, Ridgway *et al*., 1996, *Protein Eng*. 9: 617-21; and Merchant *et al*., 1998, *Nat. Biotechnol*. 16: 677-81. Specifically, the interaction surfaces of the two C_{H3} domains are altered to increase the heterodimerisation of both heavy chains containing these two C_{H3} domains. Each of the two C_{H3} domains (of the two heavy chains) can be the "knob," while the other is the "hole." The introduction of a disulfide bridge further stabilizes the heterodimers (Merchant *et al*., 1998; Atwell *et al*., 1997, *J. Mol. Biol*. 270: 26-35) and increases the yield. In particular embodiments, the knob is on the second pair of polypeptides with a single variable domain. In other embodiments, the knob is on the first pair of polypeptides having the cross-over orientation. In yet other embodiments, the C_{H3} domains do not include a knob in hole.

[0203] In some embodiments, a binding protein of the present disclosure 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 substitutions at positions corresponding to positions 354 and 366 of human IgG1 according to EU Index. In some embodiments, the amino acid substitutions are S354C and T366W. In some embodiments, the “hole” mutation comprises substitutions at positions corresponding to

positions 349, 366, 368, and 407 of human IgG1 according to EU Index. In some embodiments, 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 C_{H1}, the first Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} 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 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 C_{H1}, the second Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} 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 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 C_{H1}, the first Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} 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 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 C_{H1}, the second Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} 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 according to EU Index, wherein the amino acid substitutions are S354C and T366W.

[0204] In some embodiments, a binding protein of the present disclosure comprises one or more mutations to improve serum half-life (*See e.g.,* Hinton, P.R. *et al.* (2006) *J. Immunol.* 176(1):346-56). In some embodiments, the mutation comprises substitutions at positions corresponding to positions 428 and 434 of human IgG1 according to EU Index, wherein the amino acid substitutions are M428L and N434S. 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 comprise amino acid substitutions at positions corresponding to positions 428 and 434 of human IgG1 according to EU Index, wherein the amino acid substitutions are M428L and N434S. In some embodiments, a binding protein of the present disclosure comprises knob and hole mutations and one or more mutations to improve serum half-life.

[0205] In some embodiments, C_{H1}, C_{H2}, C_{H3} and C_L of the trispecific binding proteins described herein may comprise any of C_{H1}, C_{H2}, C_{H3} and C_L sequences of binding proteins 1-53.

Nucleic acids

[0206] 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.

[0207] Other aspects of the present disclosure relate to isolated nucleic acid molecules comprising a nucleotide sequence encoding any of the binding proteins described herein. 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.

[0208] 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.

[0209] 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. 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.

Host cells

[0210] 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).

[0211] 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).

Use for Binding Proteins

[0212] The binding proteins can be employed in any known assay method, such as competitive binding assays, direct and indirect sandwich assays, and immunoprecipitation assays for the detection and quantitation of one or more target antigens. The binding proteins will bind the one or more target antigens with an affinity that is appropriate for the assay method being employed.

[0213] For diagnostic applications, in certain embodiments, binding proteins can be labeled with a detectable moiety. The detectable moiety can be any one that is capable of producing, either directly or indirectly, a detectable signal. For example, the detectable moiety can be a radioisotope, such as ^{3}H, ^{14}C, ^{32}P, ^{35}S, ^{125}I, ^{99}Tc, ^{111}In, or ^{67}Ga; a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin; or an enzyme, such as alkaline phosphatase, β-galactosidase, or horseradish peroxidase.

[0214] The binding proteins are also useful for *in vivo* imaging. A binding protein labeled with a detectable moiety can be administered to an animal, *e.g.,* into the bloodstream, and the presence and location of the labeled antibody in the host assayed. The binding protein can be labeled with any moiety that is detectable in an animal, whether by nuclear magnetic resonance, radiology, or other detection means known in the art.

[0215] 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.

[0216] 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.

[0217] Acceptable formulation materials are nontoxic to recipients at the dosages and concentrations employed.

[0218] 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).

[0219] 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.

[0220] 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.

[0221] 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.

[0222] 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.

[0223] 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.

[0224] 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.

[0225] 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.

[0226] 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.

[0227] 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.

[0228] 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.

[0229] 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.

[0230] 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).

[0231] 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.

[0232] 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.

[0233] 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.

[0234] 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.

[0235] 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.

[0236] In some embodiments, the present disclosure relates to a method of preventing and/or treating HIV infection in a patient. In some embodiments, the method comprises administering to the patient a therapeutically effective amount of at least one of the binding proteins described herein. 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. In some embodiments, administration of the at least one binding protein results in neutralization of one or more HIV virions. In some embodiments, administration of the at least one binding protein 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.

[0237] Without limiting the present disclosure, a number of embodiments of the present disclosure are described below for purpose of illustration.

[0238] Item 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:

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

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

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

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

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

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

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

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

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.

[0239] Item 2: 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:

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

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.

[0240] Item 3: The binding protein of item 1 or item 2, wherein the one or more HIV target proteins is selected from the group consisting of glycoprotein 120, glycoprotein 41 and glycoprotein 60.

[0241] Item 4: The binding protein of item 1 or item 2, wherein the binding protein is trispecific and capable of specifically binding three different epitopes on a single HIV target protein.

[0242] Item 5: The binding protein of item 1 or item 2, wherein the binding protein is trispecific and capable of specifically binding two different epitopes on a first HIV target protein, and one epitope on a second HIV target protein, wherein the first and second HIV target proteins are different.

[0243] Item 6: The binding protein of item 1 or item 2, wherein the binding protein is trispecific and capable of specifically binding three different antigen targets.

[0244] Item 7: The binding protein of item 1 or item 2, wherein the binding protein is capable of inhibiting the function of one or more HIV target proteins.

[0245] Item 8: The binding protein of any one of items 1-7, wherein V_{L1} comprises a CDR-L1, CDR-L2, and CDR-L3 comprising a sequence as set forth in SEQ ID NOs: 266, 267, and 268, respectively; a sequence as set forth in SEQ ID NOs: 269, 270, and 271, respectively; a sequence as set forth in SEQ ID NOs: 500, 501, and 274, respectively; a sequence as set forth in SEQ ID NOs: 275, 276, and 277, respectively; a sequence as set forth in SEQ ID NOs: 281, 282, and 283, respectively; or a sequence as set forth in SEQ ID NOs: 278, 279, and 280, respectively.

[0246] Item 9: The binding protein of any one of items 1-7, wherein V_{L1} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, and 521.

[0247] Item 10: The binding protein of any one of items 1-9, wherein V_{L1} comprises a light chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, and 521.

[0248] Item 11: The binding protein of any one of items 1-10, wherein V_{L2} comprises a CDR-L1, CDR-L2, and CDR-L3 comprising a sequence as set forth in SEQ ID NOs: 266, 267, and 268, respectively; a sequence as set forth in SEQ ID NOs: 269, 270, and 271, respectively; a sequence as set forth in SEQ ID NOs: 500, 501, and 274, respectively; a sequence as set forth in SEQ ID NOs: 275, 276, and 277, respectively; a sequence as set forth in SEQ ID NOs: 281, 282, and 283, respectively; or a sequence as set forth in SEQ ID NOs: 278, 279, and 280, respectively.

[0249] Item 12: The binding protein of any one of items 1-10, wherein V_{L2} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, and 521.

[0250] Item 13: The binding protein of any one of items 1-12, wherein V_{L2} comprises a light chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, and 521.

[0251] Item 14: The binding protein of any one of items 1-13, wherein V_{L3} comprises a CDR-L1, CDR-L2, and CDR-L3 comprising a sequence as set forth in SEQ ID NOs: 266, 267, and 268, respectively; a sequence as set forth in SEQ ID NOs: 269, 270, and 271, respectively; a sequence as set forth in SEQ ID NOs: 500, 501, and 274, respectively; a sequence as set forth in SEQ ID NOs: 275, 276, and 277, respectively; a sequence as set forth in SEQ ID NOs: 281, 282, and 283, respectively; or a sequence as set forth in SEQ ID NOs: 278, 279, and 280, respectively.

[0252] Item 15: The binding protein of any one of items 1-13, wherein V_{L3} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, and 521.

[0253] Item 16: The binding protein of any one of items 1-15, wherein V_{L3} comprises a light chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, and 521.

[0254] Item 17: The binding protein of any one of items 1-16, wherein V_{H1} comprises a CDR-H1, CDR-H2, and CDR-H3 comprising a sequence as set forth in SEQ ID NOs: 248, 497, and 250, respectively; a sequence as set forth in SEQ ID NOs: 251, 252, and 253, respectively; a sequence as set forth in SEQ ID NOs: 254, 255, and 256, respectively; a sequence as set forth in SEQ ID NOs: 254, 255, and 498, respectively; a sequence as set forth in SEQ ID NOs: 257, 258, and 259, respectively; a sequence as set forth in SEQ ID NOs: 263, 264, and 265, respectively; or a sequence as set forth in SEQ ID NOs: 499, 261, and 262, respectively.

[0255] Item 18: The binding protein of any one of items 1-16, wherein V_{H1} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 502, 503, 504, 505, 506, 507, and 508.

[0256] Item 19: The binding protein of any one of items 1-18, wherein V_{H1} comprises a heavy chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 502, 503, 504, 505, 506, 507, and 508.

[0257] Item 20: The binding protein of any one of items 1-19, wherein V_{H2} comprises a CDR-H1, CDR-H2, and CDR-H3 comprising a sequence as set forth in SEQ ID NOs: 248, 497, and 250, respectively; a sequence as set forth in SEQ ID NOs: 251, 252, and 253, respectively; a sequence as set forth in SEQ ID NOs: 254, 255, and 256, respectively; a sequence as set forth in SEQ ID NOs: 254, 255, and 498, respectively; a sequence as set forth in SEQ ID NOs: 257, 258, and 259, respectively; a sequence as set forth in SEQ ID NOs: 263, 264, and 265, respectively; or a sequence as set forth in SEQ ID NOs: 499, 261, and 262, respectively.

[0258] Item 21: The binding protein of any one of items 1-19, wherein V_{H2} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 502, 503, 504, 505, 506, 507, and 508.

[0259] Item 22: The binding protein of any one of items 1-21, wherein V_{H2} comprises a heavy chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 502, 503, 504, 505, 506, 507, and 508.

[0260] Item 23: The binding protein of any one of items 1-22, wherein V_{H3} comprises a CDR-H1, CDR-H2, and CDR-H3 comprising a sequence as set forth in SEQ ID NOs: 248, 497, and 250, respectively; a sequence as set forth in SEQ ID NOs: 251, 252, and 253, respectively; a sequence as set forth in SEQ ID NOs: 254, 255, and 256, respectively; a sequence as set forth in SEQ ID NOs: 254, 255, and 498, respectively; a sequence as set forth in SEQ ID NOs: 257, 258, and 259, respectively; a sequence as set forth in SEQ ID NOs: 263, 264, and 265, respectively; or a sequence as set forth in SEQ ID NOs: 499, 261, and 262, respectively.

[0261] Item 24: The binding protein of any one of items 1-22, wherein V_{H3} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 502, 503, 504, 505, 506, 507, and 508.

[0262] Item 25: The binding protein of any one of items 1-24, wherein V_{H3} comprises a heavy chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 502, 503, 504, 505, 506, 507, and 508.

[0263] Item 26: The binding protein of any one of items 1-25, wherein V_{L1} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 500, a CDR-L2 comprising the sequence

of SEQ ID NO: 501, and a CDR-L3 comprising the sequence of SEQ ID NO: 274; V_{L2} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 275, a CDR-L2 comprising the sequence of SEQ ID NO: 276, and a CDR-L3 comprising the sequence of SEQ ID NO: 277; V_{L3} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 266, a CDR-L2 comprising the sequence of SEQ ID NO: 267, and a CDR-L3 comprising the sequence of SEQ ID NO: 268; V_{H1} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 254, a CDR-H2 comprising the sequence of SEQ ID NO: 255, and a CDR-H3 comprising the sequence of SEQ ID NO: 256; V_{H2} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 257, a CDR-H2 comprising the sequence of SEQ ID NO: 258, and a CDR-H3 comprising the sequence of SEQ ID NO: 259; and V_{H3} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 248, a CDR-H2 comprising the sequence of SEQ ID NO: 497, and a CDR-H3 comprising the sequence of SEQ ID NO: 250.

[0264] Item 27: The binding protein of any one of items 1-25, wherein V_{L1} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 518; V_{L2} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 519; V_{L3} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 512; V_{H1} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 504; V_{H2} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 506; and V_{H3} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 502.

[0265] Item 28: The binding protein of any one of items 1-27, wherein V_{L1} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 518; V_{L2} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 519; V_{L3} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 512; V_{H1} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 504; V_{H2} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 506; and V_{H3} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 502.

[0266] Item 29: The binding protein of any one of items 1-25, wherein V_{L1} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 500, a CDR-L2 comprising the sequence

of SEQ ID NO: 501, and a CDR-L3 comprising the sequence of SEQ ID NO: 274; V_{L2} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 275, a CDR-L2 comprising the sequence of SEQ ID NO: 276, and a CDR-L3 comprising the sequence of SEQ ID NO: 277; V_{L3} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 269, a CDR-L2 comprising the sequence of SEQ ID NO: 270, and a CDR-L3 comprising the sequence of SEQ ID NO: 271; V_{H1} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 254, a CDR-H2 comprising the sequence of SEQ ID NO: 255, and a CDR-H3 comprising the sequence of SEQ ID NO: 256; V_{H2} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 257, a CDR-H2 comprising the sequence of SEQ ID NO: 258, and a CDR-H3 comprising the sequence of SEQ ID NO: 259; and V_{H3} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 251, a CDR-H2 comprising the sequence of SEQ ID NO: 252, and a CDR-H3 comprising the sequence of SEQ ID NO: 253.

[0267] Item 30: The binding protein of any one of items 1-25, wherein V_{L1} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 518; V_{L2} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 519; V_{L3} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 513; V_{H1} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 504; V_{H2} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 506; and V_{H3} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 503.

[0268] Item 31: The binding protein of any one of items 1-25 and 29-30, wherein V_{L1} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 518; V_{L2} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 519; V_{L3} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 513; V_{H1} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 504; V_{H2} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 506; and V_{H3} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 503.

[0269] Item 32: The binding protein of any one of items 1-25, wherein V_{L1} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 275, a CDR-L2 comprising the sequence

of SEQ ID NO: 276, and a CDR-L3 comprising the sequence of SEQ ID NO: 277; V_{L2} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 500, a CDR-L2 comprising the sequence of SEQ ID NO: 501, and a CDR-L3 comprising the sequence of SEQ ID NO: 274; V_{L3} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 269, a CDR-L2 comprising the sequence of SEQ ID NO: 270, and a CDR-L3 comprising the sequence of SEQ ID NO: 271; V_{H1} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 257, a CDR-H2 comprising the sequence of SEQ ID NO: 258, and a CDR-H3 comprising the sequence of SEQ ID NO: 259; V_{H2} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 254, a CDR-H2 comprising the sequence of SEQ ID NO: 255, and a CDR-H3 comprising the sequence of SEQ ID NO: 256; and V_{H3} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 251, a CDR-H2 comprising the sequence of SEQ ID NO: 252, and a CDR-H3 comprising the sequence of SEQ ID NO: 253.

[0270] Item 33: The binding protein of any one of items 1-25, wherein V_{L1} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 519; V_{L2} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 518; V_{L3} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 513; V_{H1} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 506; V_{H2} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 504; and V_{H3} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 503.

[0271] Item 34: The binding protein of any one of items 1-25 and 32-33, wherein V_{L1} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 519; V_{L2} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 518; V_{L3} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 513; V_{H1} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 506; V_{H2} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 504; and V_{H3} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 503.

[0272] Item 35: The binding protein of item 1, wherein the second polypeptide chain further comprises 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.

[0273] Item 36: The binding protein of item 1, wherein the third polypeptide chain further comprises 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.

[0274] Item 37: The binding protein of item 1, wherein 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 first Fc region comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 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 C_{H1}, the second Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} 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 according to EU Index, wherein the amino acid substitutions are Y349C, T366S, L368A, and Y407V.

[0275] Item 38: The binding protein of item 1, wherein 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 first Fc region comprises amino acid substitutions at positions corresponding to positions 349, 366, 368, and 407 of human IgG1 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 C_{H1}, the second Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} 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 according to EU Index, wherein the amino acid substitutions are S354C and T366W.

[0276] Item 39: The binding protein of any one of items 1, 37, and 38, wherein 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, and 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 comprise amino acid substitutions at positions corresponding to positions 428 and 434 of human IgG1 according to EU Index, wherein the amino acid substitutions are M428L and N434S.

[0277] Item 40: The binding protein of item 2, wherein the C_{H3} domain of the second polypeptide chain comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 according to EU Index, wherein the amino acid substitutions are S354C and T366W; and wherein the 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 according to EU Index, wherein the amino acid substitutions are Y349C, T366S, L368A, and Y407V.

[0278] Item 41: The binding protein of item 2, wherein the 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 according to EU Index, wherein the amino acid substitutions are Y349C, T366S, L368A, and Y407V; and wherein the C_{H3} domain of the third polypeptide chain comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 according to EU Index, wherein the amino acid substitutions are S354C and T366W.

[0279] Item 42: The binding protein of any one of items 2, 40, and 41, wherein the C_{H3} domains of the second and the third polypeptide chains both comprise amino acid substitutions at positions corresponding to positions 428 and 434 of human IgG1 according to EU Index, wherein the amino acid substitutions are M428L and N434S.

[0280] Item 43: The binding protein of item 1 or item 2, wherein at least one of L_1, L_2, L_3, or L_4 is independently 0 amino acids in length.

[0281] Item 44: The binding protein of item 1 or item 2, wherein L_1, L_2, L_3, or L_4 are each independently at least one amino acid in length.

[0282] Item 45: The binding protein of any one of items 1-44, wherein L_1 comprises Asp-Lys-Thr-His-Thr (SEQ ID NO: 525).

[0283] Item 46: A binding protein comprising four polypeptide chains that form three antigen binding sites, 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:

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

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

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

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 the immunoglobulin C_{H1} heavy chain constant domain; 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:

(a) V_{L1}, V_{L2} and V_{L3} are each independently a variable domain derived from an amino acid sequence as set forth in any one of SEQ ID NOs: 2, 4, 10, 12, 18, 20, 26, 28, 34, 36, 42, 44, 50, 52, 58, 60, 66, 68, 74, 76, 82, 84, 90, 92, 98, 100, 106, 108, 114, 116, 122, 124, 130, 132, 138, 140, 146, 148, 154, 156, 162, 164, 170, 172, 178, 180, 186, 188, 194, 196, 202, 204, 210,212, 218, 220, 226, 228, 233, 235, 241, 243; or

(b) V_{L1}, V_{L2} and V_{L3} each independently comprise light chain complementarity determining regions of a variable domain comprising an amino acid sequence as set forth in any one of SEQ ID NOs:266-283; and

wherein:

(a) V_{H1}, V_{H2}, and V_{H3} are each independently a variable domain derived from an amino acid sequence as set forth in any one of SEQ ID NOs: 1, 3, 9, 11, 17, 10, 25, 27, 33, 35, 41, 43, 49, 51, 57, 59, 65, 67, 73, 75, 81, 83, 89, 91, 97, 99, 105, 107, 113, 115, 121, 123, 129, 131, 137, 139, 145, 147, 153, 155, 161, 163, 169, 171, 177, 179, 185, 187, 193, 195, 201, 203, 209, 211, 217, 219, 225, 227, 232, 234, 240, 242; or

(b) V_{H1}, V_{H2}, and V_{H3} each independently comprise heavy chain complementarity determining regions of a variable domain comprising an amino acid sequence as set forth in any one of SEQ ID NOs: 248-265.

[0284] Item 47: A binding protein comprising four polypeptide chains that form three antigen binding sites, 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 the 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:

(a) V_{L1}, V_{L2} and V_{L3} are each independently a variable domain derived from an amino acid sequence as set forth in any one of SEQ ID NOs: 2, 4, 10, 12, 18, 20, 26, 28, 34, 36, 42, 44, 50, 52, 58, 60, 66, 68, 74, 76, 82, 84, 90, 92, 98, 100, 106, 108, 114, 116, 122, 124,

130, 132, 138, 140, 146, 148, 154, 156, 162, 164, 170, 172, 178, 180, 186, 188, 194, 196, 202, 204, 210,212, 218, 220, 226, 228, 233, 235, 241, 243; or

(b) V_{L1}, V_{L2} and V_{L3} each independently comprise light chain complementarity determining regions of a variable domain comprising an amino acid sequence as set forth in any one of SEQ ID NOs:266-283; and

wherein:

(a) V_{H1}, V_{H2}, and V_{H3} are each independently a variable domain derived from an amino acid sequence as set forth in any one of SEQ ID NOs: 1, 3, 9, 11, 17, 10, 25, 27, 33, 35, 41, 43, 49, 51, 57, 59, 65, 67, 73, 75, 81, 83, 89, 91, 97, 99, 105, 107, 113, 115, 121, 123, 129, 131, 137, 139, 145, 147, 153, 155, 161, 163, 169, 171, 177, 179, 185, 187, 193, 195, 201, 203, 209, 211, 217, 219, 225, 227, 232, 234, 240, 242; or

(b) V_{H1}, V_{H2}, and V_{H3} each independently comprise heavy chain complementarity determining regions of a variable domain comprising an amino acid sequence as set forth in any one of SEQ ID NOs: 248-265.

[0285] Item 48: The binding protein of item 46, wherein the second polypeptide chain further comprises 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.

[0286] Item 49: The binding protein of item 46, wherein the third polypeptide chain further comprises 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.

[0287] Item 50: The binding protein of item 46, wherein 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 first Fc region comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 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 C_{H1}, the second Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} 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 according to EU Index, wherein the amino acid substitutions are Y349C, T366S, L368A, and Y407V.

[0288] Item 51: The binding protein of item 46, wherein 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 first Fc region comprises amino acid substitutions at positions corresponding to positions 349, 366, 368, and 407 of human IgG1 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 C_{H1}, the second Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} 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 according to EU Index, wherein the amino acid substitutions are S354C and T366W.

[0289] Item 52: The binding protein of any one of items 46, 50, and 51, wherein 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, and 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 comprise amino acid substitutions at positions corresponding to positions 428 and 434 of human IgG1 according to EU Index, wherein the amino acid substitutions are M428L and N434S.

[0290] Item 53: The binding protein of item 47, wherein the C_{H3} domain of the second polypeptide chain comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 according to EU Index, wherein the amino acid substitutions are S354C and T366W; and wherein the 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 according to EU Index, wherein the amino acid substitutions are Y349C, T366S, L368A, and Y407V.

[0291] Item 54: The binding protein of item 47, wherein the 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 according to EU Index, wherein the amino acid substitutions are Y349C, T366S, L368A, and Y407V; and wherein the C_{H3} domain of the third polypeptide chain comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 according to EU Index, wherein the amino acid substitutions are S354C and T366W.

[0292] Item 55: The binding protein of any one of items 47, 53, and 54, wherein the C_{H3} domains of the second and the third polypeptide chains both comprise amino acid substitutions at positions corresponding to positions 428 and 434 of human IgG1 according to EU Index, wherein the amino acid substitutions are M428L and N434S.

[0293] Item 56: The binding protein of item 46 or item 47, wherein at least one of L_1, L_2, L_3 or L_4 is independently 0 amino acids in length.

[0294] Item 57: The binding protein of item 46 or item 47, wherein L_1, L_2, L_3 or L_4 are each independently at least one amino acid in length.

[0295] Item 58: The binding protein of any one of items 46-57, wherein L_1 comprises Asp-Lys-Thr-His-Thr (SEQ ID NO: 525).

[0296] Item 59: A binding protein comprising a first polypeptide chain, a second polypeptide chain, a third polypeptide chain and a fourth polypeptide chain wherein:

(a) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 4 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 4; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 3 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 3; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 1 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 1; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 2 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 2;

(b) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 12 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 12; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 11 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 11; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 9 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 9; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 10 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 10;

(c) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 20 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 20; the second polypeptide chain comprises the amino acid sequence of SEQ

ID NO: 19 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 19; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 17 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 17; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 18 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 18;

(d) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 28 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 28; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 27 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 27; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 25 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 25; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 26 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 26;

(e) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 36 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 36; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 35 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 35; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 33 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 33; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 34 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 34;

(f) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 44 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 44; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 43 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 43; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 41 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 41; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 42 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 42;

(g) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 52 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 52; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 51 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 51; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 49 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 49; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 50 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 50;

(h) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 60 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 60; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 59 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 59; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 57 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 57; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 58 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 58;

(i) the first 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; the second 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; the third 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; and the fourth 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;

(j) the first 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; the second 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; the third 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; and the fourth 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;

(k) the first 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; the second 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; the third 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; and the fourth 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;

(l) the first 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; the second 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; the third 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; and the fourth 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;

(m) the first 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; the second 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; the third 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; and the fourth 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;

(n) the first polypeptide 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; the second 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; the third 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; and the fourth 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;

(o) the first 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; the second 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; the third 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; and the fourth 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;

(p) the first 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; the second 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; the third 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; and the fourth 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;

(q) the first 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; the second 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; the third 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; and the fourth 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;

(r) the first 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; the second 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; the third 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; and the fourth 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;

(s) the first 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; the second 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; the third 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; and the fourth 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;

(t) the first 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; the second 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; the third 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; and the fourth 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;

(u) the first 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; the second 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; the third 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; and the fourth 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;

(v) the first 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; the second 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; the third 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; and the fourth 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;

(w) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 180 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 180; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 179 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 179; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 177 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 177; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 178 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 178;

(x) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 188 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 188; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 187 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 187; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 185 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 185; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 186 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 186;

(y) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 196 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 196; the second polypeptide chain comprises the amino acid sequence of SEQ

ID NO: 195 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 195; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 193 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 193; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 194 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 194;

(z) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 204 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 204; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 203 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 203; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 201 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 201; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 202 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 202;

(aa) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 212 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 212; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 211 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 211; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 209 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 209; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 210 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 210;

(bb) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 220 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 220; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 219 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 219; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 217 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 217; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 218 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 218;

(cc) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 228 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 228; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 227 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 227; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 225 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 225; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 226 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 226;

(dd) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 235 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 235; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 234 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 234; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 232 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 232; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 233 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 233; or

(ee) first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 243 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 243; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 242 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 242; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 240 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 240; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 241 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 241.

[0297] Item 60: A binding protein comprising four polypeptide chains that form three antigen binding sites that specifically bind one or more HIV target proteins and one or more T cell target proteins, wherein a first polypeptide chain comprises a structure represented by the formula:

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

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

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

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

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

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

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

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

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.

[0298] Item 61: A binding protein comprising four polypeptide chains that form three antigen binding sites that specifically bind one or more HIV target proteins and one or more T cell target proteins, wherein a first polypeptide chain comprises a structure represented by the formula:

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

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

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

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

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

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

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

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;
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.

[0299] Item 62: The binding protein of item 60 or item 61, wherein the one or more HIV target proteins are selected from the group consisting of glycoprotein 120, glycoprotein 41 and glycoprotein 160.

[0300] Item 63: The binding protein of item 60 or item 61, wherein the one or more T cell target proteins are CD3 or CD28.

[0301] Item 64: The binding protein of item 60 or item 61, wherein the binding protein is trispecific and capable of specifically binding an HIV target protein and two different epitopes on a single T cell target protein.

[0302] Item 65: The binding protein of item 60 or item 61, wherein the binding protein is trispecific and capable of specifically binding an HIV target protein and two different T cell target proteins.

[0303] Item 66: The binding protein of item 60 or item 61, wherein the binding protein is trispecific and capable of specifically binding a T cell target protein and two different epitopes on a single HIV target protein.

[0304] Item 67: The binding protein of item 60 or item 61, wherein the binding protein is trispecific and capable of specifically binding a T cell target protein and two different HIV target proteins.

[0305] Item 68: The binding protein of item 60 or item 61, wherein the first and second polypeptide chains form two antigen binding sites that specifically target two T cell target proteins, and the third and fourth polypeptide chains form an antigen binding site that specifically binds an HIV target protein.

[0306] Item 69: The binding protein of any one of items 60-68, wherein V_{L1} comprises a CDR-L1, CDR-L2, and CDR-L3 comprising a sequence as set forth in SEQ ID NOs: 266,

267, and 268, respectively; a sequence as set forth in SEQ ID NOs: 269, 270, and 271, respectively; a sequence as set forth in SEQ ID NOs: 500, 501, and 274, respectively; a sequence as set forth in SEQ ID NOs: 275, 276, and 277, respectively; a sequence as set forth in SEQ ID NOs: 281, 282, and 283, respectively; a sequence as set forth in SEQ ID NOs: 278, 279, and 280, respectively; a sequence as set forth in SEQ ID NOs: 488, 489, and 490, respectively; a sequence as set forth in SEQ ID NOs: 491, 492, and 493, respectively; or a sequence as set forth in SEQ ID NOs: 494, 495, and 496, respectively.

[0307] Item 70: The binding protein of any one of items 60-68, wherein V_{L1} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, and 524.

[0308] Item 71: The binding protein of any one of items 60-70, wherein V_{L1} comprises a light chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, and 524.

[0309] Item 72: The binding protein of any one of items 60-71, wherein V_{L2} comprises a CDR-L1, CDR-L2, and CDR-L3 comprising a sequence as set forth in SEQ ID NOs: 266, 267, and 268, respectively; a sequence as set forth in SEQ ID NOs: 269, 270, and 271, respectively; a sequence as set forth in SEQ ID NOs: 500, 501, and 274, respectively; a sequence as set forth in SEQ ID NOs: 275, 276, and 277, respectively; a sequence as set forth in SEQ ID NOs: 281, 282, and 283, respectively; a sequence as set forth in SEQ ID NOs: 278, 279, and 280, respectively; a sequence as set forth in SEQ ID NOs: 488, 489, and 490, respectively; a sequence as set forth in SEQ ID NOs: 491, 492, and 493, respectively; or a sequence as set forth in SEQ ID NOs: 494, 495, and 496, respectively.

[0310] Item 73: The binding protein of any one of items 60-71, wherein V_{L2} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, and 524.

[0311] Item 74: The binding protein of any one of items 60-73, wherein V_{L2} comprises a light chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, and 524.

[0312] Item 75: The binding protein of any one of items 60-74, wherein V_{L3} comprises a CDR-L1, CDR-L2, and CDR-L3 comprising a sequence as set forth in SEQ ID NOs: 266, 267, and 268, respectively; a sequence as set forth in SEQ ID NOs: 269, 270, and 271,

respectively; a sequence as set forth in SEQ ID NOs: 500, 501, and 274, respectively; a sequence as set forth in SEQ ID NOs: 275, 276, and 277, respectively; a sequence as set forth in SEQ ID NOs: 281, 282, and 283, respectively; a sequence as set forth in SEQ ID NOs: 278, 279, and 280, respectively; a sequence as set forth in SEQ ID NOs: 488, 489, and 490, respectively; a sequence as set forth in SEQ ID NOs: 491, 492, and 493, respectively; or a sequence as set forth in SEQ ID NOs: 494, 495, and 496, respectively.

[0313] Item 76: The binding protein of any one of items 60-74, wherein V_{L3} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, and 524.

[0314] Item 77: The binding protein of any one of items 60-76, wherein V_{L3} comprises a light chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, and 524.

[0315] Item 78: The binding protein of any one of items 60-77, wherein V_{H1} comprises a CDR-H1, CDR-H2, and CDR-H3 comprising a sequence as set forth in SEQ ID NOs: 248, 497, and 250, respectively; a sequence as set forth in SEQ ID NOs: 251, 252, and 253, respectively; a sequence as set forth in SEQ ID NOs: 254, 255, and 256, respectively; a sequence as set forth in SEQ ID NOs: 254, 255, and 498, respectively; a sequence as set forth in SEQ ID NOs: 257, 258, and 259, respectively; a sequence as set forth in SEQ ID NOs: 263, 264, and 265, respectively; a sequence as set forth in SEQ ID NOs: 499, 261, and 262, respectively; a sequence as set forth in SEQ ID NOs: 479, 480, and 481, respectively; a sequence as set forth in SEQ ID NOs: 482, 483, and 484, respectively; or a sequence as set forth in SEQ ID NOs: 485, 486, and 487, respectively.

[0316] Item 79: The binding protein of any one of items 60-77, wherein V_{H1} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 502, 503, 504, 505, 506, 507, 508, 509, 510, and 511.

[0317] Item 80: The binding protein of any one of items 60-79, wherein V_{H1} comprises a heavy chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 502, 503, 504, 505, 506, 507, 508, 509, 510, and 511.

[0318] Item 81: The binding protein of any one of items 60-80, wherein V_{H2} comprises a CDR-H1, CDR-H2, and CDR-H3 comprising a sequence as set forth in SEQ ID NOs: 248, 497, and 250, respectively; a sequence as set forth in SEQ ID NOs: 251, 252, and 253,

respectively; a sequence as set forth in SEQ ID NOs: 254, 255, and 256, respectively; a sequence as set forth in SEQ ID NOs: 254, 255, and 498, respectively; a sequence as set forth in SEQ ID NOs: 257, 258, and 259, respectively; a sequence as set forth in SEQ ID NOs: 263, 264, and 265, respectively; a sequence as set forth in SEQ ID NOs: 499, 261, and 262, respectively; a sequence as set forth in SEQ ID NOs: 479, 480, and 481, respectively; a sequence as set forth in SEQ ID NOs: 482, 483, and 484, respectively; or a sequence as set forth in SEQ ID NOs: 485, 486, and 487, respectively.

[0319] Item 82: The binding protein of any one of items 60-80, wherein V_{H2} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 502, 503, 504, 505, 506, 507, 508, 509, 510, and 511.

[0320] Item 83: The binding protein of any one of items 60-82, wherein V_{H2} comprises a heavy chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 502, 503, 504, 505, 506, 507, 508, 509, 510, and 511.

[0321] Item 84: The binding protein of any one of items 60-83, wherein V_{H3} comprises a CDR-H1, CDR-H2, and CDR-H3 comprising a sequence as set forth in SEQ ID NOs: 248, 497, and 250, respectively; a sequence as set forth in SEQ ID NOs: 251, 252, and 253, respectively; a sequence as set forth in SEQ ID NOs: 254, 255, and 256, respectively; a sequence as set forth in SEQ ID NOs: 254, 255, and 498, respectively; a sequence as set forth in SEQ ID NOs: 257, 258, and 259, respectively; a sequence as set forth in SEQ ID NOs: 263, 264, and 265, respectively; a sequence as set forth in SEQ ID NOs: 499, 261, and 262, respectively; a sequence as set forth in SEQ ID NOs: 479, 480, and 481, respectively; a sequence as set forth in SEQ ID NOs: 482, 483, and 484, respectively; or a sequence as set forth in SEQ ID NOs: 485, 486, and 487, respectively.

[0322] Item 85: The binding protein of any one of items 60-83, wherein V_{H3} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 502, 503, 504, 505, 506, 507, 508, 509, 510, and 511.

[0323] Item 86: The binding protein of any one of items 60-85, wherein V_{H3} comprises a heavy chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 502, 503, 504, 505, 506, 507, 508, 509, 510, and 511.

[0324] Item 87: The binding protein of any one of items 60-86, wherein V_{L1} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 488, a CDR-L2 comprising the sequence

of SEQ ID NO: 489, and a CDR-L3 comprising the sequence of SEQ ID NO: 490; V_{L2} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 494, a CDR-L2 comprising the sequence of SEQ ID NO: 495, and a CDR-L3 comprising the sequence of SEQ ID NO: 496; V_{L3} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 269, a CDR-L2 comprising the sequence of SEQ ID NO: 270, and a CDR-L3 comprising the sequence of SEQ ID NO: 271; V_{H1} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 479, a CDR-H2 comprising the sequence of SEQ ID NO: 480, and a CDR-H3 comprising the sequence of SEQ ID NO: 481; V_{H2} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 485, a CDR-H2 comprising the sequence of SEQ ID NO: 486, and a CDR-H3 comprising the sequence of SEQ ID NO: 487; and V_{H3} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 251, a CDR-H2 comprising the sequence of SEQ ID NO: 252, and a CDR-H3 comprising the sequence of SEQ ID NO: 253.

[0325] Item 88: The binding protein of any one of items 60-86, wherein V_{L1} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 522; V_{L2} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 524; V_{L3} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 513; V_{H1} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 509; V_{H2} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 511; and V_{H3} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 503.

[0326] Item 89: The binding protein of any one of items 60-88, wherein V_{L1} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 522; V_{L2} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 524; V_{L3} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 513; V_{H1} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 509; V_{H2} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 511; and V_{H3} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 503.

[0327] Item 90: The binding protein of any one of items 60-86, wherein V_{L1} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 494, a CDR-L2 comprising the sequence

of SEQ ID NO: 495, and a CDR-L3 comprising the sequence of SEQ ID NO: 496; V_{L2} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 488, a CDR-L2 comprising the sequence of SEQ ID NO: 489, and a CDR-L3 comprising the sequence of SEQ ID NO: 490; V_{L3} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 269, a CDR-L2 comprising the sequence of SEQ ID NO: 270, and a CDR-L3 comprising the sequence of SEQ ID NO: 271; V_{H1} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 485, a CDR-H2 comprising the sequence of SEQ ID NO: 486, and a CDR-H3 comprising the sequence of SEQ ID NO: 487; V_{H2} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 479, a CDR-H2 comprising the sequence of SEQ ID NO: 480, and a CDR-H3 comprising the sequence of SEQ ID NO: 481; and V_{H3} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 251, a CDR-H2 comprising the sequence of SEQ ID NO: 252, and a CDR-H3 comprising the sequence of SEQ ID NO: 253.

[0328] Item 91: The binding protein of any one of items 60-86, wherein V_{L1} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 524; V_{L2} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 522; V_{L3} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 513; V_{H1} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 511; V_{H2} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 509; and V_{H3} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 503.

[0329] Item 92: The binding protein of any one of items 60-86 and 90-91, wherein V_{L1} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 524; V_{L2} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 522; V_{L3} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 513; V_{H1} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 511; V_{H2} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 509; and V_{H3} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 503.

[0330] Item 93: The binding protein of item 60, wherein the second polypeptide chain further comprises 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.

[0331] Item 94: The binding protein of item 60, wherein the third polypeptide chain further comprises 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.

[0332] Item 95: The binding protein of item 60, wherein 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 first Fc region comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 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 C_{H1}, the second Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} 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 according to EU Index, wherein the amino acid substitutions are Y349C, T366S, L368A, and Y407V.

[0333] Item 96: The binding protein of item 60, wherein 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 first Fc region comprises amino acid substitutions at positions corresponding to positions 349, 366, 368, and 407 of human IgG1 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 C_{H1}, the second Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} 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 according to EU Index, wherein the amino acid substitutions are S354C and T366W.

[0334] Item 97: The binding protein of any one of items 60, 95, and 96, wherein 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, and 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 comprise amino acid substitutions at positions corresponding to positions 428 and 434 of human IgG1 according to EU Index, wherein the amino acid substitutions are M428L and N434S.

[0335] Item 98: The binding protein of item 61, wherein the C_{H3} domain of the second polypeptide chain comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 according to EU Index, wherein the amino acid substitutions are S354C and T366W; and wherein the 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 according to EU Index, wherein the amino acid substitutions are Y349C, T366S, L368A, and Y407V.

[0336] Item 99: The binding protein of item 61, wherein the 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 according to EU Index, wherein the amino acid substitutions are Y349C, T366S, L368A, and Y407V; and wherein the C_{H3} domain of the third polypeptide chain comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 according to EU Index, wherein the amino acid substitutions are S354C and T366W.

[0337] Item 100: The binding protein of any one of items 61, 98, and 99, wherein the C_{H3} domains of the second and the third polypeptide chains both comprise amino acid substitutions at positions corresponding to positions 428 and 434 of human IgG1 according to EU Index, wherein the amino acid substitutions are M428L and N434S.

[0338] Item 101: The binding protein of item 60 or item 61, wherein at least one of L_1, L_2, L_3, or L_4 is independently 0 amino acids in length.

[0339] Item 102: The binding protein of item 60 or item 61, wherein L_1, L_2, L_3, or L_4 are each independently at least one amino acid in length.

[0340] Item 103: The binding protein of any one of items 60-102, wherein L_1 is Gly-Gln-Pro-Lys-Ala-Ala-Pro (SEQ ID NO: 299).

[0341] Item 104: A binding protein comprising four polypeptide chains that form three antigen binding sites, 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:

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

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

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

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 the immunoglobulin C_{H1} heavy chain constant domain; 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:

(a) V_{L1}, V_{L2} and V_{L3} are each independently a variable domain derived from an amino acid sequence as set forth in any one of SEQ ID NOs: 303, 305, 311, 313, 319, 321, 327, 329, 335, 337, 343, 345, 351, 353, 359, 361, 367, 369, 375, 377, 383, 385, 391, 393, 399, 401, 407, 409, 415, 417, 423, 425, 431, 433, 439, 441, 447, 449, 455, 457, 463, 465, 471, 473; or

(b) V_{L1}, V_{L2} and V_{L3} each independently comprise light chain complementarity determining regions of a variable domain comprising an amino acid sequence as set forth in any one of SEQ ID NOs: 266-271, 275-277, 488-496; and

wherein:

(a) V_{H1}, V_{H2}, and V_{H3} are each independently a variable domain derived from an amino acid sequence as set forth in any one of SEQ ID NOs: 302, 304, 310, 312, 318, 320, 326, 328, 334, 336, 342, 344, 350, 352, 358, 360, 366, 368, 374, 376, 382, 384, 390, 392, 398, 400, 406, 408, 414, 416, 422, 424, 430, 432, 438, 440, 446, 448, 454, 456, 462, 464, 470, 472; or

(b) V_{H1}, V_{H2}, and V_{H3} each independently comprise heavy chain complementarity determining regions of a variable domain comprising an amino acid sequence as set forth in any one of SEQ ID NOs: 248-253, 257-259, 479-487.

[0342] Item 105: A binding protein comprising four polypeptide chains that form three antigen binding sites, 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 the 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:

(a) V_{L1}, V_{L2} and V_{L3} are each independently a variable domain derived from an amino acid sequence as set forth in any one of SEQ ID NOs: 303, 305, 311, 313, 319, 321, 327, 329, 335, 337, 343, 345, 351, 353, 359, 361, 367, 369, 375, 377, 383, 385, 391, 393, 399,

401, 407, 409, 415, 417, 423, 425, 431, 433, 439, 441, 447, 449, 455, 457, 463, 465, 471, 473; or

(b) V_{L1}, V_{L2} and V_{L3} each independently comprise light chain complementarity determining regions of a variable domain comprising an amino acid sequence as set forth in any one of SEQ ID NOs: 266-271, 275-277, 488-496; and

wherein:

(a) V_{H1}, V_{H2}, and V_{H3} are each independently a variable domain derived from an amino acid sequence as set forth in any one of SEQ ID NOs: 302, 304, 310, 312, 318, 320, 326, 328, 334, 336, 342, 344, 350, 352, 358, 360, 366, 368, 374, 376, 382, 384, 390, 392, 398, 400, 406, 408, 414, 416, 422, 424, 430, 432, 438, 440, 446, 448, 454, 456, 462, 464, 470, 472; or

(b) V_{H1}, V_{H2}, and V_{H3} each independently comprise heavy chain complementarity determining regions of a variable domain comprising an amino acid sequence as set forth in any one of SEQ ID NOs: 248-253, 257-259, 479-487.

[0343] Item 106: The binding protein of item 104, wherein the second polypeptide chain further comprises 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.

[0344] Item 107: The binding protein of item 104, wherein the third polypeptide chain further comprises 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.

[0345] Item 108: The binding protein of item 104, wherein 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 first Fc region comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 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 C_{H1}, the second Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} 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 according to EU Index, wherein the amino acid substitutions are Y349C, T366S, L368A, and Y407V.

[0346] Item 109: The binding protein of item 104, wherein 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 first Fc region comprises amino acid substitutions at positions corresponding to positions 349, 366, 368, and 407 of human IgG1 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 C_{H1}, the second Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} 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 according to EU Index, wherein the amino acid substitutions are S354C and T366W.

[0347] Item 110: The binding protein of any one of items 104, 108, and 109, wherein 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, and 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 comprise amino acid substitutions at positions corresponding to positions 428 and 434 of human IgG1 according to EU Index, wherein the amino acid substitutions are M428L and N434S.

[0348] Item 111: The binding protein of item 105, wherein the C_{H3} domain of the second polypeptide chain comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 according to EU Index, wherein the amino acid substitutions are S354C and T366W; and wherein the 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 according to EU Index, wherein the amino acid substitutions are Y349C, T366S, L368A, and Y407V.

[0349] Item 112: The binding protein of item 105, wherein the 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 according to EU Index, wherein the amino acid substitutions are Y349C, T366S, L368A, and Y407V; and wherein the C_{H3} domain of the third polypeptide chain comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 according to EU Index, wherein the amino acid substitutions are S354C and T366W.

[0350] Item 113: The binding protein of any one of items 105, 111, and 112, wherein the C_{H3} domains of the second and the third polypeptide chains both comprise amino acid substitutions at positions corresponding to positions 428 and 434 of human IgG1 according to EU Index, wherein the amino acid substitutions are M428L and N434S.

[0351] Item 114: The binding protein of item 104 or item 105, wherein at least one of L_1, L_2, L_3, or L_4 is independently 0 amino acids in length.

[0352] Item 115: The binding protein of item 104 or item 105, wherein L_1, L_2, L_3, or L_4 are each independently at least one amino acid in length.

[0353] Item 116: The binding protein of any one of items 104-115, wherein L_1 is Gly-Gln-Pro-Lys-Ala-Ala-Pro (SEQ ID NO: 299).

[0354] Item 117: A binding protein comprising a first polypeptide chain, a second polypeptide chain, a third polypeptide chain and a fourth polypeptide chain wherein:

(a) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 305 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 305; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 304 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 304; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 302 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 302; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 303 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 303;

(b) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 313 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 313; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 312 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 312; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 310 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 310; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 311 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 311;

(c) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 321 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 321; the second polypeptide chain comprises the amino acid sequence of SEQ ID

NO: 320 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 320; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 318 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 318; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 319 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 319;

(d) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 329 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 329; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 328 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 328; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 326 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 326; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 327 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 327;

(e) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 337 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 337; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 336 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 336; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 334 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 334; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 335 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 335;

(f) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 345 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 345; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 344 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 344; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 342 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 342; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 343 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 343;

(g) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 353 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 353; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 352 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:352; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 350 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 350; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 351 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 351;

(h) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 361 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 361; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 360 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 360; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 358 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 358; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 359 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 359;

(i) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 369 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 369; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 368 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 368; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 366 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 366; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 367 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 367;

(j) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 377 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 377; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 376 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 376; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 374 or an amino acid sequence that is at least 95% identical to the amino acid

sequence of SEQ ID NO: 374; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 375 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 375;

(k) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 385 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 385; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 384 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 384; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 382 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 382; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 383 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 383;

(l) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 393 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 393; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 392 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 392; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 390 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 390; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 391 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 391;

(m) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 401 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 401; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 400 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 400; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 398 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 398; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 399 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 399;

(n) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 409 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 409; the second polypeptide chain comprises the amino acid sequence of SEQ ID

NO: 408 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 408; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 406 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 406; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 407 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 407;

(p) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 417 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 417; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 416 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 416; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 414 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 414; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 415 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 415;

(q) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 425 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 425; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 424 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 424; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 422 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 422; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 423 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 423;

(r) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 433 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:433; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 432 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 432; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 430 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 430; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 431 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 431;

(s) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 441 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 441; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 440 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 440; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 438 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 438; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 439 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 439;

(t) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 449 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 449; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 448 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 448; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 446 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 446; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 447 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 447;

(u) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 457 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 457; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 456 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 456; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 454 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 454; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 455 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 455;

(v) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 465 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 465; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 464 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 464; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 462 or an amino acid sequence that is at least 95% identical to the

amino acid sequence of SEQ ID NO: 462; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 463 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 463; or

(w) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 473 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 473; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 472 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 472; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 470 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 470; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 471 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 471.

[0355] Item 118: An isolated nucleic acid molecule comprising a nucleotide sequence encoding the binding protein of any one of items 1-117.

[0356] Item 119: An expression vector comprising the nucleic acid molecule of item 118.

[0357] Item 120: An isolated host cell comprising the nucleic acid molecule of item 118.

[0358] Item 121: An isolated host cell comprising the expression vector of item 119.

[0359] Item 122: The isolated host cell of item 120 or item 121, wherein the host cell is a mammalian cell or an insect cell.

[0360] Item 123: 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 items 1-117.

[0361] Item 124: The vector system of item 123, 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.

[0362] Item 125: The vector system of item 123, wherein 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.

[0363] Item 126: The vector system of any one of items 123-125, wherein the one or more vectors are expression vectors.

[0364] Item 127: An isolated host cell comprising the vector system of any one of items 123-126.

[0365] Item 128: The isolated host cell of item 127, wherein the host cell is a mammalian cell or an insect cell.

[0366] Item 129: A method of producing a binding protein, the method comprising:

a) culturing a host cell of any one of items 120-122 and items 127-128 under conditions such that the host cell expresses the binding protein; and

b) isolating the binding protein from the host cell.

[0367] Item 130: 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 items 1-117.

[0368] Item 131: The method of item 130, wherein the binding protein is co-administered with standard anti-retroviral therapy.

[0369] Item 132: The method of item 130 or item 131, wherein administration of the at least one binding protein results in the neutralization of one or more HIV virions.

[0370] Item 133: The method of any one of items 130-132, 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.

[0371] Item 134: The method of any one of items 130-133, wherein the patient is a human.

[0372] Item 135: The binding protein of any one of items 1-117 for the prevention or treatment of an HIV infection in a patient.

[0373] Item 136: The binding protein of item 135, wherein the binding protein is co-administered with standard anti-retroviral therapy.

[0374] Item 137: The binding protein of item 135 or item 136, wherein the binding protein causes the neutralization of one or more HIV virions in the patient.

[0375] Item 138: The binding protein of any one of items 135-137, wherein the binding protein causes the elimination of one or more latently and/or chronically HIV-infected cells in the patient.

[0376] Item 139: The binding protein of any one of items 135-138, wherein the patient is a human.

EXAMPLES

[0377] The Examples that follow are illustrative of specific embodiments of the disclosure, and various uses thereof. They are set forth for explanatory purposes only, and should not be construed as limiting the scope of the invention in any way.

Example 1: production of trispecific binding proteins targeting the HIV-1 Env glycoprotein.

[0378] The HIV-1 envelope glycoprotein (Env/gp160) is located on the surface of the virus particle, and is composed of a homo-trimer comprising three non-covalently-linked transmembrane gp41 and gp120 complexes. Env enables viral entry into target cells by the binding of gp120 to HIV's main receptor (CD4) and co-receptor (CCR5 or CXCR4), followed by the induction of viral/cellular membrane fusion facilitated by conformational changes in gp41, resulting in entry of the viral capsid and delivery of the viral genome into the host cell. Additionally, Env is expressed on the surface of infected cells.

[0379] Env acts as the only target for neutralizing antibodies on the HIV-1 virion. Binding of neutralizing antibodies to viral Env inhibits viral attachment/entry. Moreover, binding of neutralizing antibodies to HIV-1 infected, Env expressing cells leads to their destruction by Antibody-Dependent Cell-Mediated Cytotoxicity (ADCC) and Complement Dependent Cytotoxicity (CDC), resulting in reduction of the latent viral reservoir. Thus, neutralizing antibodies targeting Env are an attractive area for anti-viral therapy development. However, because of the high sequence diversity and mutation rate of the HIV-1 virus, developing neutralizing antibodies targeting Env has proven challenging due to the high likelihood that a given HIV-1 strain either lacks the epitope of any given neutralizing antibody, or the strain has evolved a mutation to become resistant to the antibody. Strategies must be developed to mitigate the breakthrough of viral strains when developing novel neutralizing antibodies targeting HIV-1. The studies described herein explore the development of novel trispecific binding proteins comprising four polypeptides forming three antigen binding sites that specifically bind three different epitopes on the HIV Env glycoprotein, and use of these novel trispecific binding proteins in neutralizing HIV-1.

Methods

Binding protein production and purification

[0380] The vectors expressing the trispecific binding proteins were constructed by inserting the designed heavy and light chain genes into a mammalian expression vector.

Corresponding heavy and light chain pairing occurred spontaneously, and heterodimer formation was promoted by Knob-in-Hole mutations engineered in the Fc region.

[0381] Binding proteins were produced in Expi293 cells by cotransfection of four expression plasmids (Life Technologies, Expi293™ Expression System Kit, Cat. No. A14635). Binding proteins were purified using a two-step purification scheme. First, binding proteins were captured on protein A affinity chromatography resin, washed, and then eluted in glycine at pH 3.0. The eluted proteins were then dialyzed in PBS, concentrated, and filtered. The filtered antibodies were further purified using a Superdex 200 SEC column to obtain monomeric binding proteins.

Affinity measurements of the binding proteins

[0382] Binding affinities of anti-HIV trispecific binding proteins were measured by surface plasmon resonance (SPR) using a Biacore3000 instrument (GE Healthcare). The assay buffer used was HBS-EP (GE Healthcare).

[0383] The affinity of the indicated proteins for the MPER binding site on the HIV-1 protein gp41 was measured by surface plasmon resonance (SPR) analysis using a Biacore Instrument as follows: binding proteins were first captured on a CM5 chip coupled with anti-human Fc antibody, followed by flow through of varying concentrations (100 nM – 6.25 nM) of the MPER binding peptide (Acetyl-RRRNEQELLELDKWASLWNWFDITNWLWYIRRR-Ttds-Lys-(Biotin)-NH_2) (SEQ ID NO: 284) at 30 µL per minute, and binding was detected by measurement of association for 240 seconds, and dissociation for 300 seconds on a Biacore 3000 at 25°C. HBS-EP buffer was used for sample dilution, as well as running buffer. Regenration of the chip was done with 3 M $MgCl_2$ at 30 µL per minute. For data analysis the BIAevaluation software v.4.1 (GE Healthcare) was used. Data were fit globally using a 1:1 Langmuir model with mass transfer. After software-based curve fitting, the ON and OFF reates at each concentration of MPER binding peptide was calculated and used to obtain a binding affinity for each binding protein.

[0384] The affinity of the indicated proteins for the CD4BS binding site on the HIV-1 protein gp120 was measured by SPR as follows: recombinant HIV-1 gp120 (Thr27-Arg498) protein (HIV-1 /Clade B/C (CN54), ARCO Biosystems (Cat. # GP4-V15227)) was captured on a CM5 chip, followed by flow through of varying concentrations (100 nM – 6.25 nM) of the binding proteins, and binding was detected by measurement of association for 240 seconds, and dissociation for 300 seconds on a Biacore 3000 at 25°C. HBS-EP buffer was used for sample dilution, as well as running buffer. Regenration of the chip was done with 3

M $MgCl_2$ at 30 µL per minute. For data analysis the BIAevaluation software v.4.1 (GE Healthcare) was used. Data were fit globally using a 1:1 Langmuir model with mass transfer. After software-based curve fitting, the ON and OFF reates at each concentration of Binding Protein was calculated and used to obtain a binding affinity for each binding protein.

Conformational stability and aggregation assays

[0385] Conformational stability of the trispecific binding proteins was assessed by determining the melting point T_m and aggregation onset temperature (T_{agg}).

[0386] Melting point T_m measurements were performed by differential scanning fluorimetry (DSF). Samples were diluted in D-PBS buffer (Invitrogen) to a final concentration of 0.2 µg/µL including a 4X concentration solution of SYPRO-Orange dye (Invitrogen,5000X stock in DMSO) in D-PBS in white sem-skirt 96-well plates (BIORAD). All measurements were done in duplicate using a MyiQ2 real time PCR instrument (BIORAD). Negative first derivative curves (-d(RFU)/dT) of the melting curves were generated in the iQ5 software v2.1 (BIORAD). Data were then exported into Excel for T_m determination and graphical display.

[0387] Melting Point T_m and aggregation onset temperature (T_{agg}) were also measured by static light scattering (SLS) using a Unit instrument (Unchained Labs). 9µL of each sample was loaded undiluted into a multicuvette array. The samples were then heated from 20°C to 95°C at a heating rate of 0.3°C/minute. The barycentric mean (BCM) of the tryptophan fluorescence spectra was used to measure the protein melting curve, and determine the T_m values. The 266 nm static light scattering (SLS) signal was used to measure the aggregation curve and determine the T_{agg}. Data analysis was performed using the Unit analysis software v2.1.

Results

[0388] A novel strategy was developed for improving neutralizing antibody efficacy against HIV-1, while concomitantly limiting the likelihood of viral breakthrough due to high sequence diversity and/or viral mutation. This strategy involved the generation of trispecific binding proteins comprising four polypeptides that formed three antigen binding sites that specifically bind three different epitopes on the HIV Env glycoprotein (**FIG. 1**). Each antigen binding site comprised the V_H and V_L domain from a different HIV-1 neutralizing antibody that targeted a distinct epitope on the Env glycoprotein. The trispecific binding proteins contained a first pair of polypeptides that possessed dual variable domains having a cross-over orientation forming two distinct antigen binding sites (called the CODV Ig format), and

a second pair of polypeptides, each with a single variable domain that formed a third antigen binding site (**FIGS. 1A and 1B**).

[0389] The first pair of polypeptides (that possessed the dual variable domains) comprised a first polypeptide having the structure V_{L2}-Linker-V_{L1}-Linker-Immunoglobulin light chain constant domain, and a second polypeptide having the structure V_{H1}-Linker-V_{H2}-Linker-Immunoglobulin C_{H1}, hinge, C_{H2}, and C_{H3} heavy chain constant domains, resulting in a pair of polypeptides which had a cross over orienation that formed two distinct antigen binding sites: V_{H1}-V_{L1} and V_{H2}-V_{L2} (**FIGS. 1C and 1D,** see light and heavy chains B). The second pair of polypeptides (that each posessed a single variable domain) comprised a first polypeptide having the structure V_{H3}-Immunoglobulin C_{H1}, hinge, C_{H2}, and C_{H3} heavy chain constant domains, and a second polypeptide having the structure V_{L3}-Immunoglobulin light chain constant domain, resulting in a pair of polypetpides that formed a third antigen binding site: V_{H3}-V_{L3} (**FIGS. 1C and 1D,** see light and heavy chains A). In addition, the trispecific binding proteins were constructed to include an LS mutation. Furthermore, the trispecific binding proteins were constructed such that within one binding protein, one C_{H3} domain included a knob mutation and the other C_{H3} domain included a hole mutation to facilitate heterodimerization of the heavy chains (**FIG. 1**).

[0390] Using the above described approach for trivalent binding protein design, three trispecific binding proteins (Binding Proteins 2, 3, and 24) were generated. These trispecific binding proteins were created by grafting onto a trispecific binding protein framework the V_H and V_L domains isolated from antibodies targeting three distinct epitopes on the HIV-1 Env glycoprotein: MPER Ab (targeting the MPER epitope on gp41), CD4BS Ab “b” (targeting the CD4 Binding Site on gp120), and V1/V2 directed Ab “a” (targeting the V1/V2 domain on gp120). Binding Protein 2 was constructed such that the first pair of polypeptides (which formed two antigen binding sites) targeted the HIV-1 Env glycoprotein epitopes MPER and V1/V2, and the second pair of polypeptides (which formed the single antigen binding site) targeted the HIV-1 Env glycoprotein epitope CD4BS (Binding Protein 2 = MPER x V1/V2 / CD4BS). Binding Protein 3 was constructed such that the first pair of polypeptides (which formed two antigen binding sites) targeted the HIV-1 Env glycoprotein epitopes V1/V2 and MPER, and the second pair of polypeptides (which formed the single antigen binding site) targeted the HIV-1 Env glycoprotein epitope CD4BS (Binding Protein 3 = V1/V2 x MPER / CD4BS). Binding Protein 24 was constructed such that the first pair of polypeptides (which formed two antigen binding sites) targeted the HIV-1 Env glycoprotein epitopes V1/V2 and

CD4BS, and the second pair of polypeptides (which formed the single antigen binding site) targeted the HIV-1 Env glycoprotein epitope MPER (Binding Protein 24 = V1/V2 x CD4BS / MPER). The three trispecific binding proteins, as well as their parental antibodies, were purified over protein A affinity resin (**FIGS. 2A and 3A**) followed by size exclusion chromatography (**FIGS. 2B and 3B**) to obtain monomeric proteins suitable for further characterization. All three trispecific binding proteins were stable and formed monomers at high frequency.

[0391] To test the potential for developing binding proteins targeting two different HIV-1 Env protein epitopes (instead of three), bispecific binding proteins were designed based upon the above described CODV Ig format (*See* WO 2012/135345), using two different V_H and V_L domains from the same parental antibodies used to create the trispecific binding proteins. However, the bispecific binding proteins with these specific variable domains did not purify well as monomers, showing significantly increased aggregate formation when compared to the corresponding trispecific binding proteins (**FIG. 4A and 4B**).

[0392] Next, the binding affinity of the purified trispecific binding proteins (and their parental antibodies) was measured for the HIV-1 Env glycoprotein epitopes on gp41 and gp120. First, the binding affinity for gp41 was measured for the three trispecific binding proteins, as well as the parental MPER antibody, by Biacore assay using the MPER binding peptide (**FIG. 5**). The binding affinity for the MPER antibody was calculated to be 18.7 nM. Surprisingly, the three trispecific binding proteins all had a higher affinity for the MPER binding peptide than did the parental antibody (**Table 3**), with Binding Protein 2 having an approximately 3.1 fold higher affinity than the MPER antibody (6.05 nM vs. 18.7 nM, respectively).

Table 3: Affinity measurements for the MPER binding peptide

Antibody	Analyte	ka (1/Ms)	kd (1/s)	Rmax (RU)	KA (1/M)	KD (M)	Chi2	MW MPER (kDa)
MPER Ab	Gp41-MPER JPT	5.85E+04	1.09E-03	47.5	5.35E+07	1.87E-08	0.55	5.25
Binding Protein 2	Gp41-MPER JPT	1.15E+05	6.97E-04	29.0	1.65E+08	6.05E-09	0.27	2.29
Binding Protein 3	Gp41-MPER JPT	4.67E+04	7.79E-04	38.5	6.00E+07	1.67E-08	0.41	5.14
Binding Protein 24	Gp41-MPER JPT	6.28E+04	8.06E-04	35.5	7.80E+07	1.28E-08	0.48	5.24

[0393] Similarly, the binding affinity for the CD4 Binding Site on gp120 was measured for the three trispecific binding proteins, as well as the parental CD4BS antibody, by Biacore

assay (**FIG. 6**). The three trispecific binding proteins all had a similar affinity for the CD4 Binding Site when compared to the parental antibody (**Table 4**).

Table 4: Affinity measurements for the CD4BS binding site

Antibody	ka (1/Ms)	kd (1/s)	Rmax (RU)	KD (M)	Chi2
CD4BS Ab "b"	2.79E+05	2.32E-04	31.4	8.30E-10	1.17
Binding Protein 2	2.31E+05	2.41E-04	34.0	1.04E-09	0.74
Binding Protein 3	7.58E+04	2.75E-04	38.2	3.63E-09	0.19
Binding Protein 24	1.46E+05	2.52E-04	41.6	1.73E-09	0.38

[0394] Thus, the trispecific binding proteins were able to bind both of the tested target epitopes on the HIV-1 Env glycoprotein (**Table 5**). Moreover, all three trispecific binding proteins bound the target epitopes with affinities approximately equal to or exceeding those of their parental antibodies. Binding affinity of the V1/V2 directed Ab "a", as well as of the V1/V2 directed Ab "a" binding sites within the three trispecific binding proteins 2, 3, and 24 could not be determined by Biacore analysis because this required a specific gp120 protein antigen which was unavailable.

Table 5: Summary of binding capabilities of tested binding proteins

Sample	Binding on gp120?	Binding on gp41?
MPER Ab	No	Yes
CD4BS Ab "b"	Yes	No
V1/V2 directed Ab "a"	No	No
Binding Protein 2	Yes	Yes
Binding Protein 3	Yes	Yes
Binding Protein 24	Yes	Yes

[0395] The biophysical properties were tested for the trispecific binding proteins and parental antibodies (**Table 6**). All of the tested proteins had similar stabilities and limited propensities to form aggregates.

Table 6: Conformational stability/aggregation of the binding proteins

Sample	DSF T_m (°C)	Intrinsic AA Fluo T_m (°C)	SLS at 266nm T_{agg} (°C)
MPER Ab	69/75	68	71
CD4BS Ab "b"	69	66	68
V1/V2 directed Ab "a"	69	64	67
Binding Protein 2	60/70	54	58

Binding Protein 3	57/70	55	56
Binding Protein 24	56/71	53	54

[0396] These experiments indicated that stable, monomeric, trispecific binding proteins targeting three distinct epitopes on the HIV-1 Env glycoprotein could be constructed and efficiently purified. Furthermore, the trispecific binding proteins retained their ability to bind their target epitopes, having similar or improved affinity relative to their parental antibodies. Finally, the trispecific binding proteins had suitable biophysical properties, and showed significantly less aggregation than the corresponding bispecific binding proteins.

Example 2: characterization of the Binding Proteins

[0397] Due to the success of developing three trispecific binding proteins with appropriate biophysical properties and binding abilities (as described in Example 1), 21 additional trispecific binding proteins were developed and tested. The experiments described herein explored the ability of the 24 trispecific binding proteins to neutralize HIV-1 *in vitro*, and the pharmacokinetic properties of a number of these trispecific binding proteins *in vivo*.

[0398] Neutralization assays were performed using the TZM-bl assay which measures neutralization as a function of reductions in HIV-1 Tat-regulated firefly luciferase (Luc) reporter gene expression after a single round of infection with Env-pseudotyped viruses. The assays were performed as described in Marcella Sarzotti-Kelsoe et al., J. Immunological Methods, 409:131-146 (2014). The neutralization results of various antibodies are shown in **Tables 8-10**.

Methods

Production of Env-pseudotyped viruses

[0399] Assay stocks of Env-pseudotyped viruses were produced in 293T/17 cells by co-transfection with two plasmids: an Env expression plasmid and a plasmid expressing the entire HIV-1 genome except for Env. Co-transfection of these plasmids produced infectious pseudovirus particles which were capable of delivering the Tat gene into target cells, but infections with these pseudovirions could not themselves produce infectious viral progeny.

Viral neutralization assay

[0400] Neutralization of HIV infection using TZM-b1 cells (also known as JC53BL-13 cells) was performed as described previously (Marcella Sarzotti-Kelsoe et al., J. Immunological Methods, 409:131-146 (2014)). Briefly, a single round of infection using the Env-pseudotyped HIV-1 virions was carried out in TZM-b1 cells (a CXCR-4-positivie HeLa

cell clone). TZM-b1 cells were engineered to express CD4 and CCR5, and to contain integrated reporter genes for firefly luciferase and *E. coli* β-galactosidase under the control of an HIV long-terminal repeat. Reporter gene expression was induced *in trans* by viral Tat protein (delivered by the pseudotyped viruses) soon after single cycle infection. Luciferase activity was quantified as relative luminescence units (RLU), and was directly proportional to the number of infectious virus particles present in the initial inoculum over a wide range of values. Neutralization was measured as a function of decreased Tat-regulated Firefly luciferase (Luc) reporter gene expression after administration of varying concentrations of the indicated binding proteins. Neutralization titers were identified as the protein dilution at which RLUs were reduced by 80% compared to virus control wells after subtraction of background RLUs. The assay was performed in 96-well plates for high throughput capacity, and well-characterized reference strains were utilized for uniformity across studies.

Pharmacokinetic (PK) measurements

[0401] Female Indian rhesus macaques weighing between 3 and 6 kg were randomly assigned to groups according to body weight (two macaques per group) and were intravenously injected with the indicated concentration of binding proteins. Blood was collected from the animals before the injection on day 0, and 30 minutes, 6 hours, 1 day, 2 days, 4 days, 7 days, 14 days, 21 days and 28 days after injection. The serum concentration of each binding protein was quantified in the plasma from the collected blood using an RSC3-based ELISA assay.

Results

[0402] 21 additional trispecific binding proteins targeting three distinct HIV-1 Env glycoprotein epitopes were generated and purified as described in Example 1. These 21 additional trispecific binding proteins (Binding Proteins 1 and 4-23) were created by grafting onto a trispecific binding protein framework the V_H and V_L domains isolated from antibodies targeting distinct HIV-1 epitopes on the HIV-1 Env glycoprotein: the anti-MPER antibodies *MPER Ab "a"* and *MPER Ab "b"* (targeting the MPER epitope on gp41), the anti-CD4BS antibodies *CD4BS Ab "a"* and *CD4BS Ab "b"* (targeting the CD4 Binding Site on gp120), the anti-V1/V2 antibodies *V1/V2 directed Ab "a"* and *V1/V2 directed Ab "b"* (targeting the V1/V2 domain on gp120), and the anti-V3 antibody *V3 directed Ab* (targeting the V3 loop on gp120) (**Table 7**).

Table 7: Epitope binding site composition of the trispecific binding proteins

Binding Protein:	Epitope Binding Site:
1	MPER x V1/V2 directed / CD4BS

2	MPER x V1/V2 directed / CD4BS
3	V1/V2 directed x MPER / CD4BS
4	MPER x V1/V2 directed / CD4BS
5	MPER x V3 directed / CD4BS
6	V1/V2 directed x MPER / CD4BS
7	V3 directed x V1/V2 directed / CD4BS
8	MPER x V1/V2 directed / CD4BS
9	MPER x V1/V2 directed / CD4BS
10	V1/V2 directed x MPER / CD4BS
11	MPER x V1/V2 directed / CD4BS
12	MPER x V3 directed / CD4BS
13	MPER x V3 directed / V1/V2 directed
14	V1/V2 directed x MPER / CD4BS
15	MPER x V3 directed / V1/V2 directed
16	MPER x V3 directed / CD4BS
17	V1/V2 directed x V3 directed / CD4BS
18	V3 directed x MPER / CD4BS
19	V3 directed x V1/V2 directed / MPER
20	V3 directed x V1/V2 directed / CD4BS
21	MPER x CD4BS / V1/V2 directed
22	CD4BS x MPER / V1/V2 directed
23	CD4BS x V1/V2 directed / MPER
24	V1/V2 directed x CD4BS / MPER

[0403] The viral neutralization capabilities of five of the trispecific binding proteins (and their parental antibodies) at varying concentrations were tested against a panel of 208 different HIV-1 Env-pseudotyped viruses (**Table 8**). Binding protein-mediated neutralization of the pseudotyped HIV-1 isolates was measured using the TZM-b1 luciferase reporter gene assay. The inhibitory dose for each binding protein was calculated for each pseudotyped virus as the dilution that caused an 80% reduction in luminescence (IC_{80}) after infection. Surprisingly, the IC_{80} geometric means calculated for each of the tested trispecific binding proteins was lower than the parental antibodies, suggesting that these trispecific binding proteins were more potent at neutralizing pseudotyped HIV-1 than their parental neutralizing antibodies.

Table 8: IC_{80} measurements from viral neutralization assay

	Binding Protein:						**Parental Antibody:**				
	15	**1**	**2**	**19**	**20**	**3**	**MPER Ab**	**V1/V2 directed Ab "a"**	**V3 directed Ab**	**CD4BS Ab "b"**	**CD4BS Ab "a"**
# Viruses	208	208	208	208	208	208	208	208	208	208	208
Total VS Neutralized:											
IC_{80} <50 µg/mL	190	202	206	198	206	206	203	151	113	202	183
IC_{80} <10 µg/mL	180	199	206	180	206	206	193	149	109	200	175

IC_{80} <1.0 µg/mL	166	169	191	145	188	186	61	133	98	184	108
IC_{80} <0.1 µg/mL	122	109	136	80	144	123	10	99	72	79	10
IC_{80} <0.01 µg/mL	74	7	70	22	54	47	5	24	26	6	0
% VS Neutralized:											
IC_{80} <50 µg/mL	91	97	99	95	99	99	98	73	54	97	88
IC_{80} <10 µg/mL	87	96	99	87	99	99	93	72	52	96	84
IC_{80} <1.0 µg/mL	80	81	92	70	90	89	29	64	47	88	52
IC_{80} <0.1 µg/mL	59	52	65	38	69	59	5	48	35	38	5
IC_{80} <0.01 µg/mL	36	3	34	11	26	23	2	12	13	3	0
Median IC_{80}	0.033	0.088	0.026	0.164	0.029	0.045	1.69	0.037	0.054	0.149	0.780
Geometric Mean	0.033	0.135	0.028	0.199	0.034	0.051	1.34	0.063	0.057	0.144	0.814

[0404] Next, the viral neutralization capabilities of a larger panel of trispecific binding proteins (and their parental antibodies) at varying concentrations were tested against 20 pseudotyped viruses representing 10 different HIV-1 clades (**Table 9**). The trispecific binding proteins provided robust protection against infection with these 20 viruses (**Table 10**).

Table 9: 20 representative viruses used for viral neutralization assay

Virus	Clade
KER2008.12.SG3	A
620345.c1.SG3	AE
DJ263.8.SG3	AG
T266-60.SG3	AG
T278-50.SG3	AG
BL01.DG.SG3	B
BR07.DG.SG3	B
CNE57.SG3	B
H086.8.SG3	B
QH0692.42.SG3	B
SS1196.01.SG3	B
CNE21.SG3	BC
6471.V1.C16.SG3	C
CAP210.E8.SG3	C
DU156.12.SG3	C
DU422.01.SG3	C
TV1.29.SG3	C
ZM106.9.SG3	C
3817.v2.c59.SG3	CD
X2088.c9.SG3	G

Table 10: IC_{80} measurements from viral neutralization assay of 20 representative viruses

		Total VS Neutralized		**% VS Neutralized**			
	# Viruses	IC_{80} <50 µg/mL	IC_{80} <1 µg/mL	IC_{80} <50 µg/mL	IC_{80} <1 µg/mL	Median IC_{80}	Geometric Mean
Binding Protein 4	20	17	11	85	55	0.474	0.398
Binding Protein 5	20	14	11	70	55	0.199	0.324
Binding Protein 6	20	16	9	80	45	0.453	0.449
Binding Protein 7	20	16	9	80	45	0.523	0.312
Binding Protein 8	20	17	12	85	60	0.578	0.488
Binding Protein 9	20	14	9	70	45	0.836	0.531

Binding Protein 10	20	16	12	80	60	0.222	0.173
Binding Protein 11	20	18	15	90	75	0.310	0.181
Binding Protein 12	20	17	12	85	60	0.526	0.566
Binding Protein 13	20	19	12	95	60	0.202	0.189
Binding Protein 14	20	17	15	85	75	0.208	0.088
Binding Protein 15	20	17	10	85	50	0.345	0.378
Binding Protein 16	20	18	11	90	55	0.228	0.314
Binding Protein 17	20	17	12	85	60	0.086	0.180
Binding Protein 18	20	15	10	75	50	0.536	0.501
Binding Protein 19	20	18	11	90	55	0.563	0.538
Binding Protein 20	20	18	14	90	70	0.224	0.229
Binding Protein 21	20	15	9	75	45	0.627	0.501
Binding Protein 2	20	18	13	90	65	0.375	0.222
Binding Protein 22	20	13	8	65	40	0.856	0.634
Binding Protein 23	20	17	6	85	30	1.930	1.129
Binding Protein 3	20	18	12	90	60	0.469	0.287
Binding Protein 24	20	16	7	80	35	2.130	1.054
MPER Ab “a”	20	16	8	80	40	1.007	0.981
MPER Ab “b”	20	16	16	80	80	0.071	0.024
CD4BS Ab “b”	20	15	9	75	45	0.181	0.399
V1/V2 directed Ab “a”	20	11	9	55	45	0.060	0.094
V3 directed Ab	20	12	10	60	50	0.183	0.136
CD4BS Ab “a”	20	10	1	50	5	1.530	1.811
V1/V2 directed Ab “b”	20	9	9	45	45	0.051	0.039

[0405] Finally, the pharmacokinetics (PK) of a subset of the trispecific binding proteins and parental antibodies were tested in rhesus macaques. Briefly, 10 or 20 mg/kg of the proteins were intravenously injected into female rhesus macaques, and ELISA assays were performed on the plasma from blood samples taken prior to injection, and on the plasma from blood samples taken at many time points after the injection (up to 42 days) (**FIG. 7**). All of the trispecific binding proteins could be detected at least 14 days after IV administration, with Binding Protein 1 remaining detectable at least 35 days after injection, showing that the binding proteins were stable *in vivo*.

[0406] Taken together, this data suggested that broadly neutralizing trispecific binding proteins could be constructed which targeted three distinct epitopes on the HIV-1 Env glycoprotein. These binding proteins showed similar or increased potency/much improved neutralizing capabilities (breadth) relative to the parental neutralizing antibodies. Furthermore, these trispecific binding proteins appeared to be well tolerated *in vivo*. Without wishing to be bound by theory, the development of broadly neutralizing trispecific binding proteins targeting multiple epitopes on HIV may allow for improved anti-viral therapy relative to monospecific or bispecific antibodies, as HIV viral particles are less likely to be resistant to all three antigen binding sites on the neutralizing trispecific binding proteins than

the single or dual antigen binding sites on monospecific or bispecific neutralizing antibodies, respectively.

Example 3: characterization of T-cell engagers.

[0407] As noted above, Env is expressed on the surface of HIV-infected cells. Because of this, Env can act as an antibody target to identify infected cells, and induce Antibody-Dependent Cell-Mediated Cytotoxicity (ADCC) and Complement Dependent Cytotoxicity (CDC), resulting in reduction of the latent viral reservoir. The studies described herein explore the development of novel trispecific binding proteins (termed "T cell engagers") that contain three antigen binding sites targeting three different antigens (HIV-1 Env glycoprotein, CD3, and CD28). These novel proteins not only include antigen binding sites from neutralizing antibodies, but also the ability to bind effector T cells, bringing them into close proximity to infected target cells, thus inducing HIV-infected cell lysis.

Methods

Binding properties of T-cell engagers

[0408] The binding properties of the T-cell engagers was measured by ELISA assay using a horse radish peroxidase-conjugated anti-Fab probe to detect T-cell engager binding to the surface of ELISA plates coated with CD3, CD28, or Resurfaced Stabilized Core 3 (RSC3) protein of gp120. Human CD3ge-hIgG4 (KIH) (Cat. No: 03-01-0051) from Cambridge Biologics, MA, USA; Human CD28-hIgG4 (Cat. No: 03-01-0303) from Cambridge Biologics, MA, USA.

T-cell activation assay

[0409] CD4 and CD8 T cell activation were measured as follows: peripheral blood mononuclear cells (PBMCs) were enriched from buffy coats obtained from naïve donors (NIH blood bank) using magnetic beads (Miltenyi Biotec). These cells were co-cultured for 14-16 hours with either uninfected or HIV-1 infected CEM cells in the presence of increasing concentrations of the binding proteins (0.01-1.0 μg/mL) with brefeldin A. The cells were then stained for surface expression of T-cell markers (CD3, CD4, and CD8) and activation markers (CD25 and CD69), followed by intracellular staining for cytokines (IFN-γ, TNF-α, and IL-2) using fluorescently conjugated antibodies (BD Biosciences, eBiosciences, Biolegend). The number of CD4 and CD8 T cells expressing each cytokine or activation marker was determined by running the samples on an LSRII flow cytometer and analyzing the data with Flowjo software (Treeestar).

CD3 downregulation

[0410] CD3 downregulation after T cell activation by the T-cell engagers was measured by staining activated PBMCs with non-competing mouse anti-human CD3 antibody and quantitated using flow cytometry.

Cytotoxicity assay

[0411] Cytotoxicity of the T-cell engagers to CEM-BaL, ACH2, and J1.1 cells was monitored by flow cytometry as follows: latent cell lines (ACH2, J1.1, OM10) were obtained from the NIH AIDS Reagent Program. The activation of these cells was performed by culturing the cells in the presence or absence of TNF-α (10 ng/mL) for 14-16 hours. Activation was measured by determining the expression of cell surface HIV envelope glycoprotein by flow cytometry using an allophycocyanin-conjugated anti-HIV Env antibody (2G12). The CEM-IIIb, ACH2, J1.1 and OM10 cells were labeled with the membrane dye PKH-26 (Sigma) and used as target cells in a cytotoxicity assay. These labeled target cells were co-cultured for 14-16 hours at an E:T ratio of 10:1 with enriched human T cells as effector cells in the presence of increasing amounts of the binding proteins. The extent of cell lysis in the target cells was determined by staining with a live/dead cell marker (Life technologies) and measuring the number of dead cells in the labeled target cell population by running the samples on an LSRII flow cytometer followed by analysis using Flowjo software (Treestar).

Results

[0412] The capacity to develop T cell engagers with antigen binding sites targeting both T cell surface proteins and neutralizing epitopes on HIV-1 was explored. T cell engagers were constructed which contained two antigen binding sites targeting two different T cell surface receptors (CD3 and CD28), and a third antigen binding site targeting the HIV-1 Env glycoprotein (**FIGS. 8A and 8B**). In addition, the T cell engagers were constructed to include an LS mutation. Furthermore, the T cell engagers were constructed such that within one binding protein, one C_{H3} domain included a knob mutation and the other C_{H3} domain included a hole mutation to facilitate heterodimerization of the heavy chains (**FIGS. 8A and 8B**).

[0413] Using this approach, two T cell engagers were constructed which targeted both T cell surface proteins and the HIV-1 Env glycoprotein (Binding Protein 32 and CD3 x CD28 / CD4BS "b" Ab). These two T cell engagers were created by grafting onto a trispecific binding protein framework the V_H and V_L domains isolated from parental antibodies targeting the T cell surface proteins CD3 and CD28, and the anti-HIV-1 antibody CD4BS Ab "b"

(targeting the CD4 Binding Site on gp120). Binding Protein 32 was constructed such that the first pair of polypeptides (which formed two antigen binding sites) targeted the T cell surface receptors CD28 and CD3, and the second pair of polypeptides (which formed the single antigen binding site) targeted the HIV-1 antigen CD4BS (Binding Protein 32 = CD28 x CD3 / CD4BS). The CD3 x CD28 / CD4BS "b" Ab trispecific binding protein was constructed such that the first pair of polypeptides (which formed two antigen binding sites) targeted the T cell surface receptors CD3 and CD28, and the second pair of polypeptides (which formed the single antigen binding site) targeted the HIV-1 antigen CD4BS (**Table 11**).

Table 11: Format of T-cell engagers

Format	Name of Construct	Arm 1 Antigen	Arm 2 Antigen	Arm 3 Antigen
T cell engagers, trispecific	CD3 x CD28 / CD4BS Ab "b"	CD4BS	CD3	CD28
T cell engagers, trispecific	Binding Protein 32	CD4BS	CD28	CD3
Monospecific	CD4BS IgG4	CD4BS	CD4BS	-

[0414] The ability of the two T cell engagers to bind to each of their three target antigens was tested by ELISA assay. The T cell engagers were capable of binding both the CD3 and CD28 T cell surface proteins with the CD3 and CD28 antigen binding sites in either orientation in the bispecific arms of the T cell engagers (*i.e.*, CD3 x CD28 for CD3 x CD28 / CD4BS Ab "b" or CD28 x CD3 for Binding Protein 32). Both T cell engagers were also capable of binding to gp120 (as measured using the HIV-1 RSC3 protein, a gp120 variant lacking the V1, V2, and V3 variable regions) (**FIG. 9**).

[0415] The effect on T cell activity was next tested for both of the T cell engagers. Incubation of the T cell engagers with monocytes revealed that the T cell engagers induced robust $CD8^+$ T cell activation (**FIG. 10**). Similarly, the T cell engagers were capable of inducing significant $CD4^+$ T cell activation on PBMCs alone, or PBMCs incubated with either of the HIV-1 infected T cell lines CEM-NKr cells or CEM-BaL cells (**FIG. 11**). Additionally, both of the T cell engagers reduced cell surface expression of CD3 on activated T cells (**FIG. 12**).

[0416] Finally, the ability of the T cell engagers to induce lysis of HIV-infected cells was tested. The T cell engagers (and positive and negative control bispecific binding proteins targeting CD3 and an HIV antigen) were incubated with the HIV-1 infected T cell line CEM-BaL cells. Incubation of the T cell engagers with the infected cells induced robust cell lysis over a wide range of concentrations (**FIG. 13A**). Likewise, incubation of these T cell engagers induced lysis of the latently infected T cell line ACH2 cells (**FIG. 13B**), as well as

J1.1 cells (**FIG. 13C**). Surprisingly, the T cell engagers showed comparable or better cytotoxic activity against chronic and latent HIV-infected cell lines when compared to the bispecific binding proteins.

[0417] Taken together, the novel T cell engagers described herein retained the ability from their parental antibodies to bind their target antigens on the HIV-1 Env glycoprotein gp120 on HIV-infected cells, as well as the cell-surface exposed T cell proteins CD3 and CD28. The T cell engagers induced robust $CD4^+$ and $CD8^+$ T cell activation, and diminished CD3 surface expression. Finally, these T cell engagers induced significant lysis of HIV-1 infected T cells. Without wishing to be bound by theory, these T cell engagers may provide a novel strategy for anti-viral therapeutics by reducing/eliminating the latent viral reservoir through T cell engagement in HIV/AIDS patients.

[0418] While the present disclosure includes various embodiments, it is understood that variations and modifications will occur to those skilled in the art. Therefore, it is intended that the appended claims cover all such equivalent variations that come within the scope of the disclosure. In addition, the section headings used herein are for organizational purposes only and are not to be construed as limiting the subject matter described.

[0419] Each embodiment herein described may be combined with any other embodiment or embodiments unless clearly indicated to the contrary. In particular, any feature or embodiment indicated as being preferred or advantageous may be combined with any other feature or features or embodiment or embodiments indicated as being preferred or advantageous, unless clearly indicated to the contrary.

[0420] All references cited in this application are expressly incorporated by reference herein.

SEQUENCES

Table 1: Heavy and light chain SEQ ID NOs for binding proteins 1-53 and the target antigens to which the binding proteins are directed.

Binding Protein	SEQ ID NOs	Target
1	4, 3, 1, 2	MPER x V1/V2 directed / CD4BS
2	12, 11, 9, 10	MPER x V1/V2 directed / CD4BS
3	20, 19, 17, 18	V1/V2 directed x MPER / CD4BS
4	28, 27, 25, 26	MPER x V1/V2 directed / CD4BS
5	36, 35, 33, 34	MPER x V3 directed / CD4BS
6	44, 43, 41, 42	V1/V2 directed x MPER / CD4BS
7	52, 51, 49, 50	V3 directed x V1/V2 directed / CD4BS
8	60, 59, 57, 58	MPER x V1/V2 directed / CD4BS
9	68, 67, 65, 66	MPER x V1/V2 directed / CD4BS
10	76, 75, 73, 74	V1/V2 directed x MPER / CD4BS
11	84, 83, 81, 82	MPER x V1/V2 directed / CD4BS
12	92, 91, 89, 90	MPER x V3 directed / CD4BS
13	100, 99, 97, 98	MPER x V3 directed / V1/V2 directed
14	108, 107, 105, 106	V1/V2 directed x MPER / CD4BS
15	116, 115, 113, 114	MPER x V3 directed / V1/V2 directed
16	124, 123, 121, 122	MPER x V3 directed / CD4BS
17	132, 131, 129, 130	V1/V2 directed x V3 directed / CD4BS
18	140, 139, 137, 138	V3 directed x MPER / CD4BS
19	148, 147, 145, 146	V3 directed x V1/V2 directed / MPER
20	156, 155, 153, 154	V3 directed x V1/V2 directed / CD4BS
21	164, 163, 161, 162	MPER x CD4BS / V1/V2 directed
22	172, 171, 169, 170	CD4BS x MPER / V1/V2 directed
23	180, 179, 177, 178	CD4BS x V1/V2 directed / MPER
24	188, 187, 185, 186	V1/V2 directed x CD4BS / MPER
25	196, 195, 193, 194	MPER x V1/V2 directed / CD4BS
26	204, 203, 201, 202	MPER x V1/V2 directed / CD4BS
27	212, 211, 209, 210	MPER x V1/V2 directed / CD4BS
28	220, 219, 217, 218	MPER x V1/V2 directed / CD4BS
29	228, 227, 225, 226	MPER x V1/V2 directed / CD4BS
30	235, 234, 232, 233	MPER x V1/V2 directed / CD4BS
31	243, 242, 240, 241	MPER x V1/V2 directed / CD4BS
32	305, 304, 302, 303	CD28 x CD3 / CD4BS
33	313, 312, 310, 311	CD28 x CD3 / CD4BS
34	321, 320, 318, 319	CD28 x CD3 / V1/V2 directed
35	329, 328, 326, 327	CD28 x CD3 / V1/V2 directed
36	337, 336, 334, 335	CD28 x CD3 / CD4BS
37	345, 344, 342, 343	CD28 x CD3 / CD4BS
38	353, 352, 350, 351	CD4BS x CD3 / CD28
39	361, 360, 358, 359	CD4BS x CD3 / CD28
40	369, 368, 366, 367	CD3 x CD4BS / CD28
41	377, 376, 374, 375	CD3 x CD4BS / CD28
42	385, 384, 382, 383	CD4BS x CD3 / CD28
43	393, 392, 390, 391	CD4BS x CD3 / CD28
44	401, 400, 398, 399	CD3 x CD4BS / CD28
45	409, 408, 406, 407	CD3 x CD4BS / CD28
46	417, 416, 414, 415	V1/V2 directed x CD3 / CD28

47	425, 424, 422, 423	V1/V2 directed x CD3 / CD28
48	433, 432, 430, 431	CD3 x V1/V2 directed / CD28
49	441, 440, 438, 439	CD3 x V1/V2 directed / CD28
50	449, 448, 446, 447	V1/V2 directed x CD3 / CD28
51	457, 456, 454, 455	V1/V2 directed x CD3 / CD28
52	465, 464, 462, 463	CD3 x V1/V2 directed / CD28
53	473, 472, 470, 471	CD3 x V1/V2 directed / CD28

Table 2: Heavy and light chain sequences of binding proteins. CDR sequences are bolded and italicized.

Binding Protein 1 Amino Acid Sequences		
Heavy chain A	Qvqlvqsggqmkkpgesmriscrasgyefi***dctln***wirlapgkrpewmg***wlkp rggavnyarplqg***rvtmtrdvysdtaflelrsltvddtavyfctr***gkncdynwdfeh***wgrgtpvivssastkgpsvfplapsskstsggtaalgclvkdyfpepvtvswnsgalt sgvhtfpavlqssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkkvepkscd kthtcppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnw yvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykckvsnkalpapi ektiskakgqprepqvctlppsrdeltknqvslscavkgfypsdiavewesngqpe nnyklttppvldsdgsfflvskltvdksrwqqgnvfscsvlhealhshytqkslslspg	**SEQ ID NO: 1**
Light chain A	Eivltqspgtlslspgetaiisc***rtsqygsla***wyqqrpgqaprlviy***sgstraa***gipdrf sgsrwgpdynltisnlesgdfgvyyc***qqyef***fgqgtkvqvdikrtvaapsvfifpps deqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsst ltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 2**
Heavy chain B	Evrlvesggglvkpggslrlscsas***gfdfdnaw***mtwvrqppgkglewvgr***itgpg egwsv***dyaesvkgrftisrdntkntlylemnnvrtedtgyyfcar***tgkyydfwsgyp pgeeyfqd***wgqgtlvivssdkthtqvhltqsgpevrkpgtsvkvsckapgntlktyd lhwvrsvpgqglqwmgwishegdkkviverfkakvtidwdrstntaylqlsgltsg dtavyy***cakgskhrlrdyalydddgalnwavdvdylsnlefw***gqgtavtvssdkt htastkgpsvfplapsskstsggtaalgclvkdyfpepvtvswnsgaltsgvhtfpav lqssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkkvepkscdkthtcppcp apellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnwyvdgvevh naktkpreeqynstyrvvsvltvlhqdwlngkeykckvsnkalpapiektiskakg qprepqvytlppcrdeltknqvslwclvkgfypsdiavewesngqpennykttpp vldsdgsfflyskltvdksrwqqgnvfscsvlhealhshytqkslslspg	**SEQ ID NO: 3**
Light chain B	Dfvltqsphslsvtpgesasisckss***hslihgdrnny***lawyvqkpgrspqlliy***las***s rasgvpdrfsgsgsdkdftlkisrvetedvgtyy***cmqgrespwtf***gqgtkvdikdkt ht aseltqdpavsvalkqtvtitc***rgdslrshyas***wyqkkpgqapvllfy***gknnrps***gi pdrfsgsasgnrasltitgaqaedeadyyc***ssrdksgsrlsv***fgggtkltvldkthtrtv aapsvfifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteq dskdstyslsstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 4**
Binding Protein 1 Nucleotide Sequences		
Heavy chain A	caggtgcagctggtgcagtctggcggccagatgaagaaacccggcgagagcatgcg gatcagctgcagagccagcggctacgagttcatcgactgcaccctgaactggatcaga actggcccctggcaagcggcctgagtggatgggatggctgaagcctagaggcggagc cgtgaactacgccagacctctgcagggcagagtgaccatgacccgggacgtgtacag	**SEQ ID NO: 5**

	cgataccgccttcctggaactgcggagcctgaccgtggatgataccgccgtgtacttct gcacccggggcaagaactgcgactacaactgggacttcgagcactggggcagaggc acccctgtgatcgtgtcaagcgcgtcgaccaagggccccagcgtgttccctctggccc ctagcagcaagagcacatctggcggaacagccgccctgggctgcctcgtgaaggact actttcccgagcccgtgaccgtgtcctggaattctggcgccctgaccagcggcgtgca caccttccagctgtgctgcagtccagcggcctgtacagcctgagcagcgtcgtgaca gtgcccagcagctctctgggcacccagacctacatctgcaacgtgaaccacaagccca gcaacaccaaggtggacaagaaggtggaacccaagagctgcgacaagacccacac ctgtccccttgtcctgccccgaactgctgggaggcccttccgtgttcctgttccccc aaagcccaaggacaccctgatgatcagccggaccccgaagtgacctgcgtggtggt ggatgtgtcccacgaggaccctgaagtgaagttcaattggtacgtggacggcgtggaa gtgcacaacgccaagaccaagccaagagaggaacagtacaacagcacctaccgggt ggtgtccgtgctgaccgtgctgcaccaggactggctgaacggcaaagagtacaagtg caaggtgtccaacaaggccctgcctgcccccatcgagaaaaccatcagcaaggccaa gggccagccccgcgaaccccaggtgtgcacactgcccccaagcagggacgagctg accaagaaccaggtgtccctgagctgtgccgtgaaaggcttctacccctccgatatcgc cgtggaatgggagagcaacggccagcccgagaacaactacaagaccacccccccctg tgctggacagcgacggctcattcttcctggtgtccaagctgacagtggacaagtcccgg tggcagcagggcaacgtgttcagctgctccgtgctgcacgaggccctgcacagccact acacccagaagtccctgagcctgagccccggc	
Light chain A	Gagatcgtgctgacacagagccctggcaccctgagcctgtctccaggcgagacagc catcatcagctgccggacaagccagtacggcagcctggcctggtatcagcagaggcc tggacaggcccccagactcgtgatctacagcggcagcacaagagccgccggaatcc ccgatagattcagcggctccagatggggccctgactacaacctgaccatcagcaacct ggaaagcggcgacttcggcgtgtactactgccagcagtacgagttcttcggccagggc accaaggtgcaggtggacatcaagcgtacggtggccgctcccagcgtgttcatcttcc cacctagcgacgagcagctgaagtccggcacagcctctgtcgtgtgcctgctgaacaa cttctacccccgcgaggccaaagtgcagtggaaggtggacaacgccctgcagagcg gcaacagccaggaaagcgtgaccgagcaggacagcaaggactccacctacagcctg agcagcaccctgacactgagcaaggccgactacgagaagcacaaggtgtacgcctg cgaagtgacccaccagggcctgtctagccccgtgaccaagagcttcaaccggggcga gtgt	**SEQ ID NO: 6**
Heavy chain B	gaggttagactggtggagtcaggaggggggcttgtgaagcccggtgggtctctccgc ctgagctgttctgcctccggctttgatttcgataacgcctggatgacctgggtcaggcag cctccaggtaagggactggagtgggtgggaagaatcacaggtccaggcgagggctg gtccgtggactacgcggaatctgttaaagggcggtttacaatctcaagggacaatacca agaataccttgtatttggagatgaacaacgtgagaactgaagacaccggatattacttct gtgccagaacaggcaaatactacgacttctggtccggctatccccctggcgaggaatat tttcaagactggggtcagggaacccttgttatcgtgtcctccgacaaaacccatacccag gtgcacctgacacagagcggacccgaagtgcggaagcctggcacctctgtgaaggtg tcctgcaaggcccctggcaacaccctgaaaacctacgacctgcactgggtgcgcagc gtgccaggacagggactgcagtggatgggctggatcagccacgagggcgacaaga aagtgatcgtggaacggttcaaggccaaagtgaccatcgactgggacagaagcacca acaccgcctacctgcagctgagcggcctgacctctggcgataccgccgtgtactactg cgccaagggcagcaagcaccggctgagagactacgccctgtacgacgatgacggcg ccctgaactgggccgtggatgtggactacctgagcaacctggaattctggggccaggg cacagccgtgaccgtgtcatctgataagacccacaccgcttccaccaagggcccatcg gtcttccccctggcaccctcctccaagagcacctctgggggcacagcggccctgggct gcctggtcaaggactacttccccgaaccggtgacggtgtcgtggaactcaggcgccct gaccagcggcgtgcacaccttcccggctgtcctacagtcctcaggactctactccctca gcagcgtggtgaccgtgccctccagcagcttgggcacccagacctacatctgcaacgt gaatcacaagcccagcaacaccaaggtggacaagaaagttgagcccaaatcttgtga caaaactcacacatgcccaccgtgcccagcacctgaactcctgggggggaccgtcagt	**SEQ ID NO: 7**

	cttcctcttccccccaaaacccaaggacaccctcatgatctcccggacccctgaggtca catgcgtggtggtggacgtgagccacgaagaccctgaggtcaagttcaactggtatgtt gacggcgtggaggtgcataatgccaagacaaagccgcgggaggagcagtacaaca gcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaa ggagtacaagtgcaaggtctccaacaaagccctcccagcccccatcgagaaaaccat ctccaaagccaaagggcagccccgagaaccacaggtgtacaccctgcccccatgcc gggatgagctgaccaagaatcaagtcagcctgtggtgcctggtaaaaggcttctatccc agcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaaga ccacgcctcccgtgctggactccgacggctccttcttcctctactcaaaactcaccgtgg acaagagcaggtggcagcaggggaacgtcttctcatgctccgtgctgcatgaggctct gcacagccactacacgcagaagagcctctccctgtctccgggt	
Light chain B	gacttcgtgctgacccagagccctcacagcctgagcgtgacacctggcgagagcgcc agcatcagctgcaagagcagccactccctgatccacggcgaccggaacaactacctg gcttggtacgtgcagaagcccggcagatccccccagctgctgatctacctggccagca gcagagccagcggcgtgcccgatagattttctggcagcggcagcgacaaggacttca ccctgaagatcagccgggtggaaaccgaggacgtgggcacctactactgtatgcagg gcagagagagcccctggacctttggccagggcaccaaggtggacatcaaggacaaa acccataccgcatccgaactgactcaggaccctgccgtctctgtggcactgaagcaga ctgtgactattacttgccgaggcgactcactgcggagccactacgcttcctggtatcaga agaaacccggccaggcacctgtgctgctgttctacggaaagaacaataggccatctgg catccccgaccgcttttctggcagtgcatcagggaaccgagccagtctgaccattaccg gcgcccaggctgaggacgaagccgattactattgcagctcccgggataagagcggct ccagactgagcgtgttcggaggaggaactaaactgaccgtcctcgataagacccatac ccgtacggtggccgctcccagcgtgttcatcttcccacctagcgacgagcagctgaagt ccggcacagcctctgtcgtgtgcctgctgaacaacttctacccccgcgaggccaaagt gcagtggaaggtggacaacgccctgcagagcggcaacagccaggaaagcgtgacc gagcaggacagcaaggactccacctacagcctgagcagcaccctgacactgagcaa ggccgactacgagaagcacaaggtgtacgcctgcgaagtgacccaccagggcctgt ctagccccgtgaccaagagcttcaaccggggcgagtgt	**SEQ ID NO: 8**
Binding Protein 2 Amino Acid Sequences		
Heavy chain A	Rahlvqsgtamkkpgasvrvscqts***gytftahi***lfwfrqapgrglewvgw***ikpqy*** ***gav***nfgggfrdrvtltrdvyreiaymdirglkpddtavyycar***drsygdsswalda*** wgqgttvvvsa<u>astkgpsvfplapsskstsggtaalgclvkdyfpepvtvswnsgal tsgvhtfpavlqssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkkvepkscd kthtcppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnw yvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykckvsnkalpapi ektiskakgqprepqvctlppsrdeltknqvslscavkgfypsdiavewesngqpe nnykttppvldsdgsfflvskltvdksrwqqgnvfscsvlhealhshytqkslslspg</u>	**SEQ ID NO: 9**
Light chain A	yihvtqspsslsvsigdrvtincqts***qgvgsd***lhwyqhkpgrapkllihhtssvedgv psrfsgsgf***hts***fnltisdlqaddiatyyc***qvlqf***fgrgsrlhikr<u>tvaapsvfifppsde qlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsstltls kadyekhkvyacevthqglsspvtksfnrgec</u>	**SEQ ID NO: 10**
Heavy chain B	Evrlvesgglvkpggslrlscsasgfdfdnawmtwvrqppgkglewvgr itgpgegwsvdyaesvkgrftisrdntkntlylemnnvrtedtgyyfcartgk yydfwsgyppgeeyfqdwgqgtlvivssdkthtqvhltqsgpevrkpgtsv kvsckapgntlktydlhwvrsvpgqglqwmgwishegdkkviverfkak vtidwdrstntaylqlsgltsgdtavyycakgskhrlrdyalydddgalnwav dvdylsnlefwgqgtavtvssdkthtastkgpsvfplapsskstsggtaalgcl vkdyfpepvtvswnsgaltsgvhtfpavlqssglyslssvvtvpssslgtqtyi cnvnhkpsntkvdkkvepkscdkthtcppcpapellggpsvflfppkpkdt lmisrtpevtcvvvdvshedpevkfnwyvdgvevhnaktkpreeqynsty	**SEQ ID NO: 11**

	rvvsvltvlhqdwlngkeykckvsnkalpapiektiskakgqprepqvytlp pcrdeltknqvslwclvkgfypsdiavewesngqpennykttppvldsdgs fflyskltvdksrwqqgnvfscsvlhealhshytqkslslspg	
Light chain B	dfvltqsphslsvtpgesasisckssshslihgdrnnylawyvqkpgrspqlliylassr asgvpdrfsgsgsdkdftlkisrvetedvgtyycmqgrespwtfgqgtkvdikdkth taseltqdpavsvalkqtvtitcrgdslrshyaswyqkkpgqapvllfygknnrpsgi pdrfsgsasgnrasltitgaqaedeadyycssrdksgsrlsvfgggtkltvldkthtrtv aapsvfifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteq dskdstyslsstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 12**
Binding Protein 2 Nucleotide Sequences		
Heavy chain A	agagcccacctggtgcagtctggcaccgccatgaagaaaccaggcgcctctgtgcgg gtgtcctgtcagacaagcggctacaccttcaccgcccacatcctgttctggttccggcag gcccctggcagaggactggaatgggtgggatggatcaagccccagtatggcgccgtg aacttcggcggaggcttccgggatagagtgaccctgacccgggacgtgtaccgcgag atcgcctacatggacatccggggcctgaagcccgatgacaccgccgtgtactactgcg ccagagacagaagctacggcgacagcagctgggctctggatgcttggggccagggc acaaccgtggtggtgtctgccgcctctacaaagggccccagcgtgttccctctggcccc tagcagcaagagcacatctggcggaacagccgccctgggctgcctcgtgaaggacta ctttcccgagcccgtgaccgtgtcctggaattctggcgccctgaccagcggcgtgcac acctttccagctgtgctgcagtccagcggcctgtacagcctgagcagcgtcgtgacagt gcccagcagctctctgggcacccagacctacatctgcaacgtgaaccacaagcccag caacaccaaggtggacaagaaggtggaacccaagagctgcgacaagacccacacct gtccccttgtcctgccccgaactgctgggaggcccttccgtgttcctgttcccccaa agcccaaggacaccctgatgatcagccggacccccgaagtgacctgcgtggtggtgg atgtgtcccacgaggaccctgaagtgaagttcaattggtacgtggacggcgtggaagt gcacaacgccaagaccaagccaagagaggaacagtacaacagcacctaccgggtg gtgtccgtgctgaccgtgctgcaccaggactggctgaacggcaaagagtacaagtgc aaggtgtccaacaaggccctgcctgccccatcgagaaaaccatcagcaaggccaag ggccagccccgcgaaccccaggtgtgcacactgcccccaagcagggacgagctga ccaagaaccaggtgtccctgagctgtgccgtgaaaggcttctacccctccgatatcgcc gtggaatgggagagcaacggccagcccgagaacaactacaagaccacccccctgt gctggacagcgacggctcattcttcctggtgtccaagctgacagtggacaagtcccggt ggcagcagggcaacgtgttcagctgctccgtgctgcacgaggccctgcacagccact acacccagaagtccctgagcctgagccccggc	**SEQ ID NO: 13**
Light chain A	tacatccacgtgacccagagccccagcagcctgtccgtgtccatcggcgacagagtga ccatcaactgccagacctctcagggcgtgggcagcgacctgcactggtatcagcacaa gcctggcagagcccccaagctgctgatccaccacacaagcagcgtggaagatggcgt gcccagcagattttccggcagcggcttccacaccagcttcaacctgaccatcagcgatc tgcaggccgacgacattgccacctactattgtcaggtgctgcagttcttcggcagaggc agcagactgcacatcaagcgtacggtggccgctcccagcgtgttcatcttcccacctag cgacgagcagctgaagtccggcacagcctctgtcgtgtgcctgctgaacaacttctacc cccgcgaggccaaagtgcagtggaaggtggacaacgccctgcagagcggcaacag ccaggaaagcgtgaccgagcaggacagcaaggactccacctacagcctgagcagca ccctgacactgagcaaggccgactacgagaagcacaaggtgtacgcctgcgaagtga cccaccagggcctgtctagccccgtgaccaagagcttcaaccggggcgagtgt	**SEQ ID NO: 14**
Heavy chain B	gaggttagactggtggagtcaggaggggggcttgtgaagcccggtgggtctctccgc ctgagctgttctgcctccggctttgatttcgataacgcctggatgacctgggtcaggcag cctccaggtaagggactggagtgggtgggaagaatcacaggtccaggcgagggctg gtccgtggactacgcggaatctgttaaagggcggtttacaatctcaagggacaatacca agaataccttgtatttggagatgaacaacgtgagaactgaagacaccggatattacttct gtgccagaacaggcaaatactacgacttctggtccggctatccccctggcgaggaatat tttcaagactggggtcagggaacccttgttatcgtgtcctccgacaaaacccatacccag	**SEQ ID NO: 15**

	gtgcacctgacacagagcggacccgaagtgcggaagcctggcacctctgtgaaggtg tcctgcaaggcccctggcaacaccctgaaaacctacgacctgcactgggtgcgcagc gtgccaggacagggactgcagtggatgggctggatcagccacgagggcgacaaga aagtgatcgtggaacggttcaaggccaaagtgaccatcgactgggacagaagcacca acaccgcctacctgcagctgagcggcctgacctctggcgataccgccgtgtactactg cgccaagggcagcaagcaccggctgagagactacgccctgtacgacgatgacggcg ccctgaactgggccgtggatgtggactacctgagcaacctggaattctggggccaggg cacagccgtgaccgtgtcatctgataagacccacaccgcttccaccaagggcccatcg gtcttcccccctggcaccctcctccaagagcacctctgggggcacagcggccctgggct gcctggtcaaggactacttccccgaaccggtgacggtgtcgtggaactcaggcgccct gaccagcggcgtgcacaccttcccggctgtcctacagtcctcaggactctactccctca gcagcgtggtgaccgtgccctccagcagcttgggcacccagacctacatctgcaacgt gaatcacaagcccagcaacaccaaggtggacaagaaagttgagcccaaatcttgtga caaaactcacacatgcccaccgtgcccagcacctgaactcctgggggggaccgtcagt cttcctcttcccccaaaacccaaggacaccctcatgatctcccggaccccctgaggtca catgcgtggtggtggacgtgagccacgaagaccctgaggtcaagttcaactggtatgtt gacggcgtggaggtgcataatgccaagacaaagccgcgggaggagcagtacaaca gcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaa ggagtacaagtgcaaggtctccaacaaagccctcccagcccccatcgagaaaaccat ctccaaagccaaagggcagccccgagaaccacaggtgtacaccctgcccccatgcc gggatgagctgaccaagaatcaagtcagcctgtggtgcctggtaaaaggcttctatccc agcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaaga ccacgcctcccgtgctggactccgacggctccttcttcctctactcaaaactcaccgtgg acaagagcaggtggcagcaggggaacgtcttctcatgctccgtgctgcatgaggctct gcacagccactacacgcagaagagcctctccctgtctccgggt	
Light chain B	gacttcgtgctgacccagagccctcacagcctgagcgtgacacctggcgagagcgcc agcatcagctgcaagagcagccactccctgatccacggcgaccggaacaactacctg gcttggtacgtgcagaagcccggcagatccccccagctgctgatctacctggccagca gcagagccagcggcgtgcccgatagattttctggcagcggcagcgacaaggacttca ccctgaagatcagccgggtggaaaccgaggacgtgggcacctactactgtatgcagg gcagagagagcccctggacctttggccagggcaccaaggtggacatcaaggacaaa acccataccgcatccgaactgactcaggaccctgccgtctctgtggcactgaagcaga ctgtgactattacttgccgaggcgactcactgcggagccactacgcttcctggtatcaga agaaacccggccaggcacctgtgctgctgttctacggaaagaacaataggccatctgg catccccgaccgcttttctggcagtgcatcagggaaccgagccagtctgaccattaccg gcgcccaggctgaggacgaagccgattactattgcagctcccgggataagagcggct ccagactgagcgtgttcggaggaggaactaaactgaccgtcctcgataagacccatac ccgtacggtggccgctcccagcgtgttcatcttcccacctagcgacgagcagctgaagt ccggcacagcctctgtcgtgtgcctgctgaacaacttctacccccgcgaggccaaagt gcagtggaaggtggacaacgccctgcagagcggcaacagccaggaaagcgtgacc gagcaggacagcaaggactccacctacagcctgagcagcaccctgacactgagcaa ggccgactacgagaagcacaaggtgtacgcctgcgaagtgacccaccagggcctgt ctagccccgtgaccaagagcttcaaccggggcgagtgt	**SEQ ID NO: 16**
Binding Protein 3 Amino Acid Sequences		
Heavy chain A	rahlvqsgtamkkpgasvrvscqtsgytftahilfwfrqapgrglewvgwikpqyg avnfgggfrdrvtltrdvyreiaymdirglkpddtavyycardrsygdsswaldaw gqgttvvvsaastkgpsvfplapsskstsggtaalgclvkdyfpepvtvswnsgalts gvhtfpavlqssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkkvepkscdkt htcppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnwyv dgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykckvsnkalpapiekt iskakgqprepqvctlppsrdeltknqvslscavkgfypsdiavewesngqpenny kttppvldsdgsfflvskltvdksrwqqgnvfscsvlhealhshytqkslslspg	**SEQ ID NO: 17**
Light chain A	yihvtqspsslsvsigdrvtincqtsqgvgsdlhwyqhkpgrapkllihhtssvedgv psrfsgsgfhtsfnltisdlqaddiatyycqvlqffgrgsrlhikrtvaapsvfifppsde	**SEQ ID NO: 18**

	qlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsstltls kadyekhkvyacevthqglsspvtksfnrgec	
Heavy chain B	Qvhltqsgpevrkpgtsvkvsckapgntlktydlhwvrsvpgqglqwmg wishegdkkviverfkakvtidwdrstntaylqlsgltsgdtavyycakgsk hrlrdyalydddgalnwavdvdylsnlefwgqgtavtvssdkthtevrlves ggglvkpggslrlscsasgfdfdnawmtwvrqppgkglewvgritgpgeg wsvdyaesvkgrftisrdntkntlylemnnvrtedtgyyfcartgkyydfws gyppgeeyfqdwgqgtlvivssdkthtastkgpsvfplapsskstsggtaalg clvkdyfpepvtvswnsgaltsgvhtfpavlqssglyslssvvtvpssslgtqt yicnvnhkpsntkvdkkvepkscdkthtcppcpapellggpsvflfppkpk dtlmisrtpevtcvvvdvshedpevkfnwyvdgvevhnaktkpreeqyns tyrvvsvltvlhqdwlngkeykckvsnkalpapiektiskakgqprepqvyt lppcrdeltknqvslwclvkgfypsdiavewesngqpennykttppvldsd gsfflyskltvdksrwqqgnvfscsvlhealhshytqkslslspg	**SEQ ID NO: 19**
Light chain B	aseltqdpavsvalkqtvtitcrgdslrshyaswyqkkpgqapvllfygknnrpsgip drfsgsasgnrasltitgaqaedeadyycssrdksgsrlsvfgggtkltvldkthtdfvlt qsphslsvtpgesasisckssshslihgdrnnylawyvqkpgrspqlliylassrasgv pdrfsgsgsdkdftlkisrvetedvgtyycmqgrespwtfgqgtkvdikdkthtrtva apsvfifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqds kdstyslsstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 20**
Binding Protein 3 Nucleotide Sequences		
Heavy chain A	agagcccacctggtgcagtctggcaccgccatgaagaaaccaggcgcctctgtgcgg gtgtcctgtcagacaagcggctacaccttcaccgcccacatcctgttctggttccggcag gcccctggcagaggactggaatgggtgggatggatcaagccccagtatggcgccgtg aacttcggcggaggcttccgggatagagtgaccctgacccgggacgtgtaccgcgag atcgcctacatggacatccggggcctgaagcccgatgacaccgccgtgtactactgcg ccagagacagaagctacggcgacagcagctgggctctggatgcttggggccagggc acaaccgtggtggtgtctgccgcctctacaaagggccccagcgtgttccctctggcccc tagcagcaagagcacatctggcggaacagccgccctgggctgcctcgtgaaggacta ctttcccgagcccgtgaccgtgtcctggaattctggcgccctgaccagcggcgtgcac acctttccagctgtgctgcagtccagcggcctgtacagcctgagcagcgtcgtgacagt gcccagcagctctctgggcacccagacctacatctgcaacgtgaaccacaagcccag caacaccaaggtggacaagaaggtggaacccaagagctgcgacaagacccacacct gtccccttgtcctgccccgaactgctgggaggcccttccgtgttcctgttcccccaa agcccaaggacaccctgatgatcagccggacccccgaagtgacctgcgtggtggtgg atgtgtcccacgaggaccctgaagtgaagttcaattggtacgtggacggcgtggaagt gcacaacgccaagaccaagccaagagaggaacagtacaacagcacctaccgggtg gtgtccgtgctgaccgtgctgcaccaggactggctgaacggcaaagagtacaagtgc aaggtgtccaacaaggccctgcctgcccccatcgagaaaaccatcagcaaggccaag ggccagccccgcgaaccccaggtgtgcacactgcccccaagcagggacgagctga ccaagaaccaggtgtccctgagctgtgccgtgaaaggcttctacccctccgatatcgcc gtggaatgggagagcaacggccagcccgagaacaactacaagaccacccccctgt gctggacagcgacggctcattcttcctggtgtccaagctgacagtggacaagtcccggt ggcagcagggcaacgtgttcagctgctccgtgctgcacgaggccctgcacagccact acacccagaagtccctgagcctgagccccggc	**SEQ ID NO: 21**
Light chain A	tacatccacgtgacccagagccccagcagcctgtccgtgtccatcggcgacagagtga ccatcaactgccagacctctcagggcgtgggcagcgacctgcactggtatcagcacaa gcctggcagagcccccaagctgctgatccaccacacaagcagcgtggaagatggcgt gcccagcagattttccggcagcggcttccacaccagcttcaacctgaccatcagcgatc tgcaggccgacgacattgccacctactattgtcaggtgctgcagttcttcggcagaggc	**SEQ ID NO: 22**

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Heavy chain B	caggtgcacctgacacagagcggacccgaagtgcggaagcctggcacctct gtgaaggtgtcctgcaaggcccctggcaacaccctgaaaacctacgacctgca ctgggtgcgcagcgtgccaggacagggactgcagtggatgggctggatcag ccacgagggcgacaagaaagtgatcgtggaacggttcaaggccaaagtgac catcgactgggacagaagcaccaacaccgcctacctgcagctgagcggcctg acctctggcgataccgccgtgtactactgcgccaagggcagcaagcaccggc tgagagactacgccctgtacgacgatgacggcgccctgaactgggccgtgga tgtggactacctgagcaacctggaattctggggccagggcacagccgtgacc gtgtcatctgacaaaacccataccgaggttagactggtggagtcaggaggggg gcttgtgaagcccggtgggtctctccgcctgagctgttctgcctccggctttgatt tcgataacgcctggatgacctgggtcaggcagcctccaggtaagggactgga gtgggtgggaagaatcacaggtccaggcgagggctggtccgtggactacgc ggaatctgttaaagggcggtttacaatctcaagggacaataccaagaataccttg tatttggagatgaacaacgtgagaactgaagacaccggatattacttctgtgcca gaacaggcaaatactacgacttctggtccggctatccccctggcgaggaatattt tcaagactggggtcagggaacccttgttatcgtgtcctccgataagacccacac cgcttccaccaagggcccatcggtcttcccctggcaccctcctccaagagcac ctctgggggcacagcggccctgggctgcctggtcaaggactacttccccgaac cggtgacggtgtcgtggaactcaggcgccctgaccagcggcgtgcacacctt cccggctgtcctacagtcctcaggactctactccctcagcagcgtggtgaccgt gccctccagcagcttgggcacccagacctacatctgcaacgtgaatcacaagc ccagcaacaccaaggtggacaagaaagttgagcccaaatcttgtgacaaaact cacacatgcccaccgtgcccagcacctgaactcctgggggggaccgtcagtctt cctcttcccccaaaacccaaggacaccctcatgatctcccggaccccctgaggt cacatgcgtggtggtggacgtgagccacgaagaccctgaggtcaagttcaact ggtatgttgacggcgtggaggtgcataatgccaagacaaagccgcgggaggga gcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccagg actggctgaatggcaaggagtacaagtgcaaggtctccaacaaagccctccca gcccccatcgagaaaaccatctccaaagccaaagggcagccccgagaacca caggtgtacaccctgcccccatgccgggatgagctgaccaagaatcaagtcag cctgtggtgcctggtaaaaggcttctatcccagcgacatcgccgtggagtggga gagcaatgggcagccggagaacaactacaagaccacgcctcccgtgctgga ctccgacggctccttcttcctctactcaaaactcaccgtggacaagagcaggtg gcagcaggggaacgtcttctcatgctccgtgctgcatgaggctctgcacagcc actacacgcagaagagcctctccctgtctccgggt	**SEQ ID NO: 23**

Light chain B	gcatccgaactgactcaggaccctgccgtctctgtggcactgaagcagactgtgactat tacttgccgaggcgactcactgcggagccactacgcttcctggtatcagaagaaaccc ggccaggcacctgtgctgctgttctacggaaagaacaataggccatctggcatccccg accgcttttctggcagtgcatcagggaaccgagccagtctgaccattaccggcgccca ggctgaggacgaagccgattactattgcagctcccgggataagagcggctccagact gagcgtgttcggaggaggaactaaactgaccgtcctcgacaaaacccataccgacttc gtgctgacccagagccctcacagcctgagcgtgacacctggcgagagcgccagcatc agctgcaagagcagccactccctgatccacggcgaccggaacaactacctggcttggt acgtgcagaagcccggcagatccccccagctgctgatctacctggccagcagcagag ccagcggcgtgcccgatagattttctggcagcggcagcgacaaggacttcaccctgaa gatcagccgggtggaaaccgaggacgtgggcacctactactgtatgcagggcagag agagcccctggacctttggccagggcaccaaggtggacatcaaggataagacccata cccgtacggtggccgctcccagcgtgttcatcttcccacctagcgacgagcagctgaa gtccggcacagcctctgtcgtgtgcctgctgaacaacttctacccccgcgaggccaaa gtgcagtggaaggtggacaacgccctgcagagcggcaacagccaggaaagcgtga ccgagcaggacagcaaggactccacctacagcctgagcagcaccctgacactgagc aaggccgactacgagaagcacaaggtgtacgcctgcgaagtgacccaccagggcct gtctagccccgtgaccaagagcttcaaccggggcgagtgt	**SEQ ID NO: 24**
Binding Protein 4 Amino Acid Sequences		
Heavy chain A	qvqlvqsggqmkkpgesmriscrasgyefidctlnwirlapgkrpewmgwlkpr ggavnyarplqgrvtmtrdvysdtaflelrsltvddtavyfctrgkncdynwdfehw grgtpvivssastkgpsvfplapsskstsggtaalgclvkdyfpepvtvswnsgalts gvhtfpavlqssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkkvepkscdkt htcppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnwyv dgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykckvsnkalpapiekt iskakgqprepqvctlppsrdeltknqvslscavkgfypsdiavewesngqpenny kttppvldsdgsfflvskltvdksrwqqgnvfscsvmhealhnhytqkslslspg	**SEQ ID NO: 25**
Light chain A	Eivltqspgtlslspgetaiiscrtsqygslawyqqrpgqaprlviysgstraagipdrf sgsrwgpdynltisnlesgdfgvyycqqyeffgqgtkvqvdikrtvaapsvfifpps deqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsst ltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 26**
Heavy chain B	evrlvesggglvkpggslrlscsasgfdfdnawmtwvrqppgkglewvgri tgpgegwsvdyaesvkgrftisrdntkntlylemnnvrtedtgyyfcartgk yydfwwgyppgeeyfqdwgqgtlvivssdkthtqvhltqsgpevrkpgts vkvsckapgntlktydlhwvrsvpgqglqwmgwishegdkkviverfka kvtidwdrstntaylqlsgltsgdtavyycakgskhrlrdyalydddgalnwa vdvdylsnlefwgqgtavtvssdkthtastkgpsvfplapsskstsggtaalg clvkdyfpepvtvswnsgaltsgvhtfpavlqssglyslssvvtvpssslgtqt yicnvnhkpsntkvdkkvepkscdkthtcppcpapellggpsvflfppkpk dtlmisrtpevtcvvvdvshedpevkfnwyvdgvevhnaktkpreeqyns tyrvvsvltvlhqdwlngkeykckvsnkalpapiektiskakgqprepqvyt lppcrdeltknqvslwclvkgfypsdiavewesngqpennykttppvldsd gsfflyskltvdksrwqqgnvfscsvmhealhnhytqkslslspg	**SEQ ID NO: 27**
Light chain B	dfvltqsphslsvtpgesasisckssshslihgdrnnylawyvqkpgrspqlliylassr asgvpdrfsgsgsdkdftlkisrvetedvgtyycmqgrespwtfgqgtkvdikdkth taseltqdpavsvalkqtvtitcrgdslrshyaswyqkkpgqapvllfygknnrpsgi pdrfsgsasgnrasltitgaqaedeadyycssrdksgsrlsvfgggtkltvldkthtrtv aapsvfifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteq dskdstyslsstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 28**
Binding Protein 4 Nucleotide Sequences		
Heavy chain A	caggtgcagctggtgcagtctggcggccagatgaagaaacccggcgagagcatgcg gatcagctgcagagccagcggctacgagttcatcgactgcaccctgaactggatcaga	**SEQ ID NO: 29**

	ctggcccctggcaagcggcctgagtggatgggatggctgaagcctagaggcggagc cgtgaactacgccagacctctgcagggcagagtgaccatgacccgggacgtgtacag cgataccgccttcctggaactgcggagcctgaccgtggatgataccgccgtgtacttct gcacccggggcaagaactgcgactacaactgggacttcgagcactggggcagaggc acccctgtgatcgtgtcaagcgcgtcgaccaagggccccagcgtgttccctctggccc ctagcagcaagagcacatctggcggaacagccgccctgggctgcctcgtgaaggact actttcccgagcccgtgaccgtgtcctggaattctggcgccctgaccagcggcgtgca caccttccagctgtgctgcagtccagcggcctgtacagcctgagcagcgtcgtgaca gtgcccagcagctctctgggcacccagacctacatctgcaacgtgaaccacaagccca gcaacaccaaggtggacaagaaggtggaacccaagagctgcgacaagacccacac ctgtccccctttgtcctgccccgaactgctgggaggcccttccgtgttcctgttccccc aaagcccaaggacaccctgatgatcagccggacccccgaagtgacctgcgtggtggt ggatgtgtcccacgaggaccctgaagtgaagttcaattggtacgtggacggcgtggaa gtgcacaacgccaagaccaagccaagagaggaacagtacaacagcacctaccgggt ggtgtccgtgctgaccgtgctgcaccaggactggctgaacggcaaagagtacaagtg caaggtgtccaacaaggccctgcctgcccccatcgagaaaaccatcagcaaggccaa gggccagccccgcgaaccccaggtgtgcacactgcccccaagcagggacgagctg accaagaaccaggtgtccctgagctgtgccgtgaaaggcttctacccctccgatatcgc cgtggaatgggagagcaacggccagcccgagaacaactacaagaccacccccccctg tgctggacagcgacggctcattcttcctggtgtccaagctgacagtggacaagtcccgg tggcagcagggcaacgtgttcagctgctccgtgatgcacgaggccctgcacaaccact acacccagaagtccctgagcctgagccccggc	
Light chain A	Gagatcgtgctgacacagagccctggcaccctgagcctgtctccaggcgagacagc catcatcagctgccggacaagccagtacggcagcctggcctggtatcagcagaggcc tggacaggcccccagactcgtgatctacagcggcagcacaagagccgccggaatcc ccgatagattcagcggctccagatggggccctgactacaacctgaccatcagcaacct ggaaagcggcgacttcggcgtgtactactgccagcagtacgagttcttcggccagggc accaaggtgcaggtggacatcaagcgtacggtggccgctcccagcgtgttcatcttcc cacctagcgacgagcagctgaagtccggcacagcctctgtcgtgtgcctgctgaacaa cttctacccccgcgaggccaaagtgcagtggaaggtggacaacgccctgcagagcg gcaacagccaggaaagcgtgaccgagcaggacagcaaggactccacctacagcctg agcagcaccctgacactgagcaaggccgactacgagaagcacaaggtgtacgcctg cgaagtgacccaccagggcctgtctagccccgtgaccaagagcttcaaccggggcga gtgt	**SEQ ID NO: 30**
Heavy chain B	gaggttagactggtggagtcaggaggggggcttgtgaagcccggtgggtctctccgc ctgagctgttctgcctccggctttgatttcgataacgcctggatgacctgggtcaggcag cctccaggtaagggactggagtgggtgggaagaatcacaggtccaggcgagggctg gtccgtggactacgcggaatctgttaaagggcggtttacaatctcaagggacaatacca agaataccttgtatttggagatgaacaacgtgagaactgaagacaccggatattacttct gtgccagaacaggcaaatactacgacttctggtggggctatccccctggcgaggaata ttttcaagactggggtcagggaacccttgttatcgtgtcctccgacaaaacccatacca ggtgcacctgacacagagcggacccgaagtgcggaagcctggcacctctgtgaaggt gtcctgcaaggcccctggcaacaccctgaaaacctacgacctgcactgggtgcgcag cgtgccaggacagggactgcagtggatgggctggatcagccacgagggcgacaag aaagtgatcgtggaacggttcaaggccaaagtgaccatcgactgggacagaagcacc aacaccgcctacctgcagctgagcggcctgacctctggcgataccgccgtgtactact gcgccaagggcagcaagcaccggctgagagactacgccctgtacgacgatgacggc gccctgaactgggccgtggatgtggactacctgagcaacctggaattctggggccagg gcacagccgtgaccgtgtcatctgataagacccacaccgcttccaccaagggcccatc ggtcttcccctggcaccctcctccaagagcacctctgggggcacagcggccctggg ctgcctggtcaaggactacttccccgaaccggtgacggtgtcgtggaactcaggcgcc ctgaccagcggcgtgcacaccttcccggctgtcctacagtcctcaggactctactccct cagcagcgtggtgaccgtgccctccagcagcttgggcacccagacctacatctgcaac	**SEQ ID NO: 31**

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Light chain B	gacttcgtgctgacccagagccctcacagcctgagcgtgacacctggcgagagcgcc agcatcagctgcaagagcagccactccctgatccacggcgaccggaacaactacctg gcttggtacgtgcagaagcccggcagatccccccagctgctgatctacctggccagca gcagagccagcggcgtgcccgatagattttctggcagcggcagcgacaaggacttca ccctgaagatcagccgggtggaaaccgaggacgtgggcacctactactgtatgcagg gcagagagagcccctggacctttggccagggcaccaaggtggacatcaaggacaaa acccataccgcatccgaactgactcaggaccctgccgtctctgtggcactgaagcaga ctgtgactattacttgccgaggcgactcactgcggagccactacgcttcctggtatcaga agaaacccggccaggcacctgtgctgctgttctacggaaagaacaataggccatctgg catccccgaccgcttttctggcagtgcatcagggaaccgagccagtctgaccattaccg gcgcccaggctgaggacgaagccgattactattgcagctcccgggataagagcggct ccagactgagcgtgttcggaggaggaactaaactgaccgtcctcgataagacccatac ccgtacggtggccgctcccagcgtgttcatcttcccacctagcgacgagcagctgaagt ccggcacagcctctgtcgtgtgcctgctgaacaacttctacccccgcgaggccaaagt gcagtggaaggtggacaacgccctgcagagcggcaacagccaggaaagcgtgacc gagcaggacagcaaggactccacctacagcctgagcagcaccctgacactgagcaa ggccgactacgagaagcacaaggtgtacgcctgcgaagtgacccaccagggcctgt ctagccccgtgaccaagagcttcaaccggggcgagtgt	**SEQ ID NO: 32**
Binding Protein 5 Amino Acid Sequences		
Heavy chain A	Qvqlvqsggqmkkpgesmriscrasgyefidctlnwirlapgkrpewmgwlkpr ggavnyarplqgrvtmtrdvysdtaflelrsltvddtavyfctrgkncdynwdfehw grgtpvivssastkgpsvfplapsskstsggtaalgclvkdyfpepvtvswnsgalts gvhtfpavlqssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkkvepkscdkt htcppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnwyv dgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykckvsnkalpapiekt iskakgqprepqvctlppsrdeltknqvslscavkgfypsdiavewesngqpenny kttppvldsdgsfflvskltvdksrwqqgnvfscsvmhealhnhytqkslslspg	**SEQ ID NO: 33**
Light chain A	Eivltqspgtlslspgetaiiscrtsqygslawyqqrpgqaprlviysgstraagipdrfs gsrwgpdynltisnlesgdfgvyycqqyeffgqgtkvqvdikrtvaapsvfifppsd eqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsstlt lskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 34**
Heavy chain B	Evrlvesggglvkpggslrlscsasgfdfdnawmtwvrqppgkglewvgr itgpgegwsvdyaesvkgrftisrdntkntlylemnnvrtedtgyyfcartgk yydfwwgyppgeeyfqdwgqgtlvivssdkthtqmqlqesgpglvkpse tlsltcsvsgasisdsywswirrspgkglewigyvhksgdtnyspslksrvnl sldtsknqvslslvaataadsgkyycartlhgrriygivafnewftyfymdvw gngtqvtvssdkthtastkgpsvfplapsskstsggtaalgclvkdyfpepvtv swnsgaltsgvhtfpavlqssglyslssvvtvpssslgtqtyicnvnhkpsntk vdkkvepkscdkthtcppcpapellggpsvflfppkpkdtlmisrtpevtcv	**SEQ ID NO: 35**

	vvdvshedpevkfnwyvdgvevhnaktkpreeqynstyrvvsvltvlhqd wlngkeykckvsnkalpapiektiskakgqprepqvytlppcrdeltknqv slwclvkgfypsdiavewesngqpennykttppvldsdgsfflyskltvdks rwqqgnvfscsvmhealhnhytqkslslspg	
Light chain B	Sdisvapgetariscgekslgsravqwyqhragqapsliiynnqdrpsgiperfsgsp dspfgttatltitsveagdeadyychiwdsrvptkwvfgggttltvldkthtaseltqdp avsvalkqtvtitcrgdslrshyaswyqkkpgqapvllfygknnrpsgipdrfsgsas gnrasltitgaqaedeadyycssrdksgsrlsvfgggtkltvldkthtrtvaapsvfifp psdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstysls stltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 36**
Binding Protein 5 Nucleotide Sequences		
Heavy chain A	Caggtgcagctggtgcagtctggcggccagatgaagaaacccggcgagagcatgc ggatcagctgcagagccagcggctacgagttcatcgactgcaccctgaactggatcag actggcccctggcaagcggcctgagtggatgggatggctgaagcctagaggcggag ccgtgaactacgccagacctctgcagggcagagtgaccatgacccgggacgtgtaca gcgataccgccttcctggaactgcggagcctgaccgtggatgataccgccgtgtacttc tgcacccggggcaagaactgcgactacaactgggacttcgagcactggggcagagg caccctgtgatcgtgtcaagc gcgtcgaccaagggccccagcgtgttccctctggccctagcagcaagagcacatct ggcggaacagccgccctgggctgcctcgtgaaggactactttcccgagcccgtgacc gtgtcctggaattctggcgccctgaccagcggcgtgcacaccttccagctgtgctgca gtccagcggcctgtacagcctgagcagcgtcgtgacagtgcccagcagctctctggg cacccagacctacatctgcaacgtgaaccacaagcccagcaacaccaaggtggacaa gaaggtggaacccaagagctgcgacaagacccacacctgtccccttgtcctgcccc cgaactgctgggaggcccttccgtgttcctgttcccccaaagcccaaggacaccctg atgatcagccggacccccgaagtgacctgcgtggtggtggatgtgtcccacgaggac cctgaagtgaagttcaattggtacgtggacggcgtggaagtgcacaacgccaagacca agccaagagaggaacagtacaacagcacctaccgggtggtgtccgtgctgaccgtgc tgcaccaggactggctgaacggcaaagagtacaagtgcaaggtgtccaacaaggccc tgcctgcccccatcgagaaaaccatcagcaaggccaagggccagccccgcgaaccc caggtgtgcacactgcccccaagcagggacgagctgaccaagaaccaggtgtccctg agctgtgccgtgaaaggcttctacccctccgatatcgccgtggaatgggagagcaacg gccagcccgagaacaactacaagaccacccccctgtgctggacagcgacggctcat tcttcctggtgtccaagctgacagtggacaagtcccggtggcagcagggcaacgtgttc agctgctccgtgatgcacgaggccctgcacaaccactacacccagaagtccctgagc ctgagccccggc	
Light chain A	Gagatcgtgctgacacagagccctggcaccctgagcctgtctccaggcgagacagc catcatcagctgccggacaagccagtacggcagcctggcctggtatcagcagaggcc tggacaggcccccagactcgtgatctacagcggcagcacaagagccgccggaatcc ccgatagattcagcggctccagatggggccctgactacaacctgaccatcagcaacct ggaaagcggcgacttcggcgtgtactactgccagcagtacgagttcttcggccagggc accaaggtgcaggtggacatcaagcgtacggtggccgctcccagcgtgttcatcttcc cacctagcgacgagcagctgaagtccggcacagcctctgtcgtgtgcctgctgaacaa cttctacccccgcgaggccaaagtgcagtggaaggtggacaacgccctgcagagcg gcaacagccaggaaagcgtgaccgagcaggacagcaaggactccacctacagcctg agcagcaccctgacactgagcaaggccgactacgagaagcacaaggtgtacgcctg cgaagtgacccaccagggcctgtctagccccgtgaccaagagcttcaaccggggcga gtgt	**SEQ ID NO: 38**
Heavy chain B	gaggttagactggtggagtcaggaggggggcttgtgaagcccggtgggtctctccgc ctgagctgttctgcctccggctttgatttcgataacgcctggatgacctgggtcaggcag	**SEQ ID NO: 39**

	cctccaggtaagggactggagtgggtgggaagaatcacaggtccaggcgagggctg gtccgtggactacgcggaatctgttaaagggcggtttacaatctcaagggacaatacca agaataccttgtatttggagatgaacaacgtgagaactgaagacaccggatattacttct gtgccagaacaggcaaatactacgacttctggtggggctatccccctggcgaggaata ttttcaagactggggtcagggaacccttgttatcgtgtcctccgacaaaacccataccca gatgcagctgcaggagagcggccctggactcgtgaagcccagcgagaccctgagcc tgacatgcagcgtgagcggcgccagcatcagcgacagctactggagctggatcagga ggagccctggcaagggcctggagtggatcggctacgtgcacaagagcggcgacacc aactacagcccctccctgaagtccagggtgaacctgtccctggacaccagcaagaacc aggtgagcctgtccctggtggctgccacagctgctgacagcggcaagtactactgtgc caggaccctgcacggcaggaggatctacggcatcgtggccttcaacgagtggttcacc tacttctacatggacgtgtggggcaacggcacccaggtgaccgtgagctccgataaga cccacaccgcttccaccaagggcccatcggtcttcccctggcaccctcctccaagag cacctctgggggcacagcggccctgggctgcctggtcaaggactacttccccgaacc ggtgacggtgtcgtggaactcaggcgccctgaccagcggcgtgcacaccttcccggc tgtcctacagtcctcaggactctactccctcagcagcgtggtgaccgtgccctccagca gcttgggcacccagacctacatctgcaacgtgaatcacaagcccagcaacaccaaggt ggacaagaaagttgagcccaaatcttgtgacaaaactcacacatgcccaccgtgccca gcacctgaactcctgggggggaccgtcagtcttcctcttcccccaaaacccaaggaca ccctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtgagccacga agaccctgaggtcaagttcaactggtatgttgacggcgtggaggtgcataatgccaaga caaagccgcgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcacc gtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaa gccctcccagcccccatcgagaaaaccatctccaaagccaaagggcagccccgaga accacaggtgtacaccctgcccccatgccgggatgagctgaccaagaatcaagtcag cctgtggtgcctggtaaaaggcttctatcccagcgacatcgccgtggagtgggagagc aatgggcagccggagaacaactacaagaccacgcctcccgtgctggactccgacgg ctccttcttcctctactcaaaactcaccgtggacaagagcaggtggcagcaggggaac gtcttctcatgctccgtgatgcatgaggctctgcacaaccactacacgcagaagagcct ctccctgtctccgggt	
Light chain B	tccgacatcagcgtggcccccggagagacagccaggatctcctgcggcgagaagag cctgggaagcagggctgtgcagtggtaccaacacagggccggacaggctcccagcc tgatcatctacaacaaccaggacaggcccagcggcatccctgagaggttcagcggaa gccccgacagccccttcggaaccacagccaccctgaccatcacaagcgtggaagcc ggcgacgaggccgactactactgccacatctgggacagcagggtgcccaccaagtg ggtgtttggcggcggcaccaccctgaccgtgctggacaaaacccataccgcatccga actgactcaggaccctgccgtctctgtggcactgaagcagactgtgactattacttgccg aggcgactcactgcggagccactacgcttcctggtatcagaagaaacccggccaggc acctgtgctgctgttctacggaaagaacaataggccatctggcatccccgaccgcttttc tggcagtgcatcagggaaccgagccagtctgaccattaccggcgcccaggctgagga cgaagccgattactattgcagctcccgggataagagcggctccagactgagcgtgttc ggaggaggaactaaactgaccgtcctcgataagacccatacccgtacggtggccgct cccagcgtgttcatcttcccacctagcgacgagcagctgaagtccggcacagcctctgt cgtgtgcctgctgaacaacttctacccccgcgaggccaaagtgcagtggaaggtggac aacgccctgcagagcggcaacagccaggaaagcgtgaccgagcaggacagcaag gactccacctacagcctgagcagcaccctgacactgagcaaggccgactacgagaag cacaaggtgtacgcctgcgaagtgacccaccagggcctgtctagccccgtgaccaag agcttcaaccggggcgagtgt	**SEQ ID NO: 40**
Binding Protein 6 Amino Acid Sequences		
Heavy chain A	Qvqlvqsggqmkkpgesmriscrasgyefidctlnwirlapgkrpewmgwlkpr ggavnyarplqgrvtmtrdvysdtaflelrsltvddtavyfctrgkncdynwdfehw grgtpvivssastkgpsvfplapsskstsggtaalgclvkdyfpepvtvswnsgalts gvhtfpavlqssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkkvepkscdkt	**SEQ ID NO: 41**

	htcppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnwyv dgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykckvsnkalpapiekt iskakgqprepqvctlppsrdeltknqvslscavkgfypsdiavewesngqpenny kttppvldsdgsfflvskltvdksrwqqgnvfscsvmhealhnhytqkslslspg	
Light chain A	Eivltqspgtlslspgetaiiscrtsqygslawyqqrpgqaprlviysgstraagipdrfs gsrwgpdynltisnlesgdfgvyycqqyeffgqgtkvqvdikrtvaapsvfifppsd eqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsstlt lskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 42**
Heavy chain B	Qvhltqsgpevrkpgtsvkvsckapgntlktydlhwvrsvpgqglqwmg wishegdkkviverfkakvtidwdrstntaylqlsgltsgdtavyycakgsk hrlrdyalydddgalnwavdvdylsnlefwgqgtavtvssdkthtevrlves ggglvkpggslrlscsasgfdfdnawmtwvrqppgkglewvgritgpgeg wsvdyaesvkgrftisrdntkntlylemnnvrtedtgyyfcartgkyydfw wgyppgeeyfqdwgqgtlvivssdkthtastkgpsvfplapsskstsggtaa lgclvkdyfpepvtvswnsgaltsgvhtfpavlqssglyslssvvtvpssslgt qtyicnvnhkpsntkvdkkvepkscdkthtcppcpapellggpsvflfppk pkdtlmisrtpevtcvvvdvshedpevkfnwyvdgvevhnaktkpreeqy nstyrvvsvltvlhqdwlngkeykckvsnkalpapiektiskakgqprepq vytlppcrdeltknqvslwclvkgfypsdiavewesngqpennykttppvl dsdgsfflyskltvdksrwqqgnvfscsvmhealhnhytqkslslspg	**SEQ ID NO: 43**
Light chain B	Aseltqdpavsvalkqtvtitcrgdslrshyaswyqkkpgqapvllfygknnrpsgi pdrfsgsasgnrasltitgaqaedeadyycssrdksgsrlsvfgggtkltvldkthtdfv ltqsphslsvtpgesasiscksshslihgdrnnylawyvqkpgrspqlliylassrasg vpdrfsgsgsdkdftlkisrvetedvgtyycmqgrespwtfgqgtkvdikdkthtrtv aapsvfifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteq dskdstyslsstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 44**
Binding Protein 6 Nucleotide Sequences		
Heavy chain A	caggtgcagctggtgcagtctggcggccagatgaagaaacccggcgagagcatgcg gatcagctgcagagccagcggctacgagttcatcgactgcaccctgaactggatcaga ctggcccctggcaagcggcctgagtggatgggatggctgaagcctagaggcggagc cgtgaactacgccagacctctgcagggcagagtgaccatgacccgggacgtgtacag cgataccgccttcctggaactgcggagcctgaccgtggatgataccgccgtgtacttct gcacccggggcaagaactgcgactacaactgggacttcgagcactggggcagaggc acccctgtgatcgtgtcaagcgcgtcgaccaagggccccagcgtgttccctctggccc ctagcagcaagagcacatctggcggaacagccgccctgggctgcctcgtgaaggact actttcccgagcccgtgaccgtgtcctggaattctggcgccctgaccagcggcgtgca caccttccagctgtgctgcagtccagcggcctgtacagcctgagcagcgtcgtgaca gtgcccagcagctctctgggcacccagacctacatctgcaacgtgaaccacaagccca gcaacaccaaggtggacaagaaggtggaacccaagagctgcgacaagacccacac ctgtccccttgtcctgccccgaactgctgggaggcccttccgtgttcctgttccccc aaagcccaaggacaccctgatgatcagccggacccccgaagtgacctgcgtggtggt ggatgtgtcccacgaggaccctgaagtgaagttcaattggtacgtggacggcgtggaa gtgcacaacgccaagaccaagccaagagaggaacagtacaacagcacctaccgggt ggtgtccgtgctgaccgtgctgcaccaggactggctgaacggcaaagagtacaagtg caaggtgtccaacaaggccctgcctgcccccatcgagaaaaccatcagcaaggccaa gggccagccccgcgaaccccaggtgtgcacactgcccccaagcagggacgagctg accaagaaccaggtgtccctgagctgtgccgtgaaaggcttctacccctccgatatcgc cgtggaatgggagagcaacggccagcccgagaacaactacaagaccacccccccctg tgctggacagcgacggctcattcttcctggtgtccaagctgacagtggacaagtcccgg tggcagcagggcaacgtgttcagctgctccgtgatgcacgaggccctgcacaaccact acacccagaagtccctgagcctgagccccggc	**SEQ ID NO: 45**

Light chain A	gagatcgtgctgacacagagccctggcaccctgagcctgtctccaggcgagacagcc atcatcagctgccggacaagccagtacggcagcctggcctggtatcagcagaggcct ggacaggcccccagactcgtgatctacagcggcagcacaagagccgccggaatccc cgatagattcagcggctccagatggggccctgactacaacctgaccatcagcaacctg gaaagcggcgacttcggcgtgtactactgccagcagtacgagttcttcggccagggca ccaaggtgcaggtggacatcaagcgtacggtggccgctcccagcgtgttcatcttccc acctagcgacgagcagctgaagtccggcacagcctctgtcgtgtgcctgctgaacaac ttctacccccgcgaggccaaagtgcagtggaaggtggacaacgccctgcagagcgg caacagccaggaaagcgtgaccgagcaggacagcaaggactccacctacagcctga gcagcaccctgacactgagcaaggccgactacgagaagcacaaggtgtacgcctgc gaagtgacccaccagggcctgtctagccccgtgaccaagagcttcaaccggggcga gtgt	**SEQ ID NO: 46**
Heavy chain B	caggtgcacctgacacagagcggacccgaagtgcggaagcctggcacctctgtgaa ggtgtcctgcaaggcccctggcaacaccctgaaaacctacgacctgcactgggtgcg cagcgtgccaggacagggactgcagtggatgggctggatcagccacgagggcgac aagaaagtgatcgtggaacggttcaaggccaaagtgaccatcgactgggacagaagc accaacaccgcctacctgcagctgagcggcctgacctctggcgataccgccgtgtact actgcgccaagggcagcaagcaccggctgagagactacgccctgtacgacgatgac ggcgccctgaactgggccgtggatgtggactacctgagcaacctggaattctggggcc agggcacagccgtgaccgtgtcatctgacaaaacccataccgaggttagactggtgga gtcaggaggggggcttgtgaagcccggtgggtctctccgcctgagctgttctgcctcc ggctttgatttcgataacgcctggatgacctgggtcaggcagcctccaggtaagggact ggagtgggtgggaagaatcacaggtccaggcgagggctggtccgtggactacgcgg aatctgttaaagggcggtttacaatctcaagggacaataccaagaataccttgtatttgga gatgaacaacgtgagaactgaagacaccggatattacttctgtgccagaacaggcaaa tactacgacttctggtggggctatccccctggcgaggaatattttcaagactggggtcag ggaacccttgttatcgtgtcctccgataagacccacaccgcttccaccaagggcccatc ggtcttcccccctggcaccctcctccaagagcacctctgggggcacagcggccctggg ctgcctggtcaaggactacttccccgaaccggtgacggtgtcgtggaactcaggcgcc ctgaccagcggcgtgcacaccttcccggctgtcctacagtcctcaggactctactccct cagcagcgtggtgaccgtgccctccagcagcttgggcacccagacctacatctgcaac gtgaatcacaagcccagcaacaccaaggtggacaagaaagttgagcccaaatcttgtg acaaaactcacacatgcccaccgtgcccagcacctgaactcctgggggggaccgtcag tcttcctcttcccccaaaacccaaggacaccctcatgatctcccggacccctgaggtca catgcgtggtggtggacgtgagccacgaagaccctgaggtcaagttcaactggtatgtt gacggcgtggaggtgcataatgccaagacaaagccgcgggaggagcagtacaaca gcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaa ggagtacaagtgcaaggtctccaacaaagccctcccagcccccatcgagaaaaccat ctccaaagccaaagggcagccccgagaaccacaggtgtacaccctgcccccatgcc gggatgagctgaccaagaatcaagtcagcctgtggtgcctggtaaaaggcttctatccc agcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaaga ccacgcctcccgtgctggactccgacggctccttcttcctctactcaaaactcaccgtgg acaagagcaggtggcagcaggggaacgtcttctcatgctccgtgatgcatgaggctct gcacaaccactacacgcagaagagcctctccctgtctccgggt	**SEQ ID NO: 47**
Light chain B	Gcatccgaactgactcaggaccctgccgtctctgtggcactgaagcagactgt gactattacttgccgaggcgactcactgcggagccactacgcttcctggtatca gaagaaacccggccaggcacctgtgctgctgttctacggaaagaacaatagg ccatctggcatccccgaccgcttttctggcagtgcatcagggaaccgagccagt ctgaccattaccggcgcccaggctgaggacgaagccgattactattgcagctc ccgggataagagcggctccagactgagcgtgttcggaggaggaactaaactg accgtcctcgacaaaacccataccgacttcgtgctgacccagagccctcacag cctgagcgtgacacctggcgagagcgccagcatcagctgcaagagcagcca	**SEQ ID NO: 48**

	ctccctgatccacggcgaccggaacaactacctggcttggtacgtgcagaagc ccggcagatccccccagctgctgatctacctggccagcagcagagccagcgg cgtgcccgatagattttctggcagcggcagcgacaaggacttcaccctgaagat cagccgggtggaaaccgaggacgtgggcacctactactgtatgcagggcaga gagagcccctggacctttggccagggcaccaaggtggacatcaaggataaga cccatacccgtacggtggccgctcccagcgtgttcatcttcccacctagcgacg agcagctgaagtccggcacagcctctgtcgtgtgcctgctgaacaacttctacc cccgcgaggccaaagtgcagtggaaggtggacaacgccctgcagagcggc aacagccaggaaagcgtgaccgagcaggacagcaaggactccacctacagc ctgagcagcaccctgacactgagcaaggccgactacgagaagcacaaggtgt acgcctgcgaagtgacccaccagggcctgtctagccccgtgaccaagagcttc aaccggggcgagtgt	
Binding Protein 7 Amino Acid Sequences		
Heavy chain A	Qvqlvqsggqmkkpgesmriscrasgyefidctlnwirlapgkrpewmgwlkpr ggavnyarplqgrvtmtrdvysdtaflelrsltvddtavyfctrgkncdynwdfehw grgtpvivssastkgpsvfplapsskstsggtaalgclvkdyfpepvtvswnsgalts gvhtfpavlqssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkkvepkscdkt htcppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnwyv dgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykckvsnkalpapiekt iskakgqprepqvctlppsrdeltknqvslscavkgfypsdiavewesngqpenny kttppvldsdgsfflvskltvdksrwqqgnvfscsvmhealhnhytqkslslspg	**SEQ ID NO: 49**
Light chain A	Eivltqspgtlslspgetaiiscrtsqygslawyqqrpgqaprlviysgstraagipdrfs gsrwgpdynltisnlesgdfgvyycqqyeffgqgtkvqvdikrtvaapsvfifppsd eqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsstlt lskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 50**
Heavy chain B	qmqlqesgpglvkpsetlsltcsvsgasisdsywswirrspgkglewigyvh ksgdtnyspslksrvnlsldtsknqvslslvaataadsgkyycartlhgrriygi vafnewftyfymdvwgngtqvtvssdkthtQvhltqsgpevrkpgtsvkv sckapgntlktydlhwvrsvpgqglqwmgwishegdkkviverfkakvti dwdrstntaylqlsgltsgdtavyycakgskhrlrdyalydddgalnwavdv dylsnlefwgqgtavtvssdkthtastkgpsvfplapsskstsggtaalgclvk dyfpepvtvswnsgaltsgvhtfpavlqssglyslssvvtvpssslgtqtyicn vnhkpsntkvdkkvepkscdkthtcppcpapellggpsvflfppkpkdtlm isrtpevtcvvvdvshedpevkfnwyvdgvevhnaktkpreeqynstyrv vsvltvlhqdwlngkeykckvsnkalpapiektiskakgqprepqvytlpp crdeltknqvslwclvkgfypsdiavewesngqpennykttppvldsdgsf flyskltvdksrwqqgnvfscsvmhealhnhytqkslslspg	**SEQ ID NO: 51**
Light chain B	Dfvltqsphslsvtpgesasiscksshslihgdrnnylawyvqkpgrspqlliylassr asgvpdrfsgsgsdkdftlkisrvetedvgtyycmqgrespwtfgqgtkvdikdkth tsdisvapgetariscgekslgsravqwyqhragqapsliiynnqdrpsgiperfsgs pdspfgttatltitsveagdeadyychiwdsrvptkwvfgggttltvldkthtrtvaaps vfifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskd styslsstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 52**
Binding Protein 7 Nucleotide Sequences		
Heavy chain A	caggtgcagctggtgcagtctggcggccagatgaagaaacccggcgagagcatgcg gatcagctgcagagccagcggctacgagttcatcgactgcaccctgaactggatcaga ctggcccctggcaagcggcctgagtggatgggatggctgaagcctagaggcggagc cgtgaactacgccagacctctgcagggcagagtgaccatgacccgggacgtgtacag cgataccgccttcctggaactgcggagcctgaccgtggatgataccgccgtgtacttct gcacccggggcaagaactgcgactacaactgggacttcgagcactggggcagaggc	**SEQ ID NO: 53**

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Light chain A	gagatcgtgctgacacagagccctggcaccctgagcctgtctccaggcgagacagcc atcatcagctgccggacaagccagtacggcagcctggcctggtatcagcagaggcct ggacaggcccccagactcgtgatctacagcggcagcacaagagccgccggaatccc cgatagattcagcggctccagatggggccctgactacaacctgaccatcagcaacctg gaaagcggcgacttcggcgtgtactactgccagcagtacgagttcttcggccagggca ccaaggtgcaggtggacatcaagcgtacggtggccgctcccagcgtgttcatcttccc acctagcgacgagcagctgaagtccggcacagcctctgtcgtgtgcctgctgaacaac ttctacccccgcgaggccaaagtgcagtggaaggtggacaacgccctgcagagcgg caacagccaggaaagcgtgaccgagcaggacagcaaggactccacctacagcctga gcagcaccctgacactgagcaaggccgactacgagaagcacaaggtgtacgcctgc gaagtgacccaccagggcctgtctagccccgtgaccaagagcttcaaccggggcga gtgt	**SEQ ID NO: 54**
Heavy chain B	cagatgcagctgcaggagagcggccctggactcgtgaagcccagcgagaccctgag cctgacatgcagcgtgagcggcgccagcatcagcgacagctactggagctggatcag gaggagccctggcaagggcctggagtggatcggctacgtgcacaagagcggcgac accaactacagcccctccctgaagtccagggtgaacctgtccctggacaccagcaaga accaggtgagcctgtccctggtggctgccacagctgctgacagcggcaagtactactg tgccaggaccctgcacggcaggaggatctacggcatcgtggccttcaacgagtggttc acctacttctacatggacgtgtggggcaacggcacccaggtgaccgtgagctccgaca aaacccatacccaggtgcacctgacacagagcggacccgaagtgcggaagcctggc acctctgtgaaggtgtcctgcaaggcccctggcaacaccctgaaaacctacgacctgc actgggtgcgcagcgtgccaggacagggactgcagtggatgggctggatcagccac gagggcgacaagaaagtgatcgtggaacggttcaaggccaaagtgaccatcgactgg gacagaagcaccaacaccgcctacctgcagctgagcggcctgacctctggcgatacc gccgtgtactactgcgccaagggcagcaagcaccggctgagagactacgccctgtac gacgatgacggcgccctgaactgggccgtggatgtggactacctgagcaacctggaa ttctggggccagggcacagccgtgaccgtgtcatctgataagacccacaccgcttcca ccaagggcccatcggtcttcccctggcaccctcctccaagagcacctctgggggcac agcggccctgggctgcctggtcaaggactacttccccgaaccggtgacggtgtcgtgg aactcaggcgccctgaccagcggcgtgcacaccttcccggctgtcctacagtcctcag gactctactccctcagcagcgtggtgaccgtgccctccagcagcttgggcacccagac ctacatctgcaacgtgaatcacaagcccagcaacaccaaggtggacaagaaagttga gcccaaatcttgtgacaaaactcacacatgcccaccgtgcccagcacctgaactcctgg ggggaccgtcagtcttcctcttcccccaaaacccaaggacaccctcatgatctcccgg	**SEQ ID NO: 55**

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Light chain B	Gacttcgtgctgacccagagccctcacagcctgagcgtgacacctggcgaga gcgccagcatcagctgcaagagcagccactccctgatccacggcgaccggaa caactacctggcttggtacgtgcagaagcccggcagatccccccagctgctga tctacctggccagcagcagagccagcggcgtgcccgatagattttctggcagc ggcagcgacaaggacttcaccctgaagatcagccgggtggaaaccgaggac gtgggcacctactactgtatgcagggcagagagagcccctggacctttggcca gggcaccaaggtggacatcaaggacaaaacccatacctccgacatcagcgtg gcccccggagagacagccaggatctcctgcggcgagaagagcctgggaag cagggctgtgcagtggtaccaacacagggccggacaggctcccagcctgatc atctacaacaaccaggacaggcccagcggcatccctgagaggttcagcggaa gccccgacagccccttcggaaccacagccaccctgaccatcacaagcgtgga agccggcgacgaggccgactactactgccacatctgggacagcagggtgcc caccaagtgggtgtttggcggcggcaccaccctgaccgtgctggataagaccc atacccgtacggtggccgctcccagcgtgttcatcttcccacctagcgacgagc agctgaagtccggcacagcctctgtcgtgtgcctgctgaacaacttctaccccc gcgaggccaaagtgcagtggaaggtggacaacgccctgcagagcggcaac agccaggaaagcgtgaccgagcaggacagcaaggactccacctacagcctg agcagcaccctgacactgagcaaggccgactacgagaagcacaaggtgtac gcctgcgaagtgacccaccagggcctgtctagccccgtgaccaagagcttcaa ccggggcgagtgt	**SEQ ID NO: 56**
Binding Protein 8 Amino Acid Sequences		
Heavy chain A	Rahlvqsgtamkkpgasvrvscqtsgytftahilfwfrqapgrglewvgwikpqy gavnfgggfrdrvtltrdvyreiaymdirglkpddtavyycardrsygdsswalda wgqgttvvvsaastkgpsvfplapsskstsggtaalgclvkdyfpepvtvswnsgal tsgvhtfpavlqssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkkvepkscd kthtcppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnw yvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykckvsnkalpapi ektiskakgqprepqvctlppsrdeltknqvslscavkgfypsdiavewesngqpe nnykttppvldsdgsfflvskltvdksrwqqgnvfscsvlhealhshytqkslslspg	**SEQ ID NO: 57**
Light chain A	Yihvtqspsslsvsigdrvtincqtsqgvgsdlhwyqhkpgrapkllihhtssvedg vpsrfsgsgfhtsfnltisdlqaddiatyycqvlqffgrgsrlhikrtvaapsvfifppsd eqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsstlt lskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 58**
Heavy chain B	Evrlvesggglvkpggslrlscsasgfdfdnawmtwvrqppgkglewvgr itgpgegwsvdyaesvkgrftisrdntkntlylemnnvrtedtgyyfcartgk yydfwwgyppgeeyfqdwgqgtlvivssdkthtqvqlvesgggvvqpgt slrlscaasqfrfdgygmhwvrqapgkglewvasishdgikkyhaekvwg rftisrdnskntlylqmnslrpedtalyycakdlredeceewwsdyydfgkq lpcaksrgglvgiadnwgqgtmvtvssdkthtastkgpsvfplapsskstsg gtaalgclvkdyfpepvtvswnsgaltsgvhtfpavlqssglyslssvvtvpss slgtqtyicnvnhkpsntkvdkkvepkscdkthtcppcpapellggpsvflf	**SEQ ID NO: 59**

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Light chain B	Qsvltqppsvsaapgqkvtiscsgntsnignnfvswyqqrpgrapqlliyetdkrps gipdrfsasksgtsgtlaitglqtgdeadyycatwaaslssarvfgtgtkvivldkthtas eltqdpavsvalkqtvtitcrgdslrshyaswyqkkpgqapvllfygknnrpsgipdr fsgsasgnrasltitgaqaedeadyycssrdksgsrlsvfgggtkltvldkthtrtvaap svfifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdsk dstyslsstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 60**
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Heavy chain A	agagcccacctggtgcagtctggcaccgccatgaagaaaccaggcgcctctgtgcgg gtgtcctgtcagacaagcggctacaccttcaccgcccacatcctgttctggttccggca ggcccctggcagaggactggaatgggtgggatggatcaagccccagtatggcgccg tgaacttcggcggaggcttccgggatagagtgaccctgacccgggacgtgtaccgcg agatcgcctacatggacatccggggcctgaagcccgatgacaccgccgtgtactactg cgccagagacagaagctacggcgacagcagctgggctctggatgcttggggccagg gcacaaccgtggtggtgtctgccgcctctacaaagggccccagcgtgttccctctggc ccctagcagcaagagcacatctggcggaacagccgccctgggctgcctcgtgaagg actactttcccgagcccgtgaccgtgtcctggaattctggcgccctgaccagcggcgtg cacaccttccagctgtgctgcagtccagcggcctgtacagcctgagcagcgtcgtga cagtgcccagcagctctctgggcacccagacctacatctgcaacgtgaaccacaagc ccagcaacaccaaggtggacaagaaggtggaacccaagagctgcgacaagaccca cacctgtccccttgtcctgccccgaactgctgggaggcccttccgtgttcctgttccc cccaaagcccaaggacaccctgatgatcagccggaccccgaagtgacctgcgtggt ggtggatgtgtcccacgaggaccctgaagtgaagttcaattggtacgtggacggcgtg gaagtgcacaacgccaagaccaagccaagagaggaacagtacaacagcacctacc gggtggtgtccgtgctgaccgtgctgcaccaggactggctgaacggcaaagagtaca agtgcaaggtgtccaacaaggccctgcctgcccccatcgagaaaaccatcagcaagg ccaagggccagccccgcgaaccccaggtgtgcacactgcccccaagcagggacga gctgaccaagaaccaggtgtccctgagctgtgccgtgaaaggcttctacccctccgat atcgccgtggaatgggagagcaacggccagcccgagaacaactacaagaccaccc cccctgtgctggacagcgacggctcattcttcctggtgtccaagctgacagtggacaag tcccggtggcagcagggcaacgtgttcagctgctccgtgatgcacgaggccctgcac aaccactacacccagaagtccctgagcctgagccccggcaag	**SEQ ID NO: 61**
Light chain A	Tacatccacgtgacccagagccccagcagcctgtccgtgtccatcggcgaca gagtgaccatcaactgccagacctctcagggcgtgggcagcgacctgcactg gtatcagcacaagcctggcagagcccccaagctgctgatccaccacacaagc agcgtggaagatggcgtgcccagcagattttccggcagcggcttccacacca gcttcaacctgaccatcagcgatctgcaggccgacgacattgccacctactatt gtcaggtgctgcagttcttcggcagaggcagcagactgcacatcaagcgtacg gtggccgctcccagcgtgttcatcttcccacctagcgacgagcagctgaagtcc ggcacagcctctgtcgtgtgcctgctgaacaacttctacccccgcgaggccaa agtgcagtggaaggtggacaacgccctgcagagcggcaacagccaggaaa gcgtgaccgagcaggacagcaaggactccacctacagcctgagcagcaccc tgacactgagcaaggccgactacgagaagcacaaggtgtacgcctgcgaagt gacccaccagggcctgtctagccccgtgaccaagagcttcaaccggggcga gtgt	**SEQ ID NO: 62**
Heavy chain B	gaggttagactggtggagtcaggaggggggcttgtgaagcccggtgggtctctccgc ctgagctgttctgcctccggctttgatttcgataacgcctggatgacctgggtcaggcag cctccaggtaagggactggagtgggtgggaagaatcacaggtccaggcgagggctg	**SEQ ID NO: 63**

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Light chain B	Cagtctgtgctgacgcagccgccctcagtgtctgcggccccaggacagaaggtcaccatctcctgctctggaaacacctccaacattggcaataattttgtgtcctggtatcaacagcgccccggcagagccccccaactcctcatttatgaaactgacaagcgaccctcagggattcctgaccgattctctgcttccaagtctggtacgtcaggcaccctggccatcaccgggctgcagactggggacgaggccgattattactgcgccacatgggctgccagcctgagttccgcgcgtgtcttcggaactgggaccaaggtcatcgtcctggacaaaacccataccgcatccgaactgactcaggaccctgccgtctctgtggcactgaagcagactgtgactattacttgccgaggcgactcactgcggagccactacgcttcctggtatcagaagaaacccggccaggcacctgtgctgctgttctacggaaagaacaataggccatctggcatccccgaccgcttttctggcagtgcatcagggaaccgagccagtctgaccattaccggcgcccaggctgaggacgaagccgattactattgcagctcccgggataagagcggctccagactgagcgtgttcggaggaggaactaaactgaccgtcctcgataagacccatacccgtacggtggccgctcccagcgtgttcatcttcccacctagcgacgagcagctgaagtccggcacagcctctgtcgtgtgcctgctgaacaacttctacccccgcgaggccaaagtgcagtggaaggtggacaacgccctgcagagcggcaacagccaggaaagcgtgaccgagcaggacagcaaggactccacctacagcctgagcagcaccctgacactgagcaaggccgactacgagaagcacaaggtgtacgcctgcgaagtgacccaccagggcctgtctagccccgtgaccaagagcttcaaccggggcgagtgt	**SEQ ID NO: 64**
Binding Protein 9 Amino Acid Sequences		
Heavy chain A	Qvqlvqsggqmkkpgesmriscrasgyefidctlnwirlapgkrpewmgwlkprggavnyarplqgrvtmtrdvysdtaflelrsltvddtavyfctrgkncdynwdfehw	**SEQ ID NO: 65**

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Light chain A	Eivltqspgtlslspgetaiiscrtsqygslawyqqrpgqaprlviysgstraagipdrfs gsrwgpdynltisnlesgdfgvyycqqyeffgqgtkvqvdikrtvaapsvfifppsd eqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsstlt lskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 66**
Heavy chain B	Evrlvesggglvkpggslrlscsasgfdfdnawmtwvrqppgkglewvgr itgpgegwsvdyaesvkgrftisrdntkntlylemnnvrtedtgyyfcartgk yydfwwgyppgeeyfqdwgqgtlvivssdkthtqvqlvesgggvvqpgt slrlscaasqfrfdgygmhwvrqapgkglewvasishdgikkyhaekvwg rftisrdnskntlylqmnslrpedtalyycakdlredeceewwsdyydfgkq lpcaksrgglvgiadnwgqgtmvtvssdkthtastkgpsvfplapsskstsg gtaalgclvkdyfpepvtvswnsgaltsgvhtfpavlqssglyslssvvtvpss slgtqtyicnvnhkpsntkvdkkvepkscdkthtcppcpapellggpsvflf ppkpkdtlmisrtpevtcvvvdvshedpevkfnwyvdgvevhnaktkpr eeqynstyrvvsvltvlhqdwlngkeykckvsnkalpapiektiskakgqpr epqvytlppcrdeltknqvslwclvkgfypsdiavewesngqpennykttp pvldsdgsfflyskltvdksrwqqgnvfscsvmhealhnhytqkslslspg	**SEQ ID NO: 67**
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Binding Protein 9 Nucleotide Sequences		
Heavy chain A	caggtgcagctggtgcagtctggcggccagatgaagaaacccggcgagagcatgcg gatcagctgcagagccagcggctacgagttcatcgactgcaccctgaactggatcaga ctggcccctggcaagcggcctgagtggatgggatggctgaagcctagaggcggagc cgtgaactacgccagacctctgcagggcagagtgaccatgacccgggacgtgtacag cgataccgccttcctggaactgcggagcctgaccgtggatgataccgccgtgtacttct gcacccggggcaagaactgcgactacaactgggacttcgagcactggggcagaggc acccctgtgatcgtgtcaagcgcgtcgaccaagggccccagcgtgttccctctggccc ctagcagcaagagcacatctggcggaacagccgccctgggctgcctcgtgaaggact actttcccgagcccgtgaccgtgtcctggaattctggcgccctgaccagcggcgtgca caccttccagctgtgctgcagtccagcggcctgtacagcctgagcagcgtcgtgaca gtgcccagcagctctctgggcacccagacctacatctgcaacgtgaaccacaagccca gcaacaccaaggtggacaagaaggtggaacccaagagctgcgacaagacccacac ctgtccccttgtcctgccccgaactgctgggaggcccttccgtgttcctgttccccc aaagcccaaggacaccctgatgatcagccggaccccgaagtgacctgcgtggtggt ggatgtgtcccacgaggaccctgaagtgaagttcaattggtacgtggacggcgtggaa gtgcacaacgccaagaccaagccaagagaggaacagtacaacagcacctaccgggt ggtgtccgtgctgaccgtgctgcaccaggactggctgaacggcaaagagtacaagtg caaggtgtccaacaaggccctgcctgcccccatcgagaaaaccatcagcaaggccaa gggccagccccgcgaaccccaggtgtgcacactgcccccaagcagggacgagctg accaagaaccaggtgtccctgagctgtgccgtgaaaggcttctacccctccgatatcgc cgtggaatgggagagcaacggccagcccgagaacaactacaagaccacccccccctg	**SEQ ID NO: 69**

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Light chain A	gagatcgtgctgacacagagccctggcaccctgagcctgtctccaggcgagacagcc atcatcagctgccggacaagccagtacggcagcctggcctggtatcagcagaggcct ggacaggcccccagactcgtgatctacagcggcagcacaagagccgccggaatccc cgatagattcagcggctccagatggggccctgactacaacctgaccatcagcaacctg gaaagcggcgacttcggcgtgtactactgccagcagtacgagttcttcggccagggca ccaaggtgcaggtggacatcaagcgtacggtggccgctcccagcgtgttcatcttccc acctagcgacgagcagctgaagtccggcacagcctctgtcgtgtgcctgctgaacaac ttctacccccgcgaggccaaagtgcagtggaaggtggacaacgccctgcagagcgg caacagccaggaaagcgtgaccgagcaggacagcaaggactccacctacagcctga gcagcaccctgacactgagcaaggccgactacgagaagcacaaggtgtacgcctgc gaagtgacccaccagggcctgtctagccccgtgaccaagagcttcaaccggggcga gtgt	**SEQ ID NO: 70**
Heavy chain B	gaggttagactggtggagtcaggaggggggcttgtgaagcccggtgggtctctccgc ctgagctgttctgcctccggctttgatttcgataacgcctggatgacctgggtcaggcag cctccaggtaagggactggagtgggtgggaagaatcacaggtccaggcgagggctg gtccgtggactacgcggaatctgttaaagggcggtttacaatctcaagggacaatacca agaataccttgtatttggagatgaacaacgtgagaactgaagacaccggatattacttct gtgccagaacaggcaaatactacgacttctggtggggctatccccctggcgaggaata ttttcaagactggggtcagggaacccttgttatcgtgtcctccgacaaaacccatacca ggtgcagttggtggagtctgggggaggcgtggtccagcctgggacgtccctgagact ctcctgtgcagcctctcaattcaggtttgatggttatggcatgcactgggtccgccaggc cccaggcaaggggctggagtgggtggcatctatatcacatgatggaattaaaaagtatc acgcagaaaaagtgtggggccgcttcaccatctccagagacaattccaagaacacact gtatctacaaatgaacagcctgcgacctgaggacacggctctctactactgtgcgaaag atttgcgagaagacgaatgtgaagagtggtggtcggattattacgattttgggaaacaac tcccttgcgcaaagtcacgcggcggcttggttggaattgctgataactggggccaagg gacaatggtcaccgtctcttcagataagacccacaccgcttccaccaagggcccatcg gtcttcccctggcaccctcctccaagagcacctctgggggcacagcggccctgggct gcctggtcaaggactacttccccgaaccggtgacggtgtcgtggaactcaggcgccct gaccagcggcgtgcacaccttcccggctgtcctacagtcctcaggactctactccctca gcagcgtggtgaccgtgccctccagcagcttgggcacccagacctacatctgcaacgt gaatcacaagcccagcaacaccaaggtggacaagaaagttgagcccaaatcttgtga caaaactcacacatgcccaccgtgcccagcacctgaactcctgggggggaccgtcagt cttcctcttcccccaaaacccaaggacaccctcatgatctcccggaccccctgaggtca catgcgtggtggtggacgtgagccacgaagaccctgaggtcaagttcaactggtatgtt gacggcgtggaggtgcataatgccaagacaaagccgcgggaggagcagtacaaca gcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaa ggagtacaagtgcaaggtctccaacaaagccctcccagcccccatcgagaaaaccat ctccaaagccaaagggcagccccgagaaccacaggtgtacaccctgcccccatgcc gggatgagctgaccaagaatcaagtcagcctgtggtgcctggtaaaaggcttctatccc agcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaaga ccacgcctcccgtgctggactccgacggctccttcttcctctactcaaaactcaccgtgg acaagagcaggtggcagcaggggaacgtcttctcatgctccgtgatgcatgaggctct gcacaaccactacacgcagaagagcctctccctgtctccgggt	**SEQ ID NO: 71**
Light chain B	cagtctgtgctgacgcagccgccctcagtgtctgcggccccaggacagaaggtcacc atctcctgctctggaaacacctccaacattggcaataattttgtgtcctggtatcaacagc gccccggcagagccccccaactcctcatttatgaaactgacaagcgaccctcagggat tcctgaccgattctctgcttccaagtctggtacgtcaggcaccctggccatcaccgggct gcagactggggacgaggccgattattactgcgccacatgggctgccagcctgagttcc	**SEQ ID NO: 72**

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Binding Protein 10 Amino Acid Sequences		
Heavy chain A	Qvqlvqsggqmkkpgesmriscrasgyefidctlnwirlapgkrpewmgwlkpr ggavnyarplqgrvtmtrdvysdtaflelrsltvddtavyfctrgkncdynwdfehw grgtpvivssastkgpsvfplapsskstsggtaalgclvkdyfpepvtvswnsgalts gvhtfpavlqssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkkvepkscdkt htcppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnwyv dgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykckvsnkalpapiekt iskakgqprepqvctlppsrdeltknqvslscavkgfypsdiavewesngqpenny kttppvldsdgsfflvskltvdksrwqqgnvfscsvmhealhnhytqkslslspg	**SEQ ID NO: 73**
Light chain A	Eivltqspgtlslspgetaiiscrtsqygslawyqqrpgqaprlviysgstraagipdrfs gsrwgpdynltisnlesgdfgvyycqqyeffgqgtkvqvdikrtvaapsvfifppsd eqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsstlt lskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 74**
Heavy chain B	qvqlvesgggvvqpgtslrlscaasqfrfdgygmhwvrqapgkglewvas ishdgikkyhaekvwgrftisrdnskntlylqmnslrpedtalyycakdlred eceewwsdyydfgkqlpcaksrgglvgiadnwgqgtmvtvssdkthtevr lvesggglvkpggslrlscsasgfdfdnawmtwvrqppgkglewvgritgp gegwsvdyaesvkgrftisrdntkntlylemnnvrtedtgyyfcartgkyyd fwwgyppgeeyfqdwgqgtlvivssdkthtastkgpsvfplapsskstsgg taalgclvkdyfpepvtvswnsgaltsgvhtfpavlqssglyslssvvtvpsss lgtqtyicnvnhkpsntkvdkkvepkscdkthtcppcpapellggpsvflfp pkpkdtlmisrtpevtcvvvdvshedpevkfnwyvdgvevhnaktkpree qynstyrvvsvltvlhqdwlngkeykckvsnkalpapiektiskakgqpre pqvytlppcrdeltknqvslwclvkgfypsdiavewesngqpennykttpp vldsdgsfflyskltvdksrwqqgnvfscsvmhealhnhytqkslslspg	**SEQ ID NO: 75**
Light chain B	aseltqdpavsvalkqtvtitcrgdslrshyaswyqkkpgqapvllfygknnrpsgip drfsgsasgnrasltitgaqaedeadyycssrdksgsrlsvfgggtkltvldkthtqsvlt qppsvsaapgqkvtiscsgntsnignnfvswyqqrpgrapqlliyetdkrpsgipdr fsasksgtsgtlaitglqtgdeadyycatwaaslssarvfgtgtkvivldkthtrtvaaps vfifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskd styslsstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 76**
Binding Protein 10 Nucleotide Sequences		
Heavy chain A	caggtgcagctggtgcagtctggcggccagatgaagaaacccggcgagagcatgcg gatcagctgcagagccagcggctacgagttcatcgactgcaccctgaactggatcaga ctggcccctggcaagcggcctgagtggatgggatggctgaagcctagaggcggagc cgtgaactacgccagacctctgcagggcagagtgaccatgacccgggacgtgtacag	**SEQ ID NO: 77**

	cgataccgccttcctggaactgcggagcctgaccgtggatgataccgccgtgtacttct gcacccggggcaagaactgcgactacaactgggacttcgagcactggggcagaggc acccctgtgatcgtgtcaagcgcgtcgaccaagggccccagcgtgttccctctggccc ctagcagcaagagcacatctggcggaacagccgccctgggctgcctcgtgaaggact actttcccgagcccgtgaccgtgtcctggaattctggcgccctgaccagcggcgtgca caccttccagctgtgctgcagtccagcggcctgtacagcctgagcagcgtcgtgaca gtgcccagcagctctctgggcacccagacctacatctgcaacgtgaaccacaagccc agcaacaccaaggtggacaagaaggtggaacccaagagctgcgacaagacccaca cctgtccccttgtcctgccccgaactgctgggaggcccttccgtgttcctgttccccc caaagcccaaggacaccctgatgatcagccggacccccgaagtgacctgcgtggtg gtggatgtgtcccacgaggaccctgaagtgaagttcaattggtacgtggacggcgtgg aagtgcacaacgccaagaccaagccaagagaggaacagtacaacagcacctaccg ggtggtgtccgtgctgaccgtgctgcaccaggactggctgaacggcaaagagtacaa gtgcaaggtgtccaacaaggccctgcctgcccccatcgagaaaaccatcagcaaggc caagggccagccccgcgaaccccaggtgtgcacactgcccccaagcagggacgag ctgaccaagaaccaggtgtccctgagctgtgccgtgaaaggcttctacccctccgatat cgccgtggaatgggagagcaacggccagcccgagaacaactacaagaccacccccc cctgtgctggacagcgacggctcattcttcctggtgtccaagctgacagtggacaagtc ccggtggcagcagggcaacgtgttcagctgctccgtgatgcacgaggccctgcacaa ccactacacccagaagtccctgagcctgagccccggc	
Light chain A	gagatcgtgctgacacagagccctggcaccctgagcctgtctccaggcgagacagcc atcatcagctgccggacaagccagtacggcagcctggcctggtatcagcagaggcct ggacaggcccccagactcgtgatctacagcggcagcacaagagccgccggaatccc cgatagattcagcggctccagatggggccctgactacaacctgaccatcagcaacctg gaaagcggcgacttcggcgtgtactactgccagcagtacgagttcttcggccagggca ccaaggtgcaggtggacatcaagcgtacggtggccgctcccagcgtgttcatcttccc acctagcgacgagcagctgaagtccggcacagcctctgtcgtgtgcctgctgaacaac ttctacccccgcgaggccaaagtgcagtggaaggtggacaacgccctgcagagcgg caacagccaggaaagcgtgaccgagcaggacagcaaggactccacctacagcctg agcagcaccctgacactgagcaaggccgactacgagaagcacaaggtgtacgcctg cgaagtgacccaccagggcctgtctagccccgtgaccaagagcttcaaccggggcg agtgt	**SEQ ID NO:78**
Heavy chain B	caggtgcagttggtggagtctgggggaggcgtggtccagcctgggacgtccctgaga ctctcctgtgcagcctctcaattcaggtttgatggttatggcatgcactgggtccgccag gccccaggcaaggggctggagtgggtggcatctatatcacatgatggaattaaaaagt atcacgcagaaaaagtgtggggccgcttcaccatctccagagacaattccaagaacac actgtatctacaaatgaacagcctgcgacctgaggacacggctctctactactgtgcga aagatttgcgagaagacgaatgtgaagagtggtggtcggattattacgattttgggaaa caactcccttgcgcaaagtcacgcggcggcttggttggaattgctgataactggggcc aagggacaatggtcaccgtctcttcagacaaaacccataccgaggttagactggtgga gtcaggaggggggcttgtgaagcccggtgggtctctccgcctgagctgttctgcctcc ggctttgatttcgataacgcctggatgacctgggtcaggcagcctccaggtaagggact ggagtgggtgggaagaatcacaggtccaggcgagggctggtccgtggactacgcgg aatctgttaaagggcggtttacaatctcaagggacaataccaagaataccttgtatttgga gatgaacaacgtgagaactgaagacaccggatattacttctgtgccagaacaggcaaa tactacgacttctggtccggctatccccctggcgaggaatattttcaagactggggtcag ggaacccttgttatcgtgtcctccgataagacccacaccgcttccaccaagggcccatc ggtcttcccccctggcaccctcctccaagagcacctctgggggcacagcggccctggg ctgcctggtcaaggactacttccccgaaccggtgacggtgtcgtggaactcaggcgcc ctgaccagcggcgtgcacaccttcccggctgtcctacagtcctcaggactctactccct cagcagcgtggtgaccgtgccctccagcagcttgggcacccagacctacatctgcaa	**SEQ ID NO: 79**

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Light chain B	gcatccgaactgactcaggaccctgccgtctctgtggcactgaagcagactgt gactattacttgccgaggcgactcactgcggagccactacgcttcctggtatca gaagaaacccggccaggcacctgtgctgctgttctacggaaagaacaatagg ccatctggcatccccgaccgcttttctggcagtgcatcagggaaccgagccagt ctgaccattaccggcgcccaggctgaggacgaagccgattactattgcagctc ccgggataagagcggctccagactgagcgtgttcggaggaggaactaaactg accgtcctcgacaaaaacccatacc cagtctgtgctgacgcagccgccctcagtgtctgcggccccaggacagaagg tcaccatctcctgctctggaaacacctccaacattggcaataattttgtgtcctggt atcaacagcgccccggcagagcccccccaactcctcatttatgaaactgacaag cgaccctcagggattcctgaccgattctctgcttccaagtctggtacgtcaggca ccctggccatcaccgggctgcagactggggacgaggccgattattactgcgc cacatgggctgccagcctgagttccgcgcgtgtcttcggaactgggaccaagg tcatcgtcctg gataagacccatacccgtacggtggccgctcccagcgtgttcatcttcccacct agcgacgagcagctgaagtccggcacagcctctgtcgtgtgcctgctgaacaa cttctacccccgcgaggccaaagtgcagtggaaggtggacaacgccctgcag agcggcaacagccaggaaagcgtgaccgagcaggacagcaaggactccac ctacagcctgagcagcaccctgacactgagcaaggccgactacgagaagca caaggtgtacgcctgcgaagtgacccaccagggcctgtctagccccgtgacc aagagcttcaaccggggcgagtgt	**SEQ ID NO: 80**
Binding Protein 11 Amino Acid Sequences		
Heavy chain A	Rahlvqsgtamkkpgasvrvscqtsgytftahilfwfrqapgrglewvgwikpqy gavnfgggfrdrvtltrdvyreiaymdirglkpddtavyycardrsygdsswalda wgqgttvvvsaastkgpsvfplapsskstsggtaalgclvkdyfpepvtvswnsgal tsgvhtfpavlqssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkkvepkscd kthtcppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnw yvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykckvsnkalpapi ektiskakgqprepqvctlppsrdeltknqvslscavkgfypsdiavewesngqpe nnykttppvldsdgsfflvskltvdksrwqqgnvfscsvmhealhnhytqkslslsp g	**SEQ ID NO: 81**
Light chain A	yihvtqspsslsvsigdrvtincqtsqgvgsdlhwyqhkpgrapkllihhtssvedgv psrfsgsgfhtsfnltisdlqaddiatyycqvlqffgrgsrlhikrtvaapsvfifppsde qlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsstltls kadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 82**
Heavy chain B	evrlvesggglvkpggslrlscsasgfdfdnawmtwvrqppgkglewvgri tgpgegwsvdyaesvkgrftisrdntkntlylemnnvrtedtgyyfcartgk yydfwwgyppgeeyfqdwgqgtlvivssdkthtqvhltqsgpevrkpgts	**SEQ ID NO: 83**

	vkvsckapgntlktydlhwvrsvpgqglqwmgwishegdkkviverfka kvtidwdrstntaylqlsgltsgdtavyycakgskhrlrdyalydddgalnwa vdvdylsnlefwgqgtavtvssdkthtastkgpsvfplapsskstsggtaalg clvkdyfpepvtvswnsgaltsgvhtfpavlqssglyslssvvtvpssslgtqt yicnvnhkpsntkvdkkvepkscdkthtcppcpapellggpsvflfppkpk dtlmisrtpevtcvvvdvshedpevkfnwyvdgvevhnaktkpreeqyns tyrvvsvltvlhqdwlngkeykckvsnkalpapiektiskakgqprepqvyt lppcrdeltknqvslwclvkgfypsdiavewesngqpennykttppvldsd gsfflyskltvdksrwqqgnvfscsvmhealhnhytqkslslspg	
Light chain B	dfvltqsphslsvtpgesasisckssshslihgdrnnylawyvqkpgrspqlliylassr asgvpdrfsgsgsdkdftlkisrvetedvgtyycmqgrespwtfgqgtkvdikdkth taseltqdpavsvalkqtvtitcrgdslrshyaswyqkkpgqapvllfygknnrpsgi pdrfsgsasgnrasltitgaqaedeadyycssrdksgsrlsvfgggtkltvldkthtrtv aapsvfifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteq dskdstyslsstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 84**
Binding Protein 11 Nucleotide Sequences		
Heavy chain A	agagcccacctggtgcagtctggcaccgccatgaagaaaccaggcgcctctgtgcgg gtgtcctgtcagacaagcggctacaccttcaccgcccacatcctgttctggttccggcag gcccctggcagaggactggaatgggtgggatggatcaagccccagtatggcgccgtg aacttcggcggaggcttccgggatagagtgaccctgacccgggacgtgtaccgcgag atcgcctacatggacatccggggcctgaagcccgatgacaccgccgtgtactactgcg ccagagacagaagctacggcgacagcagctgggctctggatgcttggggccagggc acaaccgtggtggtgtctgccgcctctacaaagggccccagcgtgttccctctggcccc tagcagcaagagcacatctggcggaacagccgccctgggctgcctcgtgaaggacta ctttcccgagcccgtgaccgtgtcctggaattctggcgccctgaccagcggcgtgcac acctttccagctgtgctgcagtccagcggcctgtacagcctgagcagcgtcgtgacagt gcccagcagctctctgggcacccagacctacatctgcaacgtgaaccacaagcccag caacaccaaggtggacaagaaggtggaacccaagagctgcgacaagacccacacct gtccccttgtcctgccccgaactgctgggaggcccttccgtgttcctgttcccccaa agcccaaggacaccctgatgatcagccggacccccgaagtgacctgcgtggtggtgg atgtgtcccacgaggaccctgaagtgaagttcaattggtacgtggacggcgtggaagt gcacaacgccaagaccaagccaagagaggaacagtacaacagcacctaccgggtg gtgtccgtgctgaccgtgctgcaccaggactggctgaacggcaaagagtacaagtgc aaggtgtccaacaaggccctgcctgcccccatcgagaaaaccatcagcaaggccaag ggccagccccgcgaaccccaggtgtgcacactgcccccaagcagggacgagctga ccaagaaccaggtgtccctgagctgtgccgtgaaaggcttctacccctccgatatcgcc gtggaatgggagagcaacggccagcccgagaacaactacaagaccacccccccctgt gctggacagcgacggctcattcttcctggtgtccaagctgacagtggacaagtcccggt ggcagcagggcaacgtgttcagctgctccgtgatgcacgaggccctgcacaaccact acacccagaagtccctgagcctgagccccggcaag	**SEQ ID NO: 85**
Light chain A	tacatccacgtgacccagagccccagcagcctgtccgtgtccatcggcgacag agtgaccatcaactgccagacctctcagggcgtgggcagcgacctgcactggt atcagcacaagcctggcagagcccccaagctgctgatccaccacacaagcag cgtggaagatggcgtgcccagcagattttccggcagcggcttccacaccagct tcaacctgaccatcagcgatctgcaggccgacgacattgccacctactattgtca ggtgctgcagttcttcggcagaggcagcagactgcacatcaagcgtacggtgg ccgctcccagcgtgttcatcttcccacctagcgacgagcagctgaagtccggc acagcctctgtcgtgtgcctgctgaacaacttctacccccgcgaggccaaagtg cagtggaaggtggacaacgccctgcagagcggcaacagccaggaaagcgt gaccgagcaggacagcaaggactccacctacagcctgagcagcaccctgac	**SEQ ID NO: 86**

	actgagcaaggccgactacgagaagcacaaggtgtacgcctgcgaagtgacc caccagggcctgtctagccccgtgaccaagagcttcaaccggggcgagtgt	
Heavy chain B	gaggttagactggtggagtcaggaggggggcttgtgaagcccggtgggtctctccgc ctgagctgttctgcctccggctttgatttcgataacgcctggatgacctgggtcaggcag cctccaggtaagggactggagtgggtgggaagaatcacaggtccaggcgagggctg gtccgtggactacgcggaatctgttaaagggcggtttacaatctcaagggacaatacca agaataccttgtatttggagatgaacaacgtgagaactgaagacaccggatattacttct gtgccagaacaggcaaatactacgacttctggtggggctatccccctggcgaggaata ttttcaagactggggtcagggaacccttgttatcgtgtcctccgacaaaacccatacccca ggtgcacctgacacagagcggacccgaagtgcggaagcctggcacctctgtgaaggt gtcctgcaaggcccctggcaacaccctgaaaacctacgacctgcactgggtgcgcag cgtgccaggacagggactgcagtggatgggctggatcagccacgagggcgacaag aaagtgatcgtggaacggttcaaggccaaagtgaccatcgactgggacagaagcacc aacaccgcctacctgcagctgagcggcctgacctctggcgataccgccgtgtactact gcgccaagggcagcaagcaccggctgagagactacgccctgtacgacgatgacggc gccctgaactgggccgtggatgtggactacctgagcaacctggaattctggggccagg gcacagccgtgaccgtgtcatctgataagacccacaccgcttccaccaagggcccatc ggtcttcccctggcaccctcctccaagagcacctctgggggcacagcggccctggg ctgcctggtcaaggactacttccccgaaccggtgacggtgtcgtggaactcaggcgcc ctgaccagcggcgtgcacaccttcccggctgtcctacagtcctcaggactctactccct cagcagcgtggtgaccgtgccctccagcagcttgggcacccagacctacatctgcaac gtgaatcacaagcccagcaacaccaaggtggacaagaaagttgagcccaaatcttgtg acaaaactcacacatgcccaccgtgcccagcacctgaactcctgggggggaccgtcag tcttcctcttcccccaaaacccaaggacaccctcatgatctcccggaccccctgaggtca catgcgtggtggtggacgtgagccacgaagaccctgaggtcaagttcaactggtatgtt gacggcgtggaggtgcataatgccaagacaaagccgcgggaggagcagtacaaca gcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaa ggagtacaagtgcaaggtctccaacaaagccctcccagcccccatcgagaaaaccat ctccaaagccaaagggcagccccgagaaccacaggtgtacaccctgcccccatgcc gggatgagctgaccaagaatcaagtcagcctgtggtgcctggtaaaaggcttctatccc agcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaaga ccacgcctcccgtgctggactccgacggctccttcttcctctactcaaaactcaccgtgg acaagagcaggtggcagcaggggaacgtcttctcatgctccgtgatgcatgaggctct gcacaaccactacacgcagaagagcctctccctgtctccgggt	**SEQ ID NO: 87**
Light chain B	gacttcgtgctgacccagagccctcacagcctgagcgtgacacctggcgaga gcgccagcatcagctgcaagagcagccactccctgatccacggcgaccggaa caactacctggcttggtacgtgcagaagcccggcagatccccccagctgctga tctacctggccagcagcagagccagcggcgtgcccgatagattttctggcagc ggcagcgacaaggacttcaccctgaagatcagccgggtggaaaccgaggac gtgggcacctactactgtatgcagggcagagagagcccctggacctttggcca gggcaccaaggtggacatcaaggacaaaacccataccgcatccgaactgact caggaccctgccgtctctgtggcactgaagcagactgtgactattacttgccga ggcgactcactgcggagccactacgcttcctggtatcagaagaaacccggcca ggcacctgtgctgctgttctacggaaagaacaataggccatctggcatccccga ccgcttttctggcagtgcatcagggaaccgagccagtctgaccattaccggcgc ccaggctgaggacgaagccgattactattgcagctcccgggataagagcggct ccagactgagcgtgttcggaggaggaactaaactgaccgtcctcgataagacc catacccgtacggtggccgctcccagcgtgttcatcttcccacctagcgacgag cagctgaagtccggcacagcctctgtcgtgtgcctgctgaacaacttctacccc cgcgaggccaaagtgcagtggaaggtggacaacgccctgcagagcggcaa cagccaggaaagcgtgaccgagcaggacagcaaggactccacctacagcct gagcagcaccctgacactgagcaaggccgactacgagaagcacaaggtgta	**SEQ ID NO: 88**

	cgcctgcgaagtgacccaccagggcctgtctagccccgtgaccaagagcttca accggggcgagtgt	
Binding Protein 12 Amino Acid Sequences		
Heavy chain A	Rahlvqsgtamkkpgasvrvscqtsgytftahilfwfrqapgrglewvgwikpqy gavnfgggfrdrvtltrdvyreiaymdirglkpddtavyycardrsygdsswalda wgqgttvvvsaastkgpsvfplapsskstsggtaalgclvkdyfpepvtvswnsgal tsgvhtfpavlqssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkkvepkscd kthtcppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnw yvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykckvsnkalpapi ektiskakgqprepqvctlppsrdeltknqvslscavkgfypsdiavewesngqpe nnykttppvldsdgsfflvskltvdksrwqqgnvfscsvmhealhnhytqkslslsp g	**SEQ ID NO: 89**
Light chain A	yihvtqspsslsvsigdrvtincqtsqgvgsdlhwyqhkpgrapkllihhtssvedgv psrfsgsgfhtsfnltisdlqaddiatyycqvlqffgrgsrlhikrtvaapsvfifppsde qlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsstltls kadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO:90**
Heavy chain B	evrlvesggglvkpggslrlscsasgfdfdnawmtwvrqppgkglewvgri tgpgegwsvdyaesvkgrftisrdntkntlylemnnvrtedtgyyfcartgk yydfwwgyppgeeyfqdwgqgtlvivssdkthtqmqlqesgpglvkpse tlsltcsvsgasisdsywswirrspgkglewigyvhksgdtnyspslksrvnl sldtsknqvslslvaataadsgkyycartlhgrriygivafnewftyfymdvw gngtqvtvssdkthtastkgpsvfplapsskstsggtaalgclvkdyfpepvtv swnsgaltsgvhtfpavlqssglyslssvvtvpssslgtqtyicnvnhkpsntk vdkkvepkscdkthtcppcpapellggpsvflfppkpkdtlmisrtpevtcv vvdvshedpevkfnwyvdgvevhnaktkpreeqynstyrvvsvltvlhqd wlngkeykckvsnkalpapiektiskakgqprepqvytlppcrdeltknqv slwclvkgfypsdiavewesngqpennykttppvldsdgsfflyskltvdks rwqqgnvfscsvmhealhnhytqkslslspg	**SEQ ID NO: 91**
Light chain B	sdisvapgetariscgekslgsravqwyqhragqapsliiynnqdrpsgiperfsgsp dspfgttatltitsveagdeadyychiwdsrvptkwvfgggttltvldkthtaseltqdp avsvalkqtvtitcrgdslrshyaswyqkkpgqapvllfygknnrpsgipdrfsgsas gnrasltitgaqaedeadyycssrdksgsrlsvfgggtkltvldkthtrtvaapsvfifp psdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstysls stltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 92**
Binding Protein 12 Nucleotide Sequences		
Heavy chain A	agagcccacctggtgcagtctggcaccgccatgaagaaaccaggcgcctctgtgcgg gtgtcctgtcagacaagcggctacaccttcaccgcccacatcctgttctggttccggcag gcccctggcagaggactggaatgggtgggatggatcaagccccagtatggcgccgtg aacttcggcggaggcttccgggatagagtgaccctgacccgggacgtgtaccgcgag atcgcctacatggacatccggggcctgaagcccgatgacaccgccgtgtactactgcg ccagagacagaagctacggcgacagcagctgggctctggatgcttggggccagggc acaaccgtggtggtgtctgccgcctctacaaagggccccagcgtgttccctctggcccc tagcagcaagagcacatctggcggaacagccgccctgggctgcctcgtgaaggacta ctttcccgagcccgtgaccgtgtcctggaattctggcgccctgaccagcggcgtgcac acctttccagctgtgctgcagtccagcggcctgtacagcctgagcagcgtcgtgacagt gcccagcagctctctgggcacccagacctacatctgcaacgtgaaccacaagcccag caacaccaaggtggacaagaaggtggaacccaagagctgcgacaagacccacacct gtccccttgtcctgccccgaactgctgggaggcccttccgtgttcctgttcccccaa agcccaaggacaccctgatgatcagccggacccccgaagtgacctgcgtggtggtgg atgtgtcccacgaggaccctgaagtgaagttcaattggtacgtggacggcgtggaagt gcacaacgccaagaccaagccaagagaggaacagtacaacagcacctaccgggtg	**SEQ ID NO: 93**

	gtgtccgtgctgaccgtgctgcaccaggactggctgaacggcaaagagtacaagtgc aaggtgtccaacaaggccctgcctgcccccatcgagaaaaccatcagcaaggccaag ggccagccccgcgaaccccaggtgtgcacactgcccccaagcagggacgagctga ccaagaaccaggtgtccctgagctgtgccgtgaaaggcttctacccctccgatatcgcc gtggaatgggagagcaacggccagcccgagaacaactacaagaccacccccccctgt gctggacagcgacggctcattcttcctggtgtccaagctgacagtggacaagtcccggt ggcagcagggcaacgtgttcagctgctccgtgatgcacgaggccctgcacaaccact acacccagaagtccctgagcctgagccccggcaag	
Light chain A	tacatccacgtgacccagagccccagcagcctgtccgtgtccatcggcgacag agtgaccatcaactgccagacctctcagggcgtgggcagcgacctgcactggt atcagcacaagcctggcagagcccccaagctgctgatccaccacacaagcag cgtggaagatggcgtgcccagcagattttccggcagcggcttccacaccagct tcaacctgaccatcagcgatctgcaggccgacgacattgccacctactattgtca ggtgctgcagttcttcggcagaggcagcagactgcacatcaagcgtacggtgg ccgctcccagcgtgttcatcttcccacctagcgacgagcagctgaagtccggc acagcctctgtcgtgtgcctgctgaacaacttctacccccgcgaggccaaagtg cagtggaaggtggacaacgccctgcagagcggcaacagccaggaaagcgt gaccgagcaggacagcaaggactccacctacagcctgagcagcaccctgac actgagcaaggccgactacgagaagcacaaggtgtacgcctgcgaagtgacc caccagggcctgtctagccccgtgaccaagagcttcaaccggggcgagtgt	**SEQ ID NO: 94**
Heavy chain B	gaggttagactggtggagtcaggaggggggcttgtgaagcccggtgggtctctccgc ctgagctgttctgcctccggctttgatttcgataacgcctggatgacctgggtcaggcag cctccaggtaagggactggagtgggtgggaagaatcacaggtccaggcgagggctg gtccgtggactacgcggaatctgttaaagggcggtttacaatctcaagggacaatacca agaataccttgtatttggagatgaacaacgtgagaactgaagacaccggatattacttct gtgccagaacaggcaaatactacgacttctggtggggctatccccctggcgaggaata ttttcaagactggggtcagggaacccttgttatcgtgtcctccgacaaaacccatacccca gatgcagctgcaggagagcggccctggactcgtgaagcccagcgagaccctgagcc tgacatgcagcgtgagcggcgccagcatcagcgacagctactggagctggatcagga ggagccctggcaagggcctggagtggatcggctacgtgcacaagagcggcgacacc aactacagcccctccctgaagtccagggtgaacctgtccctggacaccagcaagaacc aggtgagcctgtccctggtggctgccacagctgctgacagcggcaagtactactgtgc caggaccctgcacggcaggaggatctacggcatcgtggccttcaacgagtggttcacc tacttctacatggacgtgtggggcaacggcacccaggtgaccgtgagctccgataaga cccacaccgcttccaccaagggcccatcggtcttcccccctggcaccctcctccaagag cacctctgggggcacagcggccctgggctgcctggtcaaggactacttccccgaacc ggtgacggtgtcgtggaactcaggcgccctgaccagcggcgtgcacaccttcccggc tgtcctacagtcctcaggactctactccctcagcagcgtggtgaccgtgccctccagca gcttgggcacccagacctacatctgcaacgtgaatcacaagcccagcaacaccaaggt ggacaagaaagttgagcccaaatcttgtgacaaaactcacacatgcccaccgtgccca gcacctgaactcctgggggggaccgtcagtcttcctcttcccccaaaacccaaggaca ccctcatgatctcccggaccccctgaggtcacatgcgtggtggtggacgtgagccacga agaccctgaggtcaagttcaactggtatgttgacggcgtggaggtgcataatgccaaga caaagccgcgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcacc gtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaa gccctcccagccccccatcgagaaaaccatctccaaagccaaagggcagccccgaga accacaggtgtacaccctgcccccatgccgggatgagctgaccaagaatcaagtcag cctgtggtgcctggtaaaaggcttctatcccagcgacatcgccgtggagtgggagagc aatgggcagccggagaacaactacaagaccacgcctcccgtgctggactccgacgg ctccttcttcctctactcaaaactcaccgtggacaagagcaggtggcagcaggggaac gtcttctcatgctccgtgatgcatgaggctctgcacaaccactacacgcagaagagcct ctccctgtctccgggt	**SEQ ID NO: 95**

Light chain B	tccgacatcagcgtggcccccggagagacagccaggatctcctgcggcgag aagagcctgggaagcagggctgtgcagtggtaccaacacagggccggacag gctcccagcctgatcatctacaacaaccaggacaggcccagcggcatccctga gaggttcagcggaagccccgacagccccttcggaaccacagccaccctgacc atcacaagcgtggaagccggcgacgaggccgactactactgccacatctggg acagcagggtgcccaccaagtgggtgtttggcggcggcaccaccctgaccgt gctggacaaaacccataccgcatccgaactgactcaggaccctgccgtctctgt ggcactgaagcagactgtgactattacttgccgaggcgactcactgcggagcc actacgcttcctggtatcagaagaaacccggccaggcacctgtgctgctgttcta cggaaagaacaataggccatctggcatccccgaccgcttttctggcagtgcatc agggaaccgagccagtctgaccattaccggcgcccaggctgaggacgaagc cgattactattgcagctcccgggataagagcggctccagactgagcgtgttcgg aggaggaactaaactgaccgtcctcgataagacccatacccgtacggtggccg ctcccagcgtgttcatcttcccacctagcgacgagcagctgaagtccggcaca gcctctgtcgtgtgcctgctgaacaacttctacccccgcgaggccaaagtgcag tggaaggtggacaacgccctgcagagcggcaacagccaggaaagcgtgacc gagcaggacagcaaggactccacctacagcctgagcagcaccctgacactga gcaaggccgactacgagaagcacaaggtgtacgcctgcgaagtgacccacc agggcctgtctagccccgtgaccaagagcttcaaccggggcgagtgt	**SEQ ID NO: 96**
Binding Protein 13 Amino Acid Sequences		
Heavy chain A	qvhltqsgpevrkpgtsvkvsckapgntlktydlhwvrsvpgqglqwmgwishe gdkkviverfkakvtidwdrstntaylqlsgltsgdtavyycakgskhrlrdyalydd dgalnwavdvdylsnlefwgqgtavtvssastkgpsvfplapsskstsggtaalgcl vkdyfpepvtvswnsgaltsgvhtfpavlqssglyslssvvtvpssslgtqtyicnvn hkpsntkvdkkvepkscdkthtcppcpapellggpsvflfppkpkdtlmisrtpevt cvvvdvshedpevkfnwyvdgvevhnaktkpreeqynstyrvvsvltvlhqdwl ngkeykckvsnkalpapiektiskakgqprepqvctlppsrdeltknqvslscavkg fypsdiavewesngqpennykttppvldsdgsfflvskltvdksrwqqgnvfscsv mhealhnhytqkslslspg	**SEQ ID NO: 97**
Light chain A	dfvltqsphslsvtpgesasisckssshslihgdrnnylawyvqkpgrspqlliylassr asgvpdrfsgsgsdkdftlkisrvetedvgtyycmqgrespwtfgqgtkvdikrtva apsvfifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqd skdstyslsstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 98**
Heavy chain B	evrlvesggglvkpggslrlscsasgfdfdnawmtwvrqppgkglewvgr itgpgegwsvdyaesvkgrftisrdntkntlylemnnvrtedtgyyfcartgk yydfwwgyppgeeyfqdwgqgtlvivssdkthtqmqlqesgpglvkpse tlsltcsvsgasisdsywswirrspgkglewigyvhksgdtnyspslksrvnl sldtsknqvslslvaataadsgkyycartlhgrriygivafnewftyfymdv wgngtqvtvssdkthtastkgpsvfplapsskstsggtaalgclvkdyfpepv tvswnsgaltsgvhtfpavlqssglyslssvvtvpssslgtqtyicnvnhkpsn tkvdkkvepkscdkthtcppcpapellggpsvflfppkpkdtlmisrtpevt cvvvdvshedpevkfnwyvdgvevhnaktkpreeqynstyrvvsvltvlh qdwlngkeykckvsnkalpapiektiskakgqprepqvytlppcrdeltkn qvslwclvkgfypsdiavewesngqpennykttppvldsdgsfflyskltv dksrwqqgnvfscsvmhealhnhytqkslslspg	**SEQ ID NO: 99**
Light chain B	sdisvapgetariscgekslgsravqwyqhragqapsliiynnqdrpsgiperfsgsp dspfgttatltitsveagdeadyychiwdsrvptkwvfgggttltvldkthtaseltqd pavsvalkqtvtitcrgdslrshyaswyqkkpgqapvllfygknnrpsgipdrfsgs asgnrasltitgaqaedeadyycssrdksgsrlsvfgggtkltvldkthtrtvaapsvfif ppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstys	**SEQ ID NO: 100**

	lsstltlskadyekhkvyacevthqglsspvtksfnrgec	
Binding Protein 13 Nucleotide Sequences		
Heavy chain A	caggtgcacctgacacagagcggacccgaagtgcggaagcctggcacctctgtgaa ggtgtcctgcaaggcccctggcaacaccctgaaaacctacgacctgcactgggtgcg cagcgtgccaggacagggactgcagtggatgggctggatcagccacgagggcgac aagaaagtgatcgtggaacggttcaaggccaaagtgaccatcgactgggacagaagc accaacaccgcctacctgcagctgagcggcctgacctctggcgataccgccgtgtact actgcgccaagggcagcaagcaccggctgagagactacgccctgtacgacgatgac ggcgccctgaactgggccgtggatgtggactacctgagcaacctggaattctggggc cagggcacagccgtgaccgtgtcatctgcttcgaccaagggccccagcgtgttccctc tggcccctagcagcaagagcacatctggcggaacagccgccctgggctgcctcgtga aggactactttcccgagcccgtgaccgtgtcctggaattctggcgccctgaccagcgg cgtgcacaccttccagctgtgctgcagtccagcggcctgtacagcctgagcagcgtc gtgacagtgcccagcagctctctgggcacccagacctacatctgcaacgtgaaccaca agcccagcaacaccaaggtggacaagaaggtggaacccaagagctgcgacaagac ccacacctgtccccttgtcctgcccccgaactgctgggaggcccttccgtgttcctgtt ccccccaaagcccaaggacaccctgatgatcagccggaccccgaagtgacctgcg tggtggtggatgtgtcccacgaggaccctgaagtgaagttcaattggtacgtggacgg cgtggaagtgcacaacgccaagaccaagccaagagaggaacagtacaacagcacct accgggtggtgtccgtgctgaccgtgctgcaccaggactggctgaacggcaaagagt acaagtgcaaggtgtccaacaaggccctgcctgcccccatcgagaaaaccatcagca aggccaagggccagccccgcgaaccccaggtgtgcacactgcccccaagcaggga cgagctgaccaagaaccaggtgtccctgagctgtgccgtgaaaggcttctacccctcc gatatcgccgtggaatgggagagcaacggccagcccgagaacaactacaagaccac ccccccctgtgctggacagcgacggctcattcttcctggtgtccaagctgacagtggaca agtcccggtggcagcagggcaacgtgttcagctgctccgtgatgcacgaggccctgc acaaccactacacccagaagtccctgagcctgagccccggcaag	**SEQ ID NO: 101**
Light chain A	gacttcgtgctgacccagagccctcacagcctgagcgtgacacctggcgagagcgcc agcatcagctgcaagagcagccactccctgatccacggcgaccggaacaactacctg gcttggtacgtgcagaagcccggcagatccccccagctgctgatctacctggccagca gcagagccagcggcgtgcccgatagattttctggcagcggcagcgacaaggacttca ccctgaagatcagccgggtggaaaccgaggacgtgggcacctactactgtatgcagg gcagagagagcccctggacctttggccagggcaccaaggtggacatcaagcgtacg gtggccgctcccagcgtgttcatcttcccacctagcgacgagcagctgaagtccggca cagcctctgtcgtgtgcctgctgaacaacttctacccccgcgaggccaaagtgcagtg gaaggtggacaacgccctgcagagcggcaacagccaggaaagcgtgaccgagca ggacagcaaggactccacctacagcctgagcagcaccctgacactgagcaaggccg actacgagaagcacaaggtgtacgcctgcgaagtgacccaccagggcctgtctagcc ccgtgaccaagagcttcaaccggggcgagtgt	**SEQ ID NO: 102**
Heavy chain B	gaggttagactggtggagtcaggaggggggcttgtgaagcccggtgggtctctccgc ctgagctgttctgcctccggctttgatttcgataacgcctggatgacctgggtcaggcag cctccaggtaagggactggagtgggtgggaagaatcacaggtccaggcgagggctg gtccgtggactacgcggaatctgttaaagggcggtttacaatctcaagggacaataccа agaataccttgtatttggagatgaacaacgtgagaactgaagacaccggatattacttct gtgccagaacaggcaaatactacgacttctggtggggctatcccccctggcgaggaata ttttcaagactggggtcagggaacccttgttatcgtgtcctccgacaaaacccatаccca gatgcagctgcaggagagcggccctggactcgtgaagcccagcgagaccctgagcc tgacatgcagcgtgagcggcgccagcatcagcgacagctactggagctggatcagg aggagccctggcaagggcctggagtggatcggctacgtgcacaagagcggcgaca ccaactacagcccctccctgaagtccagggtgaacctgtccctggacaccagcaaga accaggtgagcctgtccctggtggctgccacagctgctgacagcggcaagtactactg tgccaggaccctgcacggcaggaggatctacggcatcgtggccttcaacgagtggttc	**SEQ ID NO: 103**

	acctacttctacatggacgtgtggggcaacggcacccaggtgaccgtgagctccgata agacccacaccgcttccaccaagggcccatcggtcttccccctggcaccctcctccaa gagcacctctgggggcacagcggccctgggctgcctggtcaaggactacttccccga accggtgacggtgtcgtggaactcaggcgccctgaccagcggcgtgcacaccttccc ggctgtcctacagtcctcaggactctactccctcagcagcgtggtgaccgtgccctcca gcagcttgggcacccagacctacatctgcaacgtgaatcacaagcccagcaacacca aggtggacaagaaagttgagcccaaatcttgtgacaaaactcacacatgcccaccgtg cccagcacctgaactcctgggggggaccgtcagtcttcctcttcccccaaaacccaag gacaccctcatgatctcccggaccctgaggtcacatgcgtggtggtggacgtgagcc acgaagaccctgaggtcaagttcaactggtatgttgacggcgtggaggtgcataatgc caagacaaagccgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcc tcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaa caaagccctcccagcccccatcgagaaaaccatctccaaagccaaagggcagcccc gagaaccacaggtgtacaccctgcccccatgccgggatgagctgaccaagaatcaag tcagcctgtggtgcctggtaaaaggcttctatcccagcgacatcgccgtggagtggga gagcaatgggcagccggagaacaactacaagaccacgcctcccgtgctggactccg acggctccttcttcctctactcaaaactcaccgtggacaagagcaggtggcagcaggg gaacgtcttctcatgctccgtgatgcatgaggctctgcacaaccactacacgcagaaga gcctctccctgtctccgggt	
Light chain B	tccgacatcagcgtggccccggagagacagccaggatctcctgcggcgag aagagcctgggaagcagggctgtgcagtggtaccaacacagggccggacag gctcccagcctgatcatctacaacaaccaggacaggcccagcggcatccctg agaggttcagcggaagccccgacagccccttcggaaccacagccaccctga ccatcacaagcgtggaagccggcgacgaggccgactactactgccacatctg ggacagcagggtgcccaccaagtgggtgtttggcggcggcaccaccctgac cgtgctggacaaaacccataccgcatccgaactgactcaggaccctgccgtct ctgtggcactgaagcagactgtgactattacttgccgaggcgactcactgcgga gccactacgcttcctggtatcagaagaaacccggccaggcacctgtgctgctgt tctacggaaagaacaataggccatctggcatccccgaccgcttttctggcagtg catcagggaaccgagccagtctgaccattaccggcgcccaggctgaggacg aagccgattactattgcagctcccgggataagagcggctccagactgagcgtg ttcggaggaggaactaaactgaccgtcctcgataagacccatacccgtacggt ggccgctcccagcgtgttcatcttcccacctagcgacgagcagctgaagtccg gcacagcctctgtcgtgtgcctgctgaacaacttctacccccgcgaggccaaa gtgcagtggaaggtggacaacgccctgcagagcggcaacagccaggaaag cgtgaccgagcaggacagcaaggactccacctacagcctgagcagcaccct gacactgagcaaggccgactacgagaagcacaaggtgtacgcctgcgaagt gacccaccagggcctgtctagccccgtgaccaagagcttcaaccggggcga gtgt	**SEQ ID NO: 104**
Binding Protein 14 Amino Acid Sequences		
Heavy chain A	Rahlvqsgtamkkpgasvrvscqtsgytftahilfwfrqapgrglewvgwikpqy gavnfgggfrdrvtltrdvyreiaymdirglkpddtavyycardrsygdsswalda wgqgttvvvsaastkgpsvfplapsskstsggtaalgclvkdyfpepvtvswnsgal tsgvhtfpavlqssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkkvepkscd kthtcppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnw yvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykckvsnkalpapi ektiskakgqprepqvctlppsrdeltknqvslscavkgfypsdiavewesngqpe nnykttppvldsdgsfflvskltvdksrwqqgnvfscsvmhealhnhytqkslslsp g	**SEQ ID NO: 105**
Light chain A	yihvtqspsslsvsigdrvtincqtsqgvgsdlhwyqhkpgrapkllihhtssvedg vpsrfsgsgfhtsfnltisdlqaddiatyycqvlqffgrgsrlhikrtvaapsvfifppsd	**SEQ ID NO: 106**

	eqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsstlt lskadyekhkvyacevthqglsspvtksfnrgec	
Heavy chain B	Qvhltqsgpevrkpgtsvkvsckapgntlktydlhwvrsvpgqglqwmg wishegdkkviverfkakvtidwdrstntaylqlsgltsgdtavyycakgsk hrlrdyalydddgalnwavdvdylsnlefwgqgtavtvssdkthtevrlves ggglvkpggslrlscsasgfdfdnawmtwvrqppgkglewvgritgpgeg wsvdyaesvkgrftisrdntkntlylemnnvrtedtgyyfcartgkyydfw wgyppgeeyfqdwgqgtlvivssdkthtastkgpsvfplapsskstsggtaa lgclvkdyfpepvtvswnsgaltsgvhtfpavlqssglyslssvvtvpssslgt qtyicnvnhkpsntkvdkkvepkscdkthtcppcpapellggpsvflfppk pkdtlmisrtpevtcvvvdvshedpevkfnwyvdgvevhnaktkpreeq ynstyrvvsvltvlhqdwlngkeykckvsnkalpapiektiskakgqprep qvytlppcrdeltknqvslwclvkgfypsdiavewesngqpennykttppv ldsdgsfflyskltvdksrwqqgnvfscsvmhealhnhytqkslslspg	**SEQ ID NO: 107**
Light chain B	aseltqdpavsvalkqtvtitcrgdslrshyaswyqkkpgqapvllfygknnrpsgi pdrfsgsasgnrasltitgaqaedeadyycssrdksgsrlsvfgggtkltvldkthtdfv ltqsphslsvtpgesasisckssshslihgdrnnylawyvqkpgrspqlliylassrasg vpdrfsgsgsdkdftlkisrvetedvgtyycmqgrespwtfgqgtkvdikdkthtrt vaapsvfifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvte qdskdstyslsstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 108**
Binding Protein 14 Nucleotide Sequences		
Heavy chain A	agagcccacctggtgcagtctggcaccgccatgaagaaaccaggcgcctctgtgcgg gtgtcctgtcagacaagcggctacaccttcaccgcccacatcctgttctggttccggca ggcccctggcagaggactggaatgggtgggatggatcaagccccagtatggcgccg tgaacttcggcggaggcttccgggatagagtgaccctgacccgggacgtgtaccgcg agatcgcctacatggacatccggggcctgaagcccgatgacaccgccgtgtactactg cgccagagacagaagctacggcgacagcagctgggctctggatgcttggggccagg gcacaaccgtggtggtgtctgccgcctctacaaagggccccagcgtgttccctctggc ccctagcagcaagagcacatctggcggaacagccgccctgggctgcctcgtgaagg actactttcccgagcccgtgaccgtgtcctggaattctggcgccctgaccagcggcgtg cacacctttccagctgtgctgcagtccagcggcctgtacagcctgagcagcgtcgtga cagtgcccagcagctctctgggcacccagacctacatctgcaacgtgaaccacaagc ccagcaacaccaaggtggacaagaaggtggaacccaagagctgcgacaagaccca cacctgtccccccttgtcctgccccgaactgctgggaggcccttccgtgttcctgttccc cccaaagcccaaggacaccctgatgatcagccggaccccgaagtgacctgcgtggt ggtggatgtgtcccacgaggaccctgaagtgaagttcaattggtacgtggacggcgtg gaagtgcacaacgccaagaccaagccaagagaggaacagtacaacagcacctacc gggtggtgtccgtgctgaccgtgctgcaccaggactggctgaacggcaaagagtaca agtgcaaggtgtccaacaaggccctgcctgcccccatcgagaaaaccatcagcaagg ccaagggccagccccgcgaaccccaggtgtgcacactgcccccaagcagggacga gctgaccaagaaccaggtgtccctgagctgtgccgtgaaaggcttctacccctccgat atcgccgtggaatgggagagcaacggccagcccgagaacaactacaagaccaccc cccctgtgctggacagcgacggctcattcttcctggtgtccaagctgacagtggacaag tcccggtggcagcagggcaacgtgttcagctgctccgtgatgcacgaggccctgcac aaccactacacccagaagtccctgagcctgagccccggcaag	**SEQ ID NO: 109**
Light chain A	tacatccacgtgacccagagccccagcagcctgtccgtgtccatcggcgacag agtgaccatcaactgccagacctctcagggcgtgggcagcgacctgcactggt atcagcacaagcctggcagagcccccaagctgctgatccaccacacaagcag cgtggaagatggcgtgcccagcagattttccggcagcggcttccacaccagct tcaacctgaccatcagcgatctgcaggccgacgacattgccacctactattgtc aggtgctgcagttcttcggcagaggcagcagactgcacatcaagcgtacggtg	**SEQ ID NO: 110**

	gccgctcccagcgtgttcatcttcccacctagcgacgagcagctgaagtccgg cacagcctctgtcgtgtgcctgctgaacaacttctacccccgcgaggccaaagt gcagtggaaggtggacaacgccctgcagagcggcaacagccaggaaagcg tgaccgagcaggacagcaaggactccacctacagcctgagcagcaccctga cactgagcaaggccgactacgagaagcacaaggtgtacgcctgcgaagtga cccaccagggcctgtctagccccgtgaccaagagcttcaaccggggcgagtg t	
Heavy chain B	caggtgcacctgacacagagcggacccgaagtgcggaagcctggcacctctgtgaa ggtgtcctgcaaggcccctggcaacaccctgaaaacctacgacctgcactgggtgcg cagcgtgccaggacagggactgcagtggatgggctggatcagccacgagggcgac aagaaagtgatcgtggaacggttcaaggccaaagtgaccatcgactgggacagaagc accaacaccgcctacctgcagctgagcggcctgacctctggcgataccgccgtgtact actgcgccaagggcagcaagcaccggctgagagactacgccctgtacgacgatgac ggcgccctgaactgggccgtggatgtggactacctgagcaacctggaattctggggc cagggcacagccgtgaccgtgtcatctgacaaaacccataccgaggttagactggtg gagtcaggaggggggcttgtgaagcccggtgggtctctccgcctgagctgttctgcct ccggctttgatttcgataacgcctggatgacctgggtcaggcagcctccaggtaaggg actggagtgggtgggaagaatcacaggtccaggcgagggctggtccgtggactacg cggaatctgttaaagggcggtttacaatctcaagggacaataccaagaataccttgtattt ggagatgaacaacgtgagaactgaagacaccggatattacttctgtgccagaacaggc aaatactacgacttctggtggggctatcccctggcgaggaatattttcaagactggggt cagggaacccttgttatcgtgtcctccgataagacccacaccgcttccaccaagggcc catcggtcttcccctggcaccctcctccaagagcacctctgggggcacagcggccct gggctgcctggtcaaggactacttccccgaaccggtgacggtgtcgtggaactcagg cgccctgaccagcggcgtgcacaccttcccggctgtcctacagtcctcaggactctact ccctcagcagcgtggtgaccgtgccctccagcagcttgggcacccagacctacatctg caacgtgaatcacaagcccagcaacaccaaggtggacaagaaagttgagcccaaatc ttgtgacaaaactcacacatgcccaccgtgcccagcacctgaactcctgggggggacc gtcagtcttcctcttcccccaaaacccaaggacaccctcatgatctcccggaccccctg aggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtcaagttcaact ggtatgttgacggcgtggaggtgcataatgccaagacaaagccgcgggaggagcag tacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctga atggcaaggagtacaagtgcaaggtctccaacaaagccctcccagccccatcgaga aaaccatctccaaagccaaagggcagccccgagaaccacaggtgtacaccctgccc ccatgccgggatgagctgaccaagaatcaagtcagcctgtggtgcctggtaaaaggct tctatcccagcgacatcgccgtggagtgggagagcaatgggcagccggagaacaac tacaagaccacgcctcccgtgctggactccgacggctccttcttcctctactcaaaactc accgtggacaagagcaggtggcagcaggggaacgtcttctcatgctccgtgatgcat gaggctctgcacaaccactacacgcagaagagcctctccctgtctccgggt	**SEQ ID NO: 111**
Light chain B	gcatccgaactgactcaggaccctgccgtctctgtggcactgaagcagactgt gactattacttgccgaggcgactcactgcggagccactacgcttcctggtatca gaagaaacccggccaggcacctgtgctgctgttctacggaaagaacaatagg ccatctggcatccccgaccgcttttctggcagtgcatcagggaaccgagccagt ctgaccattaccggcgcccaggctgaggacgaagccgattactattgcagctc ccgggataagagcggctccagactgagcgtgttcggaggaggaactaaactg accgtcctcgacaaaacccataccgacttcgtgctgacccagagccctcacag cctgagcgtgacacctggcgagagcgccagcatcagctgcaagagcagcca ctccctgatccacggcgaccggaacaactacctggcttggtacgtgcagaagc ccggcagatccccccagctgctgatctacctggccagcagcagagccagcgg cgtgcccgatagattttctggcagcggcagcgacaaggacttcaccctgaaga tcagccgggtggaaaccgaggacgtgggcacctactactgtatgcagggcag agagagcccctggacctttggccagggcaccaaggtggacatcaaggataag	**SEQ ID NO: 112**

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Binding Protein 15 Amino Acid Sequences		
Heavy chain A	qvhltqsgpevrkpgtsvkvsckapgntlktydlhwvrsvpgqglqwmgwishe gdkkviverfkakvtidwdrstntaylqlsgltsgdtavyycakgskhrlrdyalydd dgalnwavdvdylsnlefwgqgtavtvssastkgpsvfplapsskstsggtaalgcl vkdyfpepvtvswnsgaltsgvhtfpavlqssglyslssvvtvpssslgtqtyicnvn hkpsntkvdkkvepkscdkthtcppcpapellggpsvflfppkpkdtlmisrtpevt cvvvdvshedpevkfnwyvdgvevhnaktkpreeqynstyrvvsvltvlhqdwl ngkeykckvsnkalpapiektiskakgqprepqvctlppsrdeltknqvslscavkg fypsdiavewesngqpennykttppvldsdgsfflvskltvdksrwqqgnvfscsv mhealhnhytqkslslspg	**SEQ ID NO: 113**
Light chain A	dfvltqsphslsvtpgesasisckssshslihgdrnnylawyvqkpgrspqlliylassr asgvpdrfsgsgsdkdftlkisrvetedvgtyycmqgrespwtfgqgtkvdikrtva apsvfifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqds kdstyslsstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 114**
Heavy chain B	Evrlvesggglvkpggslrlscsasgfdfdnawmtwvrqppgkglewvgr itgpgegwsvdyaesvkgrftisrdntkntlylemnnvrtedtgyyfcartgk yydfwsgyppgeeyfqdwgqgtlvivssdkthtqmqlqesgpglvkpset lsltcsvsgasisdsywswirrspgkglewigyvhksgdtnyspslksrvnls ldtsknqvslslvaataadsgkyycartlhgrriygivafnewftyfymdvw gngtqvtvssdkthtastkgpsvfplapsskstsggtaalgclvkdyfpepvtv swnsgaltsgvhtfpavlqssglyslssvvtvpssslgtqtyicnvnhkpsntk vdkkvepkscdkthtcppcpapellggpsvflfppkpkdtlmisrtpevtcv vvdvshedpevkfnwyvdgvevhnaktkpreeqynstyrvvsvltvlhqd wlngkeykckvsnkalpapiektiskakgqprepqvytlppcrdeltknqv slwclvkgfypsdiavewesngqpennykttppvldsdgsfflyskltvdks rwqqgnvfscsvmhealhnhytqkslslspg	**SEQ ID NO: 115**
Light chain B	sdisvapgetariscgekslgsravqwyqhragqapsliiynnqdrpsgiperfsgsp dspfgttatltitsveagdeadyychiwdsrvptkwvfgggttltvldkthtaseltqdp avsvalkqtvtitcrgdslrshyaswyqkkpgqapvllfygknnrpsgipdrfsgsas gnrasltitgaqaedeadyycssrdksgsrlsvfgggtkltvldkthtrtvaapsvfifp psdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstysls stltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 116**
Binding Protein 15 Nucleotide Sequences		
Heavy chain A	caggtgcacctgacacagagcggacccgaagtgcggaagcctggcacctctgtgaa ggtgtcctgcaaggcccctggcaacaccctgaaaacctacgacctgcactgggtgcg cagcgtgccaggacagggactgcagtggatgggctggatcagccacgagggcgac aagaaagtgatcgtggaacggttcaaggccaaagtgaccatcgactgggacagaagc accaacaccgcctacctgcagctgagcggcctgacctctggcgataccgccgtgtact actgcgccaagggcagcaagcaccggctgagagactacgccctgtacgacgatgac ggcgccctgaactgggccgtggatgtggactacctgagcaacctggaattctggggcc agggcacagccgtgaccgtgtcatctgcttcgaccaagggccccagcgtgttccctct ggcccctagcagcaagagcacatctggcggaacagccgccctgggctgcctcgtga aggactactttcccgagcccgtgaccgtgtcctggaattctggcgccctgaccagcgg cgtgcacaccttccagctgtgctgcagtccagcggcctgtacagcctgagcagcgtc	**SEQ ID NO: 117**

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Light chain A	gacttcgtgctgacccagagccctcacagcctgagcgtgacacctggcgagagcgcc agcatcagctgcaagagcagccactccctgatccacggcgaccggaacaactacctg gcttggtacgtgcagaagcccggcagatccccccagctgctgatctacctggccagca gcagagccagcggcgtgcccgatagattttctggcagcggcagcgacaaggacttca ccctgaagatcagccgggtggaaaccgaggacgtgggcacctactactgtatgcagg gcagagagagccccctggacctttggccagggcaccaaggtggacatcaagcgtacg gtggccgctcccagcgtgttcatcttcccacctagcgacgagcagctgaagtccggca cagcctctgtcgtgtgcctgctgaacaacttctacccccgcgaggccaaagtgcagtgg aaggtggacaacgccctgcagagcggcaacagccaggaaagcgtgaccgagcagg acagcaaggactccacctacagcctgagcagcaccctgacactgagcaaggccgact acgagaagcacaaggtgtacgcctgcgaagtgacccaccagggcctgtctagccccg tgaccaagagcttcaaccggggcgagtgt	**SEQ ID NO: 118**
Heavy chain B	gaggttagactggtggagtcaggaggggggcttgtgaagcccggtgggtctctccgc ctgagctgttctgcctccggctttgatttcgataacgcctggatgacctgggtcaggcag cctccaggtaagggactggagtgggtgggaagaatcacaggtccaggcgagggctg gtccgtggactacgcggaatctgttaaagggcggtttacaatctcaagggacaatacca agaataccttgtatttggagatgaacaacgtgagaactgaagacaccggatattacttct gtgccagaacaggcaaatactacgacttctggtccggctatcccctggcgaggaatat tttcaagactggggtcagggaacccttgttatcgtgtcctccgacaaaacccatacccag atgcagctgcaggagagcggccctggactcgtgaagcccagcgagaccctgagcct gacatgcagcgtgagcggcgccagcatcagcgacagctactggagctggatcagga ggagccctggcaagggcctggagtggatcggctacgtgcacaagagcggcgacacc aactacagccctccctgaagtccagggtgaacctgtccctggacaccagcaagaacc aggtgagcctgtccctggtggctgccacagctgctgacagcggcaagtactactgtgc caggaccctgcacggcaggaggatctacggcatcgtggccttcaacgagtggttcacc tacttctacatggacgtgtggggcaacggcacccaggtgaccgtgagctccgataaga cccacaccgcttccaccaagggcccatcggtcttcccccctggcaccctcctccaagag cacctctgggggcacagcggccctgggctgcctggtcaaggactacttccccgaacc ggtgacggtgtcgtggaactcaggcgccctgaccagcggcgtgcacaccttcccggc tgtcctacagtcctcaggactctactccctcagcagcgtggtgaccgtgccctccagca gcttgggcacccagacctacatctgcaacgtgaatcacaagcccagcaacaccaaggt ggacaagaaagttgagcccaaatcttgtgacaaaactcacacatgcccaccgtgccca gcacctgaactcctgggggggaccgtcagtcttcctcttcccccaaaacccaaggaca ccctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtgagccacga agaccctgaggtcaagttcaactggtatgttgacggcgtggaggtgcataatgccaaga caaagccgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcacc gtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaa gccctcccagcccccatcgagaaaaccatctccaaagccaaagggcagccccgaga	**SEQ ID NO: 119**

	accacaggtgtacaccctgcccccatgccgggatgagctgaccaagaatcaagtcag cctgtggtgcctggtaaaaggcttctatcccagcgacatcgccgtggagtgggagagc aatgggcagccggagaacaactacaagaccacgcctcccgtgctggactccgacgg ctccttcttcctctactcaaaactcaccgtggacaagagcaggtggcagcaggggaac gtcttctcatgctccgtgatgcatgaggctctgcacaaccactacacgcagaagagcct ctccctgtctccgggt	
Light chain B	tccgacatcagcgtggccccccggagagacagccaggatctcctgcggcgag aagagcctgggaagcagggctgtgcagtggtaccaacacagggccggacag gctcccagcctgatcatctacaacaaccaggacaggcccagcggcatccctga gaggttcagcggaagccccgacagccccttcggaaccacagccaccctgacc atcacaagcgtggaagccggcgacgaggccgactactactgccacatctggg acagcagggtgcccaccaagtgggtgtttggcggcggcaccaccctgaccgt gctggacaaaacccataccgcatccgaactgactcaggaccctgccgtctctgt ggcactgaagcagactgtgactattacttgccgaggcgactcactgcggagcc actacgcttcctggtatcagaagaaacccggccaggcacctgtgctgctgttcta cggaaagaacaataggccatctggcatccccgaccgcttttctggcagtgcatc agggaaccgagccagtctgaccattaccggcgcccaggctgaggacgaagc cgattactattgcagctcccgggataagagcggctccagactgagcgtgttcgg aggaggaactaaactgaccgtcctcgataagacccatacccgtacggtggccg ctcccagcgtgttcatcttcccacctagcgacgagcagctgaagtccggcaca gcctctgtcgtgtgcctgctgaacaacttctacccccgcgaggccaaagtgcag tggaaggtggacaacgccctgcagagcggcaacagccaggaaagcgtgacc gagcaggacagcaaggactccacctacagcctgagcagcaccctgacactga gcaaggccgactacgagaagcacaaggtgtacgcctgcgaagtgacccacc agggcctgtctagccccgtgaccaagagcttcaaccggggcgagtgt	**SEQ ID NO: 120**
Binding Protein 16 Amino Acid Sequences		
Heavy chain A	Rahlvqsgtamkkpgasvrvscqtsgytftahilfwfrqapgrglewvgwikpqy gavnfgggfrdrvtltrdvyreiaymdirglkpddtavyycardrsygdsswalda wgqgttvvvsaastkgpsvfplapsskstsggtaalgclvkdyfpepvtvswnsgal tsgvhtfpavlqssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkkvepkscd kthtcppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnw yvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykckvsnkalpapi ektiskakgqprepqvctlppsrdeltknqvslscavkgfypsdiavewesngqpe nnykttppvldsdgsfflvskltvdksrwqqgnvfscsvmhealhnhytqkslslsp g	**SEQ ID NO: 121**
Light chain A	yihvtqspsslsvsigdrvtincqtsqgvgsdlhwyqhkpgrapkllihhtssvedgv psrfsgsgfhtsfnltisdlqaddiatyycqvlqffgrgsrlhikrtvaapsvfifppsde qlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsstltls kadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 122**
Heavy chain B	Evrlvesggglvkpggslrlscsasgfdfdnawmtwvrqppgkglewvgr itgpgegwsvdyaesvkgrftisrdntkntlylemnnvrtedtgyyfcartgk yydfwsgyppgeeyfqdwgqgtlvivssdkthtqmqlqesgpglvkpset lsltcsvsgasisdsywswirrspgkglewigyvhksgdtnyspslksrvnls ldtsknqvslslvaataadsgkyycartlhgrriygivafnewftyfymdvw gngtqvtvssdkthtastkgpsvfplapsskstsggtaalgclvkdyfpepvtv swnsgaltsgvhtfpavlqssglyslssvvtvpssslgtqtyicnvnhkpsntk vdkkvepkscdkthtcppcpapellggpsvflfppkpkdtlmisrtpevtcv vvdvshedpevkfnwyvdgvevhnaktkpreeqynstyrvvsvltvlhqd wlngkeykckvsnkalpapiektiskakgqprepqvytlppcrdeltknqv slwclvkgfypsdiavewesngqpennykttppvldsdgsfflyskltvdks	**SEQ ID NO: 123**

	rwqqgnvfscsvmhealhnhytqkslslspg	
Light chain B	sdisvapgetariscgekslgsravqwyqhragqapsliiynnqdrpsgiperfsgsp dspfgttatltitsveagdeadyychiwdsrvptkwvfgggttltvldkthtaseltqdp avsvalkqtvtitcrgdslrshyaswyqkkpgqapvllfygknnrpsgipdrfsgsas gnrasltitgaqaedeadyycssrdksgsrlsvfgggtkltvldkthtrtvaapsvfifp psdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstysls stltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 124**
Binding Protein 16 Nucleotide Sequences		
Heavy chain A	agagcccacctggtgcagtctggcaccgccatgaagaaaccaggcgcctctgtgcgg gtgtcctgtcagacaagcggctacaccttcaccgcccacatcctgttctggttccggcag gcccctggcagaggactggaatgggtgggatggatcaagccccagtatggcgccgtg aacttcggcggaggcttccgggatagagtgaccctgacccgggacgtgtaccgcgag atcgcctacatggacatccggggcctgaagcccgatgacaccgccgtgtactactgcg ccagagacagaagctacggcgacagcagctgggctctggatgcttggggccagggc acaaccgtggtggtgtctgccgcctctacaaagggccccagcgtgttccctctggcccc tagcagcaagagcacatctggcggaacagccgccctgggctgcctcgtgaaggacta ctttcccgagcccgtgaccgtgtcctggaattctggcgccctgaccagcggcgtgcac acctttccagctgtgctgcagtccagcggcctgtacagcctgagcagcgtcgtgacagt gcccagcagctctctgggcacccagacctacatctgcaacgtgaaccacaagcccag caacaccaaggtggacaagaaggtggaacccaagagctgcgacaagacccacacct gtccccttgtcctgccccgaactgctgggaggcccttccgtgttcctgttcccccaa agcccaaggacaccctgatgatcagccggacccccgaagtgacctgcgtggtggtgg atgtgtcccacgaggaccctgaagtgaagttcaattggtacgtggacggcgtggaagt gcacaacgccaagaccaagccaagagaggaacagtacaacagcacctaccgggtg gtgtccgtgctgaccgtgctgcaccaggactggctgaacggcaaagagtacaagtgc aaggtgtccaacaaggccctgcctgcccccatcgagaaaaccatcagcaaggccaag ggccagccccgcgaaccccaggtgtgcacactgcccccaagcagggacgagctga ccaagaaccaggtgtccctgagctgtgccgtgaaaggcttctacccctccgatatcgcc gtggaatgggagagcaacggccagcccgagaacaactacaagaccacccccctgt gctggacagcgacggctcattcttcctggtgtccaagctgacagtggacaagtcccggt ggcagcagggcaacgtgttcagctgctccgtgatgcacgaggccctgcacaaccact acacccagaagtccctgagcctgagccccggcaag	**SEQ ID NO: 125**
Light chain A	tacatccacgtgacccagagccccagcagcctgtccgtgtccatcggcgacag agtgaccatcaactgccagacctctcagggcgtgggcagcgacctgcactggt atcagcacaagcctggcagagcccccaagctgctgatccaccacacaagcag cgtggaagatggcgtgcccagcagattttccggcagcggcttccacaccagct tcaacctgaccatcagcgatctgcaggccgacgacattgccacctactattgtca ggtgctgcagttcttcggcagaggcagcagactgcacatcaagcgtacggtgg ccgctcccagcgtgttcatcttcccacctagcgacgagcagctgaagtccggc acagcctctgtcgtgtgcctgctgaacaacttctacccccgcgaggccaaagtg cagtggaaggtggacaacgccctgcagagcggcaacagccaggaaagcgt gaccgagcaggacagcaaggactccacctacagcctgagcagcaccctgac actgagcaaggccgactacgagaagcacaaggtgtacgcctgcgaagtgacc caccagggcctgtctagccccgtgaccaagagcttcaaccggggcgagtgt	**SEQ ID NO: 126**
Heavy chain B	gaggttagactggtggagtcaggaggggggcttgtgaagcccggtgggtctctccgc ctgagctgttctgcctccggctttgatttcgataacgcctggatgacctgggtcaggcag cctccaggtaagggactggagtgggtgggaagaatcacaggtccaggcgagggctg gtccgtggactacgcggaatctgttaaagggcggtttacaatctcaagggacaatacca agaataccttgtatttggagatgaacaacgtgagaactgaagacaccggatattacttct gtgccagaacaggcaaatactacgacttctggtccggctatcccctggcgaggaatat tttcaagactggggtcagggaacccttgttatcgtgtcctccgacaaaacccatacccag atgcagctgcaggagagcggccctggactcgtgaagcccagcgagaccctgagcct	**SEQ ID NO: 127**

	gacatgcagcgtgagcggcgccagcatcagcgacagctactggagctggatcagga ggagccctggcaagggcctggagtggatcggctacgtgcacaagagcggcgacacc aactacagcccctccctgaagtccagggtgaacctgtccctggacaccagcaagaacc aggtgagcctgtccctggtggctgccacagctgctgacagcggcaagtactactgtgc caggaccctgcacggcaggaggatctacggcatcgtggccttcaacgagtggttcacc tacttctacatggacgtgtggggcaacggcacccaggtgaccgtgagctccgataaga cccacaccgcttccaccaagggcccatcggtcttcccctggcaccctcctccaagag cacctctgggggcacagcggccctgggctgcctggtcaaggactacttccccgaacc ggtgacggtgtcgtggaactcaggcgccctgaccagcggcgtgcacaccttcccggc tgtcctacagtcctcaggactctactccctcagcagcgtggtgaccgtgccctccagca gcttgggcacccagacctacatctgcaacgtgaatcacaagcccagcaacaccaaggt ggacaagaaagttgagcccaaatcttgtgacaaaactcacacatgcccaccgtgccca gcacctgaactcctgggggggaccgtcagtcttcctcttcccccaaaacccaaggaca ccctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtgagccacga agaccctgaggtcaagttcaactggtatgttgacggcgtggaggtgcataatgccaaga caaagccgcgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcacc gtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaa gccctcccagccccatcgagaaaaccatctccaaagccaaagggcagccccgaga accacaggtgtacaccctgcccccatgccgggatgagctgaccaagaatcaagtcag cctgtggtgcctggtaaaaggcttctatcccagcgacatcgccgtggagtgggagagc aatgggcagccggagaacaactacaagaccacgcctcccgtgctggactccgacgg ctccttcttcctctactcaaaactcaccgtggacaagagcaggtggcagcaggggaac gtcttctcatgctccgtgatgcatgaggctctgcacaaccactacacgcagaagagcct ctccctgtctccgggt	
Light chain B	tccgacatcagcgtggcccccggagagacagccaggatctcctgcggcgag aagagcctgggaagcagggctgtgcagtggtaccaacacagggccggacag gctcccagcctgatcatctacaacaaccaggacaggcccagcggcatccctga gaggttcagcggaagccccgacagccccttcggaaccacagccaccctgacc atcacaagcgtggaagccggcgacgaggccgactactactgccacatctggg acagcagggtgcccaccaagtgggtgtttggcggcggcaccaccctgaccgt gctggacaaaacccataccgcatccgaactgactcaggaccctgccgtctctgt ggcactgaagcagactgtgactattacttgccgaggcgactcactgcggagcc actacgcttcctggtatcagaagaaacccggccaggcacctgtgctgctgttcta cggaaagaacaataggccatctggcatccccgaccgcttttctggcagtgcatc agggaaccgagccagtctgaccattaccggcgcccaggctgaggacgaagc cgattactattgcagctcccgggataagagcggctccagactgagcgtgttcgg aggaggaactaaactgaccgtcctcgataagacccatacccgtacggtggccg ctcccagcgtgttcatcttcccacctagcgacgagcagctgaagtccggcaca gcctctgtcgtgtgcctgctgaacaacttctacccccgcgaggccaaagtgcag tggaaggtggacaacgccctgcagagcggcaacagccaggaaagcgtgacc gagcaggacagcaaggactccacctacagcctgagcagcaccctgacactga gcaaggccgactacgagaagcacaaggtgtacgcctgcgaagtgacccacc agggcctgtctagccccgtgaccaagagcttcaaccggggcgagtgt	**SEQ ID NO: 128**
Binding Protein 17 Amino Acid Sequences		
Heavy chain A	Rahlvqsgtamkkpgasvrvscqtsgytftahilfwfrqapgrglewvgwikpqy gavnfgggfrdrvtltrdvyreiaymdirglkpddtavyycardrsygdsswalda wgqgttvvvsaastkgpsvfplapsskstsggtaalgclvkdyfpepvtvswnsgal tsgvhtfpavlqssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkkvepkscd kthtcppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnw yvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykckvsnkalpapi ektiskakgqprepqvctlppsrdeltknqvslscavkgfypsdiavewesngqpe nnykttppvldsdgsfflvskltvdksrwqqgnvfscsvmhealhnhytqkslslsp	**SEQ ID NO: 129**

	g	
Light chain A	yihvtqspsslsvsigdrvtincqtsqgvgsdlhwyqhkpgrapkllihhtssvedgv psrfsgsgfhtsfnltisdlqaddiatyycqvlqffgrgsrlhikrtvaapsvfifppsde qlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsstltls kadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 130**
Heavy chain B	qvhltqsgpevrkpgtsvkvsckapgntlktydlhwvrsvpgqglqwmg wishegdkkviverfkakvtidwdrstntaylqlsgltsgdtavyycakgsk hrlrdyalydddgalnwavdvdylsnlefwgqgtavtvssdkthtqmqlqe sgpglvkpsetlsltcsvsgasisdsyswswirrspgkglewigyvhksgdtn yspslksrvnlsldtsknqvslslvaataadsgkyycartlhgrriygivafne wftyfymdvwgngtqvtvssdkthtastkgpsvfplapsskstsggtaalgc lvkdyfpepvtvswnsgaltsgvhtfpavlqssglyslssvvtvpssslgtqty icnvnhkpsntkvdkkvepkscdkthtcppcpapellggpsvflfppkpkd tlmisrtpevtcvvvdvshedpevkfnwyvdgvevhnaktkpreeqynst yrvvsvltvlhqdwlngkeykckvsnkalpapiektiskakgqprepqvytl ppcrdeltknqvslwclvkgfypsdiavewesngqpennykttppvldsdg sfflyskltvdksrwqqgnvfscsvmhealhnhytqkslslspg	**SEQ ID NO: 131**
Light chain B	sdisvapgetariscgekslgsravqwyqhragqapsliiynnqdrpsgiperfsgsp dspfgttatltitsveagdeadyychiwdsrvptkwvfgggttltvldkthtdfvltqsp hslsvtpgesasiscksshslihgdrnnylawyvqkpgrspqlliylassrasgvpdrf sgsgsdkdftlkisrvetedvgtyycmqgrespwtfgqgtkvdikdkthtrtvaaps vfifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskd styslsstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 132**
Binding Protein 17 Nucleotide Sequences		
Heavy chain A	agagcccacctggtgcagtctggcaccgccatgaagaaaccaggcgcctctgtgcgg gtgtcctgtcagacaagcggctacaccttcaccgcccacatcctgttctggttccggcag gcccctggcagaggactggaatgggtgggatggatcaagccccagtatggcgccgtg aacttcggcggaggcttccgggatagagtgaccctgacccgggacgtgtaccgcgag atcgcctacatggacatccggggcctgaagcccgatgacaccgccgtgtactactgcg ccagagacagaagctacggcgacagcagctgggctctggatgcttggggccagggc acaaccgtggtggtgtctgccgcctctacaaagggccccagcgtgttccctctggcccc tagcagcaagagcacatctggcggaacagccgccctgggctgcctcgtgaaggacta ctttcccgagcccgtgaccgtgtcctggaattctggcgccctgaccagcggcgtgcac acctttccagctgtgctgcagtccagcggcctgtacagcctgagcagcgtcgtgacagt gcccagcagctctctgggcacccagacctacatctgcaacgtgaaccacaagcccag caacaccaaggtggacaagaaggtggaacccaagagctgcgacaagacccacacct gtccccttgtcctgccccgaactgctgggaggcccttccgtgttcctgttcccccaa agcccaaggacaccctgatgatcagccggacccccgaagtgacctgcgtggtggtgg atgtgtcccacgaggaccctgaagtgaagttcaattggtacgtggacggcgtggaagt gcacaacgccaagaccaagccaagagaggaacagtacaacagcacctaccgggtg gtgtccgtgctgaccgtgctgcaccaggactggctgaacggcaaagagtacaagtgc aaggtgtccaacaaggccctgcctgccccatcgagaaaaccatcagcaaggccaag ggccagccccgcgaaccccaggtgtgcacactgcccccaagcagggacgagctga ccaagaaccaggtgtccctgagctgtgccgtgaaaggcttctacccctccgatatcgcc gtggaatgggagagcaacggccagcccgagaacaactacaagaccacccccctgt gctggacagcgacggctcattcttcctggtgtccaagctgacagtggacaagtcccggt ggcagcagggcaacgtgttcagctgctccgtgatgcacgaggccctgcacaaccact acacccagaagtccctgagcctgagccccggcaag	**SEQ ID NO: 133**
Light chain A	tacatccacgtgacccagagccccagcagcctgtccgtgtccatcggcgacag agtgaccatcaactgccagacctctcagggcgtgggcagcgacctgcactggt	**SEQ ID NO: 134**

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Heavy chain B	caggtgcacctgacacagagcggacccgaagtgcggaagcctggcacctctgtgaa ggtgtcctgcaaggcccctggcaacaccctgaaaacctacgacctgcactgggtgcg cagcgtgccaggacagggactgcagtggatgggctggatcagccacgagggcgac aagaaagtgatcgtggaacggttcaaggccaaagtgaccatcgactgggacagaagc accaacaccgcctacctgcagctgagcggcctgacctctggcgataccgccgtgtact actgcgccaagggcagcaagcaccggctgagagactacgccctgtacgacgatgac ggcgccctgaactgggccgtggatgtggactacctgagcaacctggaattctggggcc agggcacagccgtgaccgtgtcatctgacaaaacccatacccagatgcagctgcagg agagcggccctggactcgtgaagcccagcgagaccctgagcctgacatgcagcgtg agcggcgccagcatcagcgacagctactggagctggatcaggaggagccctggcaa gggcctggagtggatcggctacgtgcacaagagcggcgacaccaactacagccct ccctgaagtccagggtgaacctgtccctggacaccagcaagaaccaggtgagcctgt ccctggtggctgccacagctgctgacagcggcaagtactactgtgccaggaccctgca cggcaggaggatctacggcatcgtggccttcaacgagtggttcacctacttctacatgg acgtgtggggcaacggcacccaggtgaccgtgagctccgataagacccacaccgctt ccaccaagggcccatcggtcttcccccctggcaccctcctccaagagcacctctggggg cacagcggccctgggctgcctggtcaaggactacttccccgaaccggtgacggtgtc gtggaactcaggcgccctgaccagcggcgtgcacaccttcccggctgtcctacagtcc tcaggactctactccctcagcagcgtggtgaccgtgccctccagcagcttgggcaccc agacctacatctgcaacgtgaatcacaagcccagcaacaccaaggtggacaagaaag ttgagcccaaatcttgtgacaaaactcacacatgcccaccgtgcccagcacctgaactc ctgggggggaccgtcagtcttcctcttcccccaaaacccaaggacaccctcatgatctc ccggacccctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggt caagttcaactggtatgttgacggcgtggaggtgcataatgccaagacaaagccgcgg gaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccag gactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagccctcccagcc cccatcgagaaaaccatctccaaagccaaagggcagccccgagaaccacaggtgta caccctgcccccatgccgggatgagctgaccaagaatcaagtcagcctgtggtgcctg gtaaaaggcttctatcccagcgacatcgccgtggagtgggagagcaatgggcagccg gagaacaactacaagaccacgcctcccgtgctggactccgacggctccttcttcctcta ctcaaaactcaccgtggacaagagcaggtggcagcaggggaacgtcttctcatgctcc gtgatgcatgaggctctgcacaaccactacacgcagaagagcctctccctgtctccgg gt	**SEQ ID NO: 135**
Light chain B	tccgacatcagcgtggcccccggagagacagccaggatctcctgcggcgag aagagcctgggaagcagggctgtgcagtggtaccaacacagggccggacag gctcccagcctgatcatctacaacaaccaggacaggcccagcggcatccctga gaggttcagcggaagccccgacagccccttcggaaccacagccaccctgacc atcacaagcgtggaagccggcgacgaggccgactactactgccacatctggg acagcagggtgcccaccaagtgggtgtttggcggcggcaccaccctgaccgt gctggacaaaacccataccgacttcgtgctgacccagagccctcacagcctga gcgtgacacctggcgagagcgccagcatcagctgcaagagcagccactccct gatccacggcgaccggaacaactacctggcttggtacgtgcagaagcccggc	**SEQ ID NO: 136**

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Binding Protein 18 Amino Acid Sequences		
Heavy chain A	Rahlvqsgtamkkpgasvrvscqtsgytftahilfwfrqapgrglewvgwikpqy gavnfgggfrdrvtltrdvyreiaymdirglkpddtavyycardrsygdsswalda wgqgttvvvsaastkgpsvfplapsskstsggtaalgclvkdyfpepvtvswnsgal tsgvhtfpavlqssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkkvepkscd kthtcppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnw yvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykckvsnkalpapi ektiskakgqprepqvctlppsrdeltknqvslscavkgfypsdiavewesngqpe nnykttppvldsdgsfflvskltvdksrwqqgnvfscsvmhealhnhytqkslslsp g	**SEQ ID NO: 137**
Light chain A	yihvtqspsslsvsigdrvtincqtsqgvgsdlhwyqhkpgrapkllihhtssvedgv psrfsgsgfhtsfnltisdlqaddiatyycqvlqffgrgsrlhikrtvaapsvfifppsde qlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsstltl skadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 138**
Heavy chain B	qmqlqesgpglvkpsetlsltcsvsgasisdsywswirrspgkglewigyvh ksgdtnyspslksrvnlsldtsknqvslslvaataadsgkyycartlhgrriygi vafnewftyfymdvwgngtqvtvssdkthtevrlvesggglvkpggslrls csasgfdfdnawmtwvrqppgkglewvgritgpgegwsvdyaesvkgrf tisrdntkntlylemnnvrtedtgyyfcartgkyydfwsgyppgeeyfqdw gqgtlvivssdkthtastkgpsvfplapsskstsggtaalgclvkdyfpepvtv swnsgaltsgvhtfpavlqssglyslssvvtvpssslgtqtyicnvnhkpsntk vdkkvepkscdkthtcppcpapellggpsvflfppkpkdtlmisrtpevtcv vvdvshedpevkfnwyvdgvevhnaktkpreeqynstyrvvsvltvlhqd wlngkeykckvsnkalpapiektiskakgqprepqvytlppcrdeltknqv slwclvkgfypsdiavewesngqpennykttppvldsdgsfflyskltvdks rwqqgnvfscsvmhealhnhytqkslslspg	**SEQ ID NO: 139**
Light chain B	aseltqdpavsvalkqtvtitcrgdslrshyaswyqkkpgqapvllfygknnrpsgip drfsgsasgnrasltitgaqaedeadyycssrdksgsrlsvfgggtkltvldkthtsdis vapgetariscgekslgsravqwyqhragqapsliiynnqdrpsgiperfsgspdsp fgttatltitsveagdeadyychiwdsrvptkwvfgggttltvldkthtrtvaapsvfif ppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstys lsstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 140**
Binding Protein 18 Nucleotide Sequences		
Heavy chain A	agagcccacctggtgcagtctggcaccgccatgaagaaaccaggcgcctctgtgcgg gtgtcctgtcagacaagcggctacaccttcaccgcccacatcctgttctggttccggcag gcccctggcagaggactggaatgggtgggatggatcaagccccagtatggcgccgtg aacttcggcggaggcttccgggatagagtgaccctgacccgggacgtgtaccgcgag atcgcctacatggacatccggggcctgaagcccgatgacaccgccgtgtactactgcg ccagagacagaagctacggcgacagcagctgggctctggatgcttggggccagggc acaaccgtggtggtgtctgccgcctctacaaagggccccagcgtgttccctctggcccc	**SEQ ID NO: 141**

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Light chain A	tacatccacgtgacccagagccccagcagcctgtccgtgtccatcggcgacag agtgaccatcaactgccagacctctcagggcgtgggcagcgacctgcactggt atcagcacaagcctggcagagcccccaagctgctgatccaccacacaagcag cgtggaagatggcgtgcccagcagattttccggcagcggcttccacaccagct tcaacctgaccatcagcgatctgcaggccgacgacattgccacctactattgtca ggtgctgcagttcttcggcagaggcagcagactgcacatcaagcgtacggtgg ccgctcccagcgtgttcatcttcccacctagcgacgagcagctgaagtccggc acagcctctgtcgtgtgcctgctgaacaacttctacccccgcgaggccaaagtg cagtggaaggtggacaacgccctgcagagcggcaacagccaggaaagcgt gaccgagcaggacagcaaggactccacctacagcctgagcagcaccctgac actgagcaaggccgactacgagaagcacaaggtgtacgcctgcgaagtgacc caccagggcctgtctagccccgtgaccaagagcttcaaccggggcgagtgt	**SEQ ID NO: 142**
Heavy chain B	cagatgcagctgcaggagagcggccctggactcgtgaagcccagcgagaccctgag cctgacatgcagcgtgagcggcgccagcatcagcgacagctactggagctggatcag gaggagccctggcaagggcctggagtggatcggctacgtgcacaagagcggcgac accaactacagcccctccctgaagtccagggtgaacctgtccctggacaccagcaaga accaggtgagcctgtccctggtggctgccacagctgctgacagcggcaagtactactg tgccaggaccctgcacggcaggaggatctacggcatcgtggccttcaacgagtggttc acctacttctacatggacgtgtggggcaacggcacccaggtgaccgtgagctccgaca aaacccataccgaggttagactggtggagtcaggaggggggcttgtgaagcccggtg ggtctctccgcctgagctgttctgcctccggctttgatttcgataacgcctggatgacctg ggtcaggcagcctccaggtaagggactggagtgggtgggaagaatcacaggtccag gcgagggctggtccgtggactacgcggaatctgttaaagggcggtttacaatctcaag ggacaataccaagaataccttgtatttggagatgaacaacgtgagaactgaagacacc ggatattacttctgtgccagaacaggcaaatactacgacttctggtccggctatccccct ggcgaggaatattttcaagactggggtcagggaacccttgttatcgtgtcctccgataag acccacaccgcttccaccaagggcccatcggtcttcccctggcaccctcctccaaga gcacctctgggggcacagcggccctgggctgcctggtcaaggactacttccccgaac cggtgacggtgtcgtggaactcaggcgccctgaccagcggcgtgcacaccttcccgg ctgtcctacagtcctcaggactctactccctcagcagcgtggtgaccgtgccctccagc agcttgggcacccagacctacatctgcaacgtgaatcacaagcccagcaacaccaag gtggacaagaaagttgagcccaaatcttgtgacaaaactcacacatgcccaccgtgcc cagcacctgaactcctgggggggaccgtcagtcttcctcttcccccaaaacccaagga caccctcatgatctcccggaccctgaggtcacatgcgtggtggtggacgtgagccac gaagaccctgaggtcaagttcaactggtatgttgacggcgtggaggtgcataatgccaa	**SEQ ID NO: 143**

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Light chain B	gcatccgaactgactcaggaccctgccgtctctgtggcactgaagcagactgtg actattacttgccgaggcgactcactgcggagccactacgcttcctggtatcaga agaaacccggccaggcacctgtgctgctgttctacggaaagaacaataggcca tctggcatccccgaccgcttttctggcagtgcatcagggaaccgagccagtctg accattaccggcgcccaggctgaggacgaagccgattactattgcagctcccg ggataagagcggctccagactgagcgtgttcggaggaggaactaaactgacc gtcctcgacaaaacccatacctccgacatcagcgtggcccccggagagacag ccaggatctcctgcggcgagaagagcctgggaagcagggctgtgcagtggta ccaacacagggccggacaggctcccagcctgatcatctacaacaaccaggac aggcccagcggcatccctgagaggttcagcggaagccccgacagccccttcg gaaccacagccaccctgaccatcacaagcgtggaagccggcgacgaggccg actactactgccacatctgggacagcagggtgcccaccaagtgggtgtttggc ggcggcaccaccctgaccgtgctggataagacccatacccgtacggtggccg ctcccagcgtgttcatcttcccacctagcgacgagcagctgaagtccggcaca gcctctgtcgtgtgcctgctgaacaacttctacccccgcgaggccaaagtgcag tggaaggtggacaacgccctgcagagcggcaacagccaggaaagcgtgacc gagcaggacagcaaggactccacctacagcctgagcagcaccctgacactga gcaaggccgactacgagaagcacaaggtgtacgcctgcgaagtgacccacc agggcctgtctagccccgtgaccaagagcttcaaccggggcgagtgt	**SEQ ID NO: 144**
Binding Protein 19 Amino Acid Sequences		
Heavy chain A	evrlvesggglvkpggslrlscsasgfdfdnawmtwvrqppgkglewvgritgpg egwsvdyaesvkgrftisrdntkntlylemnnvrtedtgyyfcartgkyydfwsgy ppgeeyfqdwgqgtlvivssastkgpsvfplapsskstsggtaalgclvkdyfpepv tvswnsgaltsgvhtfpavlqssglyslssvvtvpssslgtqtyicnvnhkpsntkvd kkvepkscdkthtcppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshe dpevkfnwyvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykckv snkalpapiektiskakgqprepqvctlppsrdeltknqvslscavkgfypsdiave wesngqpennykttppvldsdgsfflvskltvdksrwqqgnvfscsvmhealhnh ytqkslslspg	**SEQ ID NO: 145**
Light chain A	aseltqdpavsvalkqtvtitcrgdslrshyaswyqkkpgqapvllfygknnrpsgip drfsgsasgnrasltitgaqaedeadyycssrdksgsrlsvfgggtkltvlsqpkaaps vtlfppsseelqankatlvclisdfypgavtvawkadsspvkagvetttpskqsnnky aassylsltpeqwkshrsyscqvthegstvektvaptecs	**SEQ ID NO: 146**
Heavy chain B	qmqlqesgpglvkpsetlsltcsvsgasisdsywswirrspgkglewigyvh ksgdtnyspslksrvnlsldtsknqvslslvaataadsgkyycartlhgrriygi vafnewftyfymdvwgngtqvtvssdkthtQvhltqsgpevrkpgtsvkv sckapgntlktydlhwvrsvpgqglqwmgwishegdkkviverfkakvti dwdrstntaylqlsgltsgdtavyycakgskhrlrdyalydddgalnwavdv dylsnlefwgqgtavtvssdkthtastkgpsvfplapsskstsggtaalgclvk dyfpepvtvswnsgaltsgvhtfpavlqssglyslssvvtvpssslgtqtyicn	**SEQ ID NO: 147**

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Light chain B	dfvltqsphslsvtpgesasisckssshslihgdrnnylawyvqkpgrspqlliylassr asgvpdrfsgsgsdkdftlkisrvetedvgtyycmqgrespwtfgqgtkvdikdkth tsdisvapgetariscgekslgsravqwyqhragqapsliiynnqdrpsgiperfsgs pdspfgttatltitsveagdeadyychiwdsrvptkwvfgggttltvldkthtrtvaaps vfifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskd styslsstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 148**
Binding Protein 19 Nucleotide Sequences		
Heavy chain A	gaggttagactggtggagtcaggaggggggcttgtgaagcccggtgggtctctccgc ctgagctgttctgcctccggctttgatttcgataacgcctggatgacctgggtcaggcag cctccaggtaagggactggagtgggtgggaagaatcacaggtccaggcgagggctg gtccgtggactacgcggaatctgttaaagggcggtttacaatctcaagggacaataccа agaataccttgtatttggagatgaacaacgtgagaactgaagacaccggatattacttct gtgccagaacaggcaaatactacgacttctggtccggctatccccctggcgaggaatat tttcaagactggggtcagggaacccttgttatcgtgtcctccgcgtcgaccaagggccc cagcgtgttccctctggccccctagcagcaagagcacatctggcggaacagccgccct gggctgcctcgtgaaggactactttcccgagcccgtgaccgtgtcctggaattctggcg ccctgaccagcggcgtgcacaccttccagctgtgctgcagtccagcggcctgtacag cctgagcagcgtcgtgacagtgcccagcagctctctgggcacccagacctacatctgc aacgtgaaccacaagcccagcaacaccaaggtggacaagaaggtggaacccaaga gctgcgacaagacccacacctgtccccctttgtcctgcccccgaactgctgggaggccc ttccgtgttcctgttcccccaaagcccaaggacaccctgatgatcagccggacccccg aagtgacctgcgtggtggtggatgtgtcccacgaggaccctgaagtgaagttcaattgg tacgtggacggcgtggaagtgcacaacgccaagaccaagccaagagaggaacagta caacagcacctaccgggtggtgtccgtgctgaccgtgctgcaccaggactggctgaac ggcaaagagtacaagtgcaaggtgtccaacaaggccctgcctgcccccatcgagaaa accatcagcaaggccaagggccagccccgcgaaccccaggtgtgcacactgccccc aagcagggacgagctgaccaagaaccaggtgtccctgagctgtgccgtgaaaggctt ctacccctccgatatcgccgtggaatgggagagcaacggccagcccgagaacaacta caagaccacccccccctgtgctggacagcgacggctcattcttcctggtgtccaagctga cagtggacaagtcccggtggcagcagggcaacgtgttcagctgctccgtgatgcacg aggccctgcacaaccactacacccagaagtccctgagcctgagccccggcaag	**SEQ ID NO: 149**
Light chain A	gcatccgaactgactcaggaccctgccgtctctgtggcactgaagcagactgtg actattacttgccgaggcgactcactgcggagccactacgcttcctggtatcaga agaaacccggccaggcacctgtgctgctgttctacggaaagaacaataggcca tctggcatccccgaccgcttttctggcagtgcatcagggaaccgagccagtctg accattaccggcgcccaggctgaggacgaagccgattactattgcagctcccg ggataagagcggctccagactgagcgtgttcggaggaggaactaaactgacc gtcctcagtcagcccaaggctgccccctcggtcactctgttcccgccctcgagt gaggagcttcaagccaacaaggccacactggtgtgtctcataagtgacttctac ccgggagccgtgacagtggcctggaaggcagatagcagccccgtcaaggcg ggagtggagaccaccacaccctccaaacaaagcaacaacaagtacgcggcc agcagctacctgagcctgacgcctgagcagtggaagtcccacagaagctaca gctgccaggtcacgcatgaagggagcaccgtggagaagacagtggccccta cagaatgttca	**SEQ ID NO: 150**
Heavy chain B	cagatgcagctgcaggagagcggccctggactcgtgaagcccagcgagaccctgag cctgacatgcagcgtgagcggcgccagcatcagcgacagctactggagctggatcag	**SEQ ID NO: 151**

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Light chain B	gacttcgtgctgacccagagccctcacagcctgagcgtgacacctggcgaga gcgccagcatcagctgcaagagcagccactccctgatccacggcgaccggaa caactacctggcttggtacgtgcagaagcccggcagatccccccagctgctga tctacctggccagcagcagagccagcggcgtgcccgatagattttctggcagc ggcagcgacaaggacttcaccctgaagatcagccgggtggaaaccgaggac gtgggcacctactactgtatgcagggcagagagagcccctggacctttggcca gggcaccaaggtggacatcaaggacaaaacccatacctccgacatcagcgtg gcccccggagagacagccaggatctcctgcggcgagaagagcctgggaag cagggctgtgcagtggtaccaacacagggccggacaggctcccagcctgatc atctacaacaaccaggacaggcccagcggcatccctgagaggttcagcggaa gccccgacagccccttcggaaccacagccaccctgaccatcacaagcgtgga agccggcgacgaggccgactactactgccacatctgggacagcagggtgcc caccaagtgggtgtttggcggcggcaccaccctgaccgtgctggataagaccc atacccgtacggtggccgctcccagcgtgttcatcttcccacctagcgacgagc agctgaagtccggcacagcctctgtcgtgtgcctgctgaacaacttctacccccc gcgaggccaaagtgcagtggaaggtggacaacgccctgcagagcggcaac agccaggaaagcgtgaccgagcaggacagcaaggactccacctacagcctg agcagcaccctgacactgagcaaggccgactacgagaagcacaaggtgtac gcctgcgaagtgacccaccagggcctgtctagccccgtgaccaagagcttcaa ccggggcgagtgt	**SEQ ID NO: 152**
Binding Protein 20 Amino Acid Sequences		
Heavy chain A	Rahlvqsgtamkkpgasvrvscqtsgytftahilfwfrqapgrglewvgwikpqy	**SEQ ID NO:**

	gavnfgggfrdrvtltrdvyreiaymdirglkpddtavyycardrsygdsswalda wgqgttvvvsaastkgpsvfplapsskstsggtaalgclvkdyfpepvtvswnsgal tsgvhtfpavlqssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkkvepkscd kthtcppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnw yvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykckvsnkalpapi ektiskakgqprepqvctlppsrdeltknqvslscavkgfypsdiavewesngqpe nnykttppvldsdgsfflvskltvdksrwqqgnvfscsvmhealhnhytqkslslsp g	**153**
Light chain A	yihvtqspsslsvsigdrvtincqtsqgvgsdlhwyqhkpgrapkllihhtssvedgv psrfsgsgfhtsfnltisdlqaddiatyycqvlqffgrgsrlhikrtvaapsvfifppsde qlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsstltls kadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 154**
Heavy chain B	qmqlqesgpglvkpsetlsltcsvsgasisdsywswirrspgkglewigyvh ksgdtnyspslksrvnlsldtsknqvslslvaataadsgkyycartlhgrriygi vafnewftyfymdvwgngtqvtvssdkthtQvhltqsgpevrkpgtsvkv sckapgntlktydlhwvrsvpgqglqwmgwishegdkkviverfkakvti dwdrstntaylqlsgltsgdtavyycakgskhrlrdyalydddgalnwavdv dylsnlefwgqgtavtvssdkthtastkgpsvfplapsskstsggtaalgclvk dyfpepvtvswnsgaltsgvhtfpavlqssglyslssvvtvpssslgtqtyicn vnhkpsntkvdkkvepkscdkthtcppcpapellggpsvflfppkpkdtlm isrtpevtcvvvdvshedpevkfnwyvdgvevhnaktkpreeqynstyrv vsvltvlhqdwlngkeykckvsnkalpapiektiskakgqprepqvytlpp crdeltknqvslwclvkgfypsdiavewesngqpennykttppvldsdgsf flyskltvdksrwqqgnvfscsvmhealhnhytqkslslspg	**SEQ ID NO: 155**
Light chain B	dfvltqsphslsvtpgesasisckssshslihgdrnnylawyvqkpgrspqlliylassr asgvpdrfsgsgsdkdftlkisrvetedvgtyycmqgrespwtfgqgtkvdikdkth tsdisvapgetariscgekslgsravqwyqhragqapsliiynnqdrpsgiperfsgs pdspfgttatltitsveagdeadyychiwdsrvptkwvfgggttltvldkthtrtvaaps vfifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskd styslsstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 156**
Binding Protein 20 Nucleotide Sequences		
Heavy chain A	agagcccacctggtgcagtctggcaccgccatgaagaaaccaggcgcctctgtgcgg gtgtcctgtcagacaagcggctacaccttcaccgcccacatcctgttctggttccggca ggcccctggcagaggactggaatgggtgggatggatcaagccccagtatggcgccg tgaacttcggcggaggcttccgggatagagtgaccctgacccgggacgtgtaccgcg agatcgcctacatggacatccggggcctgaagcccgatgacaccgccgtgtactactg cgccagagacagaagctacggcgacagcagctgggctctggatgcttggggccagg gcacaaccgtggtggtgtctgccgcctctacaaagggccccagcgtgttccctctggc ccctagcagcaagagcacatctggcggaacagccgccctgggctgcctcgtgaagg actactttcccgagcccgtgaccgtgtcctggaattctggcgccctgaccagcggcgtg cacacctttccagctgtgctgcagtccagcggcctgtacagcctgagcagcgtcgtga cagtgcccagcagctctctgggcacccagacctacatctgcaacgtgaaccacaagcc cagcaacaccaaggtggacaagaaggtggaacccaagagctgcgacaagacccac acctgtccccttgtcctgccccgaactgctgggaggcccttccgtgttcctgttcccc ccaaagcccaaggacaccctgatgatcagccggaccccgaagtgacctgcgtggtg gtggatgtgtcccacgaggaccctgaagtgaagttcaattggtacgtggacggcgtgg aagtgcacaacgccaagaccaagccaagagaggaacagtacaacagcacctaccgg gtggtgtccgtgctgaccgtgctgcaccaggactggctgaacggcaaagagtacaagt gcaaggtgtccaacaaggccctgcctgcccccatcgagaaaaccatcagcaaggcca agggccagccccgcgaaccccaggtgtgcacactgcccccaagcagggacgagct gaccaagaaccaggtgtccctgagctgtgccgtgaaaggcttctacccctccgatatcg ccgtggaatgggagagcaacggccagcccgagaacaactacaagaccacccccccct	**SEQ ID NO: 157**

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Light chain A	tacatccacgtgacccagagccccagcagcctgtccgtgtccatcggcgacag agtgaccatcaactgccagacctctcagggcgtgggcagcgacctgcactggt atcagcacaagcctggcagagcccccaagctgctgatccaccacacaagcag cgtggaagatggcgtgcccagcagattttccggcagcggcttccacaccagct tcaacctgaccatcagcgatctgcaggccgacgacattgccacctactattgtca ggtgctgcagttcttcggcagaggcagcagactgcacatcaagcgtacggtgg ccgctcccagcgtgttcatcttcccacctagcgacgagcagctgaagtccggc acagcctctgtcgtgtgcctgctgaacaacttctacccccgcgaggccaaagtg cagtggaaggtggacaacgccctgcagagcggcaacagccaggaaagcgt gaccgagcaggacagcaaggactccacctacagcctgagcagcaccctgac actgagcaaggccgactacgagaagcacaaggtgtacgcctgcgaagtgacc caccagggcctgtctagccccgtgaccaagagcttcaaccggggcgagtgt	**SEQ ID NO: 158**
Heavy chain B	cagatgcagctgcaggagagcggccctggactcgtgaagcccagcgagaccctgag cctgacatgcagcgtgagcggcgccagcatcagcgacagctactggagctggatcag gaggagccctggcaagggcctggagtggatcggctacgtgcacaagagcggcgac accaactacagcccctccctgaagtccagggtgaacctgtccctggacaccagcaaga accaggtgagcctgtccctggtggctgccacagctgctgacagcggcaagtactactg tgccaggaccctgcacggcaggaggatctacggcatcgtggccttcaacgagtggttc acctacttctacatggacgtgtggggcaacggcacccaggtgaccgtgagctccgaca aaacccatacccaggtgcacctgacacagagcggacccgaagtgcggaagcctggc acctctgtgaaggtgtcctgcaaggcccctggcaacaccctgaaaacctacgacctgc actgggtgcgcagcgtgccaggacagggactgcagtggatgggctggatcagccac gagggcgacaagaaagtgatcgtggaacggttcaaggccaaagtgaccatcgactg ggacagaagcaccaacaccgcctacctgcagctgagcggcctgacctctggcgatac cgccgtgtactactgcgccaagggcagcaagcaccggctgagagactacgccctgta cgacgatgacggcgccctgaactgggccgtggatgtggactacctgagcaacctgga attctggggccagggcacagccgtgaccgtgtcatctgataagacccacaccgcttcc accaagggcccatcggtcttcccccctggcaccctcctccaagagcacctctgggggca cagcggccctgggctgcctggtcaaggactacttccccgaaccggtgacggtgtcgtg gaactcaggcgccctgaccagcggcgtgcacaccttcccggctgtcctacagtcctca ggactctactccctcagcagcgtggtgaccgtgccctccagcagcttgggcacccaga cctacatctgcaacgtgaatcacaagcccagcaacaccaaggtggacaagaaagttga gcccaaatcttgtgacaaaactcacacatgcccaccgtgcccagcacctgaactcctgg ggggaccgtcagtcttcctcttcccccaaaacccaaggacaccctcatgatctcccgg acccctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtcaag ttcaactggtatgttgacggcgtggaggtgcataatgccaagacaaagccgcgggag gagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggact ggctgaatggcaaggagtacaagtgcaaggtctccaacaaagccctcccagccccca tcgagaaaaccatctccaaagccaaagggcagccccgagaaccacaggtgtacacc ctgccccatgccgggatgagctgaccaagaatcaagtcagcctgtggtgcctggtaa aaggcttctatcccagcgacatcgccgtggagtgggagagcaatgggcagccggag aacaactacaagaccacgcctcccgtgctggactccgacggctccttcttcctctactca aaactcaccgtggacaagagcaggtggcagcaggggaacgtcttctcatgctccgtg atgcatgaggctctgcacaaccactacacgcagaagagcctctccctgtctccgggt	**SEQ ID NO: 159**
Light chain B	gacttcgtgctgacccagagccctcacagcctgagcgtgacacctggcgaga gcgccagcatcagctgcaagagcagccactccctgatccacggcgaccgga acaactacctggcttggtacgtgcagaagcccggcagatcccccagctgctg atctacctggccagcagcagagccagcggcgtgcccgatagattttctggcag	**SEQ ID NO: 160**

	cggcagcgacaaggacttcaccctgaagatcagccgggtggaaaccgagga cgtgggcacctactactgtatgcagggcagagagagcccctggacctttggcc agggcaccaaggtggacatcaaggacaaaacccatacctccgacatcagcgt ggcccccggagagacagccaggatctcctgcggcgagaagagcctgggaa gcagggctgtgcagtggtaccaacacagggccggacaggctcccagcctgat catctacaacaaccaggacaggcccagcggcatccctgagaggttcagcgga agccccgacagccccttcggaaccacagccaccctgaccatcacaagcgtgg aagccggcgacgaggccgactactactgccacatctgggacagcagggtgc ccaccaagtgggtgtttggcggcggcaccaccctgaccgtgctggataagacc catacccgtacggtggccgctcccagcgtgttcatcttcccacctagcgacgag cagctgaagtccggcacagcctctgtcgtgtgcctgctgaacaacttctacccc cgcgaggccaaagtgcagtggaaggtggacaacgccctgcagagcggcaa cagccaggaaagcgtgaccgagcaggacagcaaggactccacctacagcct gagcagcaccctgacactgagcaaggccgactacgagaagcacaaggtgta cgcctgcgaagtgacccaccagggcctgtctagccccgtgaccaagagcttca accggggcgagtgt	
Binding Protein 21 Amino Acid Sequences		
Heavy chain A	qvhltqsgpevrkpgtsvkvsckapgntlktydlhwvrsvpgqglqwmgwishe gdkkviverfkakvtidwdrstntaylqlsgltsgdtavyycakgskhrlrdyalydd dgalnwavdvdylsnlefwgqgtavtvssastkgpsvfplapsskstsggtaalgcl vkdyfpepvtvswnsgaltsgvhtfpavlqssglyslssvvtvpssslgtqtyicnvn hkpsntkvdkkvepkscdkthtcppcpapellggpsvflfppkpkdtlmisrtpevt cvvvdvshedpevkfnwyvdgvevhnaktkpreeqynstyrvvsvltvlhqdwl ngkeykckvsnkalpapiektiskakgqprepqvctlppsrdeltknqvslscavkg fypsdiavewesngqpennykttppvldsdgsfflvskltvdksrwqqgnvfscsv mhealhnhytqkslslspg	**SEQ ID NO: 161**
Light chain A	dfvltqsphslsvtpgesasisckssshslihgdrnnylawyvqkpgrspqlliylassr asgvpdrfsgsgsdkdftlkisrvetedvgtyycmqgrespwtfgqgtkvdikrtva apsvfifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqds kdstyslsstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 162**
Heavy chain B	Evrlvesggglvkpggslrlscsasgfdfdnawmtwvrqppgkglewvgr itgpgegwsvdyaesvkgrftisrdntkntlylemnnvrtedtgyyfcartgk yydfwsgyppgeeyfqdwgqgtlvivssdktht rahlvqsgtamkkpgasvrvscqtsgytftahilfwfrqapgrglewvgwik pqygavnfgggfrdrvtltrdvyreiaymdirglkpddtavyycardrsygd sswaldawgqgttvvvsadkthtastkgpsvfplapsskstsggtaalgclvk dyfpepvtvswnsgaltsgvhtfpavlqssglyslssvvtvpssslgtqtyicn vnhkpsntkvdkkvepkscdkthtcppcpapellggpsvflfppkpkdtlm isrtpevtcvvvdvshedpevkfnwyvdgvevhnaktkpreeqynstyrv vsvltvlhqdwlngkeykckvsnkalpapiektiskakgqprepqvytlpp crdeltknqvslwclvkgfypsdiavewesngqpennykttppvldsdgsf flyskltvdksrwqqgnvfscsvmhealhnhytqkslslspg	**SEQ ID NO: 163**
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Binding Protein 21 Nucleotide Sequences		

Heavy chain A	caggtgcacctgacacagagcggacccgaagtgcggaagcctggcacctctgtgaa ggtgtcctgcaaggcccctggcaacaccctgaaaacctacgacctgcactgggtgcg cagcgtgccaggacagggactgcagtggatgggctggatcagccacgagggcgac aagaaagtgatcgtggaacggttcaaggccaaagtgaccatcgactgggacagaagc accaacaccgcctacctgcagctgagcggcctgacctctggcgataccgccgtgtact actgcgccaagggcagcaagcaccggctgagagactacgccctgtacgacgatgac ggcgccctgaactgggccgtggatgtggactacctgagcaacctggaattctggggcc agggcacagccgtgaccgtgtcatctgcttcgaccaagggccccagcgtgttccctct ggcccctagcagcaagagcacatctggcggaacagccgccctgggctgcctcgtga aggactactttcccgagcccgtgaccgtgtcctggaattctggcgccctgaccagcgg cgtgcacacctttccagctgtgctgcagtccagcggcctgtacagcctgagcagcgtc gtgacagtgcccagcagctctctgggcacccagacctacatctgcaacgtgaaccaca agcccagcaacaccaaggtggacaagaaggtggaacccaagagctgcgacaagac ccacacctgtccccttgtcctgcccccgaactgctgggaggcccttccgtgttcctgtt ccccccaaagcccaaggacaccctgatgatcagccggaccccccgaagtgacctgcgt ggtggtggatgtgtcccacgaggaccctgaagtgaagttcaattggtacgtggacggc gtggaagtgcacaacgccaagaccaagccaagagaggaacagtacaacagcaccta ccgggtggtgtccgtgctgaccgtgctgcaccaggactggctgaacggcaaagagta caagtgcaaggtgtccaacaaggccctgcctgcccccatcgagaaaaccatcagcaa ggccaagggccagccccgcgaaccccaggtgtgcacactgcccccaagcagggac gagctgaccaagaaccaggtgtccctgagctgtgccgtgaaaggcttctacccctccg atatcgccgtggaatgggagagcaacggccagcccgagaacaactacaagaccacc ccccctgtgctggacagcgacggctcattcttcctggtgtccaagctgacagtggacaa gtcccggtggcagcagggcaacgtgttcagctgctccgtgatgcacgaggccctgca caaccactacacccagaagtccctgagcctgagccccggcaag	**SEQ ID NO: 165**
Light chain A	gacttcgtgctgacccagagccctcacagcctgagcgtgacacctggcgagagcgcc agcatcagctgcaagagcagccactccctgatccacggcgaccggaacaactacctg gcttggtacgtgcagaagcccggcagatccccccagctgctgatctacctggccagca gcagagccagcggcgtgcccgatagattttctggcagcggcagcgacaaggacttca ccctgaagatcagccgggtggaaaccgaggacgtgggcacctactactgtatgcagg gcagagagagcccctggacctttggccagggcaccaaggtggacatcaagcgtacg gtggccgctcccagcgtgttcatcttcccacctagcgacgagcagctgaagtccggca cagcctctgtcgtgtgcctgctgaacaacttctacccccgcgaggccaaagtgcagtgg aaggtggacaacgccctgcagagcggcaacagccaggaaagcgtgaccgagcagg acagcaaggactccacctacagcctgagcagcaccctgacactgagcaaggccgact acgagaagcacaaggtgtacgcctgcgaagtgacccaccagggcctgtctagccccg tgaccaagagcttcaaccggggcgagtgt	**SEQ ID NO: 166**
Heavy chain B	gaggttagactggtggagtcaggaggggggcttgtgaagcccggtgggtctctccgc ctgagctgttctgcctccggctttgatttcgataacgcctggatgacctgggtcaggcag cctccaggtaagggactggagtgggtgggaagaatcacaggtccaggcgagggctg gtccgtggactacgcggaatctgttaaagggcggtttacaatctcaagggacaatacca agaataccttgtatttggagatgaacaacgtgagaactgaagacaccggatattacttct gtgccagaacaggcaaatactacgacttctggtccggctatccccctggcgaggaatat tttcaagactggggtcagggaacccttgttatcgtgtcctccgacaaaacccataccaga gcccacctggtgcagtctggcaccgccatgaagaaaccaggcgcctctgtgcgggtg tcctgtcagacaagcggctacaccttcaccgcccacatcctgttctggttccggcaggc ccctggcagaggactggaatgggtgggatggatcaagccccagtatggcgccgtgaa cttcggcggaggcttccgggatagagtgaccctgacccgggacgtgtaccgcgagat cgcctacatggacatccggggcctgaagcccgatgacaccgccgtgtactactgcgc cagagacagaagctacggcgacagcagctgggctctggatgcttggggccagggca caaccgtggtggtgtctgccgataagacccacaccgcttccaccaagggcccatcggt cttccccctggcaccctcctccaagagcacctctgggggcacagcggccctgggctg	**SEQ ID NO: 167**

	cctggtcaaggactacttccccgaaccggtgacggtgtcgtggaactcaggcgccctg accagcggcgtgcacaccttcccggctgtcctacagtcctcaggactctactccctcag cagcgtggtgaccgtgccctccagcagcttgggcacccagacctacatctgcaacgtg aatcacaagcccagcaacaccaaggtggacaagaaagttgagcccaaatcttgtgaca aaactcacacatgcccaccgtgcccagcacctgaactcctgggggggaccgtcagtctt cctcttccccccaaaacccaaggacaccctcatgatctcccggaccccctgaggtcacat gcgtggtggtggacgtgagccacgaagaccctgaggtcaagttcaactggtatgttga cggcgtggaggtgcataatgccaagacaaagccgcgggaggagcagtacaacagc acgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaagg agtacaagtgcaaggtctccaacaaagccctcccagcccccatcgagaaaaccatctc caaagccaaagggcagccccgagaaccacaggtgtacaccctgcccccatgccggg atgagctgaccaagaatcaagtcagcctgtggtgcctggtaaaaggcttctatcccagc gacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaagaccac gcctcccgtgctggactccgacggctccttcttcctctactcaaaactcaccgtggacaa gagcaggtggcagcaggggaacgtcttctcatgctccgtgatgcatgaggctctgcac aaccactacacgcagaagagcctctccctgtctccgggt	
Light chain B	tacatccacgtgacccagagccccagcagcctgtccgtgtccatcggcgacagagtga ccatcaactgccagacctctcagggcgtgggcagcgacctgcactggtatcagcacaa gcctggcagagcccccaagctgctgatccaccacacaagcagcgtggaagatggcgt gcccagcagattttccggcagcggcttccacaccagcttcaacctgaccatcagcgatc tgcaggccgacgacattgccacctactattgtcaggtgctgcagttcttcggcagaggc agcagactgcacatcaaggacaaaacccataccgcatccgaactgactcaggaccct gccgtctctgtggcactgaagcagactgtgactattacttgccgaggcgactcactgcg gagccactacgcttcctggtatcagaagaaacccggccaggcacctgtgctgctgttct acggaaagaacaataggccatctggcatccccgaccgcttttctggcagtgcatcagg gaaccgagccagtctgaccattaccggcgcccaggctgaggacgaagccgattacta ttgcagctcccgggataagagcggctccagactgagcgtgttcggaggaggaactaa actgaccgtcctcgataagacccatacccgtacggtggccgctcccagcgtgttcatctt cccacctagcgacgagcagctgaagtccggcacagcctctgtcgtgtgcctgctgaac aacttctacccccgcgaggccaaagtgcagtggaaggtggacaacgccctgcagagc ggcaacagccaggaaagcgtgaccgagcaggacagcaaggactccacctacagcct gagcagcaccctgacactgagcaaggccgactacgagaagcacaaggtgtacgcct gcgaagtgacccaccagggcctgtctagccccgtgaccaagagcttcaaccggggc gagtgt	**SEQ ID NO: 168**
Binding Protein 22 Amino Acid Sequences		
Heavy chain A	qvhltqsgpevrkpgtsvkvsckapgntlktydlhwvrsvpgqglqwmgwishe gdkkviverfkakvtidwdrstntaylqlsgltsgdtavyycakgskhrlrdyalydd dgalnwavdvdylsnlefwgqgtavtvssastkgpsvfplapsskstsggtaalgcl vkdyfpepvtvswnsgaltsgvhtfpavlqssglyslssvvtvpssslgtqtyicnvn hkpsntkvdkkvepkscdkthtcppcpapellggpsvflfppkpkdtlmisrtpevt cvvvdvshedpevkfnwyvdgvevhnaktkpreeqynstyrvvsvltvlhqdwl ngkeykckvsnkalpapiektiskakgqprepqvctlppsrdeltknqvslscavkg fypsdiavewesngqpennykttppvldsdgsfflvskltvdksrwqqgnvfscsv mhealhnhytqkslslspg	**SEQ ID NO: 169**
Light chain A	dfvltqsphslsvtpgesasisckssshslihgdrnnylawyvqkpgrspqlliylassr asgvpdrfsgsgsdkdftlkisrvetedvgtyycmqgrespwtfgqgtkvdikrtva apsvfifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqds kdstyslsstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 170**
Heavy chain B	rahlvqsgtamkkpgasvrvscqtsgytftahilfwfrqapgrglewvgwik pqygavnfgggfrdrvtltrdvyreiaymdirglkpddtavyycardrsygd sswaldawgqgttvvvsadkthtevrlvesggglvkpggslrlscsasgfdfd	**SEQ ID NO: 171**

	nawmtwvrqppgkglewvgritgpgegwsvdyaesvkgrftisrdntknt lylemnnvrtedtgyyfcartgkyydfwsgyppgeeyfqdwgqgtlvivss dkthtastkgpsvfplapsskstsggtaalgclvkdyfpepvtvswnsgalts gvhtfpavlqssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkkvepk scdkthtcppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshed pevkfnwyvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkey kckvsnkalpapiektiskakgqprepqvytlppcrdeltknqvslwclvkg fypsdiavewesngqpennykttppvldsdgsf	
Light chain B	aseltqdpavsvalkqtvtitcrgdslrshyaswyqkkpgqapvllfygknnrpsgip drfsgsasgnrasltitgaqaedeadyycssrdksgsrlsvfgggtkltvl dktht Yihvtqspsslsvsigdrvtincqtsqgvgsdlhwyqhkpgrapkllihhtssvedg vpsrfsgsgfhtsfnltisdlqaddiatyycqvlqffgrgsrlhik dkthtrtvaapsvfifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgns qesvteqdskdstyslsstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 172**
Binding Protein 22 Nucleotide Sequences		
Heavy chain A	caggtgcacctgacacagagcggacccgaagtgcggaagcctggcacctctgtgaa ggtgtcctgcaaggcccctggcaacaccctgaaaacctacgacctgcactgggtgcg cagcgtgccaggacagggactgcagtggatgggctggatcagccacgagggcgac aagaaagtgatcgtggaacggttcaaggccaaagtgaccatcgactgggacagaagc accaacaccgcctacctgcagctgagcggcctgacctctggcgataccgccgtgtact actgcgccaagggcagcaagcaccggctgagagactacgccctgtacgacgatgac ggcgccctgaactgggccgtggatgtggactacctgagcaacctggaattctggggcc agggcacagccgtgaccgtgtcatctgcttcgaccaagggccccagcgtgttccctct ggcccctagcagcaagagcacatctggcggaacagccgccctgggctgcctcgtga aggactactttcccgagcccgtgaccgtgtcctggaattctggcgccctgaccagcgg cgtgcacaccttccagctgtgctgcagtccagcggcctgtacagcctgagcagcgtc gtgacagtgcccagcagctctctgggcacccagacctacatctgcaacgtgaaccaca agcccagcaacaccaaggtggacaagaaggtggaacccaagagctgcgacaagac ccacacctgtccccttgtcctgcccccgaactgctgggaggcccttccgtgttcctgtt ccccccaaagcccaaggacaccctgatgatcagccggaccccgaagtgacctgcgt ggtggtggatgtgtcccacgaggaccctgaagtgaagttcaattggtacgtggacggc gtggaagtgcacaacgccaagaccaagccaagagaggaacagtacaacagcaccta ccgggtggtgtccgtgctgaccgtgctgcaccaggactggctgaacggcaaagagta caagtgcaaggtgtccaacaaggccctgcctgcccccatcgagaaaaccatcagcaa ggccaagggccagccccgcgaaccccaggtgtgcacactgcccccaagcagggac gagctgaccaagaaccaggtgtccctgagctgtgccgtgaaaggcttctacccctccg atatcgccgtggaatgggagagcaacggccagcccgagaacaactacaagaccacc ccccctgtgctggacagcgacggctcattcttcctggtgtccaagctgacagtggacaa gtcccggtggcagcagggcaacgtgttcagctgctccgtgatgcacgaggccctgca caaccactacacccagaagtccctgagcctgagccccggcaag	**SEQ ID NO: 173**
Light chain A	gacttcgtgctgacccagagccctcacagcctgagcgtgacacctggcgagagcgcc agcatcagctgcaagagcagccactccctgatccacggcgaccggaacaactacctg gcttggtacgtgcagaagcccggcagatccccccagctgctgatctacctggccagca gcagagccagcggcgtgcccgatagattttctggcagcggcagcgacaaggacttca ccctgaagatcagccgggtggaaaccgaggacgtgggcacctactactgtatgcagg gcagagagagcccctggacctttggccagggcaccaaggtggacatcaagcgtacg gtggccgctcccagcgtgttcatcttcccacctagcgacgagcagctgaagtccggca cagcctctgtcgtgtgcctgctgaacaacttctacccccgcgaggccaaagtgcagtgg aaggtggacaacgccctgcagagcggcaacagccaggaaagcgtgaccgagcagg acagcaaggactccacctacagcctgagcagcaccctgacactgagcaaggccgact acgagaagcacaaggtgtacgcctgcgaagtgacccaccagggcctgtctagccccg	**SEQ ID NO: 174**

	tgaccaagagcttcaaccggggcgagtgt	
Heavy chain B	agagcccacctggtgcagtctggcaccgccatgaagaaaccaggcgcctctgtgcgg gtgtcctgtcagacaagcggctacaccttcaccgcccacatcctgttctggttccggcag gcccctggcagaggactggaatgggtgggatggatcaagccccagtatggcgccgtg aacttcggcggaggcttccgggatagagtgaccctgacccgggacgtgtaccgcgag atcgcctacatggacatccggggcctgaagcccgatgacaccgccgtgtactactgcg ccagagacagaagctacggcgacagcagctgggctctggatgcttggggccagggc acaaccgtggtggtgtctgccgacaaaacccataccgaggttagactggtggagtcag gaggggggcttgtgaagcccggtgggtctctccgcctgagctgttctgcctccggcttt gatttcgataacgcctggatgacctgggtcaggcagcctccaggtaagggactggagt gggtgggaagaatcacaggtccaggcgagggctggtccgtggactacgcggaatct gttaaagggcggtttacaatctcaagggacaataccaagaataccttgtatttggagatg aacaacgtgagaactgaagacaccggatattacttctgtgccagaacaggcaaatacta cgacttctggtccggctatccccctggcgaggaatattttcaagactggggtcagggaa cccttgttatcgtgtcctccgataagacccacaccgcttccaccaagggcccatcggtct tccccctggcaccctcctccaagagcacctctgggggcacagcggccctgggctgcc tggtcaaggactacttccccgaaccggtgacggtgtcgtggaactcaggcgccctgac cagcggcgtgcacaccttcccggctgtcctacagtcctcaggactctactccctcagca gcgtggtgaccgtgccctccagcagcttgggcacccagacctacatctgcaacgtgaa tcacaagcccagcaacaccaaggtggacaagaaagttgagcccaaatcttgtgacaaa actcacacatgcccaccgtgcccagcacctgaactcctgggggaccgtcagtcttcct cttcccccaaaacccaaggacaccctcatgatctcccggaccccctgaggtcacatgc gtggtggtggacgtgagccacgaagaccctgaggtcaagttcaactggtatgttgacg gcgtggaggtgcataatgccaagacaaagccgcgggaggagcagtacaacagcac gtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggag tacaagtgcaaggtctccaacaaagccctcccagcccccatcgagaaaaccatctcca aagccaaagggcagccccgagaaccacaggtgtacaccctgcccccatgccgggat gagctgaccaagaatcaagtcagcctgtggtgcctggtaaaaggcttctatcccagcga catcgccgtggagtgggagagcaatgggcagccggagaacaactacaagaccacgc ctcccgtgctggactccgacggctccttcttcctctactcaaaactcaccgtggacaaga gcaggtggcagcaggggaacgtcttctcatgctccgtgatgcatgaggctctgcacaa ccactacacgcagaagagcctctccctgtctccgggt	**SEQ ID NO: 175**
Light chain B	gcatccgaactgactcaggaccctgccgtctctgtggcactgaagcagactgtgg actattacttgccgaggcgactcactgcggagccactacgcttcctggtatcagaa agaaacccggccaggcacctgtgctgctgttctacggaaagaacaataggcca tctggcatccccgaccgcttttctggcagtgcatcagggaaccgagccagtctg accattaccggcgcccaggctgaggacgaagccgattactattgcagctcccg ggataagagcggctccagactgagcgtgttcggaggaggaactaaactgacc gtcctcgacaaaacccatacctacatccacgtgacccagagccccagcagcct gtccgtgtccatcggcgacagagtgaccatcaactgccagacctctcagggcg tgggcagcgacctgcactggtatcagcacaagcctggcagagcccccaagct gctgatccaccacacaagcagcgtggaagatggcgtgcccagcagattttccg gcagcggcttccacaccagcttcaacctgaccatcagcgatctgcaggccgac gacattgccacctactattgtcaggtgctgcagttcttcggcagaggcagcaga ctgcacatcaaggataagacccatacccgtacggtggccgctcccagcgtgtt catcttcccacctagcgacgagcagctgaagtccggcacagcctctgtcgtgtg cctgctgaacaacttctacccccgcgaggccaaagtgcagtggaaggtggac aacgccctgcagagcggcaacagccaggaaagcgtgaccgagcaggacag caaggactccacctacagcctgagcagcaccctgacactgagcaaggccgac tacgagaagcacaaggtgtacgcctgcgaagtgacccaccagggcctgtcta gccccgtgaccaagagcttcaaccggggcgagtgt	**SEQ ID NO: 176**

Binding Protein 23 Amino Acid Sequences		
Heavy chain A	evrlvesggglvkpggslrlscsasgfdfdnawmtwvrqppgkglewvgritgpg egwsvdyaesvkgrftisrdntkntlylemnnvrtedtgyyfcartgkyydfwsgy ppgeeyfqdwgqgtlvivssastkgpsvfplapsskstsggtaalgclvkdyfpepv tvswnsgaltsgvhtfpavlqssglyslssvvtvpssslgtqtyicnvnhkpsntkvd kkvepkscdkthtcppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshe dpevkfnwyvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykckv snkalpapiektiskakgqprepqvctlppsrdeltknqvslscavkgfypsdiave wesngqpennykttppvldsdgsfflvskltvdksrwqqgnvfscsvmhealhnh ytqkslslspg	**SEQ ID NO: 177**
Light chain A	Aseltqdpavsvalkqtvtitcrgdslrshyaswyqkkpgqapvllfygknnrpsgi pdrfsgsasgnrasltitgaqaedeadyycssrdksgsrlsvfgggtkltvlsqpkaap svtlfppsseelqankatlvclisdfypgavtvawkadsspvkagvetttpskqsnnk yaassylsltpeqwkshrsyscqvthegstvektvaptecs	**SEQ ID NO: 178**
Heavy chain B	rahlvqsgtamkkpgasvrvscqtsgytftahilfwfrqapgrglewvgwik pqygavnfgggfrdrvtltrdvyreiaymdirglkpddtavyycardrsygd sswaldawgqgttvvvsadkthtQvhltqsgpevrkpgtsvkvsckapgnt lktydlhwvrsvpgqglqwmgwishegdkkviverfkakvtidwdrstnt aylqlsgltsgdtavyycakgskhrlrdyalydddgalnwavdvdylsnlef wgqgtavtvssdkthtastkgpsvfplapsskstsggtaalgclvkdyfpepv tvswnsgaltsgvhtfpavlqssglyslssvvtvpssslgtqtyicnvnhkpsn tkvdkkvepkscdkthtcppcpapellggpsvflfppkpkdtlmisrtpevt cvvvdvshedpevkfnwyvdgvevhnaktkpreeqynstyrvvsvltvlh qdwlngkeykckvsnkalpapiektiskakgqprepqvytlppcrdeltkn qvslwclvkgfypsdiavewesngqpennykttppvldsdgsfflyskltvd ksrwqqgnvfscsvmhealhnhytqkslslspg	**SEQ ID NO: 179**
Light chain B	dfvltqsphslsvtpgesasisckssshslihgdrnnylawyvqkpgrspqlliylassr asgvpdrfsgsgsdkdftlkisrvetedvgtyycmqgrespwtfgqgtkvdikdkth t yihvtqspsslsvsigdrvtincqtsqgvgsdlhwyqhkpgrapkllihhtssvedgv psrfsgsgfhtsfnltisdlqaddiatyycqvlqffgrgsrlhikdkthtrtvaapsvfifp psdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstysls stltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 180**
Binding Protein 23 Nucleotide Sequences		
Heavy chain A	gaggttagactggtggagtcaggaggggggcttgtgaagcccggtgggtctctccgc ctgagctgttctgcctccggctttgatttcgataacgcctggatgacctgggtcaggcag cctccaggtaagggactggagtgggtgggaagaatcacaggtccaggcgagggctg gtccgtggactacgcggaatctgttaaagggcggtttacaatctcaagggacaataccа agaataccttgtatttggagatgaacaacgtgagaactgaagacaccggatattacttct gtgccagaacaggcaaatactacgacttctggtccggctatccccctggcgaggaatat tttcaagactggggtcagggaacccttgttatcgtgtcctccgcgtcgaccaagggccc cagcgtgttccctctggcccctagcagcaagagcacatctggcggaacagccgccct gggctgcctcgtgaaggactactttcccgagcccgtgaccgtgtcctggaattctggcg ccctgaccagcggcgtgcacaccttccagctgtgctgcagtccagcggcctgtacag cctgagcagcgtcgtgacagtgcccagcagctctctgggcacccagacctacatctgc aacgtgaaccacaagcccagcaacaccaaggtggacaagaaggtggaacccaaga gctgcgacaagacccacacctgtccccttgtcctgcccccgaactgctgggaggccc ttccgtgttcctgttcccccaaagcccaaggacaccctgatgatcagccggacccccg aagtgacctgcgtggtggtggatgtgtcccacgaggaccctgaagtgaagttcaattgg tacgtggacggcgtggaagtgcacaacgccaagaccaagccaagagaggaacagta caacagcacctaccgggtggtgtccgtgctgaccgtgctgcaccaggactggctgaac	**SEQ ID NO: 181**

	ggcaaagagtacaagtgcaaggtgtccaacaaggccctgcctgcccccatcgagaaa accatcagcaaggccaagggccagccccgcgaaccccaggtgtgcacactgccccc aagcagggacgagctgaccaagaaccaggtgtccctgagctgtgccgtgaaaggctt ctacccctccgatatcgccgtggaatgggagagcaacggccagcccgagaacaacta caagaccacccccccctgtgctggacagcgacggctcattcttcctggtgtccaagctga cagtggacaagtcccggtggcagcagggcaacgtgttcagctgctccgtgatgcacg aggccctgcacaaccactacacccagaagtccctgagcctgagccccggcaag	
Light chain A	gcatccgaactgactcaggaccctgccgtctctgtggcactgaagcagactgtg actattacttgccgaggcgactcactgcggagccactacgcttcctggtatcaga agaaacccggccaggcacctgtgctgctgttctacggaaagaacaataggcca tctggcatccccgaccgcttttctggcagtgcatcagggaaccgagccagtctg accattaccggcgcccaggctgaggacgaagccgattactattgcagctcccg ggataagagcggctccagactgagcgtgttcggaggaggaactaaactgacc gtcctcagtcagcccaaggctgccccctcggtcactctgttcccgccctcgagt gaggagcttcaagccaacaaggccacactggtgtgtctcataagtgacttctac ccgggagccgtgacagtggcctggaaggcagatagcagccccgtcaaggcg ggagtggagaccaccacaccctccaaacaaagcaacaacaagtacgcggcc agcagctacctgagcctgacgcctgagcagtggaagtcccacagaagctaca gctgccaggtcacgcatgaagggagcaccgtggagaagacagtggccccta cagaatgttca	**SEQ ID NO: 182**
Heavy chain B	agagcccacctggtgcagtctggcaccgccatgaagaaaccaggcgcctctgtgcgg gtgtcctgtcagacaagcggctacaccttcaccgcccacatcctgttctggttccggcag gcccctggcagaggactggaatgggtgggatggatcaagccccagtatggcgccgtg aacttcggcggaggcttccgggatagagtgaccctgacccgggacgtgtaccgcgag atcgcctacatggacatccggggcctgaagcccgatgacaccgccgtgtactactgcg ccagagacagaagctacggcgacagcagctgggctctggatgcttggggccagggc acaaccgtggtggtgtctgccgacaaaacccatacccaggtgcacctgacacagagc ggacccgaagtgcggaagcctggcacctctgtgaaggtgtcctgcaaggccccctggc aacaccctgaaaacctacgacctgcactgggtgcgcagcgtgccaggacagggactg cagtggatgggctggatcagccacgagggcgacaagaaagtgatcgtggaacggttc aaggccaaagtgaccatcgactgggacagaagcaccaacaccgcctacctgcagctg agcggcctgacctctggcgataccgccgtgtactactgcgccaagggcagcaagcac cggctgagagactacgccctgtacgacgatgacggcgccctgaactgggccgtggat gtggactacctgagcaacctggaattctggggccagggcacagccgtgaccgtgtcat ctgataagacccacaccgcttccaccaagggcccatcggtcttcccccctggcaccctcc tccaagagcacctctgggggcacagcggccctgggctgcctggtcaaggactacttcc ccgaaccggtgacggtgtcgtggaactcaggcgccctgaccagcggcgtgcacacct tcccggctgtcctacagtcctcaggactctactccctcagcagcgtggtgaccgtgccct ccagcagcttgggcacccagacctacatctgcaacgtgaatcacaagcccagcaaca ccaaggtggacaagaaagttgagcccaaatcttgtgacaaaactcacacatgcccacc gtgcccagcacctgaactcctgggggggaccgtcagtcttcctcttcccccaaaaccca aggacaccctcatgatctcccggaccccctgaggtcacatgcgtggtggtggacgtgag ccacgaagaccctgaggtcaagttcaactggtatgttgacggcgtggaggtgcataatg ccaagacaaagccgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtc ctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctcca acaaagccctcccagcccccatcgagaaaaccatctccaaagccaaagggcagccc cgagaaccacaggtgtacaccctgcccccatgccgggatgagctgaccaagaatcaa gtcagcctgtggtgcctggtaaaaggcttctatcccagcgacatcgccgtggagtggg agagcaatgggcagccggagaacaactacaagaccacgcctcccgtgctggactcc gacggctccttcttcctctactcaaaactcaccgtggacaagagcaggtggcagcagg ggaacgtcttctcatgctccgtgatgcatgaggctctgcacaaccactacacgcagaag agcctctccctgtctccgggt	**SEQ ID NO: 183**

Light chain B	gacttcgtgctgacccagagccctcacagcctgagcgtgacacctggcgaga gcgccagcatcagctgcaagagcagccactccctgatccacggcgaccggaa caactacctggcttggtacgtgcagaagcccggcagatccccccagctgctga tctacctggccagcagcagagccagcggcgtgcccgatagattttctggcagc ggcagcgacaaggacttcaccctgaagatcagccgggtggaaaccgaggac gtgggcacctactactgtatgcagggcagagagagcccctggacctttggcca gggcaccaaggtggacatcaaggacaaaacccatacctacatccacgtgacc cagagccccagcagcctgtccgtgtccatcggcgacagagtgaccatcaactg ccagacctctcagggcgtgggcagcgacctgcactggtatcagcacaagcct ggcagagcccccaagctgctgatccaccacacaagcagcgtggaagatggc gtgcccagcagattttccggcagcggcttccacaccagcttcaacctgaccatc agcgatctgcaggccgacgacattgccacctactattgtcaggtgctgcagttct tcggcagaggcagcagactgcacatcaaggataagacccatacccgtacggt ggccgctcccagcgtgttcatcttcccacctagcgacgagcagctgaagtccg gcacagcctctgtcgtgtgcctgctgaacaacttctacccccgcgaggccaaa gtgcagtggaaggtggacaacgccctgcagagcggcaacagccaggaaag cgtgaccgagcaggacagcaaggactccacctacagcctgagcagcaccctg acactgagcaaggccgactacgagaagcacaaggtgtacgcctgcgaagtga cccaccagggcctgtctagccccgtgaccaagagcttcaaccggggcgagtg t	**SEQ ID NO: 184**
Binding Protein 24 Amino Acid Sequences		
Heavy chain A	evrlvesggglvkpggslrlscsasgfdfdnawmtwvrqppgkglewvgritgpge gwsvdyaesvkgrftisrdntkntlylemnnvrtedtgyyfcartgkyydfwsgypp geeyfqdwgqgtlvivssastkgpsvfplapsskstsggtaalgclvkdyfpepvtvs wnsgaltsgvhtfpavlqssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkkve pkscdkthtcppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpev kfnwyvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykckvsnkal papiektiskakgqprepqvctlppsrdeltknqvslscavkgfypsdiavewesngq pennykttppvldsdgsfflvskltvdksrwqqgnvfscsvmhealhnhytqkslsls pg	**SEQ ID NO: 185**
Light chain A	aseltqdpavsvalkqtvtitcrgdslrshyaswyqkkpgqapvllfygknnrpsgip drfsgsasgnrasltitgaqaedeadyycssrdksgsrlsvfgggtkltvlsqpkaapsv tlfppsseelqankatlvclisdfypgavtvawkadsspvkagvetttpskqsnnkya assylsltpeqwkshrsyscqvthegstvektvaptecs	**SEQ ID NO: 186**
Heavy chain B	Qvhltqsgpevrkpgtsvkvsckapgntlktydlhwvrsvpgqglqwmg wishegdkkviverfkakvtidwdrstntaylqlsgltsgdtavyycakgskh rlrdyalydddgalnwavdvdylsnlefwgqgtavtvss dkthtrahlvqsgtamkkpgasvrvscqtsgytftahilfwfrqapgrglewv gwikpqygavnfgggfrdrvtltrdvyreiaymdirglkpddtavyycardrs ygdsswaldawgqgttvvvsadkthtastkgpsvfplapsskstsggtaalgc lvkdyfpepvtvswnsgaltsgvhtfpavlqssglyslssvvtvpssslgtqtyi cnvnhkpsntkvdkkvepkscdkthtcppcpapellggpsvflfppkpkdtl misrtpevtcvvvdvshedpevkfnwyvdgvevhnaktkpreeqynstyr vvsvltvlhqdwlngkeykckvsnkalpapiektiskakgqprepqvytlpp crdeltknqvslwclvkgfypsdiavewesngqpennykttppvldsdgsffl yskltvdksrwqqgnvfscsvmhealhnhytqkslslspg	**SEQ ID NO: 187**
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	ltlskadyekhkvyacevthqglsspvtksfnrgec	
Binding Protein 24 Nucleotide Sequences		
Heavy chain A	gaggttagactggtggagtcaggaggggggcttgtgaagcccggtgggtctctccgcc tgagctgttctgcctccggctttgatttcgataacgcctggatgacctgggtcaggcagcc tccaggtaagggactggagtgggtgggaagaatcacaggtccaggcgagggctggtc cgtggactacgcggaatctgttaaagggcggtttacaatctcaagggacaataccaaga ataccttgtatttggagatgaacaacgtgagaactgaagacaccggatattacttctgtgc cagaacaggcaaatactacgacttctggtccggctatccccctggcgaggaatattttca agactggggtcagggaacccttgttatcgtgtcctccgcgtcgaccaagggccccagcg tgttccctctggcccctagcagcaagagcacatctggcggaacagccgccctgggctg cctcgtgaaggactactttcccgagcccgtgaccgtgtcctggaattctggcgccctgac cagcggcgtgcacacctttccagctgtgctgcagtccagcggcctgtacagcctgagca gcgtcgtgacagtgcccagcagctctctgggcacccagacctacatctgcaacgtgaac cacaagcccagcaacaccaaggtggacaagaaggtggaacccaagagctgcgacaa gacccacacctgtccccccttgtcctgcccccgaactgctgggaggcccttccgtgttcct gttcccccccaaagcccaaggacaccctgatgatcagccggaccccccgaagtgacctgc gtggtggtggatgtgtcccacgaggaccctgaagtgaagttcaattggtacgtggacgg cgtggaagtgcacaacgccaagaccaagccaagagaggaacagtacaacagcaccta ccgggtggtgtccgtgctgaccgtgctgcaccaggactggctgaacggcaaagagtac aagtgcaaggtgtccaacaaggccctgcctgccccccatcgagaaaaccatcagcaagg ccaagggccagccccgcgaaccccaggtgtgcacactgcccccaagcagggacgag ctgaccaagaaccaggtgtccctgagctgtgccgtgaaaggcttctacccctccgatatc gccgtggaatgggagagcaacggccagcccgagaacaactacaagaccacccccccc tgtgctggacagcgacggctcattcttcctggtgtccaagctgacagtggacaagtcccg gtggcagcagggcaacgtgttcagctgctccgtgatgcacgaggccctgcacaaccac tacacccagaagtccctgagcctgagccccggcaag	**SEQ ID NO: 189**
Light chain A	gcatccgaactgactcaggaccctgccgtctctgtggcactgaagcagactgtg actattacttgccgaggcgactcactgcggagccactacgcttcctggtatcaga agaaacccggccaggcacctgtgctgctgttctacggaaagaacaataggccat ctggcatccccgaccgcttttctggcagtgcatcagggaaccgagccagtctga ccattaccggcgcccaggctgaggacgaagccgattactattgcagctcccgg gataagagcggctccagactgagcgtgttcggaggaggaactaaactgaccgt cctcagtcagcccaaggctgccccctcggtcactctgttcccgccctcgagtgag gagcttcaagccaacaaggccacactggtgtgtctcataagtgacttctacccgg gagccgtgacagtggcctggaaggcagatagcagccccgtcaaggcgggagt ggagaccaccacaccctccaaacaaagcaacaacaagtacgcggccagcagc tacctgagcctgacgcctgagcagtggaagtcccacagaagctacagctgcca ggtcacgcatgaagggagcaccgtggagaagacagtggcccctacagaatgtt ca	**SEQ ID NO: 190**
Heavy chain B	tacatccacgtgacccagagccccagcagcctgtccgtgtccatcggcgacagagtga ccatcaactgccagacctctcagggcgtgggcagcgacctgcactggtatcagcacaa gcctggcagagcccccaagctgctgatccaccacacaagcagcgtggaagatggcgt gcccagcagattttccggcagcggcttccacaccagcttcaacctgaccatcagcgatct gcaggccgacgacattgccacctactattgtcaggtgctgcagttcttcggcagaggca gcagactgcacatcaaggacaaaacccataccgacttcgtgctgacccagagccctca cagcctgagcgtgacacctggcgagagcgccagcatcagctgcaagagcagccactc cctgatccacggcgaccggaacaactacctggcttggtacgtgcagaagcccggcaga tccccccagctgctgatctacctggccagcagcagagccagcggcgtgcccgatagatt ttctggcagcggcagcgacaaggacttcaccctgaagatcagccgggtggaaaccga ggacgtgggcacctactactgtatgcagggcagagagagcccctggacctttggccag ggcaccaaggtggacatcaaggataagacccatacccgtacggtggccgctcccagc gtgttcatcttcccacctagcgacgagcagctgaagtccggcacagcctctgtcgtgtgc	**SEQ ID NO: 191**

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Light chain B	tacatccacgtgacccagagccccagcagcctgtccgtgtccatcggcgacag agtgaccatcaactgccagacctctcagggcgtgggcagcgacctgcactggt atcagcacaagcctggcagagcccccaagctgctgatccaccacacaagcagc gtggaagatggcgtgcccagcagattttccggcagcggcttccacaccagcttc aacctgaccatcagcgatctgcaggccgacgacattgccacctactattgtcagg tgctgcagttcttcggcagaggcagcagactgcacatcaaggacaaaacccata ccgacttcgtgctgacccagagccctcacagcctgagcgtgacacctggcgag agcgccagcatcagctgcaagagcagccactccctgatccacggcgaccgga acaactacctggcttggtacgtgcagaagcccggcagatccccccagctgctga tctacctggccagcagcagagccagcggcgtgcccgatagattttctggcagcg gcagcgacaaggacttcaccctgaagatcagccgggtggaaaccgaggacgt gggcacctactactgtatgcagggcagagagagccccctggacctttggccagg gcaccaaggtggacatcaaggataagacccatacccgtacggtggccgctccc agcgtgttcatcttcccacctagcgacgagcagctgaagtccggcacagcctct gtcgtgtgcctgctgaacaacttctacccccgcgaggccaaagtgcagtggaag gtggacaacgccctgcagagcggcaacagccaggaaagcgtgaccgagcag gacagcaaggactccacctacagcctgagcagcaccctgacactgagcaagg ccgactacgagaagcacaaggtgtacgcctgcgaagtgacccaccagggcct gtctagccccgtgaccaagagcttcaaccggggcgagtgt	**SEQ ID NO: 192**
Binding Protein 25 Amino Acid Sequences		
Heavy chain A	qvqlvqsggqmkkpgesmriscrasgyefi***dctln***wirlapgkrpewmg***wlkprg gavnyarplqg***rvtmtrdvysdtaflelrsltvddtavyfctr***gkncdynwdfeh***wgr gtpvivssastkgpsvfplapsskstsggtaalgclvkdyfpepvtvswnsgaltsgvh tfpavlqssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkkvepkscdkthtcp pcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnwyvdgve vhnaktkpreeqynstyrvvsvltvlhqdwlngkeykckvsnkalpapiektiskak gqprepqvctlppsrdeltknqvslscavkgfypsdiavewesngqpennykttppv ldsdgsfflvskltvdksrwqqgnvfscsvlhealhshytqkslslspg	**SEQ ID NO:193**
Light chain A	eivltqspgtlslspgetaiisc***rtsqygsla***wyqqrpgqaprlviy***sgstraa***gipdrfs gsrwgpdynltisnlesgdfgvyyc***qqyef***fgqgtkvqvdikrtvaapsvfifppsde qlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsstltls kadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 194**
Heavy chain B	evrlvesggglvkpggslrlscsasgfdfdnawmtwvrqppgkglewvgrit gpgegwsvdyaesvkgrftisrdntkntlylemnnvrtedtgyyfcartgkyy dfwsgyppgeeyfqdwgqgtlvivssdkthtqvqlvesgggvvqpgtslrls caasqfrfdgygmhwvrqapgkglewvasishdgikkyhaekvwgrftisr dnskntlylqmnslrpedtalyycakdlredeceewwsdyydfgkqlpcaks rgglvgiadnwgqgtmvtvssdkthtastkgpsvfplapsskstsggtaalgcl vkdyfpepvtvswnsgaltsgvhtfpavlqssglyslssvvtvpssslgtqtyic nvnhkpsntkvdkkvepkscdkthtcppcpapellggpsvflfppkpkdtl misrtpevtcvvvdvshedpevkfnwyvdgvevhnaktkpreeqynstyr vvsvltvlhqdwlngkeykckvsnkalpapiektiskakgqprepqvytlpp crdeltknqvslwclvkgfypsdiavewesngqpennykttppvldsdgsffl yskltvdksrwqqgnvfscsvlhealhshytqkslslspg	**SEQ ID NO: 195**
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Binding Protein 25 Nucleotide Sequences		
Heavy chain A	caggtgcagctggtgcagtctggcggccagatgaagaaacccggcgagagcatgcgg atcagctgcagagccagcggctacgagttcatcgactgcaccctgaactggatcagact ggcccctggcaagcggcctgagtggatgggatggctgaagcctagaggcggagccgt gaactacgccagacctctgcagggcagagtgaccatgacccgggacgtgtacagcgat accgccttcctggaactgcggagcctgaccgtggatgataccgccgtgtacttctgcacc cggggcaagaactgcgactacaactgggacttcgagcactggggcagaggcacccct gtgatcgtgtcaagcgcgtcgaccaagggccccagcgtgttccctctggcccctagcag caagagcacatctggcggaacagccgccctgggctgcctcgtgaaggactactttcccg agcccgtgaccgtgtcctggaattctggcgccctgaccagcggcgtgcacaccttttcca gctgtgctgcagtccagcggcctgtacagcctgagcagcgtcgtgacagtgcccagca gctctctgggcacccagacctacatctgcaacgtgaaccacaagcccagcaacaccaa ggtggacaagaaggtggaacccaagagctgcgacaagacccacacctgtccccttgt cctgccccgaactgctgggaggcccttccgtgttcctgttcccccaaagcccaagga caccctgatgatcagccggaccccgaagtgacctgcgtggtggtggatgtgtcccacg aggaccctgaagtgaagttcaattggtacgtggacggcgtggaagtgcacaacgccaa gaccaagccaagagaggaacagtacaacagcacctaccgggtggtgtccgtgctgac cgtgctgcaccaggactggctgaacggcaaagagtacaagtgcaaggtgtccaacaag gccctgcctgcccccatcgagaaaaccatcagcaaggccaagggccagccccgcgaa ccccaggtgtgcacactgcccccaagcagggacgagctgaccaagaaccaggtgtcc ctgagctgtgccgtgaaaggcttctacccctccgatatcgccgtggaatgggagagcaa cggccagcccgagaacaactacaagaccacccccccctgtgctggacagcgacggctc attcttcctggtgtccaagctgacagtggacaagtcccggtggcagcagggcaacgtgtt cagctgctccgtgctgcatgaggctctgcacagccactacacgcagaagagcctctccc tgtctccgggt	**SEQ ID NO: 197**
Light chain A	Gagatcgtgctgacacagagccctggcaccctgagcctgtctccaggcgagacagcc atcatcagctgccggacaagccagtacggcagcctggcctggtatcagcagaggcctg gacaggcccccagactcgtgatctacagcggcagcacaagagccgccggaatccccg atagattcagcggctccagatggggccctgactacaacctgaccatcagcaacctggaa agcggcgacttcggcgtgtactactgccagcagtacgagttcttcggccagggcaccaa ggtgcaggtggacatcaagcgtacggtggccgctcccagcgtgttcatcttcccacctag cgacgagcagctgaagtccggcacagcctctgtcgtgtgcctgctgaacaacttctaccc ccgcgaggccaaagtgcagtggaaggtggacaacgccctgcagagcggcaacagcc aggaaagcgtgaccgagcaggacagcaaggactccacctacagcctgagcagcacc ctgacactgagcaaggccgactacgagaagcacaaggtgtacgcctgcgaagtgacc caccagggcctgtctagccccgtgaccaagagcttcaaccggggcgagtgt	**SEQ ID NO: 198**
Heavy chain B	gaggttagactggtggagtcaggaggggggcttgtgaagcccggtgggtctctccgcct gagctgttctgcctccggctttgatttcgataacgcctggatgacctgggtcaggcagcct ccaggtaagggactggagtgggtgggaagaatcacaggtccaggcgagggctggtcc gtggactacgcggaatctgttaaagggcggtttacaatctcaagggacaataccaagaat accttgtatttggagatgaacaacgtgagaactgaagacaccggatattacttctgtgcca gaacaggcaaatactacgacttctggtccggctatccccctggcgaggaatattttcaag actggggtcagggaacccttgttatcgtgtcctccgacaaaacccatacccaggtgcagt tggtggagtctgggggaggcgtggtccagcctgggacgtccctgagactctcctgtgca gcctctcaattcaggtttgatggttatggcatgcactgggtccgccaggccccaggcaag gggctggagtgggtggcatctatatcacatgatggaattaaaaagtatcacgcagaaaaa gtgtggggccgcttcaccatctccagagacaattccaagaacacactgtatctacaaatg aacagcctgcgacctgaggacacggctctctactactgtgcgaaagatttgcgagaaga cgaatgtgaagagtggtggtcggattattacgattttgggaaacaactcccttgcgcaaag	**SEQ ID NO: 199**

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Light chain B	cagtctgtgctgacgcagccgccctcagtgtctgcggccccaggacagaaggt caccatctcctgctctggaaacacctccaacattggcaataattttgtgtcctggtat caacagcgccccggcagagccccccaactcctcatttatgaaactgacaagcga ccctcagggattcctgaccgattctctgcttccaagtctggtacgtcaggcaccct ggccatcaccgggctgcagactggggacgaggccgattattactgcgccacat gggctgccagcctgagttccgcgcgtgtcttcggaactgggaccaaggtcatcg tcctggacaaaacccataccgcatccgaactgactcaggaccctgccgtctctgt ggcactgaagcagactgtgactattacttgccgaggcgactcactgcggagcca ctacgcttcctggtatcagaagaaacccggccaggcacctgtgctgctgttctac ggaaagaacaataggccatctggcatccccgaccgcttttctggcagtgcatcag ggaaccgagccagtctgaccattaccggcgcccaggctgaggacgaagccga ttactattgcagctcccgggataagagcggctccagactgagcgtgttcggagg aggaactaaactgaccgtcctcgataagacccatacccgtacggtggccgctcc cagcgtgttcatcttcccacctagcgacgagcagctgaagtccggcacagcctct gtcgtgtgcctgctgaacaacttctacccccgcgaggccaaagtgcagtggaag gtggacaacgccctgcagagcggcaacagccaggaaagcgtgaccgagcag gacagcaaggactccacctacagcctgagcagcaccctgacactgagcaagg ccgactacgagaagcacaaggtgtacgcctgcgaagtgacccaccagggcct gtctagccccgtgaccaagagcttcaaccggggcgagtgt	**SEQ ID NO: 200**
Binding Protein 26 Amino Acid Sequences		
Heavy chain A	Rahlvqsgtamkkpgasvrvscqts***gytftahi***lfwfrqapgrglewvgw***ikpqyg*** ***av***nfgggfrdrvtltrdvyreiaymdirglkpddtavyycar***drsygdsswalda***wg qgttvvvsaastkgpsvfplapsskstsggtaalgclvkdyfpepvtvswnsgaltsgv htfpavlqssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkkvepkscdkthtc ppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnwyvdgv evhnaktkpreeqynstyrvvsvltvlhqdwlngkeykckvsnkalpapiektiska kgqprepqvctlppsrdeltknqvslscavkgfypsdiavewesngqpennykttpp vldsdgsfflvskltvdksrwqqgnvfscsvlhealhshytqkslslspg	**SEQ ID NO: 201**
Light chain A	yihvtqspsslsvsigdrvtincqts***qgvgsd***lhwyqhkpgrapkllihhtssvedgvp srfsgsgf***hts***fnltisdlqaddiatyyc***qvlqff***grgsrlhikrtvaapsvfifppsdeql ksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsstltlska dyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO:202**

Heavy chain B	evrlvesggglvkpggslrlscsasgfdfdnawmtwvrqppgkglewvgrit gpgegwsvdyaesvkgrftisrdntkntlylemnnvrtedtgyyfcartgkyy dfwsgyppgeeyfqdwgqgtlvivssdkthtqvqlvesgggvvqpgtslrls caasqfrfdgygmhwvrqapgkglewvasishdgikkyhaekvwgrftisr dnskntlylqmnslrpedtalyycakdlredeceewwsdyydfgkqlpcaks rgglvgiadnwgqgtmvtvssdkthtastkgpsvfplapsskstsggtaalgcl vkdyfpepvtvswnsgaltsgvhtfpavlqssglyslssvvtvpssslgtqtyic nvnhkpsntkvdkkvepkscdkthtcppcpapellggpsvflfppkpkdtl misrtpevtcvvvdvshedpevkfnwyvdgvevhnaktkpreeqynstyr vvsvltvlhqdwlngkeykckvsnkalpapiektiskakgqprepqvytlpp crdeltknqvslwclvkgfypsdiavewesngqpennykttppvldsdgsffl yskltvdksrwqqgnvfscsvlhealhshytqkslslspg	**SEQ ID NO: 203**
Light chain B	qsvltqppsvsaapgqkvtiscsgntsnignnfvswyqqrpgrapqlliyetdkrpsgi pdrfsasksgtsgtlaitglqtgdeadyycatwaaslssarvfgtgtkvivldkthtaselt qdpavsvalkqtvtitcrgdslrshyaswyqkkpgqapvllfygknnrpsgipdrfsg sasgnrasltitgaqaedeadyycssrdksgsrlsvfgggtkltvldkthtrtvaapsvfif ppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstysl sstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 204**
Binding Protein 26 Nucleotide Sequences		
Heavy chain A	agagcccacctggtgcagtctggcaccgccatgaagaaaccaggcgcctctgtgcggg tgtcctgtcagacaagcggctacaccttcaccgcccacatcctgttctggttccggcagg cccctggcagaggactggaatgggtgggatggatcaagccccagtatggcgccgtgaa cttcggcggaggcttccgggatagagtgaccctgacccgggacgtgtaccgcgagatc gcctacatggacatccggggcctgaagcccgatgacaccgccgtgtactactgcgcca gagacagaagctacggcgacagcagctgggctctggatgcttggggccagggcacaa ccgtggtggtgtctgccgcctctacaaagggccccagcgtgttccctctggcccctagca gcaagagcacatctggcggaacagccgccctgggctgcctcgtgaaggactactttccc gagcccgtgaccgtgtcctggaattctggcgccctgaccagcggcgtgcacaccttcc agctgtgctgcagtccagcggcctgtacagcctgagcagcgtcgtgacagtgcccagc agctctctgggcacccagacctacatctgcaacgtgaaccacaagcccagcaacacca aggtggacaagaaggtggaacccaagagctgcgacaagacccacacctgtccccctg tcctgccccgaactgctgggaggcccttccgtgttcctgttcccccaaagcccaagga caccctgatgatcagccggacccccgaagtgacctgcgtggtggtggatgtgtcccacg aggaccctgaagtgaagttcaattggtacgtggacggcgtggaagtgcacaacgccaa gaccaagccaagaggaggaacagtacaacagcacctaccgggtggtgtccgtgctgac cgtgctgcaccaggactggctgaacggcaaagagtacaagtgcaaggtgtccaacaag gccctgcctgcccccatcgagaaaaccatcagcaaggccaagggccagccccgcgaa ccccaggtgtgcacactgcccccaagcagggacgagctgaccaagaaccaggtgtcc ctgagctgtgccgtgaaaggcttctacccctccgatatcgccgtggaatgggagagcaa cggccagcccgagaacaactacaagaccacccccctgtgctggacagcgacggctc attcttcctggtgtccaagctgacagtggacaagtcccggtggcagcagggcaacgtgtt cagctgctccgtgctgcatgaggctctgcacagccactacacgcagaagagcctctccc tgtctccgggt	**SEQ ID NO: 205**
Light chain A	tacatccacgtgacccagagccccagcagcctgtccgtgtccatcggcgacagagtga ccatcaactgccagacctctcagggcgtgggcagcgacctgcactggtatcagcacaa gcctggcagagcccccaagctgctgatccaccacacaagcagcgtggaagatggcgt gcccagcagattttccggcagcggcttccacaccagcttcaacctgaccatcagcgatct gcaggccgacgacattgccacctactattgtcaggtgctgcagttcttcggcagaggcag cagactgcacatcaagcgtacggtggccgctcccagcgtgttcatcttcccacctagcga cgagcagctgaagtccggcacagcctctgtcgtgtgcctgctgaacaacttctacccccg cgaggccaaagtgcagtggaaggtggacaacgccctgcagagcggcaacagccagg aaagcgtgaccgagcaggacagcaaggactccacctacagcctgagcagcaccctga cactgagcaaggccgactacgagaagcacaaggtgtacgcctgcgaagtgacccacc	**SEQ ID NO: 206**

	agggcctgtctagccccgtgaccaagagcttcaaccggggcgagtgt	
Heavy chain B	gaggttagactggtggagtcaggaggggggcttgtgaagcccggtgggtctctccgcct gagctgttctgcctccggctttgatttcgataacgcctggatgacctgggtcaggcagcct ccaggtaagggactggagtgggtgggaagaatcacaggtccaggcgagggctggtcc gtggactacgcggaatctgttaaagggcggtttacaatctcaagggacaataccaagaat accttgtatttggagatgaacaacgtgagaactgaagacaccggatattacttctgtgcca gaacaggcaaatactacgacttctggtccggctatccccctggcgaggaatattttcaag actggggtcagggaacccttgttatcgtgtcctccgacaaaacccatacccaggtgcagt tggtggagtctgggggaggcgtggtccagcctgggacgtccctgagactctcctgtgca gcctctcaattcaggtttgatggttatggcatgcactgggtccgccaggccccaggcaag gggctggagtgggtggcatctatatcacatgatggaattaaaaagtatcacgcagaaaaa gtgtggggccgcttcaccatctccagagacaattccaagaacacactgtatctacaaatg aacagcctgcgacctgaggacacggctctctactactgtgcgaaagatttgcgagaaga cgaatgtgaagagtggtggtcggattattacgattttgggaaacaactcccttgcgcaaag tcacgcggcggcttggttggaattgctgataactggggccaagggacaatggtcaccgt ctcttcagataagacccacaccgcttccaccaagggcccatcggtcttcccctggcacc ctcctccaagagcacctctgggggcacagcggccctgggctgcctggtcaaggactac ttccccgaaccggtgacggtgtcgtggaactcaggcgccctgaccagcggcgtgcaca ccttcccggctgtcctacagtcctcaggactctactccctcagcagcgtggtgaccgtgc cctccagcagcttgggcacccagacctacatctgcaacgtgaatcacaagcccagcaac accaaggtggacaagaaagttgagcccaaatcttgtgacaaaactcacacatgcccacc gtgcccagcacctgaactcctgggggaccgtcagtcttcctcttcccccaaaacccaa ggacaccctcatgatctcccggaccccctgaggtcacatgcgtggtggtggacgtgagcc acgaagaccctgaggtcaagttcaactggtatgttgacggcgtggaggtgcataatgcc aagacaaagccgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctc accgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaaca aagccctcccagcccccatcgagaaaaccatctccaaagccaaagggcagccccgag aaccacaggtgtacaccctgcccccatgccgggatgagctgaccaagaatcaagtcag cctgtggtgcctggtaaaaggcttctatcccagcgacatcgccgtggagtgggagagca atgggcagccggagaacaactacaagaccacgcctcccgtgctggactccgacggctc cttcttcctctactcaaaactcaccgtggacaagagcaggtggcagcaggggaacgtctt ctcatgctccgtgctgcatgaggctctgcacagccactacacgcagaagagcctctccct gtctccgggt	**SEQ ID NO: 207**
Light chain B	cagtctgtgctgacgcagccgccctcagtgtctgcggccccaggacagaaggtcaccat ctcctgctctggaaacacctccaacattggcaataattttgtgtcctggtatcaacagcgcc ccggcagagccccccaactcctcatttatgaaactgacaagcgaccctcagggattcctg accgattctctgcttccaagtctggtacgtcaggcaccctggccatcaccgggctgcaga ctggggacgaggccgattattactgcgccacatgggctgccagcctgagttccgcgcgt gtcttcggaactgggaccaaggtcatcgtcctggacaaaacccataccgcatccgaact gactcaggaccctgccgtctctgtggcactgaagcagactgtgactattacttgccgagg cgactcactgcggagccactacgcttcctggtatcagaagaaacccggccaggcacct gtgctgctgttctacggaaagaacaataggccatctggcatccccgaccgcttttctggca gtgcatcagggaaccgagccagtctgaccattaccggcgcccaggctgaggacgaag ccgattactattgcagctcccgggataagagcggctccagactgagcgtgttcggagga ggaactaaactgaccgtcctcgataagacccataccgtacggtggccgctcccagcgt gttcatcttcccacctagcgacgagcagctgaagtccggcacagcctctgtcgtgtgcct gctgaacaacttctacccccgcgaggccaaagtgcagtggaaggtggacaacgccctg cagagcggcaacagccaggaaagcgtgaccgagcaggacagcaaggactccaccta cagcctgagcagcaccctgacactgagcaaggccgactacgagaagcacaaggtgta cgcctgcgaagtgacccaccagggcctgtctagccccgtgaccaagagcttcaaccgg ggcgagtgt	**SEQ ID NO: 208**
Binding Protein 27 Amino Acid Sequences		
Heavy chain A	Rahlvqsgtamkkpgasvrvscqts***gytftahi***lfwfrqapgrglewvgw***ikpqyg*** ***av***nfgggfrdrvtltrdvyreiaymdirglkpddtavyycar***drsygdsswalda***wg	**SEQ ID NO: 209**

	qgttvvvsaastkgpsvfplapsskstsggtaalgclvkdyfpepvtvswnsgaltsgv htfpavlqssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkkvepkscdkthtc ppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnwyvdgv evhnaktkpreeqynstyrvvsvltvlhqdwlngkeykckvsnkalpapiektiska kgqprepqvctlppsrdeltknqvslscavkgfypsdiavewesngqpennykttpp vldsdgsfflvskltvdksrwqqgnvfscsvlhealhshytqkslslspg	
Light chain A	yihvtqspsslsvsigdrvtincqtsqgvgsdlhwyqhkpgrapkllihhtssvedgv psrfsgsgfhtsfqltisdlqaddiatyycqvlqffgrgsrlhikrtvaapsvfifppsdeq lksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsstltlsk adyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 210**
Heavy chain B	Evrlvesggglvkpggslrlscsasgfdfdnawmtwvrqppgkglewvgri tgpgegwsvdyaesvkgrftisrdntkntlylemnnvrtedtgyyfcartgky ydfwsgyppgeeyfqdwgqgtlvivssdkthtqvhltqsgpevrkpgtsvk vsckapgntlktydlhwvrsvpgqglqwmgwishegdkkviverfkakvti dwdrstntaylqlsgltsgdtavyycakgskhrlrdyalydddgalnwavdvd ylsnlefwgqgtavtvssdkthtastkgpsvfplapsskstsggtaalgclvkdy fpepvtvswnsgaltsgvhtfpavlqssglyslssvvtvpssslgtqtyicnvnh kpsntkvdkkvepkscdkthtcppcpapellggpsvflfppkpkdtlmisrtp evtcvvvdvshedpevkfnwyvdgvevhnaktkpreeqynstyrvvsvltv lhqdwlngkeykckvsnkalpapiektiskakgqprepqvytlppcrdeltk nqvslwclvkgfypsdiavewesngqpennykttppvldsdgsfflyskltv dksrwqqgnvfscsvlhealhshytqkslslspg	**SEQ ID NO: 211**
Light chain B	dfvltqsphslsvtpgesasisckssshslihgdrnnylawyvqkpgrspqlliylassra sgvpdrfsgsgsdkdftlkisrvetedvgtyycmqgrespwtfgqgtkvdikdkthta seltqdpavsvalkqtvtitcrgdslrshyaswyqkkpgqapvllfygknnrpsgipdr fsgsasgnrasltitgaqaedeadyycssrdksgsrlsvfgggtkltvldkthtrtvaaps vfifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdst yslsstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 212**
Binding Protein 27 Nucleotide Sequences		
Heavy chain A	agagcccacctggtgcagtctggcaccgccatgaagaaaccaggcgcctctgtgcgg gtgtcctgtcagacaagcggctacaccttcaccgcccacatcctgttctggttccggcag gcccctggcagaggactggaatgggtgggatggatcaagccccagtatggcgccgt gaacttcggcggaggcttccgggatagagtgaccctgacccgggacgtgtaccgcga gatcgcctacatggacatccggggcctgaagcccgatgacaccgccgtgtactactgc gccagagacagaagctacggcgacagcagctgggctctggatgcttggggccaggg cacaaccgtggtggtgtctgccgcctctacaaagggccccagcgtgttccctctggccc ctagcagcaagagcacatctggcggaacagccgccctgggctgcctcgtgaaggact actttcccgagcccgtgaccgtgtcctggaattctggcgccctgaccagcggcgtgca caccttccagctgtgctgcagtccagcggcctgtacagcctgagcagcgtcgtgaca gtgcccagcagctctctgggcacccagacctacatctgcaacgtgaaccacaagccca gcaacaccaaggtggacaagaaggtggaacccaagagctgcgacaagacccacac ctgtccccttgtcctgcccccgaactgctgggaggcccttccgtgttcctgttccccc aaagcccaaggacaccctgatgatcagccggacccccgaagtgacctgcgtggtggt ggatgtgtcccacgaggaccctgaagtgaagttcaattggtacgtggacggcgtggaa gtgcacaacgccaagaccaagccaagagaggaacagtacaacagcacctaccgggt ggtgtccgtgctgaccgtgctgcaccaggactggctgaacggcaaagagtacaagtg caaggtgtccaacaaggccctgcctgcccccatcgagaaaaccatcagcaaggccaa gggccagccccgcgaaccccaggtgtgcacactgcccccaagcagggacgagctg accaagaaccaggtgtccctgagctgtgccgtgaaaggcttctacccctccgatatcgc cgtggaatgggagagcaacggccagcccgagaacaactacaagaccacccccccctg tgctggacagcgacggctcattcttcctggtgtccaagctgacagtggacaagtcccgg	**SEQ ID NO: 213**

	tggcagcagggcaacgtgttcagctgctccgtgctgcacgaggccctgcacagccact acacccagaagtccctgagcctgagccccggc	
Light chain A	tacatccacgtgacccagagccccagcagcctgtccgtgtccatcggcgacagagtga ccatcaactgccagacctctcagggcgtgggcagcgacctgcactggtatcagcacaa gcctggcagagcccccaagctgctgatccaccacacaagcagcgtggaagatggcgt gcccagcagattttccggcagcggcttccacaccagcttccagctgaccatcagcgatc tgcaggccgacgacattgccacctactattgtcaggtgctgcagttcttcggcagaggc agcagactgcacatcaagcgtacggtggccgctcccagcgtgttcatcttcccacctag cgacgagcagctgaagtccggcacagcctctgtcgtgtgcctgctgaacaacttctacc cccgcgaggccaaagtgcagtggaaggtggacaacgccctgcagagcggcaacag ccaggaaagcgtgaccgagcaggacagcaaggactccacctacagcctgagcagca ccctgacactgagcaaggccgactacgagaagcacaaggtgtacgcctgcgaagtga cccaccagggcctgtctagccccgtgaccaagagcttcaaccggggcgagtgt	**SEQ ID NO: 214**
Heavy chain B	gaggttagactggtggagtcaggaggggggcttgtgaagcccggtgggtctctccgc ctgagctgttctgcctccggctttgatttcgataacgcctggatgacctgggtcaggcag cctccaggtaagggactggagtgggtgggaagaatcacaggtccaggcgagggctg gtccgtggactacgcggaatctgttaaagggcggtttacaatctcaagggacaatacca agaataccttgtatttggagatgaacaacgtgagaactgaagacaccggatattacttct gtgccagaacaggcaaatactacgacttctggtccggctatccccctggcgaggaatat tttcaagactggggtcagggaacccttgttatcgtgtcctccgacaaaacccatacccag gtgcacctgacacagagcggacccgaagtgcggaagcctggcacctctgtgaaggtg tcctgcaaggcccctggcaacaccctgaaaacctacgacctgcactgggtgcgcagc gtgccaggacagggactgcagtggatgggctggatcagccacgagggcgacaaga aagtgatcgtggaacggttcaaggccaaagtgaccatcgactgggacagaagcacca acaccgcctacctgcagctgagcggcctgacctctggcgataccgccgtgtactactg cgccaagggcagcaagcaccggctgagagactacgccctgtacgacgatgacggcg ccctgaactgggccgtggatgtggactacctgagcaacctggaattctggggccagg gcacagccgtgaccgtgtcatctgataagacccacaccgcttccaccaagggcccatc ggtcttcccccctggcaccctcctccaagagcacctctgggggcacagcggccctggg ctgcctggtcaaggactacttccccgaaccggtgacggtgtcgtggaactcaggcgcc ctgaccagcggcgtgcacaccttcccggctgtcctacagtcctcaggactctactccct cagcagcgtggtgaccgtgccctccagcagcttgggcacccagacctacatctgcaac gtgaatcacaagcccagcaacaccaaggtggacaagaaagttgagcccaaatcttgtg acaaaactcacacatgcccaccgtgcccagcacctgaactcctgggggggaccgtcag tcttcctcttccccccaaaacccaaggacaccctcatgatctcccggaccccctgaggtca catgcgtggtggtggacgtgagccacgaagaccctgaggtcaagttcaactggtatgtt gacggcgtggaggtgcataatgccaagacaaagccgcgggaggagcagtacaaca gcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaa ggagtacaagtgcaaggtctccaacaaagccctcccagcccccatcgagaaaaccat ctccaaagccaaagggcagccccgagaaccacaggtgtacaccctgcccccatgcc gggatgagctgaccaagaatcaagtcagcctgtggtgcctggtaaaaggcttctatccc agcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaaga ccacgcctcccgtgctggactccgacggctccttcttcctctactcaaaactcaccgtgg acaagagcaggtggcagcaggggaacgtcttctcatgctccgtgctgcatgaggctct gcacagccactacacgcagaagagcctctccctgtctccgggt	**SEQ ID NO: 215**
Light chain B	gacttcgtgctgacccagagccctcacagcctgagcgtgacacctggcgagagcgcc agcatcagctgcaagagcagccactccctgatccacggcgaccggaacaactacctg gcttggtacgtgcagaagcccggcagatccccccagctgctgatctacctggccagca gcagagccagcggcgtgcccgatagattttctggcagcggcagcgacaaggacttca ccctgaagatcagccgggtggaaaccgaggacgtgggcacctactactgtatgcagg gcagagagagcccctggacctttggccagggcaccaaggtggacatcaaggacaaa acccataccgcatccgaactgactcaggaccctgccgtctctgtggcactgaagcaga ctgtgactattacttgccgaggcgactcactgcggagccactacgcttcctggtatcaga agaaacccggccaggcacctgtgctgctgttctacggaaagaacaataggccatctgg	**SEQ ID NO: 216**

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Binding Protein 28 Amino Acid Sequences		
Heavy chain A	Rahlvqsgtamkkpgasvrvscqts***gytftahi***lfwfrqapgrglewvgw***ikpqy gav***nfgggfrdrvtltrdvyreiaymdirglkpddtavyycar***drsygdsswalda*** wgqgttvvvsaastkgpsvfplapsskstsggtaalgclvkdyfpepvtvswnsgal tsgvhtfpavlqssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkkvepkscd kthtcppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnw yvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykckvsnkalpapi ektiskakgqprepqvctlppsrdeltknqvslscavkgfypsdiavewesngqpe nnykttppvldsdgsfflvskltvdksrwqqgnvfscsvlhealhshytqkslslspg	**SEQ ID NO: 217**
Light chain A	yihvtqspsslsvsigdrvtincqtsqgvgsdlhwyqhkpgrapkllihhtssveegv psrfsgsgfhtsfnltisdlqaddiatyycqvlqffgrgsrlhikrtvaapsvfifppsde qlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsstltl skadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 218**
Heavy chain B	Evrlvesggglvkpggslrlscsasgfdfdnawmtwvrqppgkglewvgr itgpgegwsvdyaesvkgrftisrdntkntlylemnnvrtedtgyyfcartgk yydfwsgyppgeeyfqdwgqgtlvivssdkthtqvhltqsgpevrkpgtsv kvsckapgntlktydlhwvrsvpgqglqwmgwishegdkkviverfkak vtidwdrstntaylqlsgltsgdtavyycakgskhrlrdyalydddgalnwav dvdylsnlefwgqgtavtvssdkthtastkgpsvfplapsskstsggtaalgcl vkdyfpepvtvswnsgaltsgvhtfpavlqssglyslssvvtvpssslgtqtyi cnvnhkpsntkvdkkvepkscdkthtcppcpapellggpsvflfppkpkdt lmisrtpevtcvvvdvshedpevkfnwyvdgvevhnaktkpreeqynsty rvvsvltvlhqdwlngkeykckvsnkalpapiektiskakgqprepqvytlp pcrdeltknqvslwclvkgfypsdiavewesngqpennykttppvldsdgs fflyskltvdksrwqqgnvfscsvlhealhshytqkslslspg	**SEQ ID NO: 219**
Light chain B	dfvltqsphslsvtpgesasiscksshslihgdrnnylawyvqkpgrspqlliylassr asgvpdrfsgsgsdkdftlkisrvetedvgtyycmqgrespwtfgqgtkvdikdkth taseltqdpavsvalkqtvtitcrgdslrshyaswyqkkpgqapvllfygknnrpsgi pdrfsgsasgnrasltitgaqaedeadyycssrdksgsrlsvfgggtkltvldkthtrtv aapsvfifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteq dskdstyslsstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 220**
Binding Protein 28 Nucleotide Sequences		
Heavy chain A	agagcccacctggtgcagtctggcaccgccatgaagaaaccaggcgcctctgtgcgg gtgtcctgtcagacaagcggctacaccttcaccgcccacatcctgttctggttccggca ggcccctggcagaggactggaatgggtgggatggatcaagccccagtatggcgccg tgaacttcggcggaggcttccgggatagagtgaccctgacccgggacgtgtaccgcg agatcgcctacatggacatccggggcctgaagcccgatgacaccgccgtgtactactg cgccagagacagaagctacggcgacagcagctgggctctggatgcttggggccagg gcacaaccgtggtggtgtctgccgcctctacaaagggccccagcgtgttccctctggc ccctagcagcaagagcacatctggcggaacagccgccctgggctgcctcgtgaagg actactttcccgagcccgtgaccgtgtcctggaattctggcgccctgaccagcggcgtg	**SEQ ID NO: 221**

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Light chain A	tacatccacgtgacccagagccccagcagcctgtccgtgtccatcggcgacagagtg accatcaactgccagacctctcagggcgtgggcagcgacctgcactggtatcagcac aagcctggcagagcccccaagctgctgatccaccacacaagcagcgtggaagaagg cgtgcccagcagattttccggcagcggcttccacaccagcttcaacctgaccatcagc gatctgcaggccgacgacattgccacctactattgtcaggtgctgcagttcttcggcaga ggcagcagactgcacatcaagcgtacggtggccgctcccagcgtgttcatcttcccac ctagcgacgagcagctgaagtccggcacagcctctgtcgtgtgcctgctgaacaactt ctacccccgcgaggccaaagtgcagtggaaggtggacaacgccctgcagagcggc aacagccaggaaagcgtgaccgagcaggacagcaaggactccacctacagcctga gcagcaccctgacactgagcaaggccgactacgagaagcacaaggtgtacgcctgc gaagtgacccaccagggcctgtctagccccgtgaccaagagcttcaaccggggcga gtgt	**SEQ ID NO: 222**
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Light chain B	gacttcgtgctgacccagagccctcacagcctgagcgtgacacctggcgagagcgcc agcatcagctgcaagagcagccactccctgatccacggcgaccggaacaactacctg gcttggtacgtgcagaagcccggcagatccccccagctgctgatctacctggccagca gcagagccagcggcgtgcccgatagattttctggcagcggcagcgacaaggacttca ccctgaagatcagccgggtggaaaccgaggacgtgggcacctactactgtatgcagg gcagagagagcccctggacctttggccagggcaccaaggtggacatcaaggacaaa acccataccgcatccgaactgactcaggaccctgccgtctctgtggcactgaagcaga ctgtgactattacttgccgaggcgactcactgcggagccactacgcttcctggtatcaga agaaacccggccaggcacctgtgctgctgttctacggaaagaacaataggccatctgg catccccgaccgcttttctggcagtgcatcagggaaccgagccagtctgaccattaccg gcgcccaggctgaggacgaagccgattactattgcagctcccgggataagagcggct ccagactgagcgtgttcggaggaggaactaaactgaccgtcctcgataagacccatac ccgtacggtggccgctcccagcgtgttcatcttcccacctagcgacgagcagctgaag tccggcacagcctctgtcgtgtgcctgctgaacaacttctacccccgcgaggccaaagt gcagtggaaggtggacaacgccctgcagagcggcaacagccaggaaagcgtgacc gagcaggacagcaaggactccacctacagcctgagcagcaccctgacactgagcaa ggccgactacgagaagcacaaggtgtacgcctgcgaagtgacccaccagggcctgt ctagccccgtgaccaagagcttcaaccggggcgagtgt	**SEQ ID NO: 224**
Binding Protein 29 Amino Acid Sequences		
Heavy chain A	Rahlvqsgtamkkpgasvrvscqts***gytftahi***lfwfrqapgrglewvgw***ikpqy gav***nfgggfrdrvtltrdvyreiaymdirglkpddtavyycar***drsygdsswalda*** wgqgttvvvsaastkgpsvfplapsskstsggtaalgclvkdyfpepvtvswnsgal tsgvhtfpavlqssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkkvepkscd kthtcppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnw yvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykckvsnkalpapi ektiskakgqprepqvctlppsrdeltknqvslscavkgfypsdiavewesngqpe nnykttppvldsdgsfflvskltvdksrwqqgnvfscsvlhealhshytqkslslspg	**SEQ ID NO: 225**
Light chain A	yihvtqspsslsvsigdrvtincqtsqgvgsdlhwyqhkpgrapkllihhtssvedav psrfsgsgfhtsfnltisdlqaddiatyycqvlqffgrgsrlhikrtvaapsvfifppsde qlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsstltl skadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 226**
Heavy chain B	Evrlvesggglvkpggslrlscsasgfdfdnawmtwvrqppgkglewvgr itgpgegwsvdyaesvkgrftisrdntkntlylemnnvrtedtgyyfcartgk yydfwsgyppgeeyfqdwgqgtlvivssdkthtqvhltqsgpevrkpgtsv kvsckapgntlktydlhwvrsvpgqglqwmgwishegdkkviverfkak vtidwdrstntaylqlsgltsgdtavyycakgskhrlrdyalydddgalnwav dvdylsnlefwgqgtavtvssdkthtastkgpsvfplapsskstsggtaalgcl vkdyfpepvtvswnsgaltsgvhtfpavlqssglyslssvvtvpssslgtqtyi cnvnhkpsntkvdkkvepkscdkthtcppcpapellggpsvflfppkpkdt lmisrtpevtcvvvdvshedpevkfnwyvdgvevhnaktkpreeqynsty rvvsvltvlhqdwlngkeykckvsnkalpapiektiskakgqprepqvytlp pcrdeltknqvslwclvkgfypsdiavewesngqpennykttppvldsdgs fflyskltvdksrwqqgnvfscsvlhealhshytqkslslspg	**SEQ ID NO: 227**
Light chain B	dfvltqsphslsvtpgesasiscksshslihgdrnnylawyvqkpgrspqlliylassr asgvpdrfsgsgsdkdftlkisrvetedvgtyycmqgrespwtfgqgtkvdikdkth	**SEQ ID NO: 228**

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Binding Protein 29 Nucleotide Sequences		
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Light chain A	tacatccacgtgacccagagccccagcagcctgtccgtgtccatcggcgacagagtga ccatcaactgccagacctctcagggcgtgggcagcgacctgcactggtatcagcacaa gcctggcagagcccccaagctgctgatccaccacacaagcagcgtggaagatgccgt gcccagcagattttccggcagcggcttccacaccagcttcaacctgaccatcagcgatc tgcaggccgacgacattgccacctactattgtcaggtgctgcagttcttcggcagaggc agcagactgcacatcaagcgtacggtggccgctcccagcgtgttcatcttcccacctag cgacgagcagctgaagtccggcacagcctctgtcgtgtgcctgctgaacaacttctacc cccgcgaggccaaagtgcagtggaaggtggacaacgccctgcagagcggcaacag ccaggaaagcgtgaccgagcaggacagcaaggactccacctacagcctgagcagca ccctgacactgagcaaggccgactacgagaagcacaaggtgtacgcctgcgaagtga cccaccagggcctgtctagccccgtgaccaagagcttcaaccggggcgagtgt	**SEQ ID NO: 230**
Heavy chain B	gaggttagactggtggagtcaggaggggggcttgtgaagcccggtgggtctctccgc ctgagctgttctgcctccggctttgatttcgataacgcctggatgacctgggtcaggcag cctccaggtaagggactggagtgggtgggaagaatcacaggtccaggcgagggctg gtccgtggactacgcggaatctgttaaagggcggtttacaatctcaagggacaatacca agaataccttgtatttggagatgaacaacgtgagaactgaagacaccggatattacttct gtgccagaacaggcaaatactacgacttctggtccggctatccccctggcgaggaatat tttcaagactggggtcagggaacccttgttatcgtgtcctccgacaaaacccatacccag gtgcacctgacacagagcggacccgaagtgcggaagcctggcacctctgtgaaggtg tcctgcaaggcccctggcaacaccctgaaaacctacgacctgcactgggtgcgcagc gtgccaggacagggactgcagtggatgggctggatcagccacgagggcgacaaga aagtgatcgtggaacggttcaaggccaaagtgaccatcgactgggacagaagcacca acaccgcctacctgcagctgagcggcctgacctctggcgataccgccgtgtactactg cgccaagggcagcaagcaccggctgagagactacgccctgtacgacgatgacggcg ccctgaactgggccgtggatgtggactacctgagcaacctggaattctggggccaggg	**SEQ ID NO: 231**

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Light chain B	gacttcgtgctgacccagagccctcacagcctgagcgtgacacctggcgagagcgcc agcatcagctgcaagagcagccactccctgatccacggcgaccggaacaactacctg gcttggtacgtgcagaagcccggcagatcccccccagctgctgatctacctggccagca gcagagccagcggcgtgcccgatagattttctggcagcggcagcgacaaggacttca ccctgaagatcagccgggtggaaaccgaggacgtgggcacctactactgtatgcagg gcagagagagcccctggacctttggccagggcaccaaggtggacatcaaggacaaa acccataccgcatccgaactgactcaggaccctgccgtctctgtggcactgaagcaga ctgtgactattacttgccgaggcgactcactgcggagccactacgcttcctggtatcaga agaaacccggccaggcacctgtgctgctgttctacggaaagaacaataggccatctgg catccccgaccgcttttctggcagtgcatcagggaaccgagccagtctgaccattaccg gcgcccaggctgaggacgaagccgattactattgcagctcccgggataagagcggct ccagactgagcgtgttcggaggaggaactaaactgaccgtcctcgataagacccatac ccgtacggtggccgctcccagcgtgttcatcttcccacctagcgacgagcagctgaagt ccggcacagcctctgtcgtgtgcctgctgaacaacttctacccccgcgaggccaaagt gcagtggaaggtggacaacgccctgcagagcggcaacagccaggaaagcgtgacc gagcaggacagcaaggactccacctacagcctgagcagcaccctgacactgagcaa ggccgactacgagaagcacaaggtgtacgcctgcgaagtgacccaccagggcctgt ctagccccgtgaccaagagcttcaaccggggcgagtgt	**SEQ ID NO: 301**
Binding Protein 30 Amino Acid Sequences		
Heavy chain A	Rahlvqsgtamkkpgasvrvscqts***gytftahi***lfwfrqapgrglewvgw***ikpqy gav***nfgggfrdrvtltrdvyreiaymdirglkpddtavyycar***drsygdsswalda*** wgqgttvvvsaastkgpsvfplapsskstsggtaalgclvkdyfpepvtvswnsgal tsgvhtfpavlqssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkkvepkscd kthtcppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnw yvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykckvsnkalpapi ektiskakgqprepqvctlppsrdeltknqvslscavkgfypsdiavewesngqpe nnykttppvldsdgsfflvskltvdksrwqqgnvfscsvlhealhshytqkslslspg	**SEQ ID NO: 232**
Light chain A	yihvtqspsslsvsigdrvtincqtsqgvgsdlhwyqhkpgrapkllihhtssveegv psrfsgsgfhtsfqltisdlqaddiatyycqvlqffgrgsrlhikrtvaapsvfifppsde qlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsstltl skadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 233**
Heavy chain B	Evrlvesggglvkpggslrlscsasgfdfdnawmtwvrqppgkglewvgr itgpgegwsvdyaesvkgrftisrdntkntlylemnnvrtedtgyyfcartgk yydfwsgyppgeeyfqdwgqgtlvivssdkthtqvhltqsgpevrkpgtsv	**SEQ ID NO: 234**

	kvsckapgntlktydlhwvrsvpgqglqwmgwishegdkkviverfkak vtidwdrstntaylqlsgltsgdtavyycakgskhrlrdyalydddgalnwav dvdylsnlefwgqgtavtvssdkthtastkgpsvfplapsskstsggtaalgcl vkdyfpepvtvswnsgaltsgvhtfpavlqssglyslssvvtvpssslgtqtyi cnvnhkpsntkvdkkvepkscdkthtcppcpapellggpsvflfppkpkdt lmisrtpevtcvvvdvshedpevkfnwyvdgvevhnaktkpreeqynsty rvvsvltvlhqdwlngkeykckvsnkalpapiektiskakgqprepqvytlp pcrdeltknqvslwclvkgfypsdiavewesngqpennykttppvldsdgs fflyskltvdksrwqqgnvfscsvlhealhshytqkslslspg	
Light chain B	dfvltqsphslsvtpgesasiscksshslihgdrnnylawyvqkpgrspqlliylassr asgvpdrfsgsgsdkdftlkisrvetedvgtyycmqgrespwtfgqgtkvdikdkth taseltqdpavsvalkqtvtitcrgdslrshyaswyqkkpgqapvllfygknnrpsgi pdrfsgsasgnrasltitgaqaedeadyycssrdksgsrlsvfgggtkltvldkthtrtv aapsvfifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteq dskdstyslsstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 235**
Binding Protein 30 Nucleotide Sequences		
Heavy chain A	agagcccacctggtgcagtctggcaccgccatgaagaaaccaggcgcctctgtgcgg gtgtcctgtcagacaagcggctacaccttcaccgcccacatcctgttctggttccggcag gcccctggcagaggactggaatgggtgggatggatcaagccccagtatggcgccgtg aacttcggcggaggcttccgggatagagtgaccctgacccgggacgtgtaccgcgag atcgcctacatggacatccggggcctgaagcccgatgacaccgccgtgtactactgcg ccagagacagaagctacggcgacagcagctgggctctggatgcttggggccagggc acaaccgtggtggtgtctgccgcctctacaaagggccccagcgtgttccctctggcccc tagcagcaagagcacatctggcggaacagccgccctgggctgcctcgtgaaggacta ctttcccgagcccgtgaccgtgtcctggaattctggcgccctgaccagcggcgtgcac acctttccagctgtgctgcagtccagcggcctgtacagcctgagcagcgtcgtgacagt gcccagcagctctctgggcacccagacctacatctgcaacgtgaaccacaagcccag caacaccaaggtggacaagaaggtggaacccaagagctgcgacaagacccacacct gtccccttgtcctgcccccgaactgctgggaggcccttccgtgttcctgttcccccaa agcccaaggacaccctgatgatcagccggaccccgaagtgacctgcgtggtggtgg atgtgtcccacgaggaccctgaagtgaagttcaattggtacgtggacggcgtggaagt gcacaacgccaagaccaagccaagagaggaacagtacaacagcacctaccgggtg gtgtccgtgctgaccgtgctgcaccaggactggctgaacggcaaagagtacaagtgc aaggtgtccaacaaggccctgcctgcccccatcgagaaaaccatcagcaaggccaag ggccagccccgcgaaccccaggtgtgcacactgcccccaagcagggacgagctga ccaagaaccaggtgtccctgagctgtgccgtgaaaggcttctacccctccgatatcgcc gtggaatgggagagcaacggccagcccgagaacaactacaagaccacccccctgt gctggacagcgacggctcattcttcctggtgtccaagctgacagtggacaagtcccggt ggcagcagggcaacgtgttcagctgctccgtgctgcacgaggccctgcacagccact acacccagaagtccctgagcctgagccccggc	**SEQ ID NO: 236**
Light chain A	tacatccacgtgacccagagccccagcagcctgtccgtgtccatcggcgacagagtga ccatcaactgccagacctctcagggcgtgggcagcgacctgcactggtatcagcacaa gcctggcagagcccccaagctgctgatccaccacacaagcagcgtggaagaaggcg tgcccagcagattttccggcagcggcttccacaccagcttccagctgaccatcagcgat ctgcaggccgacgacattgccacctactattgtcaggtgctgcagttcttcggcagagg cagcagactgcacatcaagcgtacggtggccgctcccagcgtgttcatcttcccaccta gcgacgagcagctgaagtccggcacagcctctgtcgtgtgcctgctgaacaacttctac ccccgcgaggccaaagtgcagtggaaggtggacaacgccctgcagagcggcaaca gccaggaaagcgtgaccgagcaggacagcaaggactccacctacagcctgagcag caccctgacactgagcaaggccgactacgagaagcacaaggtgtacgcctgcgaagt gacccaccagggcctgtctagccccgtgaccaagagcttcaaccggggcgagtgt	**SEQ ID NO: 237**
Heavy chain B	gaggttagactggtggagtcaggaggggggcttgtgaagcccggtgggtctctccgc	**SEQ ID NO:**

	ctgagctgttctgcctccggctttgatttcgataacgcctggatgacctgggtcaggcag cctccaggtaagggactggagtgggtgggaagaatcacaggtccaggcgagggctg gtccgtggactacgcggaatctgttaaagggcggtttacaatctcaagggacaatacca agaataccttgtatttggagatgaacaacgtgagaactgaagacaccggatattacttct gtgccagaacaggcaaatactacgacttctggtccggctatccccctggcgaggaatat tttcaagactggggtcagggaacccttgttatcgtgtcctccgacaaaacccatacccag gtgcacctgacacagagcggacccgaagtgcggaagcctggcacctctgtgaaggtg tcctgcaaggcccctggcaacaccctgaaaacctacgacctgcactgggtgcgcagc gtgccaggacagggactgcagtggatgggctggatcagccacgagggcgacaaga aagtgatcgtggaacggttcaaggccaaagtgaccatcgactgggacagaagcacca acaccgcctacctgcagctgagcggcctgacctctggcgataccgccgtgtactactg cgccaagggcagcaagcaccggctgagagactacgccctgtacgacgatgacggcg ccctgaactgggccgtggatgtggactacctgagcaacctggaattctggggccaggg cacagccgtgaccgtgtcatctgataagacccacaccgcttccaccaagggcccatcg gtcttcccccctggcaccctcctccaagagcacctctgggggcacagcggccctgggct gcctggtcaaggactacttccccgaaccggtgacggtgtcgtggaactcaggcgccct gaccagcggcgtgcacaccttcccggctgtcctacagtcctcaggactctactccctca gcagcgtggtgaccgtgccctccagcagcttgggcacccagacctacatctgcaacgt gaatcacaagcccagcaacaccaaggtggacaagaaagttgagcccaaatcttgtga caaaactcacacatgcccaccgtgcccagcacctgaactcctgggggggaccgtcagt cttcctcttcccccaaaacccaaggacaccctcatgatctcccggacccctgaggtca catgcgtggtggtggacgtgagccacgaagaccctgaggtcaagttcaactggtatgtt gacggcgtggaggtgcataatgccaagacaaagccgcgggaggagcagtacaaca gcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaa ggagtacaagtgcaaggtctccaacaaagccctcccagcccccatcgagaaaaccat ctccaaagccaaagggcagccccgagaaccacaggtgtacaccctgcccccatgcc gggatgagctgaccaagaatcaagtcagcctgtggtgcctggtaaaaggcttctatccc agcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaaga ccacgcctcccgtgctggactccgacggctccttcttcctctactcaaaactcaccgtgg acaagagcaggtggcagcaggggaacgtcttctcatgctccgtgctgcatgaggctct gcacagccactacacgcagaagagcctctccctgtctccgggt	**238**
Light chain B	Gacttcgtgctgacccagagccctcacagcctgagcgtgacacctggcgagagcgc cagcatcagctgcaagagcagccactccctgatccacggcgaccggaacaactacct ggcttggtacgtgcagaagcccggcagatccccccagctgctgatctacctggccagc agcagagccagcggcgtgcccgatagattttctggcagcggcagcgacaaggacttc accctgaagatcagccgggtggaaaccgaggacgtgggcacctactactgtatgcag ggcagagagagcccctggacctttggccagggcaccaaggtggacatcaaggacaa aacccataccgcatccgaactgactcaggaccctgccgtctctgtggcactgaagcag actgtgactattacttgccgaggcgactcactgcggagccactacgcttcctggtatcag aagaaacccggccaggcacctgtgctgctgttctacggaaagaacaataggccatctg gcatccccgaccgcttttctggcagtgcatcagggaaccgagccagtctgaccattacc ggcgcccaggctgaggacgaagccgattactattgcagctcccgggataagagcggc tccagactgagcgtgttcggaggaggaactaaactgaccgtcctcgataagacccata cccgtacggtggccgctcccagcgtgttcatcttcccacctagcgacgagcagctgaa gtccggcacagcctctgtcgtgtgcctgctgaacaacttctacccccgcgaggccaaa gtgcagtggaaggtggacaacgccctgcagagcggcaacagccaggaaagcgtga ccgagcaggacagcaaggactccacctacagcctgagcagcaccctgacactgagc aaggccgactacgagaagcacaaggtgtacgcctgcgaagtgacccaccagggcct gtctagccccgtgaccaagagcttcaaccggggcgagtgt	**SEQ ID NO: 239**
Binding Protein 31 Amino Acid Sequences		
Heavy chain A	Rahlvqsgtamkkpgasvrvscqts***gytftahi***lfwfrqapgrglewvgw***ikpqy gav***nfgggfrdrvtltrdvyreiaymdirglkpddtavyycar***drsygdsswalda*** wgqgttvvvsaastkgpsvfplapsskstsggtaalgclvkdyfpepvtvswnsgal tsgvhtfpavlqssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkkvepkscd	**SEQ ID NO: 240**

	kthtcppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnw yvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykckvsnkalpapi ektiskakgqprepqvctlppsrdeltknqvslscavkgfypsdiavewesngqpe nnykttppvldsdgsfflvskltvdksrwqqgnvfscsvlhealhshytqkslslspg	
Light chain A	Yihvtqspsslsvsigdrvtincqtsqgvgsdlhwyqhkpgrapkllihhtssveda vpsrfsgsgfhtsfqltisdlqaddiatyycqvlqffgrgsrlhikrtvaapsvfifppsd eqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsstlt lskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 241**
Heavy chain B	Evrlvesggglvkpggslrlscsasgfdfdnawmtwvrqppgkglewvgr itgpgegwsvdyaesvkgrftisrdntkntlylemnnvrtedtgyyfcartgk yydfwsgyppgeeyfqdwgqgtlvivssdkthtqvhltqsgpevrkpgtsv kvsckapgntlktydlhwvrsvpgqglqwmgwishegdkkviverfkak vtidwdrstntaylqlsgltsgdtavyycakgskhrlrdyalydddgalnwav dvdylsnlefwgqgtavtvssdkthtastkgpsvfplapsskstsggtaalgcl vkdyfpepvtvswnsgaltsgvhtfpavlqssglyslssvvtvpssslgtqtyi cnvnhkpsntkvdkkvepkscdkthtcppcpapellggpsvflfppkpkdt lmisrtpevtcvvvdvshedpevkfnwyvdgvevhnaktkpreeqynsty rvvsvltvlhqdwlngkeykckvsnkalpapiektiskakgqprepqvytlp pcrdeltknqvslwclvkgfypsdiavewesngqpennykttppvldsdgs fflyskltvdksrwqqgnvfscsvlhealhshytqkslslspg	**SEQ ID NO: 242**
Light chain B	dfvltqsphslsvtpgesasisckssshslihgdrnnylawyvqkpgrspqlliylassr asgvpdrfsgsgsdkdftlkisrvetedvgtyycmqgrespwtfgqgtkvdikdkth taseltqdpavsvalkqtvtitcrgdslrshyaswyqkkpgqapvllfygknnrpsgi pdrfsgsasgnrasltitgaqaedeadyycssrdksgsrlsvfgggtkltvldkthtrtv aapsvfifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteq dskdstyslsstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 243**
Binding Protein 31 Nucleotide Sequences		
Heavy chain A	agagcccacctggtgcagtctggcaccgccatgaagaaaccaggcgcctctgtgcgg gtgtcctgtcagacaagcggctacaccttcaccgcccacatcctgttctggttccggca ggcccctggcagaggactggaatgggtgggatggatcaagccccagtatggcgccg tgaacttcggcggaggcttccgggatagagtgaccctgacccgggacgtgtaccgcg agatcgcctacatggacatccggggcctgaagcccgatgacaccgccgtgtactactg cgccagagacagaagctacggcgacagcagctgggctctggatgcttggggccagg gcacaaccgtggtggtgtctgccgcctctacaaagggccccagcgtgttccctctggc ccctagcagcaagagcacatctggcggaacagccgccctgggctgcctcgtgaagg actactttcccgagcccgtgaccgtgtcctggaattctggcgccctgaccagcggcgtg cacaccttccagctgtgctgcagtccagcggcctgtacagcctgagcagcgtcgtga cagtgcccagcagctctctgggcacccagacctacatctgcaacgtgaaccacaagc ccagcaacaccaaggtggacaagaaggtggaacccaagagctgcgacaagaccca cacctgtccccttgtcctgccccgaactgctgggaggcccttccgtgttcctgttccc cccaaagcccaaggacaccctgatgatcagccggacccccgaagtgacctgcgtggt ggtggatgtgtcccacgaggaccctgaagtgaagttcaattggtacgtggacggcgtg gaagtgcacaacgccaagaccaagccaagagaggaacagtacaacagcacctacc gggtggtgtccgtgctgaccgtgctgcaccaggactggctgaacggcaaagagtaca agtgcaaggtgtccaacaaggccctgcctgcccccatcgagaaaaccatcagcaagg ccaagggccagccccgcgaaccccaggtgtgcacactgcccccaagcagggacga gctgaccaagaaccaggtgtccctgagctgtgccgtgaaaggcttctacccctccgata tcgccgtggaatgggagagcaacggccagcccgagaacaactacaagaccacccccc cctgtgctggacagcgacggctcattcttcctggtgtccaagctgacagtggacaagtc ccggtggcagcagggcaacgtgttcagctgctccgtgctgcacgaggccctgcacag ccactacacccagaagtccctgagcctgagccccggc	**SEQ ID NO: 244**

Light chain A	tacatccacgtgacccagagccccagcagcctgtccgtgtccatcggcgacagagtg accatcaactgccagacctctcagggcgtgggcagcgacctgcactggtatcagcac aagcctggcagagcccccaagctgctgatccaccacacaagcagcgtggaagatgc cgtgcccagcagattttccggcagcggcttccacaccagcttccagctgaccatcagc gatctgcaggccgacgacattgccacctactattgtcaggtgctgcagttcttcggcaga ggcagcagactgcacatcaagcgtacggtggccgctcccagcgtgttcatcttcccac ctagcgacgagcagctgaagtccggcacagcctctgtcgtgtgcctgctgaacaactt ctacccccgcgaggccaaagtgcagtggaaggtggacaacgccctgcagagcggc aacagccaggaaagcgtgaccgagcaggacagcaaggactccacctacagcctga gcagcaccctgacactgagcaaggccgactacgagaagcacaaggtgtacgcctgc gaagtgacccaccagggcctgtctagccccgtgaccaagagcttcaaccggggcga gtgt	**SEQ ID NO: 245**
Heavy chain B	gaggttagactggtggagtcaggaggggggcttgtgaagcccggtgggtctctccgc ctgagctgttctgcctccggctttgatttcgataacgcctggatgacctgggtcaggcag cctccaggtaagggactggagtgggtgggaagaatcacaggtccaggcgagggctg gtccgtggactacgcggaatctgttaaagggcggtttacaatctcaagggacaatacca agaataccttgtatttggagatgaacaacgtgagaactgaagacaccggatattacttct gtgccagaacaggcaaatactacgacttctggtccggctatccccctggcgaggaatat tttcaagactggggtcagggaacccttgttatcgtgtcctccgacaaaacccatacccag gtgcacctgacacagagcggacccgaagtgcggaagcctggcacctctgtgaaggt gtcctgcaaggcccctggcaacaccctgaaaacctacgacctgcactgggtgcgcag cgtgccaggacagggactgcagtggatgggctggatcagccacgagggcgacaag aaagtgatcgtggaacggttcaaggccaaagtgaccatcgactgggacagaagcacc aacaccgcctacctgcagctgagcggcctgacctctggcgataccgccgtgtactact gcgccaagggcagcaagcaccggctgagagactacgccctgtacgacgatgacgg cgccctgaactgggccgtggatgtggactacctgagcaacctggaattctggggccag ggcacagccgtgaccgtgtcatctgataagacccacaccgcttccaccaagggcccat cggtcttccccctggcaccctcctccaagagcacctctgggggcacagcggccctgg gctgcctggtcaaggactacttccccgaaccggtgacggtgtcgtggaactcaggcgc cctgaccagcggcgtgcacaccttcccggctgtcctacagtcctcaggactctactccc tcagcagcgtggtgaccgtgccctccagcagcttgggcacccagacctacatctgcaa cgtgaatcacaagcccagcaacaccaaggtggacaagaaagttgagcccaaatcttgt gacaaaactcacacatgcccaccgtgcccagcacctgaactcctgggggaccgtca gtcttcctcttcccccaaaacccaaggacaccctcatgatctcccggaccctgaggt cacatgcgtggtggtggacgtgagccacgaagaccctgaggtcaagttcaactggtat gttgacggcgtggaggtgcataatgccaagacaaagccgcgggaggagcagtacaa cagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggc aaggagtacaagtgcaaggtctccaacaaagccctcccagcccccatcgagaaaacc atctccaaagccaaagggcagccccgagaaccacaggtgtacaccctgcccccatgc cgggatgagctgaccaagaatcaagtcagcctgtggtgcctggtaaaaggcttctatcc cagcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaag accacgcctcccgtgctggactccgacggctccttcttcctctactcaaaactcaccgtg gacaagagcaggtggcagcaggggaacgtcttctcatgctccgtgctgcatgaggctc tgcacagccactacacgcagaagagcctctccctgtctccgggt	**SEQ ID NO: 246**
Light chain B	Gacttcgtgctgacccagagccctcacagcctgagcgtgacacctggcgagagcgc cagcatcagctgcaagagcagccactccctgatccacggcgaccggaacaactacct ggcttggtacgtgcagaagcccggcagatccccccagctgctgatctacctggccagc agcagagccagcggcgtgcccgatagattttctggcagcggcagcgacaaggacttc accctgaagatcagccgggtggaaaccgaggacgtgggcacctactactgtatgcag ggcagagagagcccctggacctttggccagggcaccaaggtggacatcaaggacaa aacccataccgcatccgaactgactcaggaccctgccgtctctgtggcactgaagcag actgtgactattacttgccgaggcgactcactgcggagccactacgcttcctggtatcag aagaaacccggccaggcacctgtgctgctgttctacggaaagaacaataggccatctg gcatccccgaccgcttttctggcagtgcatcagggaaccgagccagtctgaccattacc	**SEQ ID NO: 247**

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Binding Protein 32 Amino Acid Sequences		
Heavy chain A	Rahlvqsgtamkkpgasvrvscqtsgytftahilfwfrqapgrglewvgwikpqyg avnfgggfrdrvtltrdvyreiaymdirglkpddtavyycardrsygdsswaldawg qgttvvvsaastkgpsvfplapcsrstsestaalgclvkdyfpepvtvswnsgaltsgv htfpavlqssglyslssvvtvpssslgtktytcnvdhkpsntkvdkrveskygppcpp cpapeflggpsvflfppkpkdtlmisrtpevtcvvvdvsqedpevqfnwyvdgvev hnaktkpreeqfnstyrvvsvltvlhqdwlngkeykckvsnkglpssiektiskakg qprepqvytlppcqeemtknqvslwclvkgfypsdiavewesngqpennykttpp vldsdgsfflyskltvdksrwqegnvfscsvmhealhnhytqkslslslgk	**SEQ ID NO: 302**
Light chain A	Yihvtqspsslsvsigdrvtincqtsqgvgsdlhwyqhkpgrapkllihhtssvedgv psrfsgsgfhtsfnltisdlqaddiatyycqvlqffgrgsrlhikrtvaapsvfifppsdeq lksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsstltlsk adyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 303**
Heavy chain B	Qvqlvqsgaevvkpgasvkvsckas***gytftsyy***ihwvrqapgqglewigs***i ypgnvnt***nyaqkfqgratltvdtsistaymelsrlrsddtavyyc***trshygldw nfdv***wgkgttvtvsssqvqlvesgggvvqpgrslrlscaas***gftftkaw***mhw vrqapgkqlewvaq***ikdksns***yatyyadsvkgrftisrddsknlylqmnslr aedtavyyc***rgvyyalspfdy***wgqgtlvtvssrtastkgpsvfplapcsrstses taalgclvkdyfpepvtvswnsgaltsgvhtfpavlqssglyslssvvtvpsssl gtktytcnvdhkpsntkvdkrveskygppcppcpapeflggpsvflfppkp kdtlmisrtpevtcvvvdvsqedpevqfnwyvdgvevhnaktkpreeqfns tyrvvsvltvlhqdwlngkeykckvsnkglpssiektiskakgqprepqvctl ppsqeemtknqvslscavkgfypsdiavewesngqpennykttppvldsd gsfflvskltvdksrwqegnvfscsvmhealhnhytqkslslslgk	**SEQ ID NO: 304**
Light chain B	Divmtqtplslsvtpgqpasiscks***qslvhnnanty***lswylqkpgqspqsliy***kvs*** nrfsgvpdrfsgsgsgtdftlkisrveaedvgvyyc***gqgtqyp***ftfgsgtkveikgqpk aapdiqmtqspsslsasvgdrvtitcqas***qniyvw***lnwyqqkpgkapklliykasnl htgvpsrfsgsgsgtdftltisslqpediatyyc***qqgqtypyt***fgqgtkleiktkgpsrtv aapsvfifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqd skdstyslsstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 305**
Binding Protein 32 Nucleotide Sequences		
Heavy chain A	agagcccacctggtgcagtctggcaccgccatgaagaaaccaggcgcctctgtgcgggt gtcctgtcagacaagcggctacaccttcaccgcccacatcctgttctggttccggcaggcc cctggcagaggactggaatgggtgggatggatcaagccccagtatggcgccgtgaactt cggcggaggcttccgggatagagtgaccctgacccgggacgtgtaccgcgagatcgcc tacatggacatccggggcctgaagcccgatgacaccgccgtgtactactgcgccagaga cagaagctacggcgacagcagctgggctctggatgcttggggccagggcacaaccgtg gtggtgtctgccgcctctacaaagggcccctcggtgttccctctggccccttgcagcagaa gcaccagcgaatctacagccgccctgggctgcctcgtgaaggactactttcccgagcccg tgaccgtgtcctggaactctggcgctctgacaagcggcgtgcacacctttccagccgtgct ccagagcagcggcctgtactctctgagcagcgtcgtgacagtgcccagcagcagcctgg gcaccaagacctacacctgtaacgtggaccacaagcccagcaacaccaaggtggacaa gcgggtggaatctaagtacggccctccctgccctccttgcccagcccctgaatttctgggc ggaccctccgtgttcctgttccccccaaagcccaaggacaccctgatgatcagccggacc cccgaagtgacctgcgtggtggtggatgtgtcccaggaagatcccgaggtgcagttcaat	**SEQ ID NO: 306**

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Light chain A	Tacatccacgtgacccagagccccagcagcctgtccgtgtccatcggcgacagagtgac catcaactgccagacctctcagggcgtgggcagcgacctgcactggtatcagcacaagc ctggcagagcccccaagctgctgatccaccacacaagcagcgtggaagatggcgtgcc cagcagattttccggcagcggcttccacaccagcttcaacctgaccatcagcgatctgcag gccgacgacattgccacctactattgtcaggtgctgcagttcttcggcagaggcagcagac tgcacatcaagcgtacggtggccgctcccagcgtgttcatcttcccacctagcgacgagc agctgaagtccggcacagcctctgtcgtgtgcctgctgaacaacttctacccccgcgagg ccaaagtgcagtggaaggtggacaacgccctgcagagcggcaacagccaggaaagcg tgaccgagcaggacagcaaggactccacctacagcctgagcagcaccctgacactgag caaggccgactacgagaagcacaaggtgtacgcctgcgaagtgacccaccagggcctg tctagccccgtgaccaagagcttcaaccggggcgagtgt	**SEQ ID NO: 307**
Heavy chain B	caggtgcagctggtgcagtctggcgccgaggtcgtgaaacctggcgcctctgtgaaggt gtcctgcaaggccagcggctacacctttaccagctactacatccactgggtgcgccaggc ccctggacagggactggaatggatcggcagcatctaccccggcaacgtgaacaccaact acgcccagaagttccagggcagagccaccctgaccgtggacaccagcatcagcaccgc ctacatggaactgagccggctgagaagcgacgacaccgccgtgtactactgcacccggt cccactacggcctggattggaacttcgacgtgtggggcaagggcaccaccgtgacagtg tctagcagccaggtgcagctggtggaatctggcggcggagtggtgcagcctggcagaa gcctgagactgagctgtgccgccagcggcttcaccttcaccaaggcctggatgcactggg tgcgccaggcccctggaaagcagctggaatgggtggcccagatcaaggacaagagcaa cagctacgccacctactacgccgacagcgtgaagggccggttcaccatcagccgggac gacagcaagaacaccctgtacctgcagatgaacagcctgcgggccgaggacaccgccg tgtactactgtcggggcgtgtactatgccctgagccccttcgattactggggccagggaac cctcgtgaccgtgtctagtcggaccgccagcacaaagggcccatcggtgttccctctggc cccttgcagcagaagcaccagcgaatctacagccgccctgggctgcctcgtgaaggact actttcccgagcccgtgaccgtgtcctggaactctggcgctctgacaagcggcgtgcaca cctttccagccgtgctccagagcagcggcctgtactctctgagcagcgtcgtgacagtgcc cagcagcagcctgggcaccaagacctacacctgtaacgtggaccacaagcccagcaac accaaggtggacaagcgggtggaatctaagtacggccctccctgccctccttgcccagcc cctgaatttctgggcggaccctccgtgttcctgttcccccaaagcccaaggacaccctga tgatcagccggaccccgaagtgacctgcgtggtggtggatgtgtcccaggaagatccc gaggtgcagttcaattggtacgtggacggcgtggaagtgcacaacgccaagaccaagcc cagagaggaacagttcaacagcacctaccgggtggtgtccgtgctgaccgtgctgcacc aggactggctgaacggcaaagagtacaagtgcaaggtgtccaacaagggcctgcccag ctccatcgagaaaaccatcagcaaggccaagggccagccccgcgagcctcaagtgtgta ccctgccccctagccaggaagagatgaccaagaaccaggtgtccctgagctgtgccgtg aaaggcttctaccccagcgacattgccgtggaatgggagagcaacggccagcccgaga acaactacaagaccacccccccctgtgctggacagcgacggctcattcttcctggtgtccaa gctgaccgtggacaagagccggtggcaggaaggcaacgtgttcagctgctccgtgatgc acgaggccctgcacaaccactacacccagaagtccctgtctctgtccctgggcaag	**SEQ ID NO: 308**
Light chain B	gacatcgtgatgacccagaccccctgagcctgagcgtgacacctggacagcctgccag catcagctgcaagagcagccagagcctggtgcacaacaacgccaacacctacctgagct ggtatctgcagaagcccggccagagcccccagtccctgatctacaaggtgtccaacagat tcagcggcgtgcccgacagattctccggcagcggctctggcaccgacttcaccctgaag atcagccgggtggaagccgaggacgtgggcgtgtactattgtggccagggcacccagta	**SEQ ID NO: 309**

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Binding Protein 33 Amino Acid Sequences		
Heavy chain A	Rahlvqsgtamkkpgasvrvscqtsgytftahilfwfrqapgrglewvgwikpqyga vnfgggfrdrvtltrdvyreiaymdirglkpddtavyycardrsygdsswaldawgqg ttvvvsaastkgpsvfplapcsrstsestaalgclvkdyfpepvtvswnsgaltsgvhtfp avlqssglyslssvvtvpssslgtktytcnvdhkpsntkvdkrveskygppcppcpape flggpsvflfppkpkdtlmisrtpevtcvvvdvsqedpevqfnwyvdgvevhnaktk preeqfnstyrvvsvltvlhqdwlngkeykckvsnkglpssiektiskakgqprepqv ytlppcqeemtknqvslwclvkgfypsdiavewesngqpennykttppvldsdgsff lyskltvdksrwqegnvfscsvmhealhnhytqkslslslgk	**SEQ ID NO: 310**
Light chain A	Yihvtqspsslsvsigdrvtincqtsqgvgsdlhwyqhkpgrapkllihhtssvedgvp srfsgsgfhtsfnltisdlqaddiatyycqvlqffgrgsrlhikrtvaapsvfifppsdeqlks gtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsstltlskadye khkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 311**
Heavy chain B	Qvqlqesgpglvkpsqtlsltctvsgfslsdygvhwvrqppgkglewlgviwa gggtnynpslksrktiskdtsknqvslklssvtaadtavyycardkgysyyysm dywgqgttvtvsssqvqlvesgggvvqpgrslrlscaasgftftkawmhwvrq apgkqlewvaqikdksnsyatyyadsvkgrftisrddskntlylqmnslraedt avyycrgvyyalspfdywgqgtlvtvssrtastkgpsvfplapcsrstsestaalg clvkdyfpepvtvswnsgaltsgvhtfpavlqssglyslssvvtvpssslgtktyt cnvdhkpsntkvdkrveskygppcppcpapeflggpsvflfppkpkdtlmis rtpevtcvvvdvsqedpevqfnwyvdgvevhnaktkpreeqfnstyrvvsvlt vlhqdwlngkeykckvsnkglpssiektiskakgqprepqvctlppsqeemt knqvslscavkgfypsdiavewesngqpennykttppvldsdgsfflvskltv dksrwqegnvfscsvmhealhnhytqkslslslgk	**SEQ ID NO: 312**
Light chain B	Divmtqtplslsvtpgqpasisckssqslvhnnantylswylqkpgqspqsliykvsnr fsgvpdrfsgsgsgtdftlkisrveaedvgvyycgqgtqypftfgsgtkveikgqpkaa pdivltqspaslavspgqratitcrasesveyyvtslmqwyqqkpgqppkllifaasnv esgvparfsgsgsgtdftltinpveandvanyycqqsrkvpytfgqgtkleiktkgpsrt vaapsvfifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqd skdstyslsstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 313**
Binding Protein 33 Nucleotide Sequences		
Heavy chain A	agagcccacctggtgcagtctggcaccgccatgaagaaaccaggcgcctctgtgcgggt gtcctgtcagacaagcggctacaccttcaccgcccacatcctgttctggttccggcaggcc cctggcagaggactggaatgggtgggatggatcaagccccagtatggcgccgtgaactt cggcggaggcttccgggatagagtgaccctgacccgggacgtgtaccgcgagatcgcc tacatggacatccggggcctgaagcccgatgacaccgccgtgtactactgcgccagaga cagaagctacggcgacagcagctgggctctggatgcttggggccagggcacaaccgtg gtggtgtctgccgcctctacaaagggcccctcggtgttccctctggccccttgcagcagaa gcaccagcgaatctacagccgccctgggctgcctcgtgaaggactactttcccgagcccg	**SEQ ID NO: 314**

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Light chain A	Tacatccacgtgacccagagccccagcagcctgtccgtgtccatcggcgacagagtgac catcaactgccagacctctcagggcgtgggcagcgacctgcactggtatcagcacaagc ctggcagagccccaagctgctgatccaccacacaagcagcgtggaagatggcgtgcc cagcagattttccggcagcggcttccacaccagcttcaacctgaccatcagcgatctgcag gccgacgacattgccacctactattgtcaggtgctgcagttcttcggcagaggcagcagac tgcacatcaagcgtacggtggccgctcccagcgtgttcatcttcccacctagcgacgagc agctgaagtccggcacagcctctgtcgtgtgcctgctgaacaacttctacccccgcgagg ccaaagtgcagtggaaggtggacaacgccctgcagagcggcaacagccaggaaagcg tgaccgagcaggacagcaaggactccacctacagcctgagcagcaccctgacactgag caaggccgactacgagaagcacaaggtgtacgcctgcgaagtgacccaccagggcctg tctagccccgtgaccaagagcttcaaccggggcgagtgt	**SEQ ID NO: 315**
Heavy chain B	caggtgcagctgcaggaatctggccctggcctcgtgaagcctagccagaccctgagcct gacctgtaccgtgtccggcttcagcctgagcgactacggcgtgcactgggtgcgccagc cacctggaaaaggcctggaatggctgggcgtgatctgggctggcggaggcaccaacta caaccccagcctgaagtccagaaagaccatcagcaaggacaccagcaagaaccaggtg tccctgaagctgagcagcgtgacagccgccgataccgccgtgtactactgcgccagaga caagggctacagctactactacagcatggactactggggccagggcaccaccgtgaccg tgtcatcctctcaggtgcagctggtggaatctggcggcggagtggtgcagcctggcagaa gcctgagactgagctgtgccgccagcggcttcaccttcaccaaggcctggatgcactggg tgcgccaggcccctggaaagcagctggaatgggtggcccagatcaaggacaagagcaa cagctacgccacctactacgccgacagcgtgaagggccggttcaccatcagccgggac gacagcaagaacaccctgtacctgcagatgaacagcctgcgggccgaggacaccgccg tgtactactgtcggggcgtgtactatgccctgagccccttcgattactggggccagggaac cctcgtgaccgtgtctagtcggaccgcttcgaccaagggcccatcggtgttccctctggcc ccttgcagcagaagcaccagcgaatctacagccgccctgggctgcctcgtgaaggacta ctttcccgagcccgtgaccgtgtcctggaactctggcgctctgacaagcggcgtgcacac ctttccagccgtgctccagagcagcggcctgtactctctgagcagcgtcgtgacagtgccc agcagcagcctgggcaccaagacctacacctgtaacgtggaccacaagcccagcaaca ccaaggtggacaagcgggtggaatctaagtacggccctccctgccctccttgcccagccc ctgaatttctgggcggaccctccgtgttcctgttccccccaaagcccaaggacaccctgat gatcagccggaccccccgaagtgacctgcgtggtggtggatgtgtcccaggaagatcccg aggtgcagttcaattggtacgtggacggcgtggaagtgcacaacgccaagaccaagccc agagaggaacagttcaacagcacctaccgggtggtgtccgtgctgaccgtgctgcacca ggactggctgaacggcaaagagtacaagtgcaaggtgtccaacaagggcctgcccagc tccatcgagaaaaccatcagcaaggccaagggccagccccgcgagcctcaagtgtgtac cctgcccccctagccaggaagagatgaccaagaaccaggtgtccctgagctgtgccgtga aaggcttctaccccagcgacattgccgtggaatgggagagcaacggccagcccgagaa caactacaagaccacccccccctgtgctggacagcgacggctcattcttcctggtgtccaag ctgaccgtggacaagagccggtggcaggaaggcaacgtgttcagctgctccgtgatgca	**SEQ ID NO: 316**

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Light chain B	gacatcgtgatgacccagacccccctgagcctgagcgtgacacctggacagcctgccag catcagctgcaagagcagccagagcctggtgcacaacaacgccaacacctacctgagct ggtatctgcagaagcccggccagagcccccagtccctgatctacaaggtgtccaacagat tcagcggcgtgcccgacagattctccggcagcggctctggcaccgacttcaccctgaag atcagccgggtggaagccgaggacgtgggcgtgtactattgtggccagggcacccagta ccccttcacctttggcagcggcaccaaggtggaaatcaagggccagcccaaggccgcc cccgacatcgtgctgacacagagccctgctagcctggccgtgtctcctggacagagggc caccatcacctgtagagccagcgagagcgtggaatattacgtgaccagcctgatgcagtg gtatcagcagaagcccggccagccccccaagctgctgattttcgccgccagcaacgtgg aaagcggcgtgccagccagattttccggcagcggctctggcaccgacttcaccctgacca tcaaccccgtggaagccaacgacgtggccaactactactgccagcagagccggaaggt gccctacacctttggccagggcaccaagctggaaatcaagaccaagggccccagccgta cggtggccgctcccagcgtgttcatcttcccacctagcgacgagcagctgaagtccggca cagcctctgtcgtgtgcctgctgaacaacttctacccccgcgaggccaaagtgcagtgga aggtggacaacgccctgcagagcggcaacagccaggaaagcgtgaccgagcaggac agcaaggactccacctacagcctgagcagcaccctgacactgagcaaggccgactacg agaagcacaaggtgtacgcctgcgaagtgacccaccagggcctgtctagccccgtgacc aagagcttcaaccggggcgagtgt	**SEQ ID NO: 317**
Binding Protein 34 Amino Acid Sequences		
Heavy chain A	Qvhltqsgpevrkpgtsvkvsckapgntlktydlhwvrsvpgqglqwmgwisheg dkkviverfkakvtidwdrstntaylqlsgltsgdtavyycakgskhrlrdyalydddga lnwavdvdylsnlefwgqgtavtvssastkgpsvfplapcsrstsestaalgclvkdyfp epvtvswnsgaltsgvhtfpavlqssglyslssvvtvpssslgtktytcnvdhkpsntkv dkrveskygppcppcpapeflggpsvflfppkpkdtlmisrtpevtcvvvdvsqedpe vqfnwyvdgvevhnaktkpreeqfnstyrvvsvltvlhqdwlngkeykckvsnkgl pssiektiskakgqprepqvytlppcqeemtknqvslwclvkgfypsdiavewesng qpennykttppvldsdgsfflyskltvdksrwqegnvfscsvmhealhnhytqkslsls lgk	**SEQ ID NO:318**
Light chain A	Dfvltqsphslsvtpgesasisckssshslihgdrnnylawyvqkpgrspqlliylassras gvpdrfsgsgsdkdftlkisrvetedvgtyycmqgrespwtfgqgtkvdikrtvaapsv fifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstys lsstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 319**
Heavy chain B	Qvqlvqsgaevvkpgasvkvsckas***gytftsyy***ihwvrqapgqglewigs***iy pgnvnt***nyaqkfqgratltvdtsistaymelsrlrsddtavyyc***trshygldwnf dv***wgkgttvtvsssqvqlvesgggvvqpgrslrlscaas***gftftkaw***mhwvrq apgkqlewvaq***ikdksns***yatyyadsvkgrftisrddsknltlylqmnslraedt avyyc***rgvyyalspfdy***wgqgtlvtvssrtastkgpsvfplapcsrstsestaalg clvkdyfpepvtvswnsgaltsgvhtfpavlqssglyslssvvtvpssslgtktyt cnvdhkpsntkvdkrveskygppcppcpapeflggpsvflfppkpkdtlmis rtpevtcvvvdvsqedpevqfnwyvdgvevhnaktkpreeqfnstyrvvsvlt vlhqdwlngkeykckvsnkglpssiektiskakgqprepqvctlppsqeemt knqvslscavkgfypsdiavewesngqpennykttppvldsdgsfflvskltv dksrwqegnvfscsvmhealhnhytqkslslslgk	**SEQ ID NO: 320**
Light chain B	Divmtqtplslsvtpgqpasisckss***qslvhnnanty***lswylqkpgqspqsliy***kvs***nr fsgvpdrfsgsgsgtdftlkisrveaedvgvyyc***gqgtqyp***ftfgsgtkveikgqpkaap diqmtqspsslsasvgdrvtitcqas***qniyvw***lnwyqqkpgkapklliy***kas***nlhtgv psrfsgsgsgtdftltisslqpediatyyc***qqgqtypyt***fgqgtkleiktkgpsrtvaapsvf ifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstysl sstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 321**
Binding Protein 34 Nucleotide Sequences		
Heavy chain A	caggtgcacctgacacagagcggacccgaagtgcggaagcctggcacctctgtgaagg tgtcctgcaaggcccctggcaacaccctgaaaacctacgacctgcactgggtgcgcagc	**SEQ ID NO: 322**

	gtgccaggacagggactgcagtggatgggctggatcagccacgagggcgacaagaaa gtgatcgtggaacggttcaaggccaaagtgaccatcgactgggacagaagcaccaacac cgcctacctgcagctgagcggcctgacctctggcgataccgccgtgtactactgcgccaa gggcagcaagcaccggctgagagactacgccctgtacgacgatgacggcgccctgaac tgggccgtggatgtggactacctgagcaacctggaattctggggccagggcacagccgt gaccgtgtcatctgcttcgaccaagggcccctcggtgttccctctggcccccttgcagcaga agcaccagcgaatctacagccgccctgggctgcctcgtgaaggactactttcccgagccc gtgaccgtgtcctggaactctggcgctctgacaagcggcgtgcacaccctttccagccgtg ctccagagcagcggcctgtactctctgagcagcgtcgtgacagtgcccagcagcagcct gggcaccaagacctacacctgtaacgtggaccacaagcccagcaacaccaaggtggac aagcgggtggaatctaagtacggccctccctgccctccttgcccagcccctgaatttctgg gcggaccctccgtgttcctgttcccccaaagcccaaggacaccctgatgatcagccgga cccccgaagtgacctgcgtggtggtggatgtgtcccaggaagatcccgaggtgcagttca attggtacgtggacggcgtggaagtgcacaacgccaagaccaagcccagagaggaaca gttcaacagcacctaccgggtggtgtccgtgctgaccgtgctgcaccaggactggctgaa cggcaaagagtacaagtgcaaggtgtccaacaagggcctgcccagctccatcgagaaa accatcagcaaggccaagggccagccccgcgagcctcaagtgtataccctgccccctg ccaggaagagatgaccaagaaccaggtgtccctgtggtgtctcgtgaaaggcttctaccc cagcgacattgccgtggaatgggagagcaacggccagcccgagaacaactacaagacc acccccctgtgctggacagcgacggctcattcttcctgtactccaagctgaccgtggaca agagccggtggcaggaaggcaacgtgttcagctgctccgtgatgcacgaggccctgcac aaccactacacccagaagtccctgtctctgtccctgggcaag	
Light chain A	gacttcgtgctgacccagagccctcacagcctgagcgtgacacctggcgagagcgccag catcagctgcaagagcagccactccctgatccacggcgaccggaacaactacctggctt ggtacgtgcagaagcccggcagatccccccagctgctgatctacctggccagcagcaga gccagcggcgtgcccgatagattttctggcagcggcagcgacaaggacttcaccctgaa gatcagccgggtggaaaccgaggacgtgggcacctactactgtatgcagggcagagag agcccctggacctttggccagggcaccaaggtggacatcaagcgtacggtggccgctcc cagcgtgttcatcttcccacctagcgacgagcagctgaagtccggcacagcctctgtcgtg tgcctgctgaacaacttctacccccgcgaggccaaagtgcagtggaaggtggacaacgc cctgcagagcggcaacagccaggaaagcgtgaccgagcaggacagcaaggactccac ctacagcctgagcagcaccctgacactgagcaaggccgactacgagaagcacaaggtg tacgcctgcgaagtgacccaccagggcctgtctagccccgtgaccaagagcttcaaccg gggcgagtgt	**SEQ ID NO: 323**
Heavy chain B	caggtgcagctggtgcagtctggcgccgaggtcgtgaaacctggcgcctctgtgaaggt gtcctgcaaggccagcggctacacctttaccagctactacatccactgggtgcgccaggc ccctggacagggactggaatggatcggcagcatctaccccggcaacgtgaacaccaact acgcccagaagttccagggcagagccaccctgaccgtggacaccagcatcagcaccgc ctacatggaactgagccggctgagaagcgacgacaccgccgtgtactactgcacccggt cccactacggcctggattggaacttcgacgtgtggggcaagggcaccaccgtgacagtg tctagcagccaggtgcagctggtggaatctggcggcggagtggtgcagcctggcagaa gcctgagactgagctgtgccgccagcggcttcaccttcaccaaggcctggatgcactggg tgcgccaggcccctggaaagcagctggaatgggtggcccagatcaaggacaagagcaa cagctacgccacctactacgccgacagcgtgaagggccggttcaccatcagccgggac gacagcaagaacaccctgtacctgcagatgaacagcctgcgggccgaggacaccgccg tgtactactgtcggggcgtgtactatgccctgagccccttcgattactggggccagggaac cctcgtgaccgtgtctagtcggaccgccagcacaaagggcccatcggtgttccctctggc cccttgcagcagaagcaccagcgaatctacagccgccctgggctgcctcgtgaaggact actttcccgagcccgtgaccgtgtcctggaactctggcgctctgacaagcggcgtgcaca cctttccagccgtgctccagagcagcggcctgtactctctgagcagcgtcgtgacagtgcc cagcagcagcctgggcaccaagacctacacctgtaacgtggaccacaagcccagcaac accaaggtggacaagcgggtggaatctaagtacggccctccctgccctccttgcccagcc cctgaatttctgggcggaccctccgtgttcctgttcccccaaagcccaaggacaccctga tgatcagccggacccccgaagtgacctgcgtggtggtggatgtgtcccaggaagatccc	**SEQ ID NO: 324**

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Light chain B	gacatcgtgatgacccagacccccctgagcctgagcgtgacacctggacagcctgccag catcagctgcaagagcagccagagcctggtgcacaacaacgccaacacctacctgagct ggtatctgcagaagcccggccagagcccccagtccctgatctacaaggtgtccaacagat tcagcggcgtgcccgacagattctccggcagcggctctggcaccgacttcaccctgaag atcagccgggtggaagccgaggacgtgggcgtgtactattgtggccagggcacccagta ccccttcaccttggcagcggcaccaaggtggaaatcaagggccagcccaaggccgcc cccgacatccagatgacccagagccccagcagcctgtctgccagcgtgggcgacagag tgaccatcacctgtcaggccagccagaacatctacgtgtggctgaactggtatcagcaga agcccggcaaggcccccaagctgctgatctacaaggccagcaacctgcacaccggcgt gcccagcagattttctggcagcggctccggcaccgacttcaccctgacaatcagctccctg cagcccgaggacattgccacctactactgccagcagggccagacctacccctacaccttt ggccagggcaccaagctggaaatcaagaccaagggccccagccgtacggtggccgct cccagcgtgttcatcttcccacctagcgacgagcagctgaagtccggcacagcctctgtc gtgtgcctgctgaacaacttctacccccgcgaggccaaagtgcagtggaaggtggacaa cgccctgcagagcggcaacagccaggaaagcgtgaccgagcaggacagcaaggactc cacctacagcctgagcagcaccctgacactgagcaaggccgactacgagaagcacaag gtgtacgcctgcgaagtgacccaccagggcctgtctagccccgtgaccaagagcttcaac cggggcgagtgt	**SEQ ID NO: 325**
Binding Protein 35 Amino Acid Sequences		
Heavy chain A	Qvhltqsgpevrkpgtsvkvsckapgntlktydlhwvrsvpgqglqwmgwisheg dkkviverfkakvtidwdrstntaylqlsgltsgdtavyycakgskhrlrdyalydddga lnwavdvdylsnlefwgqgtavtvssastkgpsvfplapcsrstsestaalgclvkdyfp epvtvswnsgaltsgvhtfpavlqssglyslssvvtvpssslgtktytcnvdhkpsntkv dkrveskygppcppcpapeflggpsvflfppkpkdtlmisrtpevtcvvvdvsqedpe vqfnwyvdgvevhnaktkpreeqfnstyrvvsvltvlhqdwlngkeykckvsnkgl pssiektiskakgqprepqvytlppcqeemtknqvslwclvkgfypsdiavewesng qpennykttppvldsdgsfflyskltvdksrwqegnvfscsvmhealhnhytqkslsls lgk	**SEQ ID NO: 326**
Light chain A	Dfvltqsphslsvtpgesasisckssshslihgdrnnylawyvqkpgrspqlliylassras gvpdrfsgsgsdkdftlkisrvetedvgtyycmqgrespwtfgqgtkvdikrtvaapsv fifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstys lsstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO:327**
Heavy chain B	Qvqlqesgpglvkpsqtlsltctvsgfslsdygvhwvrqppgkglewlgviwa gggtnynpslksrktiskdtsknqvslklssvtaadtavyycardkgysyyysm dywgqgttvtvsssqvqlvesgggvvqpgrslrlscaasgftftkawmhwvrq apgkqlewvaqikdksnsyatyyadsvkgrftisrddskntlylqmnslraedt avyycrgvyyalspfdywgqgtlvtvssrtastkgpsvfplapcsrstsestaalg clvkdyfpepvtvswnsgaltsgvhtfpavlqssglyslssvvtvpssslgtktyt cnvdhkpsntkvdkrveskygppcppcpapeflggpsvflfppkpkdtlmis rtpevtcvvvdvsqedpevqfnwyvdgvevhnaktkpreeqfnstyrvvsvlt vlhqdwlngkeykckvsnkglpssiektiskakgqprepqvctlppsqeemt knqvslscavkgfypsdiavewesngqpennykttppvldsdgsfflvskltv dksrwqegnvfscsvmhealhnhytqkslslslgk	**SEQ ID NO: 328**
Light chain B	Divmtqtplslsvtpgqpasisckssqslvhnnantylswylqkpgqspqsliykvsnr	**SEQ ID**

	fsgvpdrfsgsgsgtdftlkisrveaedvgvyycgqgtqypftfgsgtkveikgqpkaa pdivltqspaslavspgqratitcrasesveyyvtslmqwyqqkpgqppkllifaasnv esgvparfsgsgsgtdftltinpveandvanyycqqsrkvpytfgqgtkleiktkgpsrt vaapsvfifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqd skdstyslsstltlskadyekhkvyacevthqglsspvtksfnrgec	**NO: 329**
Binding Protein 35 Nucleotide Sequences		
Heavy chain A	caggtgcacctgacacagagcggacccgaagtgcggaagcctggcacctctgtgaagg tgtcctgcaaggcccctggcaacaccctgaaaacctacgacctgcactgggtgcgcagc gtgccaggacagggactgcagtggatgggctggatcagccacgagggcgacaagaaa gtgatcgtggaacggttcaaggccaaagtgaccatcgactgggacagaagcaccaacac cgcctacctgcagctgagcggcctgacctctggcgataccgccgtgtactactgcgccaa gggcagcaagcaccggctgagagactacgccctgtacgacgatgacggcgccctgaac tgggccgtggatgtggactacctgagcaacctggaattctggggccagggcacagccgt gaccgtgtcatctgcttcgaccaagggcccctcggtgttccctctggccccttgcagcaga agcaccagcgaatctacagccgccctgggctgcctcgtgaaggactactttcccgagccc gtgaccgtgtcctggaactctggcgctctgacaagcggcgtgcacaccttccagccgtg ctccagagcagcggcctgtactctctgagcagcgtcgtgacagtgcccagcagcagcct gggcaccaagacctacacctgtaacgtggaccacaagcccagcaacaccaaggtggac aagcgggtggaatctaagtacggccctccctgccctccttgcccagcccctgaatttctgg gcggaccctccgtgttcctgttcccccccaaagcccaaggacaccctgatgatcagccgga cccccgaagtgacctgcgtggtggtggatgtgtcccaggaagatcccgaggtgcagttca attggtacgtggacggcgtggaagtgcacaacgccaagaccaagcccagagaggaaca gttcaacagcacctaccgggtggtgtccgtgctgaccgtgctgcaccaggactggctgaa cggcaaagagtacaagtgcaaggtgtccaacaagggcctgcccagctccatcgagaaa accatcagcaaggccaagggccagccccgcgagcctcaagtgtataccctgccccctg ccaggaagagatgaccaagaaccaggtgtccctgtggtgtctcgtgaaaggcttctaccc cagcgacattgccgtggaatgggagagcaacggccagcccgagaacaactacaagacc acccccccctgtgctggacagcgacggctcattcttcctgtactccaagctgaccgtggaca agagccggtggcaggaaggcaacgtgttcagctgctccgtgatgcacgaggccctgcac aaccactacacccagaagtccctgtctctgtccctgggcaag	**SEQ ID NO: 330**
Light chain A	gacttcgtgctgacccagagccctcacagcctgagcgtgacacctggcgagagcgccag catcagctgcaagagcagccactccctgatccacggcgaccggaacaactacctggctt ggtacgtgcagaagcccggcagatccccccagctgctgatctacctggccagcagcaga gccagcggcgtgcccgatagattttctggcagcggcagcgacaaggacttcaccctgaa gatcagccgggtggaaaccgaggacgtgggcacctactactgtatgcagggcagagag agcccctggacctttggccagggcaccaaggtggacatcaagcgtacggtggccgctcc cagcgtgttcatcttcccacctagcgacgagcagctgaagtccggcacagcctctgtcgtg tgcctgctgaacaacttctacccccgcgaggccaaagtgcagtggaaggtggacaacgc cctgcagagcggcaacagccaggaaagcgtgaccgagcaggacagcaaggactccac ctacagcctgagcagcaccctgacactgagcaaggccgactacgagaagcacaaggtg tacgcctgcgaagtgacccaccagggcctgtctagccccgtgaccaagagcttcaaccg gggcgagtgt	**SEQ ID NO: 331**
Heavy chain B	caggtgcagctgcaggaatctggccctggcctcgtgaagcctagccagaccctgagcct gacctgtaccgtgtccggcttcagcctgagcgactacggcgtgcactgggtgcgccagc cacctggaaaaggcctggaatggctgggcgtgatctgggctggcggaggcaccaacta caaccccagcctgaagtccagaaagaccatcagcaaggacaccagcaagaaccaggtg tccctgaagctgagcagcgtgacagccgccgataccgccgtgtactactgcgccagaga caagggctacagctactactacagcatggactactggggccagggcaccaccgtgaccg tgtcatcctctcaggtgcagctggtggaatctggcggcggagtggtgcagcctggcagaa gcctgagactgagctgtgccgccagcggcttcaccttcaccaaggcctggatgcactggg tgcgccaggcccctggaaagcagctggaatgggtggcccagatcaaggacaagagcaa cagctacgccacctactacgccgacagcgtgaagggccggttcaccatcagccgggac gacagcaagaacaccctgtacctgcagatgaacagcctgcgggccgaggacaccgccg tgtactactgtcggggcgtgtactatgccctgagccccttcgattactggggccagggaac	**SEQ ID NO: 332**

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Light chain B	gacatcgtgatgacccagacccccctgagcctgagcgtgacacctggacagcctgccag catcagctgcaagagcagccagagcctggtgcacaacaacgccaacacctacctgagct ggtatctgcagaagcccggccagagcccccagtccctgatctacaaggtgtccaacagat tcagcggcgtgcccgacagattctccggcagcggctctggcaccgacttcaccctgaag atcagccgggtggaagccgaggacgtgggcgtgtactattgtggccagggcacccagta ccccttcacctttggcagcggcaccaaggtggaaatcaagggccagcccaaggccgcc cccgacatcgtgctgacacagagccctgctagcctggccgtgtctcctggacagagggc caccatcacctgtagagccagcgagagcgtggaatattacgtgaccagcctgatgcagtg gtatcagcagaagcccggccagccccccaagctgctgattttcgccgccagcaacgtgg aaagcggcgtgccagccagattttccggcagcggctctggcaccgacttcaccctgacca tcaaccccgtggaagccaacgacgtggccaactactactgccagcagagccggaaggt gccctacacctttggccagggcaccaagctggaaatcaagaccaagggccccagccgta cggtggccgctcccagcgtgttcatcttcccacctagcgacgagcagctgaagtccggca cagcctctgtcgtgtgcctgctgaacaacttctacccccgcgaggccaaagtgcagtgga aggtggacaacgccctgcagagcggcaacagccaggaaagcgtgaccgagcaggac agcaaggactccacctacagcctgagcagcaccctgacactgagcaaggccgactacg agaagcacaaggtgtacgcctgcgaagtgacccaccagggcctgtctagccccgtgacc aagagcttcaaccggggcgagtgt	**SEQ ID NO: 333**
Binding Protein 36 Amino Acid Sequences		
Heavy chain A	Qvqlvqsggqmkkpgesmriscrasgyefidctlnwirlapgkrpewmgwlkprg gavnyarplqgrvtmtrdvysdtaflelrsltvddtavyfctrgkncdynwdfehwgrg tpvivssastkgpsvfplapcsrstsestaalgclvkdyfpepvtvswnsgaltsgvhtfp avlqssglyslssvvtvpssslgtktytcnvdhkpsntkvdkrveskygppcppcpape flggpsvflfppkpkdtlmisrtpevtcvvvdvsqedpevqfnwyvdgvevhnaktk preeqfnstyrvvsvltvlhqdwlngkeykckvsnkglpssiektiskakgqprepqv ytlppcqeemtknqvslwclvkgfypsdiavewesngqpennykttppvldsdgsff lyskltvdksrwqegnvfscsvmhealhnhytqkslslslgk	**SEQ ID NO: 334**
Light chain A	Eivltqspgtlslspgetaiiscrtsqygslawyqqrpgqaprlviysgstraagipdrfsg srwgpdynltisnlesgdfgvyycqqyeffgqgtkvqvdikrtvaapsvfifppsdeql ksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsstltlskad yekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 335**
Heavy chain B	Qvqlvqsgaevvkpgasvkvsckas***gytftsyy***ihwvrqapgqglewigs***iy*** ***pgnvnt***nyaqkfqgratltvdtsistaymelsrlrsddtavyyc***trshygldwnf*** ***dv***wgkgttvtvsssqvqlvesgggvvqpgrslrlscaas***gftftkaw***mhwvrq apgkqlewvaq***ikdksns***yatyyadsvkgrftisrddskntlylqmnslraedt avyyc***rgvyyalspfdy***wgqgtlvtvssrtastkgpsvfplapcsrstsestaalg	**SEQ ID NO: 336**

	clvkdyfpepvtvswnsgaltsgvhtfpavlqssglyslssvvtvpssslgtktyt cnvdhkpsntkvdkrveskygppcppcpapeflggpsvflfppkpkdtlmis rtpevtcvvvdvsqedpevqfnwyvdgvevhnaktkpreeqfnstyrvvsvl tvlhqdwlngkeykckvsnkglpssiektiskakgqprepqvctlppsqeemt knqvslscavkgfypsdiavewesngqpennykttppvldsdgsfflvskltv dksrwqegnvfscsvmhealhnhytqkslslslgk	
Light chain B	Divmtqtplslsvtpgqpasisckss***qslvhnnanty***lswylqkpgqspqsliy***kvs***n rfsgvpdrfsgsgsgtdftlkisrveaedvgvyyc***gqgtqyp***ftfgsgtkveikgqpkaa pdiqmtqspsslsasvgdrvtitcqas***qniyvw***lnwyqqkpgkapklliy***kas***nlhtg vpsrfsgsgsgtdftltisslqpediatyyc***qqgqtypyt***fgqgtkleiktkgpsrtvaaps vfifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdst yslsstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 337**
Binding Protein 36 Nucleotide Sequences		
Heavy chain A	caggtgcagctggtgcagtctggcggccagatgaagaaacccggcgagagcatgcgga tcagctgcagagccagcggctacgagttcatcgactgcaccctgaactggatcagactgg ccctggcaagcggcctgagtggatgggatggctgaagcctagaggcggagccgtgaa ctacgccagacctctgcagggcagagtgaccatgacccgggacgtgtacagcgataccg ccttcctggaactgcggagcctgaccgtggatgataccgccgtgtacttctgcacccggg gcaagaactgcgactacaactgggacttcgagcactggggcagaggcacccctgtgatc gtgtcaagcgcgtcgaccaagggcccctcggtgttccctctggcccccttgcagcagaagc accagcgaatctacagccgccctgggctgcctcgtgaaggactactttcccgagcccgtg accgtgtcctggaactctggcgctctgacaagcggcgtgcacacctttccagccgtgctcc agagcagcggcctgtactctctgagcagcgtcgtgacagtgcccagcagcagcctgggc accaagacctacacctgtaacgtggaccacaagcccagcaacaccaaggtggacaagc gggtggaatctaagtacggccctccctgccctccttgcccagcccctgaatttctgggcgg accctccgtgttcctgttcccccccaaagcccaaggacaccctgatgatcagccggacccc cgaagtgacctgcgtggtggtggatgtgtcccaggaagatcccgaggtgcagttcaattg gtacgtggacggcgtggaagtgcacaacgccaagaccaagcccagagaggaacagttc aacagcacctaccgggtggtgtccgtgctgaccgtgctgcaccaggactggctgaacgg caaagagtacaagtgcaaggtgtccaacaagggcctgcccagctccatcgagaaaacca tcagcaaggccaagggccagccccgcgagcctcaagtgtataccctgcccccttgccag gaagagatgaccaagaaccaggtgtccctgtggtgtctcgtgaaaggcttctaccccagc gacattgccgtggaatgggagagcaacggccagcccgagaacaactacaagaccaccc cccctgtgctggacagcgacggctcattcttcctgtactccaagctgaccgtggacaagag ccggtggcaggaaggcaacgtgttcagctgctccgtgatgcacgaggccctgcacaacc actacacccagaagtccctgtctctgtccctgggcaag	**SEQ ID NO: 338**
Light chain A	Gagatcgtgctgacacagagccctggcaccctgagcctgtctccaggcgagacagccat catcagctgccggacaagccagtacggcagcctggcctggtatcagcagaggcctgga caggcccccagactcgtgatctacagcggcagcacaagagccgccggaatccccgata gattcagcggctccagatggggccctgactacaacctgaccatcagcaacctggaaagc ggcgacttcggcgtgtactactgccagcagtacgagttcttcggccagggcaccaaggtg caggtggacatcaagcgtacggtggccgctcccagcgtgttcatcttcccacctagcgac gagcagctgaagtccggcacagcctctgtcgtgtgcctgctgaacaacttctacccccgc gaggccaaagtgcagtggaaggtggacaacgccctgcagagcggcaacagccaggaa agcgtgaccgagcaggacagcaaggactccacctacagcctgagcagcaccctgacac tgagcaaggccgactacgagaagcacaaggtgtacgcctgcgaagtgacccaccaggg cctgtctagccccgtgaccaagagcttcaaccggggcgagtgt	**SEQ ID NO: 339**
Heavy chain B	caggtgcagctggtgcagtctggcgccgaggtcgtgaaacctggcgcctctgtgaaggt gtcctgcaaggccagcggctacacctttaccagctactacatccactgggtgcgccaggc ccctggacagggactggaatggatcggcagcatctaccccggcaacgtgaacaccaact acgcccagaagttccagggcagagccaccctgaccgtggacaccagcatcagcaccgc ctacatggaactgagccggctgagaagcgacgacaccgccgtgtactactgcacccggt cccactacggcctggattggaacttcgacgtgtggggcaagggcaccaccgtgacagtg	**SEQ ID NO: 340**

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Light chain B	gacatcgtgatgacccagaccccctgagcctgagcgtgacacctggacagcctgccag catcagctgcaagagcagccagagcctggtgcacaacaacgccaacacctacctgagct ggtatctgcagaagcccggccagagcccccagtccctgatctacaaggtgtccaacagat tcagcggcgtgcccgacagattctccggcagcggctctggcaccgacttcaccctgaag atcagccgggtggaagccgaggacgtgggcgtgtactattgtggccagggcacccagta ccccttcacctttggcagcggcaccaaggtggaaatcaagggccagcccaaggccgcc cccgacatccagatgacccagagccccagcagcctgtctgccagcgtgggcgacagag tgaccatcacctgtcaggccagccagaacatctacgtgtggctgaactggtatcagcaga agcccggcaaggcccccaagctgctgatctacaaggccagcaacctgcacaccggcgt gcccagcagattttctggcagcggctccggcaccgacttcaccctgacaatcagctccctg cagcccgaggacattgccacctactactgccagcagggccagacctacccctacacctttt ggccagggcaccaagctggaaatcaagaccaagggccccagccgtacggtggccgct cccagcgtgttcatcttcccacctagcgacgagcagctgaagtccggcacagcctctgtc gtgtgcctgctgaacaacttctacccccgcgaggccaaagtgcagtggaaggtggacaa cgccctgcagagcggcaacagccaggaaagcgtgaccgagcaggacagcaaggactc cacctacagcctgagcagcaccctgacactgagcaaggccgactacgagaagcacaag gtgtacgcctgcgaagtgacccaccagggcctgtctagccccgtgaccaagagcttcaac cggggcgagtgt	**SEQ ID NO: 341**
Binding Protein 37 Amino Acid Sequences		
Heavy chain A	Qvqlvqsggqmkkpgesmriscrasgyefidctlnwirlapgkrpewmgwlkprg gavnyarplqgrvtmtrdvysdtaflelrsltvddtavyfctrgkncdynwdfehwgrg tpvivssastkgpsvfplapcsrstsestaalgclvkdyfpepvtvswnsgaltsgvhtfp avlqssglyslssvvtvpssslgtktytcnvdhkpsntkvdkrveskygppcppcpape flggpsvflfppkpkdtlmisrtpevtcvvvdvsqedpevqfnwyvdgvevhnaktk preeqfnstyrvvsvltvlhqdwlngkeykckvsnkglpssiektiskakgqprepqv ytlppcqeemtknqvslwclvkgfypsdiavewesngqpennykttppvldsdgsff lyskltvdksrwqegnvfscsvmhealhnhytqkslslslgk	**SEQ ID NO: 342**
Light chain A	Eivltqspgtlslspgetaiiscrtsqygslawyqqrpgqaprlviysgstraagipdrfsg srwgpdynltisnlesgdfgvyycqqyeffgqgtkvqvdikrtvaapsvfifppsdeql ksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsstltlskad yekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 343**

Heavy chain B	Qvqlqesgpglvkpsqtlsltctvsgfslsdygvhwvrqppgkglewlgviwa gggtnynpslksrktiskdtsknqvslklssvtaadtavyycardkgysyyysm dywgqgttvtvsssqvqlvesgggvvqpgrslrlscaasgftftkawmhwvrq apgkqlewvaqikdksnsyatyyadsvkgrftisrddsknt lylqmnslraedt avyycrgvyyalspfdywgqgtlvtvssrtastkgpsvfplapcsrstsestaalg clvkdyfpepvtvswnsgaltsgvhtfpavlqssglyslssvvtvpssslgtktyt cnvdhkpsntkvdkrveskygppcppcpapeflggpsvflfppkpkdtlmis rtpevtcvvvdvsqedpevqfnwyvdgvevhnaktkpreeqfnstyrvvsvlt vlhqdwlngkeykckvsnkglpssiektiskakgqprepqvctlppsqeemt knqvslscavkgfypsdiavewesngqpennykttppvldsdgsfflvskltv dksrwqegnvfscsvmhealhnhytqkslslslgk	**SEQ ID NO:344**
Light chain B	Divmtqtplslsvtpgqpasisckssqslvhnnantylswylqkpgqspqsliykvsnr fsgvpdrfsgsgsgtdftlkisrveaedvgvyycgqgtqypftfgsgtkveikgqpkaa pdivltqspaslavspgqratitcrasesveyyvtslmqwyqqkpgqppkllifaasnv esgvparfsgsgsgtdftltinpveandvanyycqqsrkvpytfgqgtkleiktkgpsrt vaapsvfifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqd skdstyslsstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 345**
Binding Protein 37 Nucleotide Sequences		
Heavy chain A	caggtgcagctggtgcagtctggcggccagatgaagaaacccggcgagagcatgcgga tcagctgcagagccagcggctacgagttcatcgactgcaccctgaactggatcagactgg ccctggcaagcggcctgagtggatgggatggctgaagcctagaggcggagccgtgaa ctacgccagacctctgcagggcagagtgaccatgacccgggacgtgtacagcgataccg ccttcctggaactgcggagcctgaccgtggatgataccgccgtgtacttctgcacccggg gcaagaactgcgactacaactgggacttcgagcactggggcagaggcacccctgtgatc gtgtcaagcgcgtcgaccaagggcccctcggtgttccctctggcccccttgcagcagaagc accagcgaatctacagccgccctgggctgcctcgtgaaggactactttcccgagcccgtg accgtgtcctggaactctggcgctctgacaagcggcgtgcacaccttccagccgtgctcc agagcagcggcctgtactctctgagcagcgtcgtgacagtgcccagcagcagcctgggc accaagacctacacctgtaacgtggaccacaagcccagcaacaccaaggtggacaagc gggtggaatctaagtacggccctccctgccctccttgcccagcccctgaatttctgggcgg accctccgtgttcctgttcccccaaagcccaaggacaccctgatgatcagccggacccc cgaagtgacctgcgtggtggtggatgtgtcccaggaagatcccgaggtgcagttcaattg gtacgtggacggcgtggaagtgcacaacgccaagaccaagcccagagaggaacagttc aacagcacctaccgggtggtgtccgtgctgaccgtgctgcaccaggactggctgaacgg caaagagtacaagtgcaaggtgtccaacaagggcctgcccagctccatcgagaaaacca tcagcaaggccaagggccagccccgcgagcctcaagtgtataccctgccccccttgccag gaagagatgaccaagaaccaggtgtccctgtggtgtctcgtgaaaggcttctaccccagc gacattgccgtggaatgggagagcaacggccagcccgagaacaactacaagaccaccc cccctgtgctggacagcgacggctcattcttcctgtactccaagctgaccgtggacaagag ccggtggcaggaaggcaacgtgttcagctgctccgtgatgcacgaggccctgcacaacc actacacccagaagtccctgtctctgtccctgggcaag	**SEQ ID NO: 346**
Light chain A	Gagatcgtgctgacacagagccctggcaccctgagcctgtctccaggcgagacagccat catcagctgccggacaagccagtacggcagcctggcctggtatcagcagaggcctggac aggcccccagactcgtgatctacagcggcagcacaagagccgccggaatccccgatag attcagcggctccagatggggccctgactacaacctgaccatcagcaacctggaaagcg gcgacttcggcgtgtactactgccagcagtacgagttcttcggccagggcaccaaggtgc aggtggacatcaagcgtacggtggccgctcccagcgtgttcatcttcccacctagcgacg agcagctgaagtccggcacagcctctgtcgtgtgcctgctgaacaacttctacccccgcga ggccaaagtgcagtggaaggtggacaacgccctgcagagcggcaacagccaggaaag cgtgaccgagcaggacagcaaggactccacctacagcctgagcagcaccctgacactg agcaaggccgactacgagaagcacaaggtgtacgcctgcgaagtgacccaccagggcc tgtctagccccgtgaccaagagcttcaaccggggcgagtgt	**SEQ ID NO: 347**
Heavy chain B	caggtgcagctgcaggaatctggccctggcctcgtgaagcctagccagaccctgagcct	**SEQ ID**

	gacctgtaccgtgtccggcttcagcctgagcgactacggcgtgcactgggtgcgccagcc acctggaaaaggcctggaatggctgggcgtgatctgggctggcggaggcaccaactaca accccagcctgaagtccagaaagaccatcagcaaggacaccagcaagaaccaggtgtc cctgaagctgagcagcgtgacagccgccgataccgccgtgtactactgcgccagagaca agggctacagctactactacagcatggactactggggccagggcaccaccgtgaccgtg tcatcctctcaggtgcagctggtggaatctggcggcggagtggtgcagcctggcagaagc ctgagactgagctgtgccgccagcggcttcaccttcaccaaggcctggatgcactgggtg cgccaggcccctggaaagcagctggaatgggtggcccagatcaaggacaagagcaac agctacgccacctactacgccgacagcgtgaagggccggttcaccatcagccgggacg acagcaagaacaccctgtacctgcagatgaacagcctgcgggccgaggacaccgccgt gtactactgtcggggcgtgtactatgccctgagccccttcgattactggggccagggaacc ctcgtgaccgtgtctagtcggaccgcttcgaccaagggcccatcggtgttccctctggccc cttgcagcagaagcaccagcgaatctacagccgccctgggctgcctcgtgaaggactact ttcccgagcccgtgaccgtgtcctggaactctggcgctctgacaagcggcgtgcacaccctt tccagccgtgctccagagcagcggcctgtactctctgagcagcgtcgtgacagtgcccag cagcagcctgggcaccaagacctacacctgtaacgtggaccacaagcccagcaacacc aaggtggacaagcgggtggaatctaagtacggccctccctgccctccttgcccagccct gaatttctgggcggaccctccgtgttcctgttccccccaaagcccaaggacaccctgatga tcagccggaccccgaagtgacctgcgtggtggtggatgtgtcccaggaagatcccgag gtgcagttcaattggtacgtggacggcgtggaagtgcacaacgccaagaccaagcccag agaggaacagttcaacagcacctaccgggtggtgtccgtgctgaccgtgctgcaccagg actggctgaacggcaaagagtacaagtgcaaggtgtccaacaagggcctgcccagctcc atcgagaaaaccatcagcaaggccaagggccagccccgcgagcctcaagtgtgtaccct gcccccctagccaggaagagatgaccaagaaccaggtgtccctgagctgtgccgtgaaag gcttctaccccagcgacattgccgtggaatgggagagcaacggccagcccgagaacaa ctacaagaccaccccccctgtgctggacagcgacggctcattcttcctggtgtccaagctg accgtggacaagagccggtggcaggaaggcaacgtgttcagctgctccgtgatgcacga ggccctgcacaaccactacacccagaagtccctgtctctgtccctgggcaag	**NO: 348**
Light chain B	gacatcgtgatgacccagacccccctgagcctgagcgtgacacctggacagcctgccag catcagctgcaagagcagccagagcctggtgcacaacaacgccaacacctacctgagct ggtatctgcagaagcccggccagagcccccagtccctgatctacaaggtgtccaacagat tcagcggcgtgcccgacagattctccggcagcggctctggcaccgacttcaccctgaaga tcagccgggtggaagccgaggacgtgggcgtgtactattgtggccagggcacccagtac cccttcacctttggcagcggcaccaaggtggaaatcaagggccagcccaaggccgcccc cgacatcgtgctgacacagagccctgctagcctggccgtgtctcctggacagagggcca ccatcacctgtagagccagcgagagcgtggaatattacgtgaccagcctgatgcagtggt atcagcagaagcccggccagccccccaagctgctgattttcgccgccagcaacgtggaa agcggcgtgccagccagattttccggcagcggctctggcaccgacttcaccctgaccatc aaccccgtggaagccaacgacgtggccaactactactgccagcagagccggaaggtgc cctacacctttggccagggcaccaagctggaaatcaagaccaagggccccagccgtacg gtggccgctcccagcgtgttcatcttcccacctagcgacgagcagctgaagtccggcaca gcctctgtcgtgtgcctgctgaacaacttctacccccgcgaggccaaagtgcagtggaag gtggacaacgccctgcagagcggcaacagccaggaaagcgtgaccgagcaggacagc aaggactccacctacagcctgagcagcaccctgacactgagcaaggccgactacgaga agcacaaggtgtacgcctgcgaagtgacccaccagggcctgtctagccccgtgaccaag agcttcaaccggggcgagtgt	**SEQ ID NO: 349**
Binding Protein 38 Amino Acid Sequences		
Heavy chain A	Qvqlvqsgaevvkpgasvkvsckasgytftsyyihwvrqapgqglewigsiypgnv ntnyaqkfqgratltvdtsistaymelsrlrsddtavyyctrshygldwnfdvwgkgttv tvssastkgpsvfplapcsrstsestaalgclvkdyfpepvtvswnsgaltsgvhtfpavl qssglyslssvvtvpssslgtktytcnvdhkpsntkvdkrveskygppcppcpapeflg gpsvflfppkpkdtlmisrtpevtcvvvdvsqedpevqfnwyvdgvevhnaktkpre eqfnstyrvvsvltvlhqdwlngkeykckvsnkglpssiektiskakgqprepqvytlp pcqeemtknqvslwclvkgfypsdiavewesngqpennykttppvldsdgsfflysk	**SEQ ID NO: 350**

	ltvdksrwqegnvfscsvmhealhnhytqkslslslgk	
Light chain A	Diqmtqspsslsasvgdrvtitcqasqniyvwlnwyqqkpgkapklliykasnlhtgv psrfsgsgsgtdftltisslqpediatyycqqgqtypytfgqgtkleikrtvaapsvfifpps deqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsstltl skadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 351**
Heavy chain B	Rahlvqsgtamkkpgasvrvscqtsgytftahilfwfrqapgrglewvgwikp qygavnfgggfrdrvtltrdvyreiaymdirglkpddtavyycardrsygdssw aldawgqgttvvvsasqvqlvesgggvvqpgrslrlscaasgftftkawmhw vrqapgkqlewvaqikdksnsyatyyadsvkgrftisrddskntlylqmnslra edtavyycrgvyyalspfdywgqgtlvtvssrtastkgpsvfplapcsrstsesta algclvkdyfpepvtvswnsgaltsgvhtfpavlqssglyslssvvtvpssslgtk tytcnvdhkpsntkvdkrveskygppcppcpapeflggpsvflfppkpkdtl misrtpevtcvvvdvsqedpevqfnwyvdgvevhnaktkpreeqfnstyrvv svltvlhqdwlngkeykckvsnkglpssiektiskakgqprepqvctlppsqee mtknqvslscavkgfypsdiavewesngqpennykttppvldsdgsfflvskl tvdksrwqegnvfscsvmhealhnhytqkslslslgk	**SEQ ID NO: 352**
Light chain B	Divmtqtplslsvtpgqpasisckssqslvhnnantylswylqkpgqspqsliykvsnr fsgvpdrfsgsgsgtdftlkisrveaedvgvyycgqgtqypftfgsgtkveikgqpkaa pyihvtqspsslsvsigdrvtincqtsqgvgsdlhwyqhkpgrapkllihhtssvedgv psrfsgsgfhtsfnltisdlqaddiatyycqvlqffgrgsrlhiktkgpsrtvaapsvfifpp sdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsstlt lskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 353**
Binding Protein 38 Nucleotide Sequences		
Heavy chain A	caggtgcagctggtgcagtctggcgccgaggtcgtgaaacctggcgcctctgtgaaggt gtcctgcaaggccagcggctacacctttaccagctactacatccactgggtgcgccaggc ccctggacagggactggaatggatcggcagcatctaccccggcaacgtgaacaccaact acgcccagaagttccagggcagagccaccctgaccgtggacaccagcatcagcaccgc ctacatggaactgagccggctgagaagcgacgacaccgccgtgtactactgcacccggt cccactacggcctggattggaacttcgacgtgtggggcaagggcaccaccgtgacagtgt ctagcgcgtcgaccaagggcccctcggtgttccctctggccccttgcagcagaagcacca gcgaatctacagccgccctgggctgcctcgtgaaggactactttcccgagcccgtgaccg tgtcctggaactctggcgctctgacaagcggcgtgcacaccttccagccgtgctccagag cagcggcctgtactctctgagcagcgtcgtgacagtgcccagcagcagcctgggcacca agacctacacctgtaacgtggaccacaagcccagcaacaccaaggtggacaagcgggt ggaatctaagtacggccctccctgccctccttgcccagcccctgaatttctgggcggaccc tccgtgttcctgttcccccaaagcccaaggacaccctgatgatcagccggacccccgaa gtgacctgcgtggtggtggatgtgtcccaggaagatcccgaggtgcagttcaattggtacg tggacggcgtggaagtgcacaacgccaagaccaagcccagagaggaacagttcaacag cacctaccgggtggtgtccgtgctgaccgtgctgcaccaggactggctgaacggcaaag agtacaagtgcaaggtgtccaacaagggcctgcccagctccatcgagaaaaccatcagc aaggccaagggccagccccgcgagcctcaagtgtataccctgcccccttgccaggaaga gatgaccaagaaccaggtgtccctgtggtgtctcgtgaaaggcttctaccccagcgacatt gccgtggaatgggagagcaacggccagcccgagaacaactacaagaccacccccccct gtgctggacagcgacggctcattcttcctgtactccaagctgaccgtggacaagagccggt ggcaggaaggcaacgtgttcagctgctccgtgatgcacgaggccctgcacaaccactac acccagaagtccctgtctctgtccctgggcaag	**SEQ ID NO: 354**
Light chain A	Gacatccagatgacccagagccccagcagcctgtctgccagcgtgggcgacagagtga ccatcacctgtcaggccagccagaacatctacgtgtggctgaactggtatcagcagaagc ccggcaaggcccccaagctgctgatctacaaggccagcaacctgcacaccggcgtgcc cagcagattttctggcagcggctccggcaccgacttcaccctgacaatcagctccctgcag cccgaggacattgccacctactactgccagcagggccagacctacccctacaccttggc cagggcaccaagctggaaatcaagcgtacggtggccgctcccagcgtgttcatcttccca cctagcgacgagcagctgaagtccggcacagcctctgtcgtgtgcctgctgaacaacttct	**SEQ ID NO: 355**

	accccgcgaggccaaggtgcagtggaaggtggacaatgccctgcagagcggcaaca gccaggaaagcgtgaccgagcaggacagcaaggactccacctacagcctgagcagca ccctgaccctgagcaaggccgactacgagaagcacaaggtgtacgcctgcgaagtgac ccaccagggcctgtctagccccgtgaccaagagcttcaaccggggcgagtgt	
Heavy chain B	agagcccacctggtgcagtctggcaccgccatgaagaaaccaggcgcctctgtgcgggt gtcctgtcagacaagcggctacaccttcaccgcccacatcctgttctggttccggcaggcc cctggcagaggactggaatgggtgggatggatcaagccccagtatggcgccgtgaactt cggcggaggcttccgggatagagtgaccctgacccgggacgtgtaccgcgagatcgcct acatggacatccggggcctgaagcccgatgacaccgccgtgtactactgcgccagagac agaagctacggcgacagcagctgggctctggatgcttggggccagggcacaaccgtgg tggtgtctgcctctcaggtgcagctggtggaatctggcggcggagtggtgcagcctggca gaagcctgagactgagctgtgccgccagcggcttcaccttcaccaaggcctggatgcact gggtgcgccaggcccctggaaagcagctggaatgggtggcccagatcaaggacaaga gcaacagctacgccacctactacgccgacagcgtgaagggccggttcaccatcagccgg gacgacagcaagaacaccctgtacctgcagatgaacagcctgcgggccgaggacaccg ccgtgtactactgtcggggcgtgtactatgccctgagccccttcgattactggggccaggg aaccctcgtgaccgtgtctagtcggaccgcttcgaccaagggcccatcggtgttccctctg gccccttgcagcagaagcaccagcgaatctacagccgccctgggctgcctcgtgaagga ctactttcccgagcccgtgaccgtgtcctggaactctggcgctctgacaagcggcgtgcac acctttccagccgtgctccagagcagcggcctgtactctctgagcagcgtcgtgacagtgc ccagcagcagcctgggcaccaagacctacacctgtaacgtggaccacaagcccagcaa caccaaggtggacaagcgggtggaatctaagtacggccctccctgccctccttgcccagc ccctgaatttctgggcggaccctccgtgttcctgttccccccaaagcccaaggacaccctg atgatcagccggacccccgaagtgacctgcgtggtggtggatgtgtcccaggaagatccc gaggtgcagttcaattggtacgtggacggcgtggaagtgcacaacgccaagaccaagcc cagagaggaacagttcaacagcacctaccgggtggtgtccgtgctgaccgtgctgcacc aggactggctgaacggcaaagagtacaagtgcaaggtgtccaacaagggcctgcccag ctccatcgagaaaaccatcagcaaggccaagggccagccccgcgagcctcaagtgtgta ccctgccccctagccaggaagagatgaccaagaaccaggtgtccctgagctgtgccgtg aaaggcttctaccccagcgacattgccgtggaatgggagagcaacggccagcccgaga acaactacaagaccacccccccctgtgctggacagcgacggctcattcttcctggtgtccaa gctgaccgtggacaagagccggtggcaggaaggcaacgtgttcagctgctccgtgatgc acgaggccctgcacaaccactacacccagaagtccctgtctctgtccctgggcaag	**SEQ ID NO: 356**
Light chain B	Gacatcgtgatgacccagacccccctgagcctgagcgtgacacctggacagcctgcca gcatcagctgcaagagcagccagagcctggtgcacaacaacgccaacacctacctgag ctggtatctgcagaagcccggccagagcccccagtccctgatctacaaggtgtccaacag attcagcggcgtgcccgacagattctccggcagcggctctggcaccgacttcaccctgaa gatcagccgggtggaagccgaggacgtgggcgtgtactattgtggccagggcacccagt acccttcacctttggcagcggcaccaaggtggaaatcaagggccagcccaaggccgcc ccctacatccacgtgacccagagccccagcagcctgtccgtgtccatcggcgacagagt gaccatcaactgccagacctctcagggcgtgggcagcgacctgcactggtatcagcaca agcctggcagagcccccaagctgctgatccaccacacaagcagcgtggaagatggcgt gcccagcagattttccggcagcggcttccacaccagcttcaacctgaccatcagcgatctg caggccgacgacattgccacctactattgtcaggtgctgcagttcttcggcagaggcagca gactgcacatcaagaccaagggccccagccgtacggtggccgctcccagcgtgttcatct tcccacctagcgacgagcagctgaagtccggcacagcctctgtcgtgtgcctgctgaaca acttctacccccgcgaggccaaagtgcagtggaaggtggacaacgccctgcagagcgg caacagccaggaaagcgtgaccgagcaggacagcaaggactccacctacagcctgag cagcaccctgacactgagcaaggccgactacgagaagcacaaggtgtacgcctgcgaa gtgacccaccagggcctgtctagccccgtgaccaagagcttcaaccggggcgagtgt	**SEQ ID NO: 357**
Binding Protein 39 Amino Acid Sequences		
Heavy chain A	Qvqlvqsgaevvkpgasvkvsckasgytftsyyihwvrqapgqglewigsiypgnv ntnyaqkfqgratltvdtsistaymelsrlrsddtavyyctrshygldwnfdvwgkgttv tvssastkgpsvfplapcsrstsestaalgclvkdyfpepvtvswnsgaltsgvhtfpavl	**SEQ ID NO: 358**

	qssglyslssvvtvpssslgtktytcnvdhkpsntkvdkrveskygppcppcpapeflg gpsvflfppkpkdtlmisrtpevtcvvvdvsqedpevqfnwyvdgvevhnaktkpre eqfnstyrvvsvltvlhqdwlngkeykckvsnkglpssiektiskakgqprepqvytlp pcqeemtknqvslwclvkgfypsdiavewesngqpennykttppvldsdgsfflysk ltvdksrwqegnvfscsvmhealhnhytqkslslslgk	
Light chain A	Diqmtqspsslsasvgdrvtitcqasqniyvwlnwyqqkpgkapklliykasnlhtgv psrfsgsgsgtdftltisslqpediatyycqqgqtypytfgqgtkleikrtvaapsvfifpps deqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsstltl skadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 359**
Heavy chain B	Rahlvqsgtamkkpgasvrvscqtsgytftahilfwfrqapgrglewvgwikp qygavnfgggfrdrvtltrdvyreiaymdirglkpddtavyycardrsygdssw aldawgqgttvvvsadkthtqvqlvesgggvvqpgrslrlscaasgftftkaw mhwvrqapgkqlewvaqikdksnsyatyyadsvkgrftisrddskntlylqm nslraedtavyycrgvyyalspfdywgqgtlvtvssdkthtastkgpsvfplapc srstsestaalgclvkdyfpepvtvswnsgaltsgvhtfpavlqssglyslssvvt vpssslgtktytcnvdhkpsntkvdkrveskygppcppcpapeflggpsvflfp pkpkdtlmisrtpevtcvvvdvsqedpevqfnwyvdgvevhnaktkpreeq fnstyrvvsvltvlhqdwlngkeykckvsnkglpssiektiskakgqprepqvc tlppsqeemtknqvslscavkgfypsdiavewesngqpennykttppvldsd gsfflvskltvdksrwqegnvfscsvmhealhnhytqkslslslgk	**SEQ ID NO: 360**
Light chain B	Divmtqtplslsvtpgqpasisckssqslvhnnantylswylqkpgqspqsliykvsnr fsgvpdrfsgsgsgtdftlkisrveaedvgvyycgqgtqypftfgsgtkveikdkthtyih vtqspsslsvsigdrvtincqtsqgvgsdlhwyqhkpgrapkllihhtssvedgvpsrfs gsgfhtsfnltisdlqaddiatyycqvlqffgrgsrlhikdkthtrtvaapsvfifppsdeql ksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsstltlskad yekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 361**
Binding Protein 39 Nucleotide Sequences		
Heavy chain A	caggtgcagctggtgcagtctggcgccgaggtcgtgaaacctggcgcctctgtgaaggt gtcctgcaaggccagcggctacacctttaccagctactacatccactgggtgcgccaggc ccctggacagggactggaatggatcggcagcatctaccccggcaacgtgaacaccaact acgcccagaagttccagggcagagccaccctgaccgtggacaccagcatcagcaccgc ctacatggaactgagccggctgagaagcgacgacaccgccgtgtactactgcacccggt cccactacggcctggattggaacttcgacgtgtggggcaagggcaccaccgtgacagtgt ctagcgcgtcgaccaagggcccctcggtgttccctctggcccccttgcagcagaagcacca gcgaatctacagccgccctgggctgcctcgtgaaggactactttcccgagcccgtgaccg tgtcctggaactctggcgctctgacaagcggcgtgcacaccctttccagccgtgctccagag cagcggcctgtactctctgagcagcgtcgtgacagtgcccagcagcagcctgggcacca agacctacacctgtaacgtggaccacaagcccagcaacaccaaggtggacaagcgggt ggaatctaagtacggccctccctgccctccttgcccagcccctgaatttctgggcggaccc tccgtgttcctgttcccccccaaagcccaaggacaccctgatgatcagccggaccccccgaa gtgacctgcgtggtggtggatgtgtcccaggaagatcccgaggtgcagttcaattggtacg tggacggcgtggaagtgcacaacgccaagaccaagcccagagaggaacagttcaacag cacctaccgggtggtgtccgtgctgaccgtgctgcaccaggactggctgaacggcaaag agtacaagtgcaaggtgtccaacaagggcctgcccagctccatcgagaaaaccatcagc aaggccaagggccagccccgcgagcctcaagtgtataccctgcccccttgccaggaaga gatgaccaagaaccaggtgtccctgtggtgtctcgtgaaaggcttctaccccagcgacatt gccgtggaatgggagagcaacggccagcccgagaacaactacaagaccacccccccct gtgctggacagcgacggctcattcttcctgtactccaagctgaccgtggacaagagccggt ggcaggaaggcaacgtgttcagctgctccgtgatgcacgaggccctgcacaaccactac acccagaagtccctgtctctgtccctgggcaag	**SEQ ID NO: 362**
Light chain A	gacatccagatgacccagagccccagcagcctgtctgccagcgtgggcgacagagtga ccatcacctgtcaggccagccagaacatctacgtgtggctgaactggtatcagcagaagc ccggcaaggcccccaagctgctgatctacaaggccagcaacctgcacaccggcgtgcc	**SEQ ID NO: 363**

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Heavy chain B	agagcccacctggtgcagtctggcaccgccatgaagaaaccaggcgcctctgtgcgggt gtcctgtcagacaagcggctacaccttcaccgcccacatcctgttctggttccggcaggcc cctggcagaggactggaatgggtgggatggatcaagccccagtatggcgccgtgaactt cggcggaggcttccgggatagagtgaccctgacccgggacgtgtaccgcgagatcgcct acatggacatccggggcctgaagcccgatgacaccgccgtgtactactgcgccagagac agaagctacggcgacagcagctgggctctggatgcttggggccagggcacaaccgtgg tggtgtctgccgacaaaacccatacccaggtgcagctggtggaatctggcggcggagtg gtgcagcctggcagaagcctgagactgagctgtgccgccagcggcttcaccttcaccaa ggcctggatgcactgggtgcgccaggcccctggaaagcagctggaatgggtggcccag atcaaggacaagagcaacagctacgccacctactacgccgacagcgtgaagggccggtt caccatcagccgggacgacagcaagaacaccctgtacctgcagatgaacagcctgcgg gccgaggacaccgccgtgtactactgtcggggcgtgtactatgccctgagccccttcgatt actggggccagggaaccctcgtgaccgtgtctagtgataagacccacaccgcttcgacca agggcccatcggtgttccctctggccccttgcagcagaagcaccagcgaatctacagccg ccctgggctgcctcgtgaaggactactttcccgagcccgtgaccgtgtcctggaactctgg cgctctgacaagcggcgtgcacaccttccagccgtgctccagagcagcggcctgtactc tctgagcagcgtcgtgacagtgcccagcagcagcctgggcaccaagacctacacctgta acgtggaccacaagcccagcaacaccaaggtggacaagcgggtggaatctaagtacgg ccctccctgccctccttgcccagcccctgaatttctgggcggaccctccgtgttcctgttccc cccaaagcccaaggacaccctgatgatcagccggaccccgaagtgacctgcgtggtg gtggatgtgtcccaggaagatcccgaggtgcagttcaattggtacgtggacggcgtggaa gtgcacaacgccaagaccaagcccagagaggaacagttcaacagcacctaccgggtgg tgtccgtgctgaccgtgctgcaccaggactggctgaacggcaaagagtacaagtgcaag gtgtccaacaagggcctgcccagctccatcgagaaaaccatcagcaaggccaagggcc agccccgcgagcctcaagtgtgtaccctgccccctagccaggaagagatgaccaagaac caggtgtccctgagctgtgccgtgaaaggcttctaccccagcgacattgccgtggaatgg gagagcaacggccagcccgagaacaactacaagaccacccccccctgtgctggacagcg acggctcattcttcctggtgtccaagctgaccgtggacaagagccggtggcaggaaggca acgtgttcagctgctccgtgatgcacgaggccctgcacaaccactacacccagaagtccc tgtctctgtccctgggcaag	**SEQ ID NO: 364**
Light chain B	gacatcgtgatgacccagaccccctgagcctgagcgtgacacctggacagcctgccag catcagctgcaagagcagccagagcctggtgcacaacaacgccaacacctacctgagct ggtatctgcagaagcccggccagagcccccagtccctgatctacaaggtgtccaacagat tcagcggcgtgcccgacagattctccggcagcggctctggcaccgacttcaccctgaaga tcagccgggtggaagccgaggacgtgggcgtgtactattgtggccagggcacccagtac cccttcacctttggcagcggcaccaaggtggaaatcaaggacaaaacccatacctacatc cacgtgacccagagccccagcagcctgtccgtgtccatcggcgacagagtgaccatcaa ctgccagacctctcagggcgtgggcagcgacctgcactggtatcagcacaagcctggca gagcccccaagctgctgatccaccacacaagcagcgtggaagatggcgtgcccagcag attttccggcagcggcttccacaccagcttcaacctgaccatcagcgatctgcaggccgac gacattgccacctactattgtcaggtgctgcagttcttcggcagaggcagcagactgcacat caaggataagacccatacccgtacggtggccgctcccagcgtgttcatcttcccacctagc gacgagcagctgaagtccggcacagcctctgtcgtgtgcctgctgaacaacttctaccccc gcgaggccaaagtgcagtggaaggtggacaacgccctgcagagcggcaacagccagg aaagcgtgaccgagcaggacagcaaggactccacctacagcctgagcagcaccctgac actgagcaaggccgactacgagaagcacaaggtgtacgcctgcgaagtgacccaccag	**SEQ ID NO: 365**

	ggcctgtctagccccgtgaccaagagcttcaaccggggcgagtgt	
Binding Protein 40 Amino Acid Sequences		
Heavy chain A	Qvqlvqsgaevvkpgasvkvsckasgytftsyyihwvrqapgqglewigsiypgnv ntnyaqkfqgratltvdtsistaymelsrlrsddtavyyctrshygldwnfdvwgkgttv tvssastkgpsvfplapcsrstsestaalgclvkdyfpepvtvswnsgaltsgvhtfpavl qssglyslssvvtvpssslgtktytcnvdhkpsntkvdkrveskygppcppcpapeflg gpsvflfppkpkdtlmisrtpevtcvvvdvsqedpevqfnwyvdgvevhnaktkpre eqfnstyrvvsvltvlhqdwlngkeykckvsnkglpssiektiskakgqprepqvytlp pcqeemtknqvslwclvkgfypsdiavewesngqpennykttppvldsdgsfflysk ltvdksrwqegnvfscsvmhealhnhytqkslslslgk	**SEQ ID NO: 366**
Light chain A	Diqmtqspsslsasvgdrvtitcqasqniyvwlnwyqqkpgkapklliykasnlhtgv psrfsgsgsgtdftltisslqpediatyycqqgqtypytfgqgtkleikrtvaapsvfifpps deqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsstltl skadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 367**
Heavy chain B	Qvqlvesgggvvqpgrslrlscaasgftftkawmhwvrqapgkqlewvaqi kdksnsyatyyadsvkgrftisrddskntlylqmnslraedtavyycrgvyyal spfdywgqgtlvtvsssrahlvqsgtamkkpgasvrvscqtsgytftahilfwfr qapgrglewvgwikpqygavnfgggfrdrvtltrdvyreiaymdirglkpddt avyycardrsygdsswaldawgqgttvvvsartastkgpsvfplapcsrstsest aalgclvkdyfpepvtvswnsgaltsgvhtfpavlqssglyslssvvtvpssslgt ktytcnvdhkpsntkvdkrveskygppcppcpapeflggpsvflfppkpkdtl misrtpevtcvvvdvsqedpevqfnwyvdgvevhnaktkpreeqfnstyrv vsvltvlhqdwlngkeykckvsnkglpssiektiskakgqprepqvctlppsq eemtknqvslscavkgfypsdiavewesngqpennykttppvldsdgsfflvs kltvdksrwqegnvfscsvmhealhnhytqkslslslgk	**SEQ ID NO: 368**
Light chain B	Yihvtqspsslsvsigdrvtincqtsqgvgsdlhwyqhkpgrapkllihhtssvedgvp srfsgsgfhtsfnltisdlqaddiatyycqvlqffgrgsrlhikgqpkaapdivmtqtplsl svtpgqpasisckssqslvhnnantylswylqkpgqspqsliykvsnrfsgvpdrfsgs gsgtdftlkisrveaedvgvyycgqgtqypftfgsgtkveiktkgpsrtvaapsvfifpps deqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsstltl skadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 369**
Binding Protein 40 Nucleotide Sequences		
Heavy chain A	caggtgcagctggtgcagtctggcgccgaggtcgtgaaacctggcgcctctgtgaaggt gtcctgcaaggccagcggctacacctttaccagctactacatccactgggtgcgccaggc ccctggacagggactggaatggatcggcagcatctaccccggcaacgtgaacaccaact acgcccagaagttccagggcagagccaccctgaccgtggacaccagcatcagcaccgc ctacatggaactgagccggctgagaagcgacgacaccgccgtgtactactgcacccggt cccactacggcctggattggaacttcgacgtgtggggcaagggcaccaccgtgacagtgt ctagcgcgtcgaccaagggcccctcggtgttccctctggccccttgcagcagaagcacca gcgaatctacagccgccctgggctgcctcgtgaaggactactttcccgagcccgtgaccg tgtcctggaactctggcgctctgacaagcggcgtgcacaccttccagccgtgctccagag cagcggcctgtactctctgagcagcgtcgtgacagtgcccagcagcagcctgggcacca agacctacacctgtaacgtggaccacaagcccagcaacaccaaggtggacaagcgggt ggaatctaagtacggccctccctgccctccttgcccagcccctgaatttctgggcggaccc tccgtgttcctgttcccccccaaagcccaaggacaccctgatgatcagccggacccccgaa gtgacctgcgtggtggtggatgtgtcccaggaagatcccgaggtgcagttcaattggtacg tggacggcgtggaagtgcacaacgccaagaccaagcccagagaggaacagttcaacag cacctaccgggtggtgtccgtgctgaccgtgctgcaccaggactggctgaacggcaaag agtacaagtgcaaggtgtccaacaagggcctgcccagctccatcgagaaaaccatcagc aaggccaagggccagccccgcgagcctcaagtgtataccctgcccccttgccaggaaga gatgaccaagaaccaggtgtccctgtggtgtctcgtgaaaggcttctaccccagcgacatt gccgtggaatgggagagcaacggccagcccgagaacaactacaagaccacccccccct gtgctggacagcgacggctcattcttcctgtactccaagctgaccgtggacaagagccggt	**SEQ ID NO: 370**

	ggcaggaaggcaacgtgttcagctgctccgtgatgcacgaggccctgcacaaccactac acccagaagtccctgtctctgtccctgggcaag	
Light chain A	gacatccagatgacccagagccccagcagcctgtctgccagcgtgggcgacagagtga ccatcacctgtcaggccagccagaacatctacgtgtggctgaactggtatcagcagaagc ccggcaaggcccccaagctgctgatctacaaggccagcaacctgcacaccggcgtgcc cagcagattttctggcagcggctccggcaccgacttcaccctgacaatcagctccctgcag cccgaggacattgccacctactactgccagcagggccagacctacccctacaccttggc cagggcaccaagctggaaatcaagcgtacggtggccgctcccagcgtgttcatcttccca cctagcgacgagcagctgaagtccggcacagcctctgtcgtgtgcctgctgaacaacttct accccgcgaggccaaggtgcagtggaaggtggacaatgccctgcagagcggcaaca gccaggaaagcgtgaccgagcaggacagcaaggactccacctacagcctgagcagca ccctgaccctgagcaaggccgactacgagaagcacaaggtgtacgcctgcgaagtgac ccaccagggcctgtctagccccgtgaccaagagcttcaaccggggcgagtgt	**SEQ ID NO: 371**
Heavy chain B	caggtgcagctggtggaatctggcggcggagtggtgcagcctggcagaagcctgagact gagctgtgccgccagcggcttcaccttcaccaaggcctggatgcactgggtgcgccagg cccctggaaagcagctggaatgggtggcccagatcaaggacaagagcaacagctacgc cacctactacgccgacagcgtgaagggccggttcaccatcagccgggacgacagcaag aacaccctgtacctgcagatgaacagcctgcgggccgaggacaccgccgtgtactactgt cggggcgtgtactatgccctgagccccttcgattactggggccagggaaccctcgtgacc gtgtctagtagcagagcccacctggtgcagtctggcaccgccatgaagaaaccaggcgc ctctgtgcgggtgtcctgtcagacaagcggctacaccttcaccgcccacatcctgttctggt tccggcaggcccctggcagaggactggaatgggtgggatggatcaagccccagtatgg cgccgtgaacttcggcggaggcttccgggatagagtgaccctgacccgggacgtgtacc gcgagatcgcctacatggacatccggggcctgaagcccgatgacaccgccgtgtactact gcgccagagacagaagctacggcgacagcagctgggctctggatgcttggggccaggg cacaaccgtggtggtgtctgcccggaccgccagcacaaagggcccatcggtgttccctct ggcccccttgcagcagaagcaccagcgaatctacagccgccctgggctgcctcgtgaagg actactttcccgagcccgtgaccgtgtcctggaactctggcgctctgacaagcggcgtgca caccttccagccgtgctccagagcagcggcctgtactctctgagcagcgtcgtgacagtg cccagcagcagcctgggcaccaagacctacacctgtaacgtggaccacaagcccagca acaccaaggtggacaagcgggtggaatctaagtacggccctccctgccctccttgcccag cccctgaatttctgggcggaccctccgtgttcctgttcccccaaagcccaaggacaccct gatgatcagccggacccccgaagtgacctgcgtggtggtggatgtgtcccaggaagatc ccgaggtgcagttcaattggtacgtggacggcgtggaagtgcacaacgccaagaccaag cccagagaggaacagttcaacagcacctaccgggtggtgtccgtgctgaccgtgctgca ccaggactggctgaacggcaaagagtacaagtgcaaggtgtccaacaagggcctgccc agctccatcgagaaaaccatcagcaaggccaagggccagccccgcgagcctcaagtgt gtaccctgccccctagccaggaagagatgaccaagaaccaggtgtccctgagctgtgcc gtgaaaggcttctaccccagcgacattgccgtggaatgggagagcaacggccagcccga gaacaactacaagaccacccccccctgtgctggacagcgacggctcattcttcctggtgtcc aagctgaccgtggacaagagccggtggcaggaaggcaacgtgttcagctgctccgtgat gcacgaggccctgcacaaccactacacccagaagtccctgtctctgtccctgggcaag	**SEQ ID NO: 372**
Light chain B	tacatccacgtgacccagagccccagcagcctgtccgtgtccatcggcgacaga gtgaccatcaactgccagacctctcagggcgtgggcagcgacctgcactggtatc agcacaagcctggcagagcccccaagctgctgatccaccacacaagcagcgtg gaagatggcgtgcccagcagattttccggcagcggcttccacaccagcttcaacc tgaccatcagcgatctgcaggccgacgacattgccacctactattgtcaggtgctg cagttcttcggcagaggcagcagactgcacatcaagggccagcccaaggccgc ccccgacatcgtgatgacccagacccccctgagcctgagcgtgacacctggaca gcctgccagcatcagctgcaagagcagccagagcctggtgcacaacaacgcca acacctacctgagctggtatctgcagaagcccggccagagcccccagtccctgat ctacaaggtgtccaacagattcagcggcgtgcccgacagattctccggcagcgg ctctggcaccgacttcaccctgaagatcagccgggtggaagccgaggacgtggg	**SEQ ID NO: 373**

	cgtgtactattgtggccagggcacccagtacccccttcacctttggcagcggcacca aggtggaaatcaagaccaagggccccagccgtacggtggccgctcccagcgtg ttcatcttcccacctagcgacgagcagctgaagtccggcacagcctctgtcgtgtg cctgctgaacaacttctacccccgcgaggccaaagtgcagtggaaggtggacaa cgccctgcagagcggcaacagccaggaaagcgtgaccgagcaggacagcaag gactccacctacagcctgagcagcaccctgacactgagcaaggccgactacgag aagcacaaggtgtacgcctgcgaagtgacccaccagggcctgtctagccccgtg accaagagcttcaaccggggcgagtgt	
Binding Protein 41 Amino Acid Sequences		
Heavy chain A	Qvqlvqsgaevvkpgasvkvsckasgytftsyyihwvrqapgqglewigsiypgnv ntnyaqkfqgratltvdtsistaymelsrlrsddtavyyctrshygldwnfdvwgkgttv tvssastkgpsvfplapcsrstsestaalgclvkdyfpepvtvswnsgaltsgvhtfpavl qssglyslssvvtvpssslgtktytcnvdhkpsntkvdkrveskygppcppcpapeflg gpsvflfppkpkdtlmisrtpevtcvvvdvsqedpevqfnwyvdgvevhnaktkpre eqfnstyrvvsvltvlhqdwlngkeykckvsnkglpssiektiskakgqprepqvytlp pcqeemtknqvslwclvkgfypsdiavewesngqpennykttppvldsdgsfflysk ltvdksrwqegnvfscsvmhealhnhytqkslslslgk	**SEQ ID NO: 374**
Light chain A	Diqmtqspsslsasvgdrvtitcqasqniyvwlnwyqqkpgkapklliykasnlhtgv psrfsgsgsgtdftltisslqpediatyycqqgqtypytfgqgtkleikrtvaapsvfifpps deqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsstltl skadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 375**
Heavy chain B	qvqlvesgggvvqpgrslrlscaasgftftkawmhwvrqapgkqlewvaqik dksnsyatyyadsvkgrftisrddskntlylqmnslraedtavyycrgvyyalsp fdywgqgtlvtvssdkthtrahlvqsgtamkkpgasvrvscqtsgytftahilfw frqapgrglewvgwikpqygavnfgggfrdrvtltrdvyreiaymdirglkpd dtavyycardrsygdsswaldawgqgttvvvsadkthtastkgpsvfplapcsr stsestaalgclvkdyfpepvtvswnsgaltsgvhtfpavlqssglyslssvvtvp ssslgtktytcnvdhkpsntkvdkrveskygppcppcpapeflggpsvflfppk pkdtlmisrtpevtcvvvdvsqedpevqfnwyvdgvevhnaktkpreeqfns tyrvvsvltvlhqdwlngkeykckvsnkglpssiektiskakgqprepqvctlp psqeemtknqvslscavkgfypsdiavewesngqpennykttppvldsdgsf flvskltvdksrwqegnvfscsvmhealhnhytqkslslslgk	**SEQ ID NO: 376**
Light chain B	Yihvtqspsslsvsigdrvtincqtsqgvgsdlhwyqhkpgrapkllihhtssvedgvp srfsgsgfhtsfnltisdlqaddiatyycqvlqffgrgsrlhikdkthtdivmtqtplslsvtp gqpasisckssqslvhnnantylswylqkpgqspqsliykvsnrfsgvpdrfsgsgsgt dftlkisrveaedvgvyycgqgtqypftfgsgtkveikdkthtrtvaapsvfifppsdeql ksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsstltlskad yekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 377**
Binding Protein 41 Nucleotide Sequences		
Heavy chain A	caggtgcagctggtgcagtctggcgccgaggtcgtgaaacctggcgcctctgtgaaggt gtcctgcaaggccagcggctacacctttaccagctactacatccactgggtgcgccaggc ccctggacagggactggaatggatcggcagcatctaccccggcaacgtgaacaccaact acgcccagaagttccagggcagagccaccctgaccgtggacaccagcatcagcaccgc ctacatggaactgagccggctgagaagcgacgacaccgccgtgtactactgcacccggt cccactacggcctggattggaacttcgacgtgtggggcaagggcaccaccgtgacagtgt ctagcgcgtcgaccaagggcccctcggtgttccctctggccccttgcagcagaagcacca gcgaatctacagccgccctgggctgcctcgtgaaggactactttcccgagcccgtgaccg tgtcctggaactctggcgctctgacaagcggcgtgcacaccttccagccgtgctccagag cagcggcctgtactctctgagcagcgtcgtgacagtgcccagcagcagcctgggcacca agacctacacctgtaacgtggaccacaagcccagcaacaccaaggtggacaagcgggt ggaatctaagtacggccctccctgccctccttgcccagcccctgaatttctgggcggaccc tccgtgttcctgttcccccccaaagcccaaggacaccctgatgatcagccggaccccccgaa	**SEQ ID NO: 378**

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Light chain A	gacatccagatgacccagagccccagcagcctgtctgccagcgtgggcgacagagtga ccatcacctgtcaggccagccagaacatctacgtgtggctgaactggtatcagcagaagc ccggcaaggcccccaagctgctgatctacaaggccagcaacctgcacaccggcgtgcc cagcagattttctggcagcggctccggcaccgacttcaccctgacaatcagctccctgcag cccgaggacattgccacctactactgccagcagggccagacctacccctacacctttggc cagggcaccaagctggaaatcaagcgtacggtggccgctcccagcgtgttcatcttccca cctagcgacgagcagctgaagtccggcacagcctctgtcgtgtgcctgctgaacaacttct acccccgcgaggccaaggtgcagtggaaggtggacaatgccctgcagagcggcaaca gccaggaaagcgtgaccgagcaggacagcaaggactccacctacagcctgagcagca ccctgaccctgagcaaggccgactacgagaagcacaaggtgtacgcctgcgaagtgac ccaccagggcctgtctagccccgtgaccaagagcttcaaccggggcgagtgt	**SEQ ID NO: 379**
Heavy chain B	caggtgcagctggtggaatctggcggcggagtggtgcagcctggcagaagcctgagact gagctgtgccgccagcggcttcaccttcaccaaggcctggatgcactgggtgcgccagg ccctggaaagcagctggaatgggtggcccagatcaaggacaagagcaacagctacgc cacctactacgccgacagcgtgaagggccggttcaccatcagccgggacgacagcaag aacaccctgtacctgcagatgaacagcctgcgggccgaggacaccgccgtgtactactgt cggggcgtgtactatgccctgagccccttcgattactggggccagggaaccctcgtgacc gtgtctagtgacaaaacccataccagagcccacctggtgcagtctggcaccgccatgaag aaaccaggcgcctctgtgcgggtgtcctgtcagacaagcggctacaccttcaccgcccac atcctgttctggttccggcaggcccctggcagaggactggaatgggtgggatggatcaag ccccagtatggcgccgtgaacttcggcggaggcttccgggatagagtgaccctgacccg ggacgtgtaccgcgagatcgcctacatggacatccggggcctgaagcccgatgacaccg ccgtgtactactgcgccagagacagaagctacggcgacagcagctgggctctggatgctt ggggccagggcacaaccgtggtggtgtctgccgataagacccacaccgccagcacaaa gggcccatcggtgttccctctggccccttgcagcagaagcaccagcgaatctacagccgc cctgggctgcctcgtgaaggactactttcccgagcccgtgaccgtgtcctggaactctggc gctctgacaagcggcgtgcacaccttccagccgtgctccagagcagcggcctgtactct ctgagcagcgtcgtgacagtgcccagcagcagcctgggcaccaagacctacacctgtaa cgtggaccacaagcccagcaacaccaaggtggacaagcgggtggaatctaagtacggc cctccctgccctccttgcccagcccctgaatttctgggcggaccctccgtgttcctgttcccc ccaaagcccaaggacaccctgatgatcagccggaccccgaagtgacctgcgtggtggt ggatgtgtcccaggaagatcccgaggtgcagttcaattggtacgtggacggcgtggaagt gcacaacgccaagaccaagcccagagaggaacagttcaacagcacctaccgggtggtg tccgtgctgaccgtgctgcaccaggactggctgaacggcaaagagtacaagtgcaaggt gtccaacaagggcctgcccagctccatcgagaaaaccatcagcaaggccaagggccag ccccgcgagcctcaagtgtgtaccctgccccctagccaggaagagatgaccaagaacca ggtgtccctgagctgtgccgtgaaaggcttctaccccagcgacattgccgtggaatggga gagcaacggccagcccgagaacaactacaagaccacccccccctgtgctggacagcgac ggctcattcttcctggtgtccaagctgaccgtggacaagagccggtggcaggaaggcaac gtgttcagctgctccgtgatgcacgaggccctgcacaaccactacacccagaagtccctgt ctctgtccctgggcaag	**SEQ ID NO: 380**
Light chain B	tacatccacgtgacccagagccccagcagcctgtccgtgtccatcggcgacagagtgac catcaactgccagacctctcagggcgtgggcagcgacctgcactggtatcagcacaagc ctggcagagcccccaagctgctgatccaccacacaagcagcgtggaagatggcgtgcc	**SEQ ID NO: 381**

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Binding Protein 42 Amino Acid Sequences		
Heavy chain A	Qvqlqesgpglvkpsqtlsltctvsgfslsdygvhwvrqppgkglewlgviwagggt nynpslksrktiskdtsknqvslklssvtaadtavyycardkgysyyysmdywgqgtt vtvssastkgpsvfplapcsrstsestaalgclvkdyfpepvtvswnsgaltsgvhtfpav lqssglyslssvvtvpssslgtktytcnvdhkpsntkvdkrveskygppcppcpapefl ggpsvflfppkpkdtlmisrtpevtcvvvdvsqedpevqfnwyvdgvevhnaktkpr eeqfnstyrvvsvltvlhqdwlngkeykckvsnkglpssiektiskakgqprepqvytl ppcqeemtknqvslwclvkgfypsdiavewesngqpennykttppvldsdgsfflys kltvdksrwqegnvfscsvmhealhnhytqkslslslgk	**SEQ ID NO: 382**
Light chain A	Divltqspaslavspgqratitcrasesveyyvtslmqwyqqkpgqppkllifaasnve sgvparfsgsgsgtdftltinpveandvanyycqqsrkvpytfgqgtkleikrtvaapsv fifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstys lsstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 383**
Heavy chain B	Rahlvqsgtamkkpgasvrvscqtsgytftahilfwfrqapgrglewvgwikp qygavnfgggfrdrvtltrdvyreiaymdirglkpddtavyycardrsygdssw aldawgqgttvvvsasqvqlvesgggvvqpgrslrlscaasgftftkawmhw vrqapgkqlewvaqikdksnsyatyyadsvkgrftisrddsknlylqmnslra edtavyycrgvyyalspfdywgqgtlvtvssrtastkgpsvfplapcsrstsesta algclvkdyfpepvtvswnsgaltsgvhtfpavlqssglyslssvvtvpssslgtk tytcnvdhkpsntkvdkrveskygppcppcpapeflggpsvflfppkpkdtl misrtpevtcvvvdvsqedpevqfnwyvdgvevhnaktkpreeqfnstyrvv svltvlhqdwlngkeykckvsnkglpssiektiskakgqprepqvctlppsqee mtknqvslscavkgfypsdiavewesngqpennykttppvldsdgsfflvskl tvdksrwqegnvfscsvmhealhnhytqkslslslgk	**SEQ ID NO: 384**
Light chain B	Divmtqtplslsvtpgqpasisckssqslvhnnantylswylqkpgqspqsliykvsnr fsgvpdrfsgsgsgtdftlkisrveaedvgvyycgqgtqypftfgsgtkveikgqpkaa pyihvtqspsslsvsigdrvtincqtsqgvgsdlhwyqhkpgrapkllihhtssvedgv psrfsgsgfhtsfnltisdlqaddiatyycqvlqffgrgsrlhiktkgpsrtvaapsvfifpp sdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsstlt lskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 385**
Binding Protein 42 Nucleotide Sequences		
Heavy chain A	caggtgcagctgcaggaatctggccctggcctcgtgaagcctagccagaccctgagcct gacctgtaccgtgtccggcttcagcctgagcgactacggcgtgcactgggtgcgccagc cacctggaaaaggcctggaatggctgggcgtgatctgggctggcggaggcaccaacta caaccccagcctgaagtccagaaagaccatcagcaaggacaccagcaagaaccaggtg tccctgaagctgagcagcgtgacagccgccgataccgccgtgtactactgcgccagaga caagggctacagctactactacagcatggactactggggccagggcaccaccgtgaccg tgtcatccgcgtcgaccaagggcccctcggtgttccctctggccccttgcagcagaagca ccagcgaatctacagccgccctgggctgcctcgtgaaggactactttcccgagcccgtga	**SEQ ID NO: 386**

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Light chain A	gacatcgtgctgacacagagccctgctagcctggccgtgtctcctggacagagggccac catcacctgtagagccagcgagagcgtggaatattacgtgaccagcctgatgcagtggta tcagcagaagcccggccagcccccaagctgctgattttcgccgccagcaacgtggaaa gcggcgtgccagccagattttccggcagcggctctggcaccgacttcaccctgaccatca accccgtggaagccaacgacgtggccaactactactgccagcagagccggaaggtgcc ctacacctttggccagggcaccaagctggaaatcaagcgtacggtggccgctcccagcg tgttcatcttcccacctagcgacgagcagctgaagtccggcacagcctctgtcgtgtgcct gctgaacaacttctacccccgcgaggccaaggtgcagtggaaggtggacaatgccctgc agagcggcaacagccaggaaagcgtgaccgagcaggacagcaaggactccacctaca gcctgagcagcaccctgaccctgagcaaggccgactacgagaagcacaaggtgtacgc ctgcgaagtgacccaccagggcctgtctagccccgtgaccaagagcttcaaccggggcg agtgt	**SEQ ID NO: 387**
Heavy chain B	agagcccacctggtgcagtctggcaccgccatgaagaaaccaggcgcctctgtgcgggt gtcctgtcagacaagcggctacaccttcaccgcccacatcctgttctggttccggcaggcc cctggcagaggactggaatgggtgggatggatcaagccccagtatggcgccgtgaactt cggcggaggcttccgggatagagtgaccctgacccgggacgtgtaccgcgagatcgcc tacatggacatccggggcctgaagcccgatgacaccgccgtgtactactgcgccagaga cagaagctacggcgacagcagctgggctctggatgcttggggccagggcacaaccgtg gtggtgtctgcctctcaggtgcagctggtggaatctggcggcggagtggtgcagcctggc agaagcctgagactgagctgtgccgccagcggcttcaccttcaccaaggcctggatgca ctgggtgcgccaggcccctggaaagcagctggaatgggtggcccagatcaaggacaag agcaacagctacgccacctactacgccgacagcgtgaagggccggttcaccatcagccg ggacgacagcaagaacaccctgtacctgcagatgaacagcctgcgggccgaggacacc gccgtgtactactgtcggggcgtgtactatgccctgagccccttcgattactggggccagg gaaccctcgtgaccgtgtctagtcggaccgcttcgaccaagggcccatcggtgttccctct ggcccccttgcagcagaagcaccagcgaatctacagccgccctgggctgcctcgtgaagg actactttcccgagcccgtgaccgtgtcctggaactctggcgctctgacaagcggcgtgca caccttccagccgtgctccagagcagcggcctgtactctctgagcagcgtcgtgacagtg cccagcagcagcctgggcaccaagacctacacctgtaacgtggaccacaagcccagca acaccaaggtggacaagcgggtggaatctaagtacggccctccctgccctccttgcccag cccctgaatttctgggcggaccctccgtgttcctgttcccccaaagcccaaggacaccct gatgatcagccggaccccgaagtgacctgcgtggtggtggatgtgtcccaggaagatc ccgaggtgcagttcaattggtacgtggacggcgtggaagtgcacaacgccaagaccaag cccagagaggaacagttcaacagcacctaccgggtggtgtccgtgctgaccgtgctgca ccaggactggctgaacggcaaagagtacaagtgcaaggtgtccaacaagggcctgccc agctccatcgagaaaaccatcagcaaggccaagggccagccccgcgagcctcaagtgt gtaccctgccccctagccaggaagagatgaccaagaaccaggtgtccctgagctgtgcc gtgaaaggcttctaccccagcgacattgccgtggaatgggagagcaacggccagcccg agaacaactacaagaccacccccccctgtgctggacagcgacggctcattcttcctggtgtc	**SEQ ID NO: 388**

	caagctgaccgtggacaagagccggtggcaggaaggcaacgtgttcagctgctccgtga tgcacgaggccctgcacaaccactacacccagaagtccctgtctctgtccctgggcaag	
Light chain B	gacatcgtgatgacccagacccccctgagcctgagcgtgacacctggacagcctgccag catcagctgcaagagcagccagagcctggtgcacaacaacgccaacacctacctgagct ggtatctgcagaagcccggccagagcccccagtccctgatctacaaggtgtccaacagat tcagcggcgtgcccgacagattctccggcagcggctctggcaccgacttcaccctgaag atcagccgggtggaagccgaggacgtgggcgtgtactattgtggccagggcacccagta ccccttcacctttggcagcggcaccaaggtggaaatcaagggccagcccaaggccgcc ccctacatccacgtgacccagagccccagcagcctgtccgtgtccatcggcgacagagt gaccatcaactgccagacctctcagggcgtgggcagcgacctgcactggtatcagcaca agcctggcagagcccccaagctgctgatccaccacacaagcagcgtggaagatggcgt gcccagcagattttccggcagcggcttccacaccagcttcaacctgaccatcagcgatctg caggccgacgacattgccacctactattgtcaggtgctgcagttcttcggcagaggcagca gactgcacatcaagaccaagggccccagccgtacggtggccgctcccagcgtgttcatct tcccacctagcgacgagcagctgaagtccggcacagcctctgtcgtgtgcctgctgaaca acttctacccccgcgaggccaaagtgcagtggaaggtggacaacgccctgcagagcgg caacagccaggaaagcgtgaccgagcaggacagcaaggactccacctacagcctgag cagcaccctgacactgagcaaggccgactacgagaagcacaaggtgtacgcctgcgaa gtgacccaccagggcctgtctagccccgtgaccaagagcttcaaccggggcgagtgt	**SEQ ID NO: 389**
Binding Protein 43 Amino Acid Sequences		
Heavy chain A	Qvqlqesgpglvkpsqtlsltctvsgfslsdygvhwvrqppgkglewlgviwagggt nynpslksrktiskdtsknqvslklssvtaadtavyycardkgysyyysmdywgqgtt vtvssastkgpsvfplapcsrstsestaalgclvkdyfpepvtvswnsgaltsgvhtfpav lqssglyslssvvtvpssslgtktytcnvdhkpsntkvdkrveskygppcppcpapefl ggpsvflfppkpkdtlmisrtpevtcvvvdvsqedpevqfnwyvdgvevhnaktkp reeqfnstyrvvsvltvlhqdwlngkeykckvsnkglpssiektiskakgqprepqvyt lppcqeemtknqvslwclvkgfypsdiavewesngqpennykttppvldsdgsffly skltvdksrwqegnvfscsvmhealhnhytqkslslslgk	**SEQ ID NO: 390**
Light chain A	Divltqspaslavspgqratitcrasesveyyvtslmqwyqqkpgqppkllifaasnve sgvparfsgsgsgtdftltinpveandvanyycqqsrkvpytfgqgtkleikrtvaapsv fifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstys lsstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO:391**
Heavy chain B	Rahlvqsgtamkkpgasvrvscqtsgytftahilfwfrqapgrglewvgwik pqygavnfgggfrdrvtltrdvyreiaymdirglkpddtavyycardrsygdss waldawgqgttvvvsadkthtqvqlvesgggvvqpgrslrlscaasgftftka wmhwvrqapgkqlewvaqikdksnsyatyyadsvkgrftisrddskntlylq mnslraedtavyycrgvyyalspfdywgqgtlvtvssdkthtastkgpsvfpla pcsrstsestaalgclvkdyfpepvtvswnsgaltsgvhtfpavlqssglyslssv vtvpssslgtktytcnvdhkpsntkvdkrveskygppcppcpapeflggpsvfl fppkpkdtlmisrtpevtcvvvdvsqedpevqfnwyvdgvevhnaktkpre eqfnstyrvvsvltvlhqdwlngkeykckvsnkglpssiektiskakgqprepq vctlppsqeemtknqvslscavkgfypsdiavewesngqpennykttppvld sdgsfflvskltvdksrwqegnvfscsvmhealhnhytqkslslslgk	**SEQ ID NO: 392**
Light chain B	Divmtqtplslsvtpgqpasisckssqslvhnnantylswylqkpgqspqsliykvsnr fsgvpdrfsgsgsgtdftlkisrveaedvgvyycgqgtqypftfgsgtkveikdkthtyi hvtqspsslsvsigdrvtincqtsqgvgsdlhwyqhkpgrapkllihhtssvedgvpsrf sgsgfhtsfnltisdlqaddiatyycqvlqffgrgsrlhikdkthtrtvaapsvfifppsdeq lksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsstltlska dyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 393**
Binding Protein 43 Nucleotide Sequences		
Heavy chain A	caggtgcagctgcaggaatctggccctggcctcgtgaagcctagccagaccctgagcct gacctgtaccgtgtccggcttcagcctgagcgactacggcgtgcactgggtgcgccagc cacctggaaaaggcctggaatggctgggcgtgatctgggctggcggaggcaccaacta	**SEQ ID NO: 394**

	caaccccagcctgaagtccagaaagaccatcagcaaggacaccagcaagaaccaggtg tccctgaagctgagcagcgtgacagccgccgataccgccgtgtactactgcgccagaga caagggctacagctactactacagcatggactactggggccagggcaccaccgtgaccg tgtcatccgcgtcgaccaagggcccctcggtgttccctctggccccttgcagcagaagca ccagcgaatctacagccgccctgggctgcctcgtgaaggactactttcccgagcccgtga ccgtgtcctggaactctggcgctctgacaagcggcgtgcacacctttccagccgtgctcca gagcagcggcctgtactctctgagcagcgtcgtgacagtgcccagcagcagcctgggca ccaagacctacacctgtaacgtggaccacaagcccagcaacaccaaggtggacaagcg ggtggaatctaagtacggccctccctgccctccttgcccagcccctgaatttctgggcgga ccctccgtgttcctgttccccccaaagcccaaggacaccctgatgatcagccggaccccc gaagtgacctgcgtggtggtggatgtgtcccaggaagatcccgaggtgcagttcaattggt acgtggacggcgtggaagtgcacaacgccaagaccaagcccagagaggaacagttca acagcacctaccgggtggtgtccgtgctgaccgtgctgcaccaggactggctgaacggc aaagagtacaagtgcaaggtgtccaacaagggcctgcccagctccatcgagaaaaccat cagcaaggccaagggccagccccgcgagcctcaagtgtataccctgccccccttgccag gaagagatgaccaagaaccaggtgtccctgtggtgtctcgtgaaaggcttctaccccagc gacattgccgtggaatgggagagcaacggccagcccgagaacaactacaagaccaccc cccctgtgctggacagcgacggctcattcttcctgtactccaagctgaccgtggacaagag ccggtggcaggaaggcaacgtgttcagctgctccgtgatgcacgaggccctgcacaacc actacacccagaagtccctgtctctgtccctgggcaag	
Light chain A	gacatcgtgctgacacagagccctgctagcctggccgtgtctcctggacagagggccac catcacctgtagagccagcgagagcgtggaatattacgtgaccagcctgatgcagtggta tcagcagaagcccggccagcccccaagctgctgattttcgccgccagcaacgtggaaa gcggcgtgccagccagattttccggcagcggctctggcaccgacttcaccctgaccatca accccgtggaagccaacgacgtggccaactactactgccagcagagccggaaggtgcc ctacacctttggccagggcaccaagctggaaatcaagcgtacggtggccgctcccagcg tgttcatcttcccacctagcgacgagcagctgaagtccggcacagcctctgtcgtgtgcct gctgaacaacttctacccccgcgaggccaaggtgcagtggaaggtggacaatgccctgc agagcggcaacagccaggaaagcgtgaccgagcaggacagcaaggactccacctaca gcctgagcagcaccctgaccctgagcaaggccgactacgagaagcacaaggtgtacgc ctgcgaagtgacccaccagggcctgtctagccccgtgaccaagagcttcaaccggggcg agtgt	**SEQ ID NO: 395**
Heavy chain B	agagcccacctggtgcagtctggcaccgccatgaagaaaccaggcgcctctgtgcgggt gtcctgtcagacaagcggctacaccttcaccgcccacatcctgttctggttccggcaggcc cctggcagaggactggaatgggtgggatggatcaagccccagtatggcgccgtgaactt cggcggaggcttccgggatagagtgaccctgacccgggacgtgtaccgcgagatcgcc tacatggacatccggggcctgaagcccgatgacaccgccgtgtactactgcgccagaga cagaagctacggcgacagcagctgggctctggatgcttggggccagggcacaaccgtg gtggtgtctgccgacaaaacccatacccaggtgcagctggtggaatctggcggcggagt ggtgcagcctggcagaagcctgagactgagctgtgccgccagcggcttcaccttcacca aggcctggatgcactgggtgcgccaggccccctggaaagcagctggaatgggtggccca gatcaaggacaagagcaacagctacgccacctactacgccgacagcgtgaagggccgg ttcaccatcagccgggacgacagcaagaacaccctgtacctgcagatgaacagcctgcg ggccgaggacaccgccgtgtactactgtcggggcgtgtactatgccctgagccccttcga ttactggggccagggaaccctcgtgaccgtgtctagtgataagacccacaccgcttcgac caagggcccatcggtgttccctctggcccttgcagcagaagcaccagcgaatctacagc cgccctgggctgcctcgtgaaggactactttcccgagcccgtgaccgtgtcctggaactct ggcgctctgacaagcggcgtgcacacctttccagccgtgctccagagcagcggcctgta ctctctgagcagcgtcgtgacagtgcccagcagcagcctgggcaccaagacctacacct gtaacgtggaccacaagcccagcaacaccaaggtggacaagcgggtggaatctaagta cggccctccctgccctccttgcccagcccctgaatttctgggcggaccctccgtgttcctgt tcccccaaagcccaaggacaccctgatgatcagccggaccccgaagtgacctgcgtg gtggtggatgtgtcccaggaagatcccgaggtgcagttcaattggtacgtggacggcgtg gaagtgcacaacgccaagaccaagcccagagaggaacagttcaacagcacctaccgg	**SEQ ID NO: 396**

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Heavy chain A	Qvqlqesgpglvkpsqtlsltctvsgfslsdygvhwvrqppgkglewlgviwagggt nynpslksrktiskdtsknqvslklssvtaadtavyycardkgysyyysmdywgqgtt vtvssastkgpsvfplapcsrstsestaalgclvkdyfpepvtvswnsgaltsgvhtfpav lqssglyslssvvtvpssslgtktytcnvdhkpsntkvdkrveskygppcppcpapefl ggpsvflfppkpkdtlmisrtpevtcvvvdvsqedpevqfnwyvdgvevhnaktkpr eeqfnstyrvvsvltvlhqdwlngkeykckvsnkglpssiektiskakgqprepqvytl ppcqeemtknqvslwclvkgfypsdiavewesngqpennykttppvldsdgsfflys kltvdksrwqegnvfscsvmhealhnhytqkslslslgk	**SEQ ID NO: 398**
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Binding Protein 44 Nucleotide Sequences		
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Light chain B	tacatccacgtgacccagagccccagcagcctgtccgtgtccatcggcgacaga gtgaccatcaactgccagacctctcagggcgtgggcagcgacctgcactggtatc agcacaagcctggcagagcccccaagctgctgatccaccacacaagcagcgtg gaagatggcgtgcccagcagattttccggcagcggcttccacaccagcttcaacc tgaccatcagcgatctgcaggccgacgacattgccacctactattgtcaggtgctg cagttcttcggcagaggcagcagactgcacatcaagggccagcccaaggccgc ccccgacatcgtgatgacccagacccccctgagcctgagcgtgacacctggaca gcctgccagcatcagctgcaagagcagccagagcctggtgcacaacaacgcca acacctacctgagctggtatctgcagaagcccggccagagcccccagtccctgat ctacaaggtgtccaacagattcagcggcgtgcccgacagattctccggcagcgg ctctggcaccgacttcaccctgaagatcagccgggtggaagccgaggacgtggg cgtgtactattgtggccagggcacccagtacccccttcacctttggcagcggcacca aggtggaaatcaagaccaagggccccagccgtacggtggccgctcccagcgtg ttcatcttcccacctagcgacgagcagctgaagtccggcacagcctctgtcgtgtg cctgctgaacaacttctacccccgcgaggccaaagtgcagtggaaggtggacaa cgccctgcagagcggcaacagccaggaaagcgtgaccgagcaggacagcaa ggactccacctacagcctgagcagcaccctgacactgagcaaggccgactacga gaagcacaaggtgtacgcctgcgaagtgacccaccagggcctgtctagccccgt gaccaagagcttcaaccggggcgagtgt	**SEQ ID NO: 405**
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Light chain A	Divltqspaslavspgqratitcrasesveyyvtslmqwyqqkpgqppkllifaasnve sgvparfsgsgsgtdftltinpveandvanyycqqsrkvpytfgqgtkleikrtvaapsv fifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstys lsstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 407**
Heavy chain B	qvqlvesgggvvqpgrslrlscaasgftftkawmhwvrqapgkqlewvaqik dksnsyatyyadsvkgrftisrddskntlylqmnslraedtavyycrgvyyals pfdywgqgtlvtvssdkthtrahlvqsgtamkkpgasvrvscqtsgytftahilf wfrqapgrglewvgwikpqygavnfgggfrdrvtltrdvyreiaymdirglkp ddtavyycardrsygdsswaldawgqgttvvvsadkthtastkgpsvfplapc	**SEQ ID NO: 408**

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Binding Protein 45 Nucleotide Sequences		
Heavy chain A	caggtgcagctgcaggaatctggccctggcctcgtgaagcctagccagaccctgagcct gacctgtaccgtgtccggcttcagcctgagcgactacggcgtgcactgggtgcgccagc cacctggaaaaggcctggaatggctgggcgtgatctgggctggcggaggcaccaacta caaccccagcctgaagtccagaaagaccatcagcaaggacaccagcaagaaccaggtg tccctgaagctgagcagcgtgacagccgccgataccgccgtgtactactgcgccagaga caagggctacagctactactacagcatggactactggggccagggcaccaccgtgaccg tgtcatccgcgtcgaccaagggcccctcggtgttccctctggccccttgcagcagaagca ccagcgaatctacagccgccctgggctgcctcgtgaaggactactttcccgagcccgtga ccgtgtcctggaactctggcgctctgacaagcggcgtgcacaccttccagccgtgctcca gagcagcggcctgtactctctgagcagcgtcgtgacagtgcccagcagcagcctgggca ccaagacctacacctgtaacgtggaccacaagcccagcaacaccaaggtggacaagcg ggtggaatctaagtacggccctccctgccctccttgcccagcccctgaatttctgggcgga ccctccgtgttcctgttcccccaaagcccaaggacaccctgatgatcagccggacccccc gaagtgacctgcgtggtggtggatgtgtcccaggaagatcccgaggtgcagttcaattggt acgtggacggcgtggaagtgcacaacgccaagaccaagcccagagaggaacagttca acagcacctaccgggtggtgtccgtgctgaccgtgctgcaccaggactggctgaacggc aaagagtacaagtgcaaggtgtccaacaagggcctgcccagctccatcgagaaaaccat cagcaaggccaagggccagccccgcgagcctcaagtgtataccctgcccccttgccag gaagagatgaccaagaaccaggtgtccctgtggtgtctcgtgaaaggcttctaccccagc gacattgccgtggaatgggagagcaacggccagcccgagaacaactacaagaccaccc ccctgtgctggacagcgacggctcattcttcctgtactccaagctgaccgtggacaagag ccggtggcaggaaggcaacgtgttcagctgctccgtgatgcacgaggccctgcacaacc actacacccagaagtccctgtctctgtccctgggcaag	**SEQ ID NO: 410**
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Heavy chain B	caggtgcagctggtggaatctggcggcggagtggtgcagcctggcagaagcctgagac tgagctgtgccgccagcggcttcaccttcaccaaggcctggatgcactgggtgcgccag gcccctggaaagcagctggaatgggtggcccagatcaaggacaagagcaacagctacg ccacctactacgccgacagcgtgaagggccggttcaccatcagccgggacgacagcaa gaacaccctgtacctgcagatgaacagcctgcgggccgaggacaccgccgtgtactact	**SEQ ID NO: 412**

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Light chain B	tacatccacgtgacccagagccccagcagcctgtccgtgtccatcggcgacagagtgac catcaactgccagacctctcagggcgtgggcagcgacctgcactggtatcagcacaagc ctggcagagcccccaagctgctgatccaccacacaagcagcgtggaagatggcgtgcc cagcagattttccggcagcggcttccacaccagcttcaacctgaccatcagcgatctgcag gccgacgacattgccacctactattgtcaggtgctgcagttcttcggcagaggcagcagac tgcacatcaaggacaaaacccataccgacatcgtgatgacccagacccccctgagcctg agcgtgacacctggacagcctgccagcatcagctgcaagagcagccagagcctggtgc acaacaacgccaacacctacctgagctggtatctgcagaagcccggccagagccccca gtccctgatctacaaggtgtccaacagattcagcggcgtgcccgacagattctccggcag cggctctggcaccgacttcaccctgaagatcagccgggtggaagccgaggacgtgggc gtgtactattgtggccagggcacccagtacccccttcaccctttggcagcggcaccaaggtg gaaatcaaggataagacccataccgtacggtggccgctcccagcgtgttcatcttcccac ctagcgacgagcagctgaagtccggcacagcctctgtcgtgtgcctgctgaacaacttcta cccccgcgaggccaaagtgcagtggaaggtggacaacgccctgcagagcggcaacag ccaggaaagcgtgaccgagcaggacagcaaggactccacctacagcctgagcagcac cctgacactgagcaaggccgactacgagaagcacaaggtgtacgcctgcgaagtgacc caccagggcctgtctagccccgtgaccaagagcttcaaccggggcgagtgt	**SEQ ID NO: 413**
Binding Protein 46 Amino Acid Sequences		
Heavy chain A	Qvqlvqsgaevvkpgasvkvsckasgytftsyyihwvrqapgqglewigsiypgnv ntnyaqkfqgratltvdtsistaymelsrlrsddtavyyctrshygldwnfdvwgkgttv tvssastkgpsvfplapcsrstsestaalgclvkdyfpepvtvswnsgaltsgvhtfpavl qssglyslssvvtvpssslgtktytcnvdhkpsntkvdkrveskygppcppcpapeflg gpsvflfppkpkdtlmisrtpevtcvvvdvsqedpevqfnwyvdgvevhnaktkpre eqfnstyrvvsvltvlhqdwlngkeykckvsnkglpssiektiskakgqprepqvytlp pcqeemtknqvslwclvkgfypsdiavewesngqpennykttppvldsdgsfflysk ltvdksrwqegnvfscsvmhealhnhytqkslslslgk	**SEQ ID NO: 414**
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	skadyekhkvyacevthqglsspvtksfnrgec	
Heavy chain B	Qvhltqsgpevrkpgtsvkvsckapgntlktydlhwvrsvpgqglqwmgwi shegdkkviverfkakvtidwdrstntaylqlsgltsgdtavyycakgskhrlrd yalydddgalnwavdvdylsnlefwgqgtavtvsssqvqlvesgggvvqpgr slrlscaasgftftkawmhwvrqapgkqlewvaqikdksnsyatyyadsvkg rftisrddskntlylqmnslraedtavyycrgvyyalspfdywgqgtlvtvssrta stkgpsvfplapcsrstsestaalgclvkdyfpepvtvswnsgaltsgvhtfpavl qssglyslssvvtvpssslgtktytcnvdhkpsntkvdkrveskygppcppcpa peflggpsvflfppkpkdtlmisrtpevtcvvvdvsqedpevqfnwyvdgve vhnaktkpreeqfnstyrvvsvltvlhqdwlngkeykckvsnkglpssiektis kakgqprepqvctlppsqeemtknqvslscavkgfypsdiavewesngqpe nnykttppvldsdgsfflvskltvdksrwqegnvfscsvmhealhnhytqksls lslgk	**SEQ ID NO: 416**
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Binding Protein 46 Nucleotide Sequences		
Heavy chain A	caggtgcagctggtgcagtctggcgccgaggtcgtgaaacctggcgcctctgtgaaggt gtcctgcaaggccagcggctacacctttaccagctactacatccactgggtgcgccaggc ccctggacagggactggaatggatcggcagcatctaccccggcaacgtgaacaccaact acgcccagaagttccagggcagagccaccctgaccgtggacaccagcatcagcaccgc ctacatggaactgagccggctgagaagcgacgacaccgccgtgtactactgcacccggt cccactacggcctggattggaacttcgacgtgtggggcaagggcaccaccgtgacagtg tctagcgcgtcgaccaagggcccctcggtgttccctctggccccttgcagcagaagcacc agcgaatctacagccgccctgggctgcctcgtgaaggactactttcccgagcccgtgacc gtgtcctggaactctggcgctctgacaagcggcgtgcacaccttccagccgtgctccaga gcagcggcctgtactctctgagcagcgtcgtgacagtgcccagcagcagcctgggcacc aagacctacacctgtaacgtggaccacaagcccagcaacaccaaggtggacaagcggg tggaatctaagtacggccctccctgccctccttgcccagcccctgaatttctgggcggacc ctccgtgttcctgttcccccccaaagcccaaggacaccctgatgatcagccggacccccga agtgacctgcgtggtggtggatgtgtcccaggaagatcccgaggtgcagttcaattggtac gtggacggcgtggaagtgcacaacgccaagaccaagcccagagaggaacagttcaac agcacctaccgggtggtgtccgtgctgaccgtgctgcaccaggactggctgaacggcaa agagtacaagtgcaaggtgtccaacaagggcctgcccagctccatcgagaaaaccatca gcaaggccaagggccagccccgcgagcctcaagtgtataccctgcccccttgccagga agagatgaccaagaaccaggtgtccctgtggtgtctcgtgaaaggcttctaccccagcga cattgccgtggaatgggagagcaacggccagcccgagaacaactacaagaccaccccc cctgtgctggacagcgacggctcattcttcctgtactccaagctgaccgtggacaagagcc ggtggcaggaaggcaacgtgttcagctgctccgtgatgcacgaggccctgcacaaccac tacacccagaagtccctgtctctgtccctgggcaag	**SEQ ID NO: 418**
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Heavy chain B	caggtgcacctgacacagagcggacccgaagtgcggaagcctggcacctctgtgaagg tgtcctgcaaggcccctggcaacaccctgaaaacctacgacctgcactgggtgcgcagc gtgccaggacagggactgcagtggatgggctggatcagccacgagggcgacaagaaa gtgatcgtggaacggttcaaggccaaagtgaccatcgactgggacagaagcaccaacac cgcctacctgcagctgagcggcctgacctctggcgataccgccgtgtactactgcgccaa gggcagcaagcaccggctgagagactacgccctgtacgacgatgacggcgccctgaac tgggccgtggatgtggactacctgagcaacctggaattctggggccagggcacagccgt gaccgtgtcatcttctcaggtgcagctggtggaatctggcggcggagtggtgcagcctgg cagaagcctgagactgagctgtgccgccagcggcttcaccttcaccaaggcctggatgc actgggtgcgccaggcccctggaaagcagctggaatgggtggcccagatcaaggacaa gagcaacagctacgccacctactacgccgacagcgtgaagggccggttcaccatcagcc gggacgacagcaagaacaccctgtacctgcagatgaacagcctgcgggccgaggaca ccgccgtgtactactgtcggggcgtgtactatgccctgagccccttcgattactggggcca gggaaccctcgtgaccgtgtctagtcggaccgcttcgaccaagggcccatcggtgttccc tctggcccccttgcagcagaagcaccagcgaatctacagccgccctgggctgcctcgtgaa ggactactttcccgagcccgtgaccgtgtcctggaactctggcgctctgacaagcggcgt gcacaccttccagccgtgctccagagcagcggcctgtactctctgagcagcgtcgtgac agtgcccagcagcagcctgggcaccaagacctacacctgtaacgtggaccacaagccc agcaacaccaaggtggacaagcgggtggaatctaagtacggccctccctgccctccttgc ccagcccctgaatttctgggcggaccctccgtgttcctgttcccccaaagcccaaggaca ccctgatgatcagccggaccccgaagtgacctgcgtggtggtggatgtgtcccaggaa gatcccgaggtgcagttcaattggtacgtggacggcgtggaagtgcacaacgccaagac caagcccagagaggaacagttcaacagcacctaccgggtggtgtccgtgctgaccgtgc tgcaccaggactggctgaacggcaaagagtacaagtgcaaggtgtccaacaagggcct gcccagctccatcgagaaaaccatcagcaaggccaagggccagccccgcgagcctcaa gtgtgtaccctgccccctagccaggaagagatgaccaagaaccaggtgtccctgagctgt gccgtgaaaggcttctaccccagcgacattgccgtggaatgggagagcaacggccagc ccgagaacaactacaagaccacccccccctgtgctggacagcgacggctcattcttcctgg tgtccaagctgaccgtggacaagagccggtggcaggaaggcaacgtgttcagctgctcc gtgatgcacgaggccctgcacaaccactacacccagaagtccctgtctctgtccctgggc aag	**SEQ ID NO: 420**
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Binding Protein 47 Amino Acid Sequences		
Heavy chain A	Qvqlvqsgaevvkpgasvkvsckasgytftsyyihwvrqapgqglewigsiypgnv ntnyaqkfqgratltvdtsistaymelsrlrsddtavyyctrshygldwnfdvwgkgttv tvssastkgpsvfplapcsrstsestaalgclvkdyfpepvtvswnsgaltsgvhtfpavl	**SEQ ID NO: 422**

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Light chain A	Diqmtqspsslsasvgdrvtitcqasqniyvwlnwyqqkpgkapklliykasnlhtgv psrfsgsgsgtdftltisslqpediatyycqqgqtypytfgqgtkleikrtvaapsvfifpps deqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsstltl skadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 423**
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Binding Protein 47 Nucleotide Sequences		
Heavy chain A	caggtgcagctggtgcagtctggcgccgaggtcgtgaaacctggcgcctctgtgaaggt gtcctgcaaggccagcggctacacctttaccagctactacatccactgggtgcgccaggc ccctggacagggactggaatggatcggcagcatctaccccggcaacgtgaacaccaact acgcccagaagttccagggcagagccaccctgaccgtggacaccagcatcagcaccgc ctacatggaactgagccggctgagaagcgacgacaccgccgtgtactactgcacccggt cccactacggcctggattggaacttcgacgtgtggggcaagggcaccaccgtgacagtgt ctagcgcgtcgaccaagggccccctcggtgttccctctggccccttgcagcagaagcacca gcgaatctacagccgccctgggctgcctcgtgaaggactactttcccgagcccgtgaccg tgtcctggaactctggcgctctgacaagcggcgtgcacaccttccagccgtgctccagag cagcggcctgtactctctgagcagcgtcgtgacagtgcccagcagcagcctgggcacca agacctacacctgtaacgtggaccacaagcccagcaacaccaaggtggacaagcgggt ggaatctaagtacggccctccctgccctccttgcccagcccctgaatttctgggcggaccc tccgtgttcctgttcccccaaagcccaaggacaccctgatgatcagccggacccccgaa gtgacctgcgtggtggtggatgtgtcccaggaagatcccgaggtgcagttcaattggtacg tggacggcgtggaagtgcacaacgccaagaccaagcccagagaggaacagttcaacag cacctaccgggtggtgtccgtgctgaccgtgctgcaccaggactggctgaacggcaaag agtacaagtgcaaggtgtccaacaagggcctgcccagctccatcgagaaaaccatcagc aaggccaagggccagccccgcgagcctcaagtgtataccctgcccccttgccaggaaga gatgaccaagaaccaggtgtccctgtggtgtctcgtgaaaggcttctaccccagcgacatt gccgtggaatgggagagcaacggccagcccgagaacaactacaagaccacccccccct gtgctggacagcgacggctcattcttcctgtactccaagctgaccgtggacaagagccggt ggcaggaaggcaacgtgttcagctgctccgtgatgcacgaggccctgcacaaccactac acccagaagtccctgtctctgtccctgggcaag	**SEQ ID NO: 426**
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Heavy chain B	caggtgcacctgacacagagcggacccgaagtgcggaagcctggcacctctgtgaagg tgtcctgcaaggcccctggcaacaccctgaaaacctacgacctgcactgggtgcgcagc gtgccaggacagggactgcagtggatgggctggatcagccacgagggcgacaagaaa gtgatcgtggaacggttcaaggccaaagtgaccatcgactgggacagaagcaccaacac cgcctacctgcagctgagcggcctgacctctggcgataccgccgtgtactactgcgccaa gggcagcaagcaccggctgagagactacgccctgtacgacgatgacggcgccctgaac tgggccgtggatgtggactacctgagcaacctggaattctggggccagggcacagccgt gaccgtgtcatctgacaaaacccatacccaggtgcagctggtggaatctggcggcggagt ggtgcagcctggcagaagcctgagactgagctgtgccgccagcggcttcaccttcacca aggcctggatgcactgggtgcgccaggcccctggaaagcagctggaatgggtggccca gatcaaggacaagagcaacagctacgccacctactacgccgacagcgtgaagggccgg ttcaccatcagccgggacgacagcaagaacaccctgtacctgcagatgaacagcctgcg ggccgaggacaccgccgtgtactactgtcggggcgtgtactatgccctgagccccttcga ttactggggccagggaaccctcgtgaccgtgtctagtgataagacccacaccgcttcgac caagggcccatcggtgttccctctggccccttgcagcagaagcaccagcgaatctacagc cgccctgggctgcctcgtgaaggactactttcccgagcccgtgaccgtgtcctggaactct ggcgctctgacaagcggcgtgcacaccttccagccgtgctccagagcagcggcctgta ctctctgagcagcgtcgtgacagtgcccagcagcagcctgggcaccaagacctacacct gtaacgtggaccacaagcccagcaacaccaaggtggacaagcgggtggaatctaagta cggccctccctgccctccttgcccagcccctgaatttctgggcggaccctccgtgttcctgtt ccccccaaagcccaaggacaccctgatgatcagccggaccccgaagtgacctgcgtg gtggtggatgtgtcccaggaagatcccgaggtgcagttcaattggtacgtggacggcgtg gaagtgcacaacgccaagaccaagcccagagaggaacagttcaacagcacctaccggg tggtgtccgtgctgaccgtgctgcaccaggactggctgaacggcaaagagtacaagtgca aggtgtccaacaagggcctgcccagctccatcgagaaaaccatcagcaaggccaaggg ccagccccgcgagcctcaagtgtgtaccctgccccctagccaggaagagatgaccaaga accaggtgtccctgagctgtgccgtgaaaggcttctaccccagcgacattgccgtggaatg ggagagcaacggccagcccgagaacaactacaagaccacccccccctgtgctggacagc gacggctcattcttcctggtgtccaagctgaccgtggacaagagccggtggcaggaagg caacgtgttcagctgctccgtgatgcacgaggccctgcacaaccactacacccagaagtc cctgtctctgtccctgggcaag	**SEQ ID NO: 428**
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Binding Protein 48 Amino Acid Sequences		
Heavy chain A	Qvqlvqsgaevvkpgasvkvsckasgytftsyyihwvrqapgqglewigsiypgnv ntnyaqkfqgratltvdtsistaymelsrlrsddtavyyctrshygldwnfdvwgkgttv tvssastkgpsvfplapcsrstsestaalgclvkdyfpepvtvswnsgaltsgvhtfpavl qssglyslssvvtvpssslgtktytcnvdhkpsntkvdkrveskygppcppcpapeflg gpsvflfppkpkdtlmisrtpevtcvvvdvsqedpevqfnwyvdgvevhnaktkpre eqfnstyrvvsvltvlhqdwlngkeykckvsnkglpssiektiskakgqprepqvytlp pcqeemtknqvslwclvkgfypsdiavewesngqpennykttppvldsdgsfflysk ltvdksrwqegnvfscsvmhealhnhytqkslslslgk	**SEQ ID NO: 430**
Light chain A	Diqmtqspsslsasvgdrvtitcqasqniyvwlnwyqqkpgkapklliykasnlhtgv psrfsgsgsgtdftltisslqpediatyycqqgqtypytfgqgtkleikrtvaapsvfifpps deqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsstltl skadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 431**
Heavy chain B	Qvqlvesgggvvqpgrslrlscaasgftftkawmhwvrqapgkqlewvaqi kdksnsyatyyadsvkgrftisrddskntlylqmnslraedtavyycrgvyyals pfdywgqgtlvtvsssqvhltqsgpevrkpgtsvkvsckapgntlktydlhwv rsvpgqglqwmgwishegdkkviverfkakvtidwdrstntaylqlsgltsgd tavyycakgskhrlrdyalydddgalnwavdvdylsnlefwgqgtavtvssrt astkgpsvfplapcsrstsestaalgclvkdyfpepvtvswnsgaltsgvhtfpav lqssglyslssvvtvpssslgtktytcnvdhkpsntkvdkrveskygppcppcp apeflggpsvflfppkpkdtlmisrtpevtcvvvdvsqedpevqfnwyvdgv evhnaktkpreeqfnstyrvvsvltvlhqdwlngkeykckvsnkglpssiekti skakgqprepqvctlppsqeemtknqvslscavkgfypsdiavewesngqpe nnykttppvldsdgsfflvskltvdksrwqegnvfscsvmhealhnhytqksls lslgk	**SEQ ID NO: 432**
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Binding Protein 48 Nucleotide Sequences		
Heavy chain A	caggtgcagctggtgcagtctggcgccgaggtcgtgaaacctggcgcctctgtgaaggt gtcctgcaaggccagcggctacacctttaccagctactacatccactgggtgcgccaggc ccctggacagggactggaatggatcggcagcatctaccccggcaacgtgaacaccaact acgcccagaagttccagggcagagccaccctgaccgtggacaccagcatcagcaccgc ctacatggaactgagccggctgagaagcgacgacaccgccgtgtactactgcacccggt cccactacggcctggattggaacttcgacgtgtggggcaagggcaccaccgtgacagtgt ctagcgcgtcgaccaagggcccctcggtgttccctctggccccttgcagcagaagcacca gcgaatctacagccgccctgggctgcctcgtgaaggactactttcccgagcccgtgaccg tgtcctggaactctggcgctctgacaagcggcgtgcacaccttccagccgtgctccagag cagcggcctgtactctctgagcagcgtcgtgacagtgcccagcagcagcctgggcacca agacctacacctgtaacgtggaccacaagcccagcaacaccaaggtggacaagcgggt ggaatctaagtacggccctccctgccctccttgcccagcccctgaatttctgggcggaccc tccgtgttcctgttcccccccaaagcccaaggacaccctgatgatcagccggacccccgaa gtgacctgcgtggtggtggatgtgtcccaggaagatcccgaggtgcagttcaattggtacg tggacggcgtggaagtgcacaacgccaagaccaagcccagagaggaacagttcaacag cacctaccgggtggtgtccgtgctgaccgtgctgcaccaggactggctgaacggcaaag	**SEQ ID NO: 434**

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Light chain A	gacatccagatgacccagagccccagcagcctgtctgccagcgtgggcgacagagtga ccatcacctgtcaggccagccagaacatctacgtgtggctgaactggtatcagcagaagc ccggcaaggcccccaagctgctgatctacaaggccagcaacctgcacaccggcgtgcc cagcagattttctggcagcggctccggcaccgacttcaccctgacaatcagctccctgcag cccgaggacattgccacctactactgccagcagggccagacctacccctacaccttggc cagggcaccaagctggaaatcaagcgtacggtggccgctcccagcgtgttcatcttccca cctagcgacgagcagctgaagtccggcacagcctctgtcgtgtgcctgctgaacaacttct acccccgcgaggccaaggtgcagtggaaggtggacaatgccctgcagagcggcaaca gccaggaaagcgtgaccgagcaggacagcaaggactccacctacagcctgagcagca ccctgaccctgagcaaggccgactacgagaagcacaaggtgtacgcctgcgaagtgac ccaccagggcctgtctagccccgtgaccaagagcttcaaccggggcgagtgt	**SEQ ID NO: 435**
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Light chain B	gacttcgtgctgacccagagccctcacagcctgagcgtgacacctggcgagagcgccag catcagctgcaagagcagccactccctgatccacggcgaccggaacaactacctggcttg gtacgtgcagaagcccggcagatcccccagctgctgatctacctggccagcagcagag ccagcggcgtgcccgatagattttctggcagcggcagcgacaaggacttcaccctgaag atcagccgggtggaaaccgaggacgtgggcacctactactgtatgcagggcagagaga gcccctggacctttggccagggcaccaaggtggacatcaagggccagcccaaggccgc	**SEQ ID NO: 437**

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Binding Protein 49 Amino Acid Sequences		
Heavy chain A	Qvqlvqsgaevvkpgasvkvsckasgytftsyyihwvrqapgqglewigsiypgnv ntnyaqkfqgratltvdtsistaymelsrlrsddtavyyctrshygldwnfdvwgkgttv tvssastkgpsvfplapcsrstsestaalgclvkdyfpepvtvswnsgaltsgvhtfpavl qssglyslssvvtvpssslgtktytcnvdhkpsntkvdkrveskygppcppcpapeflg gpsvflfppkpkdtlmisrtpevtcvvvdvsqedpevqfnwyvdgvevhnaktkpre eqfnstyrvvsvltvlhqdwlngkeykckvsnkglpssiektiskakgqprepqvytlp pcqeemtknqvslwclvkgfypsdiavewesngqpennykttppvldsdgsfflysk ltvdksrwqegnvfscsvmhealhnhytqkslslslgk	**SEQ ID NO: 438**
Light chain A	Diqmtqspsslsasvgdrvtitcqasqniyvwlnwyqqkpgkapkllliykasnlhtgv psrfsgsgsgtdftltisslqpediatyycqqgqtypytfgqgtkleikrtvaapsvfifpps deqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstyslsstltl skadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 439**
Heavy chain B	Qvqlvesgggvvqpgrslrlscaasgftftkawmhwvrqapgkqlewvaqi kdksnsyatyyadsvkgrftisrddsknlylqmnslraedtavyycrgvyyals pfdywgqgtlvtvssdkthtqvhltqsgpevrkpgtsvkvsckapgntlktydl hwvrsvpgqglqwmgwishegdkkviverfkakvtidwdrstntaylqlsgl tsgdtavyycakgskhrlrdyalydddgalnwavdvdylsnlefwgqgtavtv ssdkthtastkgpsvfplapcsrstsestaalgclvkdyfpepvtvswnsgaltsg vhtfpavlqssglyslssvvtvpssslgtktytcnvdhkpsntkvdkrveskygp pcppcpapeflggpsvflfppkpkdtlmisrtpevtcvvvdvsqedpevqfn wyvdgvevhnaktkpreeqfnstyrvvsvltvlhqdwlngkeykckvsnkgl pssiektiskakgqprepqvctlppsqeemtknqvslscavkgfypsdiavew esngqpennykttppvldsdgsfflvskltvdksrwqegnvfscsvmhealhn hytqkslslslgk	**SEQ ID NO: 440**
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Binding Protein 49 Nucleotide Sequences		
Heavy chain A	caggtgcagctggtgcagtctggcgccgaggtcgtgaaacctggcgcctctgtgaaggt gtcctgcaaggccagcggctacacctttaccagctactacatccactgggtgcgccaggc ccctggacagggactggaatggatcggcagcatctaccccggcaacgtgaacaccaact acgcccagaagttccagggcagagccaccctgaccgtggacaccagcatcagcaccgc ctacatggaactgagccggctgagaagcgacgacaccgccgtgtactactgcacccggt cccactacggcctggattggaacttcgacgtgtggggcaagggcaccaccgtgacagtgt ctagcgcgtcgaccaagggcccctcggtgttccctctggcccccttgcagcagaagcacca gcgaatctacagccgccctgggctgcctcgtgaaggactactttcccgagcccgtgaccg tgtcctggaactctggcgctctgacaagcggcgtgcacacctttccagccgtgctccagag	**SEQ ID NO: 442**

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Light chain A	gacatccagatgacccagagccccagcagcctgtctgccagcgtgggcgacagagtga ccatcacctgtcaggccagccagaacatctacgtgtggctgaactggtatcagcagaagc ccggcaaggcccccaagctgctgatctacaaggccagcaacctgcacaccggcgtgcc cagcagattttctggcagcggctccggcaccgacttcaccctgacaatcagctccctgcag cccgaggacattgccacctactactgccagcagggccagacctacccctacacctttggc cagggcaccaagctggaaatcaagcgtacggtggccgctcccagcgtgttcatcttccca cctagcgacgagcagctgaagtccggcacagcctctgtcgtgtgcctgctgaacaacttct acccccgcgaggccaaggtgcagtggaaggtggacaatgccctgcagagcggcaaca gccaggaaagcgtgaccgagcaggacagcaaggactccacctacagcctgagcagca ccctgaccctgagcaaggccgactacgagaagcacaaggtgtacgcctgcgaagtgac ccaccagggcctgtctagccccgtgaccaagagcttcaaccggggcgagtgt	**SEQ ID NO: 443**
Heavy chain B	caggtgcagctggtggaatctggcggcggagtggtgcagcctggcagaagcctgagact gagctgtgccgccagcggcttcaccttcaccaaggcctggatgcactgggtgcgccagg ccccctggaaagcagctggaatgggtggcccagatcaaggacaagagcaacagctacgc cacctactacgccgacagcgtgaagggccggttcaccatcagccgggacgacagcaag aacaccctgtacctgcagatgaacagcctgcgggccgaggacaccgccgtgtactactgt cggggcgtgtactatgccctgagccccttcgattactggggccagggaaccctcgtgacc gtgtctagtgacaaaacccatacccaggtgcacctgacacagagcggacccgaagtgcg gaagcctggcacctctgtgaaggtgtcctgcaaggcccctggcaacaccctgaaaaccta cgacctgcactgggtgcgcagcgtgccaggacagggactgcagtggatgggctggatc agccacgagggcgacaagaaagtgatcgtggaacggttcaaggccaaagtgaccatcg actgggacagaagcaccaacaccgcctacctgcagctgagcggcctgacctctggcgat accgccgtgtactactgcgccaagggcagcaagcaccggctgagagactacgccctgta cgacgatgacggcgccctgaactgggccgtggatgtggactacctgagcaacctggaatt ctggggccagggcacagccgtgaccgtgtcatctgataagacccacaccgccagcacaa agggcccatcggtgttccctctggcccccttgcagcagaagcaccagcgaatctacagccg ccctgggctgcctcgtgaaggactactttcccgagcccgtgaccgtgtcctggaactctgg cgctctgacaagcggcgtgcacaccttccagccgtgctccagagcagcggcctgtactc tctgagcagcgtcgtgacagtgcccagcagcagcctgggcaccaagacctacacctgta acgtggaccacaagcccagcaacaccaaggtggacaagcgggtggaatctaagtacgg ccctccctgccctccttgcccagcccctgaatttctgggcggaccctccgtgttcctgttccc cccaaagcccaaggacaccctgatgatcagccggaccccgaagtgacctgcgtggtg gtggatgtgtcccaggaagatcccgaggtgcagttcaattggtacgtggacggcgtggaa gtgcacaacgccaagaccaagcccagagaggaacagttcaacagcacctaccgggtgg tgtccgtgctgaccgtgctgcaccaggactggctgaacggcaaagagtacaagtgcaag gtgtccaacaagggcctgcccagctccatcgagaaaaccatcagcaaggccaagggcc agccccgcgagcctcaagtgtgtaccctgccccctagccaggaagagatgaccaagaac caggtgtccctgagctgtgccgtgaaaggcttctaccccagcgacattgccgtggaatgg gagagcaacggccagcccgagaacaactacaagaccacccccccctgtgctggacagcg acggctcattcttcctggtgtccaagctgaccgtggacaagagccggtggcaggaaggca	**SEQ ID NO: 444**

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Light chain B	gacttcgtgctgacccagagccctcacagcctgagcgtgacacctggcgagagcgccag catcagctgcaagagcagccactccctgatccacggcgaccggaacaactacctggcttg gtacgtgcagaagcccggcagatccccccagctgctgatctacctggccagcagcagag ccagcggcgtgcccgatagattttctggcagcggcagcgacaaggacttcaccctgaag atcagccgggtggaaaccgaggacgtgggcacctactactgtatgcagggcagagaga gcccctggacctttggccagggcaccaaggtggacatcaaggacaaaacccataccgac atcgtgatgacccagacccccctgagcctgagcgtgacacctggacagcctgccagcat cagctgcaagagcagccagagcctggtgcacaacaacgccaacacctacctgagctggt atctgcagaagcccggccagagcccccagtccctgatctacaaggtgtccaacagattca gcggcgtgcccgacagattctccggcagcggctctggcaccgacttcaccctgaagatca gccgggtggaagccgaggacgtgggcgtgtactattgtggccagggcacccagtaccc cttcacctttggcagcggcaccaaggtggaaatcaaggataagacccataccgtacggt ggccgctcccagcgtgttcatcttcccacctagcgacgagcagctgaagtccggcacagc ctctgtcgtgtgcctgctgaacaacttctacccccgcgaggccaaagtgcagtggaaggtg gacaacgccctgcagagcggcaacagccaggaaagcgtgaccgagcaggacagcaa ggactccacctacagcctgagcagcaccctgacactgagcaaggccgactacgagaag cacaaggtgtacgcctgcgaagtgacccaccagggcctgtctagccccgtgaccaagag cttcaaccggggcgagtgt	**SEQ ID NO: 445**
Binding Protein 50 Amino Acid Sequences		
Heavy chain A	Qvqlqesgpglvkpsqtlsltctvsgfslsdygvhwvrqppgkglewlgviwagggt nynpslksrktiskdtsknqvslklssvtaadtavyycardkgysyyysmdywgqgtt vtvssastkgpsvfplapcsrstsestaalgclvkdyfpepvtvswnsgaltsgvhtfpav lqssglyslssvvtvpssslgtktytcnvdhkpsntkvdkrveskygppcppcpapefl ggpsvflfppkpkdtlmisrtpevtcvvvdvsqedpevqfnwyvdgvevhnaktkpr eeqfnstyrvvsvltvlhqdwlngkeykckvsnkglpssiektiskakgqprepqvytl ppcqeemtknqvslwclvkgfypsdiavewesngqpennykttppvldsdgsfflys kltvdksrwqegnvfscsvmhealhnhytqkslslslgk	**SEQ ID NO: 446**
Light chain A	Divltqspaslavspgqratitcrasesveyyvtslmqwyqqkpgqppkllifaasnve sgvparfsgsgsgtdftltinpveandvanyycqqsrkvpytfgqgtkleikrtvaapsv fifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstys lsstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 447**
Heavy chain B	Qvhltqsgpevrkpgtsvkvsckapgntlktydlhwvrsvpgqglqwmgwi shegdkkviverfkakvtidwdrstntaylqlsgltsgdtavyycakgskhrlrd yalydddgalnwavdvdylsnlefwgqgtavtvsssqvqlvesgggvvqpgr slrlscaasgftftkawmhwvrqapgkqlewvaqikdksnsyatyyadsvkg rftisrddskntlylqmnslraedtavyycrgvyyalspfdywgqgtlvtvssrta stkgpsvfplapcsrstsestaalgclvkdyfpepvtvswnsgaltsgvhtfpavl qssglyslssvvtvpssslgtktytcnvdhkpsntkvdkrveskygppcppcpa peflggpsvflfppkpkdtlmisrtpevtcvvvdvsqedpevqfnwyvdgve vhnaktkpreeqfnstyrvvsvltvlhqdwlngkeykckvsnkglpssiektis kakgqprepqvctlppsqeemtknqvslscavkgfypsdiavewesngqpe nnykttppvldsdgsfflvskltvdksrwqegnvfscsvmhealhnhytqksls lslgk	**SEQ ID NO: 448**
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Binding Protein 50 Nucleotide Sequences		

Heavy chain A	caggtgcagctgcaggaatctggccctggcctcgtgaagcctagccagaccctgagcct gacctgtaccgtgtccggcttcagcctgagcgactacggcgtgcactgggtgcgccagcc acctggaaaaggcctggaatggctgggcgtgatctgggctggcggaggcaccaactaca accccagcctgaagtccagaaagaccatcagcaaggacaccagcaagaaccaggtgtc cctgaagctgagcagcgtgacagccgccgataccgccgtgtactactgcgccagagaca agggctacagctactactacagcatggactactggggccagggcaccaccgtgaccgtg tcatccgcgtcgaccaagggccccctcggtgttccctctggccccttgcagcagaagcacc agcgaatctacagccgccctgggctgcctcgtgaaggactactttcccgagcccgtgacc gtgtcctggaactctggcgctctgacaagcggcgtgcacacctttccagccgtgctccaga gcagcggcctgtactctctgagcagcgtcgtgacagtgcccagcagcagcctgggcacc aagacctacacctgtaacgtggaccacaagcccagcaacaccaaggtggacaagcggg tggaatctaagtacggccctccctgccctccttgcccagcccctgaatttctgggcggacc ctccgtgttcctgttcccccccaaagcccaaggacaccctgatgatcagccggacccccga agtgacctgcgtggtggtggatgtgtcccaggaagatcccgaggtgcagttcaattggtac gtggacggcgtggaagtgcacaacgccaagaccaagcccagagaggaacagttcaaca gcacctaccgggtggtgtccgtgctgaccgtgctgcaccaggactggctgaacggcaaa gagtacaagtgcaaggtgtccaacaagggcctgcccagctccatcgagaaaaccatcag caaggccaagggccagccccgcgagcctcaagtgtataccctgccccttgccaggaag agatgaccaagaaccaggtgtccctgtggtgtctcgtgaaaggcttctaccccagcgacat tgccgtggaatgggagagcaacggccagcccgagaacaactacaagaccacccccct gtgctggacagcgacggctcattcttcctgtactccaagctgaccgtggacaagagccggt ggcaggaaggcaacgtgttcagctgctccgtgatgcacgaggccctgcacaaccactac acccagaagtccctgtctctgtccctgggcaag	**SEQ ID NO: 450**
Light chain A	gacatcgtgctgacacagagccctgctagcctggccgtgtctcctggacagagggccac catcacctgtagagccagcgagagcgtggaatattacgtgaccagcctgatgcagtggtat cagcagaagcccggccagcccccaagctgctgattttcgccgccagcaacgtggaaag cggcgtgccagccagattttccggcagcggctctggcaccgacttcaccctgaccatcaa ccccgtggaagccaacgacgtggccaactactactgccagcagagccggaaggtgccc tacacctttggccagggcaccaagctggaaatcaagcgtacggtggccgctcccagcgt gttcatcttcccacctagcgacgagcagctgaagtccggcacagcctctgtcgtgtgcctg ctgaacaacttctacccccgcgaggccaaggtgcagtggaaggtggacaatgccctgca gagcggcaacagccaggaaagcgtgaccgagcaggacagcaaggactccacctacag cctgagcagcaccctgaccctgagcaaggccgactacgagaagcacaaggtgtacgcct gcgaagtgacccaccagggcctgtctagccccgtgaccaagagcttcaaccggggcga gtgt	**SEQ ID NO: 451**
Heavy chain B	caggtgcacctgacacagagcggacccgaagtgcggaagcctggcacctctgtgaagg tgtcctgcaaggcccctggcaacaccctgaaaacctacgacctgcactgggtgcgcagc gtgccaggacagggactgcagtggatgggctggatcagccacgagggcgacaagaaa gtgatcgtggaacggttcaaggccaaagtgaccatcgactgggacagaagcaccaacac cgcctacctgcagctgagcggcctgacctctggcgataccgccgtgtactactgcgccaa gggcagcaagcaccggctgagagactacgccctgtacgacgatgacggcgccctgaac tgggccgtggatgtggactacctgagcaacctggaattctggggccagggcacagccgt gaccgtgtcatcttctcaggtgcagctggtggaatctggcggcggagtggtgcagcctgg cagaagcctgagactgagctgtgccgccagcggcttcaccttcaccaaggcctggatgca ctgggtgcgccaggcccctggaaagcagctggaatgggtggcccagatcaaggacaag agcaacagctacgccacctactacgccgacagcgtgaagggccggttcaccatcagccg ggacgacagcaagaacaccctgtacctgcagatgaacagcctgcgggccgaggacacc gccgtgtactactgtcggggcgtgtactatgccctgagccccttcgattactggggccagg gaaccctcgtgaccgtgtctagtcggaccgcttcgaccaagggcccatcggtgttccctct ggcccctgcagcagaagcaccagcgaatctacagccgccctgggctgcctcgtgaagg actactttcccgagcccgtgaccgtgtcctggaactctggcgctctgacaagcggcgtgca caccttccagccgtgctccagagcagcggcctgtactctctgagcagcgtcgtgacagtg cccagcagcagcctgggcaccaagacctacacctgtaacgtggaccacaagcccagca acaccaaggtggacaagcgggtggaatctaagtacggccctccctgccctccttgcccag	**SEQ ID NO: 452**

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Light chain B	gacatcgtgatgacccagacccccctgagcctgagcgtgacacctggacagcctgccag catcagctgcaagagcagccagagcctggtgcacaacaacgccaacacctacctgagct ggtatctgcagaagcccggccagagcccccagtccctgatctacaaggtgtccaacagat tcagcggcgtgcccgacagattctccggcagcggctctggcaccgacttcaccctgaaga tcagccgggtggaagccgaggacgtgggcgtgtactattgtggccagggcacccagtac cccttcacctttggcagcggcaccaaggtggaaatcaagggccagcccaaggccgcccc cgacttcgtgctgacccagagccctcacagcctgagcgtgacacctggcgagagcgcca gcatcagctgcaagagcagccactccctgatccacggcgaccggaacaactacctggctt ggtacgtgcagaagcccggcagatccccccagctgctgatctacctggccagcagcaga gccagcggcgtgcccgatagattttctggcagcggcagcgacaaggacttcaccctgaa gatcagccgggtggaaaccgaggacgtgggcacctactactgtatgcagggcagagag agcccctggacctttggccagggcaccaaggtggacatcaagaccaagggccccagcc gtacggtggccgctcccagcgtgttcatcttcccacctagcgacgagcagctgaagtccg gcacagcctctgtcgtgtgcctgctgaacaacttctacccccgcgaggccaaagtgcagt ggaaggtggacaacgccctgcagagcggcaacagccaggaaagcgtgaccgagcag gacagcaaggactccacctacagcctgagcagcaccctgacactgagcaaggccgact acgagaagcacaaggtgtacgcctgcgaagtgacccaccagggcctgtctagccccgtg accaagagcttcaaccggggcgagtgt	**SEQ ID NO: 453**
Binding Protein 51 Amino Acid Sequences		
Heavy chain A	Qvqlqesgpglvkpsqtlsltctvsgfslsdygvhwvrqppgkglewlgviwagggt nynpslksrktiskdtsknqvslklssvtaadtavyycardkgysyyysmdywgqgtt vtvssastkgpsvfplapcsrstsestaalgclvkdyfpepvtvswnsgaltsgvhtfpav lqssglyslssvvtvpssslgtktytcnvdhkpsntkvdkrveskygppcppcpapefl ggpsvflfppkpkdtlmisrtpevtcvvvdvsqedpevqfnwyvdgvevhnaktkpr eeqfnstyrvvsvltvlhqdwlngkeykckvsnkglpssiektiskakgqprepqvytl ppcqeemtknqvslwclvkgfypsdiavewesngqpennykttppvldsdgsfflys kltvdksrwqegnvfscsvmhealhnhytqkslslslgk	**SEQ ID NO: 454**
Light chain A	Divltqspaslavspgqratitcrasesveyyvtslmqwyqqkpgqppkllifaasnve sgvparfsgsgsgtdftltinpveandvanyycqqsrkvpytfgqgtkleikrtvaapsv fifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstys lsstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 455**
Heavy chain B	Qvhltqsgpevrkpgtsvkvsckapgntlktydlhwvrsvpgqglqwmgwi shegdkkviverfkakvtidwdrstntaylqlsgltsgdtavyycakgskhrlrd yalydddgalnwavdvdylsnlefwgqgtavtvssdkthtqvqlvesgggvv qpgrslrlscaasgftftkawmhwvrqapgkqlewvaqikdksnsyatyyad svkgrftisrddsknlylqmnslraedtavyycrgvyyalspfdywgqgtlvtv ssdkthtastkgpsvfplapcsrstsestaalgclvkdyfpepvtvswnsgaltsg vhtfpavlqssglyslssvvtvpssslgtktytcnvdhkpsntkvdkrveskygp pcppcpapeflggpsvflfppkpkdtlmisrtpevtcvvvdvsqedpevqfn wyvdgvevhnaktkpreeqfnstyrvvsvltvlhqdwlngkeykckvsnkgl pssiektiskakgqprepqvctlppsqeemtknqvslscavkgfypsdiavew	**SEQ ID NO: 456**

	esngqpennykttppvldsdgsfflvskltvdksrwqegnvfscsvmhealhn hytqkslslslgk	
Light chain B	Divmtqtplslsvtpgqpasisckssqslvhnnantylswylqkpgqspqsliykvsnr fsgvpdrfsgsgsgtdftlkisrveaedvgvyycgqgtqypftfgsgtkveikdkthtdf vltqsphslsvtpgesasisckssshslihgdrnnylawyvqkpgrspqlliylassrasgv pdrfsgsgsdkdftlkisrvetedvgtyycmqgrespwtfgqgtkvdikdkthtrtvaa psvfifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskd styslsstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 457**
Binding Protein 51 Nucleotide Sequences		
Heavy chain A	caggtgcagctgcaggaatctggccctggcctcgtgaagcctagccagaccctgagcct gacctgtaccgtgtccggcttcagcctgagcgactacggcgtgcactgggtgcgccagcc acctggaaaaggcctggaatggctgggcgtgatctgggctggcggaggcaccaactaca accccagcctgaagtccagaaagaccatcagcaaggacaccagcaagaaccaggtgtc cctgaagctgagcagcgtgacagccgccgataccgccgtgtactactgcgccagagaca agggctacagctactactacagcatggactactggggccagggcaccaccgtgaccgtg tcatccgcgtcgaccaagggcccctcggtgttccctctggccccttgcagcagaagcacc agcgaatctacagccgccctgggctgcctcgtgaaggactactttcccgagcccgtgacc gtgtcctggaactctggcgctctgacaagcggcgtgcacaccttccagccgtgctccaga gcagcggcctgtactctctgagcagcgtcgtgacagtgcccagcagcagcctgggcacc aagacctacacctgtaacgtggaccacaagcccagcaacaccaaggtggacaagcggg tggaatctaagtacggccctccctgccctccttgcccagcccctgaatttctgggcggacc ctccgtgttcctgttcccccaaagcccaaggacaccctgatgatcagccggacccccga agtgacctgcgtggtggtggatgtgtcccaggaagatcccgaggtgcagttcaattggtac gtggacggcgtggaagtgcacaacgccaagaccaagcccagagaggaacagttcaaca gcacctaccgggtggtgtccgtgctgaccgtgctgcaccaggactggctgaacggcaaa gagtacaagtgcaaggtgtccaacaagggcctgcccagctccatcgagaaaaccatcag caaggccaagggccagccccgcgagcctcaagtgtataccctgccccctgccaggaag agatgaccaagaaccaggtgtccctgtggtgtctcgtgaaaggcttctaccccagcgacat tgccgtggaatgggagagcaacggccagcccgagaacaactacaagaccacccccct gtgctggacagcgacggctcattcttcctgtactccaagctgaccgtggacaagagccggt ggcaggaaggcaacgtgttcagctgctccgtgatgcacgaggccctgcacaaccactac acccagaagtccctgtctctgtccctgggcaag	**SEQ ID NO: 458**
Light chain A	gacatcgtgctgacacagagccctgctagcctggccgtgtctcctggacagagggccac catcacctgtagagccagcgagagcgtggaatattacgtgaccagcctgatgcagtggtat cagcagaagcccggccagcccccaagctgctgattttcgccgccagcaacgtggaaag cggcgtgccagccagattttccggcagcggctctggcaccgacttcaccctgaccatcaa ccccgtggaagccaacgacgtggccaactactactgccagcagagccggaaggtgccc tacacctttggccagggcaccaagctggaaatcaagcgtacggtggccgctcccagcgt gttcatcttcccacctagcgacgagcagctgaagtccggcacagcctctgtcgtgtgcctg ctgaacaacttctacccccgcgaggccaaggtgcagtggaaggtggacaatgccctgca gagcggcaacagccaggaaagcgtgaccgagcaggacagcaaggactccacctacag cctgagcagcaccctgaccctgagcaaggccgactacgagaagcacaaggtgtacgcct gcgaagtgacccaccagggcctgtctagccccgtgaccaagagcttcaaccggggcga gtgt	**SEQ ID NO: 459**
Heavy chain B	caggtgcacctgacacagagcggacccgaagtgcggaagcctggcacctctgtgaagg tgtcctgcaaggcccctggcaacaccctgaaaacctacgacctgcactgggtgcgcagc gtgccaggacagggactgcagtggatgggctggatcagccacgagggcgacaagaaa gtgatcgtggaacggttcaaggccaaagtgaccatcgactgggacagaagcaccaacac cgcctacctgcagctgagcggcctgacctctggcgataccgccgtgtactactgcgccaa gggcagcaagcaccggctgagagactacgccctgtacgacgatgacggcgccctgaac tgggccgtggatgtggactacctgagcaacctggaattctggggccagggcacagccgt gaccgtgtcatctgacaaaacccatacccaggtgcagctggtggaatctggcggcggagt	**SEQ ID NO: 460**

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Light chain B	gacatcgtgatgacccagaccccctgagcctgagcgtgacacctggacagcctgccag catcagctgcaagagcagccagagcctggtgcacaacaacgccaacacctacctgagct ggtatctgcagaagcccggccagagcccccagtccctgatctacaaggtgtccaacagat tcagcggcgtgcccgacagattctccggcagcggctctggcaccgacttcaccctgaaga tcagccgggtggaagccgaggacgtgggcgtgtactattgtggccagggcacccagtac cccttcacctttggcagcggcaccaaggtggaaatcaaggacaaaacccataccgacttc gtgctgacccagagccctcacagcctgagcgtgacacctggcgagagcgccagcatca gctgcaagagcagccactccctgatccacggcgaccggaacaactacctggcttggtac gtgcagaagcccggcagatccccccagctgctgatctacctggccagcagcagagcca gcggcgtgcccgatagattttctggcagcggcagcgacaaggacttcaccctgaagatca gccgggtggaaaccgaggacgtgggcacctactactgtatgcagggcagagagagccc ctggacctttggccagggcaccaaggtggacatcaaggataagacccataccgtacggt ggccgctcccagcgtgttcatcttcccacctagcgacgagcagctgaagtccggcacagc ctctgtcgtgtgcctgctgaacaacttctaccccgcgaggccaaagtgcagtggaaggtg gacaacgccctgcagagcggcaacagccaggaaagcgtgaccgagcaggacagcaa ggactccacctacagcctgagcagcaccctgacactgagcaaggccgactacgagaag cacaaggtgtacgcctgcgaagtgacccaccagggcctgtctagccccgtgaccaagag cttcaaccggggcgagtgt	**SEQ ID NO: 461**
Binding Protein 52 Amino Acid Sequences		
Heavy chain A	Qvqlqesgpglvkpsqtlsltctvsgfslsdygvhwvrqppgkglewlgviwagggt nynpslksrktiskdtsknqvslklssvtaadtavyycardkgysyyysmdywgqgtt vtvssastkgpsvfplapcsrstsestaalgclvkdyfpepvtvswnsgaltsgvhtfpav lqssglyslssvvtvpssslgtktytcnvdhkpsntkvdkrveskygppcppcpapefl ggpsvflfppkpkdtlmisrtpevtcvvvdvsqedpevqfnwyvdgvevhnaktkpr eeqfnstyrvvsvltvlhqdwlngkeykckvsnkglpssiektiskakgqprepqvytl ppcqeemtknqvslwclvkgfypsdiavewesngqpennykttppvldsdgsfflys kltvdksrwqegnvfscsvmhealhnhytqkslslslgk	**SEQ ID NO: 462**
Light chain A	Divltqspaslavspgqratitcrasesveyyvtslmqwyqqkpgqppkllifaasnve sgvparfsgsgsgtdftltinpveandvanyycqqsrkvpytfgqgtkleikrtvaapsv fifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstys lsstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 463**

Heavy chain B	Qvqlvesgggvvqpgrslrlscaasgftftkawmhwvrqapgkqlewvaqi kdksnsyatyyadsvkgrftisrddsknt lylqmnslraedtavyycrgvyyals pfdywgqgtlvtvsssqvhltqsgpevrkpgtsvkvsckapgntlktydlhwv rsvpgqglqwmgwishegdkkviverfkakvtidwdrstntaylqlsgltsgd tavyycakgskhrlrdyalydddgalnwavdvdylsnlefwgqgtavtvssrt astkgpsvfplapcsrstsestaalgclvkdyfpepvtvswnsgaltsgvhtfpav lqssglyslssvvtvpssslgtktytcnvdhkpsntkvdkrveskygppcppcp apeflggpsvflfppkpkdtlmisrtpevtcvvvdvsqedpevqfnwyvdgv evhnaktkpreeqfnstyrvvsvltvlhqdwlngkeykckvsnkglpssiekti skakgqprepqvctlppsqeemtknqvslscavkgfypsdiavewesngqpe nnykttppvldsdgsfflvskltvdksrwqegnvfscsvmhealhnhytqksls lslgk	**SEQ ID NO: 464**
Light chain B	Dfvltqsphslsvtpgesasisckssh slihgdrnnylawyvqkpgrspqlliylassras gvpdrfsgsgsdkdftlkisrvetedvgtyycmqgrespwtfgqgtkvdikgqpkaap divmtqtplslsvtpgqpasisckssqslvhnnantylswylqkpgqspqsliykvsnrf sgvpdrfsgsgsgtdftlkisrveaedvgvyycgqgtqypftfgsgtkveiktkgpsrtv aapsvfifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqds kdstyslsstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 465**
Binding Protein 52 Nucleotide Sequences		
Heavy chain A	caggtgcagctgcaggaatctggccctggcctcgtgaagcctagccagaccctgagcct gacctgtaccgtgtccggcttcagcctgagcgactacggcgtgcactgggtgcgccagcc acctggaaaaggcctggaatggctgggcgtgatctgggctggcggaggcaccaactaca accccagcctgaagtccagaaagaccatcagcaaggacaccagcaagaaccaggtgtc cctgaagctgagcagcgtgacagccgccgataccgccgtgtactactgcgccagagaca agggctacagctactactacagcatggactactggggccagggcaccaccgtgaccgtg tcatccgcgtcgaccaagggcccctcggtgttccctctggccccttgcagcagaagcacc agcgaatctacagccgccctgggctgcctcgtgaaggactactttcccgagcccgtgacc gtgtcctggaactctggcgctctgacaagcggcgtgcacaccttccagccgtgctccaga gcagcggcctgtactctctgagcagcgtcgtgacagtgcccagcagcagcctgggcacc aagacctacacctgtaacgtggaccacaagcccagcaacaccaaggtggacaagcggg tggaatctaagtacggccctccctgccctccttgcccagcccctgaatttctgggcggacc ctccgtgttcctgttcccccaaagcccaaggacaccctgatgatcagccggacccccga agtgacctgcgtggtggtggatgtgtcccaggaagatcccgaggtgcagttcaattggtac gtggacggcgtggaagtgcacaacgccaagaccaagcccagagaggaacagttcaaca gcacctaccgggtggtgtccgtgctgaccgtgctgcaccaggactggctgaacggcaaa gagtacaagtgcaaggtgtccaacaagggcctgcccagctccatcgagaaaaccatcag caaggccaagggccagccccgcgagcctcaagtgtataccctgccccctgccaggaag agatgaccaagaaccaggtgtccctgtggtgtctcgtgaaaggcttctaccccagcgacat tgccgtggaatgggagagcaacggccagcccgagaacaactacaagaccacccccct gtgctggacagcgacggctcattcttcctgtactccaagctgaccgtggacaagagccggt ggcaggaaggcaacgtgttcagctgctccgtgatgcacgaggccctgcacaaccactac acccagaagtccctgtctctgtccctgggcaag	**SEQ ID NO: 466**
Light chain A	gacatcgtgctgacacagagccctgctagcctggccgtgtctcctggacagagggccac catcacctgtagagccagcgagagcgtggaatattacgtgaccagcctgatgcagtggtat cagcagaagcccggccagcccccaagctgctgattttcgccgccagcaacgtggaaag cggcgtgccagccagattttccggcagcggctctggcaccgacttcaccctgaccatcaa ccccgtggaagccaacgacgtggccaactactactgccagcagagccggaaggtgccc tacacctttggccagggcaccaagctggaaatcaagcgtacggtggccgctcccagcgt gttcatcttcccacctagcgacgagcagctgaagtccggcacagcctctgtcgtgtgcctg ctgaacaacttctacccccgcgaggccaaggtgcagtggaaggtggacaatgccctgca gagcggcaacagccaggaaagcgtgaccgagcaggacagcaaggactccacctacag cctgagcagcaccctgaccctgagcaaggccgactacgagaagcacaaggtgtacgcct gcgaagtgacccaccagggcctgtctagccccgtgaccaagagcttcaaccggggcga	**SEQ ID NO: 467**

	gtgt	
Heavy chain B	caggtgcagctggtggaatctggcggcggagtggtgcagcctggcagaagcctgagact gagctgtgccgccagcggcttcaccttcaccaaggcctggatgcactgggtgcgccagg cccctggaaagcagctggaatgggtggcccagatcaaggacaagagcaacagctacgc cacctactacgccgacagcgtgaagggccggttcaccatcagccgggacgacagcaag aacaccctgtacctgcagatgaacagcctgcgggccgaggacaccgccgtgtactactgt cggggcgtgtactatgccctgagccccttcgattactggggccagggaaccctcgtgacc gtgtctagtagccaggtgcacctgacacagagcggacccgaagtgcggaagcctggca cctctgtgaaggtgtcctgcaaggcccctggcaacaccctgaaaacctacgacctgcact gggtgcgcagcgtgccaggacagggactgcagtggatgggctggatcagccacgagg gcgacaagaaagtgatcgtggaacggttcaaggccaaagtgaccatcgactgggacaga agcaccaacaccgcctacctgcagctgagcggcctgacctctggcgataccgccgtgta ctactgcgccaagggcagcaagcaccggctgagagactacgccctgtacgacgatgac ggcgccctgaactgggccgtggatgtggactacctgagcaacctggaattctggggcca gggcacagccgtgaccgtgtcatctcggaccgccagcacaaagggcccatcggtgttcc ctctggcccccttgcagcagaagcaccagcgaatctacagccgccctgggctgcctcgtga aggactactttcccgagcccgtgaccgtgtcctggaactctggcgctctgacaagcggcgt gcacacctttccagccgtgctccagagcagcggcctgtactctctgagcagcgtcgtgac agtgcccagcagcagcctgggcaccaagacctacacctgtaacgtggaccacaagccc agcaacaccaaggtggacaagcgggtggaatctaagtacggccctccctgccctccttgc ccagcccctgaatttctgggcggaccctccgtgttcctgttcccccaaagcccaaggaca ccctgatgatcagccggaccccgaagtgacctgcgtggtggtggatgtgtcccaggaa gatcccgaggtgcagttcaattggtacgtggacggcgtggaagtgcacaacgccaagac caagcccagagaggaacagttcaacagcacctaccgggtggtgtccgtgctgaccgtgc tgcaccaggactggctgaacggcaaagagtacaagtgcaaggtgtccaacaagggcctg cccagctccatcgagaaaaccatcagcaaggccaagggccagccccgcgagcctcaag tgtgtaccctgccccctagccaggaagagatgaccaagaaccaggtgtccctgagctgtg ccgtgaaaggcttctaccccagcgacattgccgtggaatgggagagcaacggccagccc gagaacaactacaagaccacccccccctgtgctggacagcgacggctcattcttcctggtgt ccaagctgaccgtggacaagagccggtggcaggaaggcaacgtgttcagctgctccgtg atgcacgaggccctgcacaaccactacacccagaagtccctgtctctgtccctgggcaag	**SEQ ID NO: 468**
Light chain B	gacttcgtgctgacccagagccctcacagcctgagcgtgacacctggcgagagcgccag catcagctgcaagagcagccactccctgatccacggcgaccggaacaactacctggcttg gtacgtgcagaagcccggcagatccccccagctgctgatctacctggccagcagcagag ccagcggcgtgcccgatagattttctggcagcggcagcgacaaggacttcaccctgaag atcagccgggtggaaaccgaggacgtgggcacctactactgtatgcagggcagagaga gcccctggacctttggccagggcaccaaggtggacatcaagggccagcccaaggccgc ccccgacatcgtgatgacccagacccccctgagcctgagcgtgacacctggacagcctg ccagcatcagctgcaagagcagccagagcctggtgcacaacaacgccaacacctacctg agctggtatctgcagaagcccggccagagcccccagtccctgatctacaaggtgtccaac agattcagcggcgtgcccgacagattctccggcagcggctctggcaccgacttcaccctg aagatcagccgggtggaagccgaggacgtgggcgtgtactattgtggccagggcaccc agtacccccttcaccctttggcagcggcaccaaggtggaaatcaagaccaagggccccagc cgtacggtggccgctcccagcgtgttcatcttcccacctagcgacgagcagctgaagtcc ggcacagcctctgtcgtgtgcctgctgaacaacttctacccccgcgaggccaaagtgcag tggaaggtggacaacgccctgcagagcggcaacagccaggaaagcgtgaccgagcag gacagcaaggactccacctacagcctgagcagcaccctgacactgagcaaggccgact acgagaagcacaaggtgtacgcctgcgaagtgacccaccagggcctgtctagccccgtg accaagagcttcaaccggggcgagtgt	**SEQ ID NO: 469**
Binding Protein 53 Amino Acid Sequences		
Heavy chain A	Qvqlqesgpglvkpsqtlsltctvsgfslsdygvhwvrqppgkglewlgviwagggt nynpslksrktiskdtsknqvslklssvtaadtavyycardkgysyyysmdywgqgtt vtvssastkgpsvfplapcsrstsestaalgclvkdyfpepvtvswnsgaltsgvhtfpav lqssglyslssvvtvpssslgtktytcnvdhkpsntkvdkrveskygppcppcpapefl	**SEQ ID NO: 470**

	ggpsvflfppkpkdtlmisrtpevtcvvvdvsqedpevqfnwyvdgvevhnaktkpr eeqfnstyrvvsvltvlhqdwlngkeykckvsnkglpssiektiskakgqprepqvytl ppcqeemtknqvslwclvkgfypsdiavewesngqpennykttppvldsdgsfflys kltvdksrwqegnvfscsvmhealhnhytqkslslslgk	
Light chain A	Divltqspaslavspgqratitcrasesveyyvtslmqwyqqkpgqppkllifaasnve sgvparfsgsgsgtdftltinpveandvanyycqqsrkvpytfgqgtkleikrtvaapsv fifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdstys lsstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 471**
Heavy chain B	Qvqlvesgggvvqpgrslrlscaasgftftkawmhwvrqapgkqlewvaqi kdksnsyatyyadsvkgrftisrddskntlylqmnslraedtavyycrgvyyals pfdywgqgtlvtvssdkthtqvhltqsgpevrkpgtsvkvsckapgntlktydl hwvrsvpgqglqwmgwishegdkkviverfkakvtidwdrstntaylqlsgl tsgdtavyycakgskhrlrdyalydddgalnwavdvdylsnlefwgqgtavtv ssdkthtastkgpsvfplapcsrstsestaalgclvkdyfpepvtvswnsgaltsg vhtfpavlqssglyslssvvtvpssslgtktytcnvdhkpsntkvdkrveskygp pcppcpapeflggpsvflfppkpkdtlmisrtpevtcvvvdvsqedpevqfn wyvdgvevhnaktkpreeqfnstyrvvsvltvlhqdwlngkeykckvsnkgl pssiektiskakgqprepqvctlppsqeemtknqvslscavkgfypsdiavew esngqpennykttppvldsdgsfflvskltvdksrwqegnvfscsvmhealhn hytqkslslslgk	**SEQ ID NO: 472**
Light chain B	Dfvltqsphslsvtpgesasisckssshslihgdrnnylawyvqkpgrspqlliylassras gvpdrfsgsgsdkdftlkisrvetedvgtyycmqgrespwtfgqgtkvdikdkthtdiv mtqtplslsvtpgqpasisckssqslvhnnantylswylqkpgqspqsliykvsnrfsg vpdrfsgsgsgtdftlkisrveaedvgvyycgqgtqypftfgsgtkveikdkthtrtvaap svfifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskdst yslsstltlskadyekhkvyacevthqglsspvtksfnrgec	**SEQ ID NO: 473**
Binding Protein 53 Nucleotide Sequences		
Heavy chain A	caggtgcagctgcaggaatctggccctggcctcgtgaagcctagccagaccctgagcct gacctgtaccgtgtccggcttcagcctgagcgactacggcgtgcactgggtgcgccagcc acctggaaaaggcctggaatggctgggcgtgatctgggctggcggaggcaccaactaca accccagcctgaagtccagaaagaccatcagcaaggacaccagcaagaaccaggtgtc cctgaagctgagcagcgtgacagccgccgataccgccgtgtactactgcgccagagaca agggctacagctactactacagcatggactactggggccagggcaccaccgtgaccgtg tcatccgcgtcgaccaagggcccctcggtgttccctctggccccttgcagcagaagcacc agcgaatctacagccgccctgggctgcctcgtgaaggactactttcccgagcccgtgacc gtgtcctggaactctggcgctctgacaagcggcgtgcacaccttccagccgtgctccaga gcagcggcctgtactctctgagcagcgtcgtgacagtgcccagcagcagcctgggcacc aagacctacacctgtaacgtggaccacaagcccagcaacaccaaggtggacaagcggg tggaatctaagtacggccctccctgccctccttgcccagcccctgaatttctgggcggacc ctccgtgttcctgttcccccaaagcccaaggacaccctgatgatcagccggacccccga agtgacctgcgtggtggtggatgtgtcccaggaagatcccgaggtgcagttcaattggtac gtggacggcgtggaagtgcacaacgccaagaccaagcccagagaggaacagttcaaca gcacctaccgggtggtgtccgtgctgaccgtgctgcaccaggactggctgaacggcaaa gagtacaagtgcaaggtgtccaacaagggcctgcccagctccatcgagaaaaccatcag caaggccaagggccagccccgcgagcctcaagtgtataccctgccccttgccaggaag agatgaccaagaaccaggtgtccctgtggtgtctcgtgaaaggcttctaccccagcgacat tgccgtggaatgggagagcaacggccagcccgagaacaactacaagaccacccccct gtgctggacagcgacggctcattcttcctgtactccaagctgaccgtggacaagagccggt ggcaggaaggcaacgtgttcagctgctccgtgatgcacgaggccctgcacaaccactac acccagaagtccctgtctctgtccctgggcaag	**SEQ ID NO: 474**
Light chain A	gacatcgtgctgacacagagccctgctagcctggccgtgtctcctggacagagggccac catcacctgtagagccagcgagagcgtggaatattacgtgaccagcctgatgcagtggtat cagcagaagcccggccagcccccaagctgctgattttcgccgccagcaacgtggaaag	**SEQ ID NO: 475**

	cggcgtgccagccagattttccggcagcggctctggcaccgacttcaccctgaccatcaa ccccgtggaagccaacgacgtggccaactactactgccagcagagccggaaggtgccc tacacctttggccagggcaccaagctggaaatcaagcgtacggtggccgctcccagcgt gttcatcttcccacctagcgacgagcagctgaagtccggcacagcctctgtcgtgtgcctg ctgaacaacttctacccccgcgaggccaaggtgcagtggaaggtggacaatgccctgca gagcggcaacagccaggaaagcgtgaccgagcaggacagcaaggactccacctacag cctgagcagcaccctgaccctgagcaaggccgactacgagaagcacaaggtgtacgcct gcgaagtgacccaccagggcctgtctagccccgtgaccaagagcttcaaccggggcga gtgt	
Heavy chain B	caggtgcagctggtggaatctggcggcggagtggtgcagcctggcagaagcctgagact gagctgtgccgccagcggcttcaccttcaccaaggcctggatgcactgggtgcgccagg cccctggaaagcagctggaatgggtggcccagatcaaggacaagagcaacagctacgc cacctactacgccgacagcgtgaagggccggttcaccatcagccgggacgacagcaag aacaccctgtacctgcagatgaacagcctgcgggccgaggacaccgccgtgtactactgt cggggcgtgtactatgccctgagccccttcgattactggggccagggaaccctcgtgacc gtgtctagtgacaaaacccatacccaggtgcacctgacacagagcggacccgaagtgcg gaagcctggcacctctgtgaaggtgtcctgcaaggcccctggcaacaccctgaaaaccta cgacctgcactgggtgcgcagcgtgccaggacagggactgcagtggatgggctggatc agccacgagggcgacaagaaagtgatcgtggaacggttcaaggccaaagtgaccatcg actgggacagaagcaccaacaccgcctacctgcagctgagcggcctgacctctggcgat accgccgtgtactactgcgccaagggcagcaagcaccggctgagagactacgccctgta cgacgatgacggcgccctgaactgggccgtggatgtggactacctgagcaacctggaatt ctggggccagggcacagccgtgaccgtgtcatctgataagacccacaccgccagcacaa agggcccatcggtgttccctctggcccccttgcagcagaagcaccagcgaatctacagccg ccctgggctgcctcgtgaaggactactttcccgagcccgtgaccgtgtcctggaactctgg cgctctgacaagcggcgtgcacaccttccagccgtgctccagagcagcggcctgtactc tctgagcagcgtcgtgacagtgcccagcagcagcctgggcaccaagacctacacctgta acgtggaccacaagcccagcaacaccaaggtggacaagcgggtggaatctaagtacgg ccctccctgccctccttgcccagcccctgaatttctgggcggaccctccgtgttcctgttccc cccaaagcccaaggacaccctgatgatcagccggaccccccgaagtgacctgcgtggtg gtggatgtgtcccaggaagatcccgaggtgcagttcaattggtacgtggacggcgtggaa gtgcacaacgccaagaccaagcccagagaggaacagttcaacagcacctaccgggtgg tgtccgtgctgaccgtgctgcaccaggactggctgaacggcaaagagtacaagtgcaag gtgtccaacaagggcctgcccagctccatcgagaaaaccatcagcaaggccaagggcc agccccgcgagcctcaagtgtgtaccctgccccctagccaggaagagatgaccaagaac caggtgtccctgagctgtgccgtgaaaggcttctaccccagcgacattgccgtggaatgg gagagcaacggccagcccgagaacaactacaagaccacccccccctgtgctggacagcg acggctcattcttcctggtgtccaagctgaccgtggacaagagccggtggcaggaaggca acgtgttcagctgctccgtgatgcacgaggccctgcacaaccactacacccagaagtccc tgtctctgtccctgggcaag	**SEQ ID NO: 476**
Light chain B	gacttcgtgctgacccagagccctcacagcctgagcgtgacacctggcgagagcgccag catcagctgcaagagcagccactccctgatccacggcgaccggaacaactacctggcttg gtacgtgcagaagcccggcagatcccccccagctgctgatctacctggccagcagcagag ccagcggcgtgcccgatagattttctggcagcggcagcgacaaggacttcaccctgaag atcagccgggtggaaaccgaggacgtgggcacctactactgtatgcagggcagagaga gcccctggacctttggccagggcaccaaggtggacatcaaggacaaaacccataccgac atcgtgatgacccagacccccctgagcctgagcgtgacacctggacagcctgccagcat cagctgcaagagcagccagagcctggtgcacaacaacgccaacacctacctgagctggt atctgcagaagcccggccagagcccccagtccctgatctacaaggtgtccaacagattca gcggcgtgcccgacagattctccggcagcggctctggcaccgacttcaccctgaagatca gccgggtggaagccgaggacgtgggcgtgtactattgtggccagggcacccagtaccc cttcacctttggcagcggcaccaaggtggaaatcaaggataagacccatacccgtacggt ggccgctcccagcgtgttcatcttcccacctagcgacgagcagctgaagtccggcacagc ctctgtcgtgtgcctgctgaacaacttctacccccgcgaggccaaagtgcagtggaaggtg	**SEQ ID NO: 477**

	gacaacgccctgcagagcggcaacagccaggaaagcgtgaccgagcaggacagcaa ggactccacctacagcctgagcagcaccctgacactgagcaaggccgactacgagaag cacaaggtgtacgcctgcgaagtgacccaccagggcctgtctagccccgtgaccaagag cttcaaccggggcgagtgt	

Table A: CDR sequences of binding proteins

Ab	CDRH1	CDRH2	CDRH3	CDRL1	CDRL2	CDRL3
CD4BS "a"	dctln (SEQ ID NO:248)	wlkprggavnyarplqg (SEQ ID NO: 249)	gkncdynwdfeh (SEQ ID NO: 250)	rtsqygsla (SEQ ID NO: 266)	sgstraa (SEQ ID NO: 267)	qqyef (SEQ ID NO: 268)
CD4BS "b"	GYTFTAHI(SEQ ID NO: 251)	IKPQYGAV(SEQ ID NO: 252)	drsygdsswalda (SEQ ID NO: 253)	QGVGSD (SEQ ID NO: 269)	HTS (SEQ ID NO: 270)	qvlqf (SEQ ID NO: 271)
MPER	gfdfdnaw(SEQ ID NO: 254)	itgpgegwsv(SEQ ID NO: 255)	tgkyydfwsgyppgeeyfqd(SEQ ID NO: 256)	rgdslrshyas (SEQ ID NO: 272)	gknnrps (SEQ ID NO: 273)	ssrdksgsrlsv (SEQ ID NO: 274)
V1/V2 dir."a"	GNTLKTYD (SEQ ID NO:257)	ISHEGDKK(SEQ ID NO: 258)	cakgskhrlrdyalydddgalnwavdvdylsnlefw (SEQ ID NO:259)	hslihgdrnny (SEQ ID NO: 275)	las (SEQ ID NO: 276)	cmqgrespwtf (SEQ ID NO: 277)
V3 dir.	SGASISDSY (SEQ ID NO: 260)	VHKSGDT (SEQ ID NO:261)	ARTLHGRRIYGIVAFNEWFTYFYMDV (SEQ ID NO: 262)	SLGSRA (SEQ ID NO: 278)	NNQ (SEQ ID NO: 279)	HIWDSRVPTKWV (SEQ ID NO: 280)
V1/V dir. "b"	QFRFDGYG (SEQ ID NO: 263)	ISHDGIKK (SEQ ID NO: 264)	CAKDLREDECEEWWSDYYDFGKQLPCAKSRGGLVGIADNW(SEQ ID NO: 265)	TSNIGNNF (SEQ ID NO: 281)	ETD (SEQ ID NO: 282)	atwaaslssarv (SEQ ID NO: 283)

Ab	CDRH1	CDRH2	CDRH3	CDRL1	CDRL2	CDRL3
Anti-CD28	GYTFTSYY (SEQ ID NO: 479)	IYPGNVNT (SEQ ID NO: 480)	trshygldwnfdv (SEQ ID NO: 481)	QNIYVW (SEQ ID NO: 488)	KAS (SEQ ID NO: 489)	qqgqtypyt (SEQ ID NO: 490)
Anti-CD28	GFSLSDYG (SEQ ID NO: 482)	IWAGGGT (SEQ ID NO: 483)	ardkgysyyysmd (SEQ ID NO: 484)	ESVEYYVTSL (SEQ ID NO: 491)	AAS (SEQ ID NO: 492)	qqsrkvpyt (SEQ ID NO: 493)
Anti-CD3	GFTFTKAW (SEQ ID NO: 485)	IKDKSNS (SEQ ID NO: 486)	rgvyyalspfdy (SEQ ID NO:487)	QSLVHNNANTY (SEQ ID NO: 494)	KVS (SEQ ID NO: 495)	gqgtqyp (SEQ ID NO: 496)

Table B: CDR sequences of parental antibodies

Ab	CDR_H1	CDR_H2	CDR_H3	CDR_L1	CDR_L2	CDR_L3
CD4BS "a"	DCTLN (SEQ ID NO: 248)	LKPRGGAVNYARPLQ (SEQ ID NO: 497)	GKNCDYNWDFEH (SEQ ID NO: 250)	RTSQYGSLA (SEQ ID NO: 266)	SGSTRAA (SEQ ID NO: 267)	QQYEF (SEQ ID NO: 268)
CD4BS "b"	GYTFTAHI (SEQ ID NO: 251)	IKPQYGAV (SEQ ID NO: 252)	DRSYGDSSWALDA (SEQ ID NO: 253)	QGVGSD (SEQ ID NO: 269)	HTS (SEQ ID NO: 270)	QVLQF (SEQ ID NO: 271)
MPER	GFDFDNAW (SEQ ID NO: 254)	ITGPGEGWSV (SEQ ID NO: 255)	TGKYYDFWSGYPPGEEYFQD (SEQ ID NO: 256)	SLRSHY (SEQ ID NO: 500)	GKN (SEQ ID NO: 501)	SSRDKSGSRLSV (SEQ ID NO: 274)
MPER_100W	GFDFDNAW (SEQ ID NO: 254)	ITGPGEGWSV (SEQ ID NO: 255)	TGKYYDFWWGYPPGEEYFQD (SEQ ID NO: 498)	SLRSHY (SEQ ID NO: 500)	GKN (SEQ ID NO: 501)	SSRDKSGSRLSV (SEQ ID NO: 274)
V1/V2 directed "a"	GNTLKTYD (SEQ ID NO: 257)	ISHEGDKK (SEQ ID NO: 258)	CAKGSKHRLRDYALYDDDGALNWAVDVDYLSNLEFW (SEQ ID NO: 259)	HSLIHGDRNNY (SEQ ID NO: 275)	LAS (SEQ ID NO: 276)	CMQGRESPWTF (SEQ ID NO: 277)
V1/V2 directed "b"	QFRFDGYG (SEQ ID NO: 263)	ISHDGIKK (SEQ ID NO: 264)	CAKDLREDECEEWWSDYYDFGKQLPCAKSRGGLVGIADNW (SEQ ID NO: 265)	TSNIGNNF (SEQ ID NO: 281)	ETD (SEQ ID NO: 282)	ATWAASLSSARV (SEQ ID NO: 283)
V3 directe	GASISDSY (SEQ ID NO: 499)	VHKSGDT (SEQ ID NO: 261)	ARTLHGRRIYGIVAFNEWFTYFYMDV	SLGSRA (SEQ ID NO: 278)	NNQ (SEQ ID NO: 279)	HIWDSRVPTKWV

d			(SEQ ID NO: 262)			(SEQ ID NO: 280)
CD28	GYTFTSYY (SEQ ID NO: 479)	IYPGNVNT (SEQ ID NO: 480)	TRSHYGLDWNFDV (SEQ ID NO: 481)	QNIYVW (SEQ ID NO: 488)	KAS (SEQ ID NO: 489)	QQGQTYPYT (SEQ ID NO: 490)
CD28_2	GFSLSDYG (SEQ ID NO: 482)	IWAGGGT (SEQ ID NO:483)	ARDKGYSYYYSMD (SEQ ID NO: 484)	ESVEYYVTSL (SEQ ID NO: 491)	AAS (SEQ ID NO: 492)	QQSRKVPYT (SEQ ID NO: 493)
CD3	GFTFTKAW (SEQ ID NO: 485)	IKDKSNS (SEQ ID NO: 486)	RGVYYALSPFDY (SEQ ID NO: 487)	QSLVHNNANTY (SEQ ID NO: 494)	KVS (SEQ ID NO: 495)	GQGTQYP (SEQ ID NO: 496)

Table C: Variable domain sequences of parental antibodies

Ab Name	V_H	V_L
CD4BS "a"	QVQLVQSGGQMKKPGESMRISCRASGYEFIDCTLNWIRLAP GKRPEWMGWLKPRGGAVNYARPLQGRVTMTRDVYSDTAF LELRSLTVDDTAVYFCTRGKNCDYNWDFEHWGRGTPVIVS S (SEQ ID NO: 502)	EIVLTQSPGTLSLSPGETAIISCRTSQYGSLAWYQQ RPGQAPRLVIYSGSTRAAGIPDRFSGSRWGPDYNL TISNLESGDFGVYYCQQYEFFGQGTKVQVDIK (SEQ ID NO: 512)
CD4BS "b"	RAHLVQSGTAMKKPGASVRVSCQTSGYTFTAHILFWFRQAP GRGLEWVGWIKPQYGAVNFGGGFRDRVTLTRDVYREIAY MDIRGLKPDDTAVYYCARDRSYGDSSWALDAWGQGTTVV VSA (SEQ ID NO: 503)	YIHVTQSPSSLSVSIGDRVTINCQTSQGVGSDLHW YQHKPGRAPKLLIHHTSSVEDGVPSRFSGSGFHTS FNLTISDLQADDIATYYCQVLQFFGRGSRLHIK (SEQ ID NO: 513)
CD4BS "b" (Δglycan)	RAHLVQSGTAMKKPGASVRVSCQTSGYTFTAHILFWFRQAP GRGLEWVGWIKPQYGAVNFGGGFRDRVTLTRDVYREIAY MDIRGLKPDDTAVYYCARDRSYGDSSWALDAWGQGTTVV VSA (SEQ ID NO: 503)	YIHVTQSPSSLSVSIGDRVTINCQTSQGVGSDLHW YQHKPGRAPKLLIHHTSSVEDGVPSRFSGSGFHTS F***Q***LTISDLQADDIATYYCQVLQFFGRGSRLHIK (SEQ ID NO: 514)
CD4BS "b" (Δisomerization D55E)	RAHLVQSGTAMKKPGASVRVSCQTSGYTFTAHILFWFRQAP GRGLEWVGWIKPQYGAVNFGGGFRDRVTLTRDVYREIAY MDIRGLKPDDTAVYYCARDRSYGDSSWALDAWGQGTTVV VSA (SEQ ID NO: 503)	YIHVTQSPSSLSVSIGDRVTINCQTSQGVGSDLHW YQHKPGRAPKLLIHHTSSVE***E***GVPSRFSGSGFHTS FNLTISDLQADDIATYYCQVLQFFGRGSRLHIK (SEQ ID NO: 515)
CD4BS "b" (Δisomerizatio	RAHLVQSGTAMKKPGASVRVSCQTSGYTFTAHILFWFRQAP GRGLEWVGWIKPQYGAVNFGGGFRDRVTLTRDVYREIAY	YIHVTQSPSSLSVSIGDRVTINCQTSQGVGSDLHW YQHKPGRAPKLLIHHTSSVED***A***VPSRFSGSGFHTS

n G56A)	MDIRGLKPDDTAVYYCARDRSYGDSSWALDAWGQGTTVVVSA (SEQ ID NO: 503)	FNLTISDLQADDIATYYCQVLQFFGRGSRLHIK (SEQ ID NO: 516)
CD4BS "b" (Δglycan / Δisomerization D55E)	RAHLVQSGTAMKKPGASVRVSCQTSGYTFTAHILFWFRQAPGRGLEWVGWIKPQYGAVNFGGGFRDRVTLTRDVYREIAYMDIRGLKPDDTAVYYCARDRSYGDSSWALDAWGQGTTVVVSA (SEQ ID NO: 503)	YIHVTQSPSSLSVSIGDRVTINCQTSQGVGSDLHWYQHKPGRAPKLLIHHTSSVE***E***GVPSRFSGSGFHTSF***Q***LTISDLQADDIATYYCQVLQFFGRGSRLHIK (SEQ ID NO: 517)
MPER	EVRLVESGGGLVKPGGSLRLSCSASGFDFDNAWMTWVRQPPGKGLEWVGRITGPGEGWSVDYAESVKGRFTISRDNTKNTLYLEMNNVRTEDTGYYFCARTGKYYDFWSGYPPGEEYFQDWGQGTLVIVSS (SEQ ID NO: 504)	ASELTQDPAVSVALKQTVTITCRGDSLRSHYASWYQKKPGQAPVLLFYGKNNRPSGIPDRFSGSASGNRASLTITGAQAEDEADYYCSSRDKSGSRLSVFGGGTKLTVL (SEQ ID NO: 518)
MPER_100W	EVRLVESGGGLVKPGGSLRLSCSASGFDFDNAWMTWVRQPPGKGLEWVGRITGPGEGWSVDYAESVKGRFTISRDNTKNTLYLEMNNVRTEDTGYYFCARTGKYYDFW***W***GYPPGEEYFQDWGQGTLVIVSS (SEQ ID NO: 505)	ASELTQDPAVSVALKQTVTITCRGDSLRSHYASWYQKKPGQAPVLLFYGKNNRPSGIPDRFSGSASGNRASLTITGAQAEDEADYYCSSRDKSGSRLSVFGGGTKLTVL (SEQ ID NO: 518)
V1/V2 directed "a"	QVHLTQSGPEVRKPGTSVKVSCKAPGNTLKTYDLHWVRSVPGQGLQWMGWISHEGDKKVIVERFKAKVTIDWDRSTNTAYLQLSGLTSGDTAVYYCAKGSKHRLRDYALYDDDGALNWAVDVDYLSNLEFWGQGTAVTVSS (SEQ ID NO: 506)	DFVLTQSPHSLSVTPGESASISCKSSHSLIHGDRNNYLAWYVQKPGRSPQLLIYLASSRASGVPDRFSGSGSGSDKDFTLKISRVETEDVGTYYCMQGRESPWTFGQGTKVDIK (SEQ ID NO: 519)
V1/V2 directed "b"	QVQLVESGGGVVQPGTSLRLSCAASQFRFDGYGMHWVRQAPGKGLEWVASISHDGIKKYHAEKVWGRFTISRDNSKNTLYLQMNSLRPEDTALYYCAKDLREDECEEWWSDYYDFGKQLPCAKSRGGLVGIADNWGQGTMVTVSS (SEQ ID NO: 507)	QSVLTQPPSVSAAPGQKVTISCSGNTSNIGNNFVSWYQQRPGRAPQLLIYETDKRPSGIPDRFSASKSGTSGTLAITGLQTGDEADYYCATWAASLSSARVFGTGTKVIVL (SEQ ID NO: 520)
V3 directed	QMQLQESGPGLVKPSETLSLTCSVSGASISDSYWSWIRRSPGKGLEWIGYVHKSGDTNYSPSLKSRVNLSLDTSKNQVSLSLVAATAADSGKYYCARTLHGRRIYGIVAFNEWFTYFYMDVWGNGTQVTVSS (SEQ ID NO: 508)	SDISVAPGETARISCGEKSLGSRAVQWYQHRAGQAPSLIIYNNQDRPSGIPERFSGSPDSPFGTTATLTITSVEAGDEADYYCHIWDSRVPTKWVFGGGTTLTVL (SEQ ID NO: 521)
CD28	QVQLVQSGAEVVKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWIGSIYPGNVNTNYAQKFQGRATLTVDTSISTAYM	DIQMTQSPSSLSASVGDRVTITCQASQNIYVWLNWYQQKPGKAPKLLIYKASNLHTGVPSRFSGSGSG

	ELSRLRSDDTAVYYCTRSHYGLDWNFDVWGKGTTVTVSS (SEQ ID NO: 509)	TDFTLTISSLQPEDIATYYCQQGQTYPYTFGQGTK LEIK (SEQ ID NO: 522)
CD28_2	QVQLQESGPGLVKPSQTLSLTCTVSGFSLSDYGVHWVRQPP GKGLEWLGVIWAGGGTNYNPSLKSRKTISKDTSKNQVSLKL SSVTAADTAVYYCARDKGYSYYYSMDYWGQGTTVTVSS (SEQ ID NO: 510)	DIVLTQSPASLAVSPGQRATITCRASESVEYYVTS LMQWYQQKPGQPPKLLIFAASNVESGVPARFSGS GSGTDFTLTINPVEANDVANYYCQQSRKVPYTFG QGTKLEIK (SEQ ID NO: 523)
CD3	QVQLVESGGGVVQPGRSLRLSCAASGFTFTKAWMHWVRQ APGKQLEWVAQIKDKSNSYATYYADSVKGRFTISRDDSKNT LYLQMNSLRAEDTAVYYCRGVYYALSPFDYWGQGTLVTV SS (SEQ ID NO: 511)	DIVMTQTPLSLSVTPGQPASISCKSSQSLVHNNAN TYLSWYLQKPGQSPQSLIYKVSNRFSGVPDRFSGS GSGTDFTLKISRVEAEDVGVYYCGQGTQYPFTFG SGTKVEIK (SEQ ID NO: 524)

CDR sequences are underlined.
Variable domain modifications are shown in bold and italicized.

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:

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

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

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

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

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

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; 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.

2. 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:

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

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.

3. The binding protein of claim 1 or claim 2, wherein the one or more HIV target protein is selected from the group consisting of glycoprotein 120, glycoprotein 41 and glycoprotein 160.

4. The binding protein of claim 1 or claim 2, wherein the binding protein is trispecific and capable of specifically binding three different epitopes on a single HIV target protein.

5. The binding protein of claim 1 or claim 2, wherein the binding protein is trispecific and capable of specifically binding two different epitopes on a first HIV target protein, and one epitope on a second HIV target protein, wherein the first and second HIV target proteins are different.

6. The binding protein of claim 1 or claim 2, wherein the binding protein is trispecific and capable of specifically binding three different antigen targets.

7. The binding protein of claim 1 or claim 2, wherein the binding protein is capable of inhibiting the function of one or more HIV target proteins.

8. The binding protein of any one of claims 1-7, wherein V_{L1} comprises a CDR-L1, CDR-L2, and CDR-L3 comprising a sequence as set forth in SEQ ID NOs: 266, 267, and 268, respectively; a sequence as set forth in SEQ ID NOs: 269, 270, and 271, respectively; a sequence as set forth in SEQ ID NOs: 500, 501, and 274, respectively; a sequence as set forth in SEQ ID NOs: 275, 276, and 277, respectively; a sequence as set forth in SEQ ID NOs: 281, 282, and 283, respectively; or a sequence as set forth in SEQ ID NOs: 278, 279, and 280, respectively.

9. The binding protein of any one of claims 1-7, wherein V_{L1} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, and 521.

10. The binding protein of any one of claims 1-9, wherein V_{L1} comprises a light chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, and 521.

11. The binding protein of any one of claims 1-10, wherein V_{L2} comprises a CDR-L1, CDR-L2, and CDR-L3 comprising a sequence as set forth in SEQ ID NOs: 266, 267, and 268, respectively; a sequence as set forth in SEQ ID NOs: 269, 270, and 271, respectively; a sequence as set forth in SEQ ID NOs: 500, 501, and 274, respectively; a sequence as set forth in SEQ ID NOs: 275, 276, and 277, respectively; a sequence as set forth in SEQ ID NOs: 281, 282, and 283, respectively; or a sequence as set forth in SEQ ID NOs: 278, 279, and 280, respectively.

12. The binding protein of any one of claims 1-10, wherein V_{L2} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, and 521.

13. The binding protein of any one of claims 1-12, wherein V_{L2} comprises a light chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, and 521.

14. The binding protein of any one of claims 1-13, wherein V_{L3} comprises a CDR-L1, CDR-L2, and CDR-L3 comprising a sequence as set forth in SEQ ID NOs: 266, 267, and 268, respectively; a sequence as set forth in SEQ ID NOs: 269, 270, and 271, respectively; a sequence as set forth in SEQ ID NOs: 500, 501, and 274, respectively; a sequence as set forth

in SEQ ID NOs: 275, 276, and 277, respectively; a sequence as set forth in SEQ ID NOs: 281, 282, and 283, respectively; or a sequence as set forth in SEQ ID NOs: 278, 279, and 280, respectively.

15. The binding protein of any one of claims 1-13, wherein V_{L3} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, and 521.

16. The binding protein of any one of claims 1-15, wherein V_{L3} comprises a light chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, and 521.

17. The binding protein of any one of claims 1-16, wherein V_{H1} comprises a CDR-H1, CDR-H2, and CDR-H3 comprising a sequence as set forth in SEQ ID NOs: 248, 497, and 250, respectively; a sequence as set forth in SEQ ID NOs: 251, 252, and 253, respectively; a sequence as set forth in SEQ ID NOs: 254, 255, and 256, respectively; a sequence as set forth in SEQ ID NOs: 254, 255, and 498, respectively; a sequence as set forth in SEQ ID NOs: 257, 258, and 259, respectively; a sequence as set forth in SEQ ID NOs: 263, 264, and 265, respectively; or a sequence as set forth in SEQ ID NOs: 499, 261, and 262, respectively.

18. The binding protein of any one of claims 1-16, wherein V_{H1} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 502, 503, 504, 505, 506, 507, and 508.

19. The binding protein of any one of claims 1-18, wherein V_{H1} comprises a heavy chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 502, 503, 504, 505, 506, 507, and 508.

20. The binding protein of any one of claims 1-19, wherein V_{H2} comprises a CDR-H1, CDR-H2, and CDR-H3 comprising a sequence as set forth in SEQ ID NOs: 248, 497, and 250, respectively; a sequence as set forth in SEQ ID NOs: 251, 252, and 253, respectively; a sequence as set forth in SEQ ID NOs: 254, 255, and 256, respectively; a sequence as set forth in SEQ ID NOs: 254, 255, and 498, respectively; a sequence as set forth in SEQ ID NOs: 257, 258, and 259, respectively; a sequence as set forth in SEQ ID NOs: 263, 264, and 265, respectively; or a sequence as set forth in SEQ ID NOs: 499, 261, and 262, respectively.

21. The binding protein of any one of claims 1-19, wherein V_{H2} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 502, 503, 504, 505, 506, 507, and 508.

22. The binding protein of any one of claims 1-21, wherein V_{H2} comprises a heavy chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 502, 503, 504, 505, 506, 507, and 508.

23. The binding protein of any one of claims 1-22, wherein V_{H3} comprises a CDR-H1, CDR-H2, and CDR-H3 comprising a sequence as set forth in SEQ ID NOs: 248, 497, and 250, respectively; a sequence as set forth in SEQ ID NOs: 251, 252, and 253, respectively; a sequence as set forth in SEQ ID NOs: 254, 255, and 256, respectively; a sequence as set forth in SEQ ID NOs: 254, 255, and 498, respectively; a sequence as set forth in SEQ ID NOs: 257, 258, and 259, respectively; a sequence as set forth in SEQ ID NOs: 263, 264, and 265, respectively; or a sequence as set forth in SEQ ID NOs: 499, 261, and 262, respectively.

24. The binding protein of any one of claims 1-22, wherein V_{H3} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 502, 503, 504, 505, 506, 507, and 508.

25. The binding protein of any one of claims 1-24, wherein V_{H3} comprises a heavy chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 502, 503, 504, 505, 506, 507, and 508.

26. The binding protein of any one of claims 1-25, wherein V_{L1} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 500, a CDR-L2 comprising the sequence of SEQ ID NO: 501, and a CDR-L3 comprising the sequence of SEQ ID NO: 274; V_{L2} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 275, a CDR-L2 comprising the sequence of SEQ ID NO: 276, and a CDR-L3 comprising the sequence of SEQ ID NO: 277; V_{L3} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 266, a CDR-L2 comprising the sequence of SEQ ID NO: 267, and a CDR-L3 comprising the sequence of SEQ ID NO: 268; V_{H1} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 254, a CDR-H2 comprising the sequence of SEQ ID NO: 255, and a CDR-H3 comprising the sequence of SEQ ID NO: 256; V_{H2} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 257, a CDR-H2 comprising the sequence of SEQ ID NO: 258, and a CDR-H3 comprising the

sequence of SEQ ID NO: 259; and V_{H3} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 248, a CDR-H2 comprising the sequence of SEQ ID NO: 497, and a CDR-H3 comprising the sequence of SEQ ID NO: 250.

27. The binding protein of any one of claims 1-25, wherein V_{L1} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 518; V_{L2} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 519; V_{L3} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 512; V_{H1} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 504; V_{H2} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 506; and V_{H3} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 502.

28. The binding protein of any one of claims 1-27, wherein V_{L1} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 518; V_{L2} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 519; V_{L3} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 512; V_{H1} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 504; V_{H2} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 506; and V_{H3} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 502.

29. The binding protein of any one of claims 1-25, wherein V_{L1} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 500, a CDR-L2 comprising the sequence of SEQ ID NO: 501, and a CDR-L3 comprising the sequence of SEQ ID NO: 274; V_{L2} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 275, a CDR-L2 comprising the sequence of SEQ ID NO: 276, and a CDR-L3 comprising the sequence of SEQ ID NO: 277; V_{L3} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 269, a CDR-L2 comprising the sequence of SEQ ID NO: 270, and a CDR-L3 comprising the sequence of SEQ ID NO: 271; V_{H1} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 254, a CDR-H2 comprising the sequence of SEQ ID NO: 255, and a CDR-H3 comprising the sequence of

SEQ ID NO: 256; V_{H2} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 257, a CDR-H2 comprising the sequence of SEQ ID NO: 258, and a CDR-H3 comprising the sequence of SEQ ID NO: 259; and V_{H3} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 251, a CDR-H2 comprising the sequence of SEQ ID NO: 252, and a CDR-H3 comprising the sequence of SEQ ID NO: 253.

30. The binding protein of any one of claims 1-25, wherein V_{L1} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 518; V_{L2} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 519; V_{L3} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 513; V_{H1} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 504; V_{H2} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 506; and V_{H3} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 503.

31. The binding protein of any one of claims 1-25 and 29-30, wherein V_{L1} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 518; V_{L2} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 519; V_{L3} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 513; V_{H1} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 504; V_{H2} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 506; and V_{H3} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 503.

32. The binding protein of any one of claims 1-25, wherein V_{L1} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 275, a CDR-L2 comprising the sequence of SEQ ID NO: 276, and a CDR-L3 comprising the sequence of SEQ ID NO: 277; V_{L2} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 500, a CDR-L2 comprising the sequence of SEQ ID NO: 501, and a CDR-L3 comprising the sequence of SEQ ID NO: 274; V_{L3} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 269, a CDR-L2 comprising the sequence of SEQ ID NO: 270, and a CDR-L3 comprising the sequence of SEQ ID NO:

271; V_{H1} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 257, a CDR-H2 comprising the sequence of SEQ ID NO: 258, and a CDR-H3 comprising the sequence of SEQ ID NO: 259; V_{H2} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 254, a CDR-H2 comprising the sequence of SEQ ID NO: 255, and a CDR-H3 comprising the sequence of SEQ ID NO: 256; and V_{H3} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 251, a CDR-H2 comprising the sequence of SEQ ID NO: 252, and a CDR-H3 comprising the sequence of SEQ ID NO: 253.

33. The binding protein of any one of claims 1-25, wherein V_{L1} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 519; V_{L2} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 518; V_{L3} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 513; V_{H1} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 506; V_{H2} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 504; and V_{H3} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 503.

34. The binding protein of any one of claims 1-25 and 32-33, wherein V_{L1} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 519; V_{L2} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 518; V_{L3} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 513; V_{H1} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 506; V_{H2} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 504; and V_{H3} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 503.

35. The binding protein of claim 1, wherein the second polypeptide chain further comprises 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.

36. The binding protein of claim 1, wherein the third polypeptide chain further comprises 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.

37. The binding protein of claim 1, wherein 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 first Fc region comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 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 C_{H1}, the second Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} 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 according to EU Index, wherein the amino acid substitutions are Y349C, T366S, L368A, and Y407V.

38. The binding protein of claim 1, wherein 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 first Fc region comprises amino acid substitutions at positions corresponding to positions 349, 366, 368, and 407 of human IgG1 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 C_{H1}, the second Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} 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 according to EU Index, wherein the amino acid substitutions are S354C and T366W.

39. The binding protein of claim 1, wherein 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, and 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 comprise amino acid

substitutions at positions corresponding to positions 428 and 434 of human IgG1 according to EU Index, wherein the amino acid substitutions are M428L and N434S.

40. The binding protein of claim 2, wherein the C_{H3} domain of the second polypeptide chain comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 according to EU Index, wherein the amino acid substitutions are S354C and T366W; and wherein the 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 according to EU Index, wherein the amino acid substitutions are Y349C, T366S, L368A, and Y407V.

41. The binding protein of claim 2, wherein the 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 according to EU Index, wherein the amino acid substitutions are Y349C, T366S, L368A, and Y407V; and wherein the C_{H3} domain of the third polypeptide chain comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 according to EU Index, wherein the amino acid substitutions are S354C and T366W.

42. The binding protein of claim 2, wherein the C_{H3} domains of the second and the third polypeptide chains both comprise amino acid substitutions at positions corresponding to positions 428 and 434 of human IgG1 according to EU Index, wherein the amino acid substitutions are M428L and N434S.

43. The binding protein of claim 1 or claim 2, wherein at least one of L_1, L_2, L_3, or L_4 is independently 0 amino acids in length.

44. The binding protein of claim 1 or claim 2, wherein L_1, L_2, L_3, or L_4 are each independently at least one amino acid in length.

45. The binding protein of any one of claims 1-44, wherein L_1 comprises Asp-Lys-Thr-His-Thr (SEQ ID NO: 525).

46. A binding protein comprising four polypeptide chains that form three antigen binding sites, 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:

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

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

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

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 the immunoglobulin C_{H1} heavy chain constant domain; 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:

(a) V_{L1}, V_{L2} and V_{L3} are each independently a variable domain derived from an amino acid sequence as set forth in any one of SEQ ID NOs: 2, 4, 10, 12, 18, 20, 26, 28, 34, 36, 42, 44, 50, 52, 58, 60, 66, 68, 74, 76, 82, 84, 90, 92, 98, 100, 106, 108, 114, 116, 122, 124, 130, 132, 138, 140, 146, 148, 154, 156, 162, 164, 170, 172, 178, 180, 186, 188, 194, 196, 202, 204, 210,212, 218, 220, 226, 228, 233, 235, 241, 243; or

(b) V_{L1}, V_{L2} and V_{L3} each independently comprise light chain complementarity determining regions of a variable domain comprising an amino acid sequence as set forth in any one of SEQ ID NOs:266-283; and

wherein:

(a) V_{H1}, V_{H2}, and V_{H3} are each independently a variable domain derived from an amino acid sequence as set forth in any one of SEQ ID NOs: 1, 3, 9, 11, 17, 10, 25, 27, 33, 35, 41, 43, 49, 51, 57, 59, 65, 67, 73, 75, 81, 83, 89, 91, 97, 99, 105, 107, 113, 115, 121, 123,

129, 131, 137, 139, 145, 147, 153, 155, 161, 163, 169, 171, 177, 179, 185, 187, 193, 195, 201, 203, 209, 211, 217, 219, 225, 227, 232, 234, 240, 242; or

(b) V_{H1}, V_{H2}, and V_{H3} each independently comprise heavy chain complementarity determining regions of a variable domain comprising an amino acid sequence as set forth in any one of SEQ ID NOs: 248-265.

47. A binding protein comprising four polypeptide chains that form three antigen binding sites, 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 the 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:

(a) V_{L1}, V_{L2} and V_{L3} are each independently a variable domain derived from an amino acid sequence as set forth in any one of SEQ ID NOs: 2, 4, 10, 12, 18, 20, 26, 28, 34, 36,

42, 44, 50, 52, 58, 60, 66, 68, 74, 76, 82, 84, 90, 92, 98, 100, 106, 108, 114, 116, 122, 124, 130, 132, 138, 140, 146, 148, 154, 156, 162, 164, 170, 172, 178, 180, 186, 188, 194, 196, 202, 204, 210,212, 218, 220, 226, 228, 233, 235, 241, 243; or

(b) V_{L1}, V_{L2} and V_{L3} each independently comprise light chain complementarity determining regions of a variable domain comprising an amino acid sequence as set forth in any one of SEQ ID NOs:266-283; and

wherein:

(a) V_{H1}, V_{H2}, and V_{H3} are each independently a variable domain derived from an amino acid sequence as set forth in any one of SEQ ID NOs: 1, 3, 9, 11, 17, 10, 25, 27, 33, 35, 41, 43, 49, 51, 57, 59, 65, 67, 73, 75, 81, 83, 89, 91, 97, 99, 105, 107, 113, 115, 121, 123, 129, 131, 137, 139, 145, 147, 153, 155, 161, 163, 169, 171, 177, 179, 185, 187, 193, 195, 201, 203, 209, 211, 217, 219, 225, 227, 232, 234, 240, 242; or

(b) V_{H1}, V_{H2}, and V_{H3} each independently comprise heavy chain complementarity determining regions of a variable domain comprising an amino acid sequence as set forth in any one of SEQ ID NOs: 248-265.

48. The binding protein of claim 46, wherein the second polypeptide chain further comprises 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.

49. The binding protein of claim 46, wherein the third polypeptide chain further comprises 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.

50. The binding protein of claim 46, wherein 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 first Fc region comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 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 C_{H1}, the second Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} 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 according to EU Index, wherein the amino acid substitutions are Y349C, T366S, L368A, and Y407V.

51. The binding protein of claim 46, wherein 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 first Fc region comprises amino acid substitutions at positions corresponding to positions 349, 366, 368, and 407 of human IgG1 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 C_{H1}, the second Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} 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 according to EU Index, wherein the amino acid substitutions are S354C and T366W.

52. The binding protein of claim 46, wherein 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, and 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 comprise amino acid substitutions at positions corresponding to positions 428 and 434 of human IgG1 according to EU Index, wherein the amino acid substitutions are M428L and N434S.

53. The binding protein of claim 47, wherein the C_{H3} domain of the second polypeptide chain comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 according to EU Index, wherein the amino acid substitutions are S354C and T366W; and wherein the 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 according to EU Index, wherein the amino acid substitutions are Y349C, T366S, L368A, and Y407V.

54. The binding protein of claim 47, wherein the 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 according to EU Index, wherein the amino acid substitutions are

Y349C, T366S, L368A, and Y407V; and wherein the C_{H3} domain of the third polypeptide chain comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 according to EU Index, wherein the amino acid substitutions are S354C and T366W.

55. The binding protein of claim 47, wherein the C_{H3} domains of the second and the third polypeptide chains both comprise amino acid substitutions at positions corresponding to positions 428 and 434 of human IgG1 according to EU Index, wherein the amino acid substitutions are M428L and N434S.

56. The binding protein of claim 46 or claim 47, wherein at least one of L_1, L_2, L_3, or L_4 is independently 0 amino acids in length.

57. The binding protein of claim 46 or claim 47, wherein L_1, L_2, L_3, or L_4 are each independently at least one amino acid in length.

58. The binding protein of any one of claims 46-57, wherein L_1 comprises Asp-Lys-Thr-His-Thr (SEQ ID NO: 525).

59. A binding protein comprising a first polypeptide chain, a second polypeptide chain, a third polypeptide chain and a fourth polypeptide chain wherein:

(a) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 4 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 4; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 3 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 3; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 1 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 1; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 2 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 2;

(b) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 12 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 12; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 11 or an amino acid sequence that is at least 95% identical to the amino acid sequence of

SEQ ID NO: 11; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 9 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 9; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 10 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 10;

(c) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 20 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 20; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 19 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 19; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 17 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 17; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 18 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 18;

(d) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 28 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 28; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 27 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 27; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 25 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 25; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 26 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 26;

(e) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 36 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 36; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 35 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 35; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 33 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 33; and the fourth polypeptide chain comprises the amino acid sequence of SEQ

ID NO: 34 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 34;

(f) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 44 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 44; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 43 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 43; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 41 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 41; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 42 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 42;

(g) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 52 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 52; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 51 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 51; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 49 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 49; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 50 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 50;

(h) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 60 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 60; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 59 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 59; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 57 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 57; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 58 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 58;

(i) the first 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; the second 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; the third 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; and the fourth 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;

(j) the first 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; the second 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; the third 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; and the fourth 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;

(k) the first 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; the second 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; the third 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; and the fourth 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;

(l) the first 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; the second 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; the third 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; and the fourth 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;

(m) the first 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; the second 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; the third 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; and the fourth 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;

(n) the first polypeptide 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; the second 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; the third 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; and the fourth 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;

(o) the first 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; the second 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; the third 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; and the fourth 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;

(p) the first 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; the second 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; the third 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; and the fourth 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;

(q) the first 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; the second 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; the third 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; and the fourth 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;

(r) the first 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; the second 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; the third 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; and the fourth 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;

(s) the first 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; the second 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; the third 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; and the fourth 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;

(t) the first 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; the second 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; the third 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; and the fourth 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;

(u) the first 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; the second 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; the third 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; and the fourth 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;

(v) the first 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; the second 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; the third 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; and the fourth 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;

(w) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 180 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 180; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 179 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 179; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 177 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 177; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 178 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 178;

(x) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 188 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 188; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 187 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 187; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 185 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 185; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 186 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 186;

(y) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 196 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 196; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 195 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 195; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 193 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 193; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 194 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 194;

(z) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 204 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ

ID NO: 204; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 203 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 203; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 201 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 201; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 202 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 202;

(aa) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 212 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 212; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 211 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 211; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 209 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 209; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 210 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 210;

(bb) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 220 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 220; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 219 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 219; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 217 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 217; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 218 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 218;

(cc) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 228 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 228; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 227 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 227; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 225 or an amino acid sequence that is at least 95% identical to the amino acid

sequence of SEQ ID NO: 225; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 226 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 226;

(dd) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 235 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 235; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 234 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 234; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 232 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 232; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 233 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 233; or

(ee) first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 243 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 243; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 242 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 242; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 240 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 240; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 241 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 241.

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

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

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

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

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

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

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 the immunoglobulin C_{H1} heavy chain constant domain; 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.

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

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

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

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

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 the 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.

62. The binding protein of claim 60 or claim 61, wherein the one or more HIV target proteins are selected from the group consisting of glycoprotein 120, glycoprotein 41 and glycoprotein 160.

63. The binding protein of claim 60 or claim 61, wherein the one or more T cell target proteins are CD3 or CD28.

64. The binding protein of claim 60 or claim 61, wherein the binding protein is trispecific and capable of specifically binding an HIV target protein and two different epitopes on a single T cell target protein.

65. The binding protein of claim 60 or claim 61, wherein the binding protein is trispecific and capable of specifically binding an HIV target protein and two different T cell target proteins.

66. The binding protein of claim 60 or claim 61, wherein the binding protein is trispecific and capable of specifically binding a T cell target protein and two different epitopes on a single HIV target protein.

67. The binding protein of claim 60 or claim 61, wherein the binding protein is trispecific and capable of specifically binding a T cell target protein and two different HIV target proteins.

68. The binding protein of claim 60 or claim 61, wherein the first and second polypeptide chains form two antigen binding sites that specifically target two T cell target proteins, and the third and fourth polypeptide chains form an antigen binding site that specifically binds an HIV target protein.

69. The binding protein of any one of claims 60-68, wherein V_{L1} comprises a CDR-L1, CDR-L2, and CDR-L3 comprising a sequence as set forth in SEQ ID NOs: 266, 267, and 268, respectively; a sequence as set forth in SEQ ID NOs: 269, 270, and 271, respectively; a

sequence as set forth in SEQ ID NOs: 500, 501, and 274, respectively; a sequence as set forth in SEQ ID NOs: 275, 276, and 277, respectively; a sequence as set forth in SEQ ID NOs: 281, 282, and 283, respectively; a sequence as set forth in SEQ ID NOs: 278, 279, and 280, respectively; a sequence as set forth in SEQ ID NOs: 488, 489, and 490, respectively; a sequence as set forth in SEQ ID NOs: 491, 492, and 493, respectively; or a sequence as set forth in SEQ ID NOs: 494, 495, and 496, respectively.

70. The binding protein of any one of claims 60-68, wherein V_{L1} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, and 524.

71. The binding protein of any one of claims 60-70, wherein V_{L1} comprises a light chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, and 524.

72. The binding protein of any one of claims 60-71, wherein V_{L2} comprises a CDR-L1, CDR-L2, and CDR-L3 comprising a sequence as set forth in SEQ ID NOs: 266, 267, and 268, respectively; a sequence as set forth in SEQ ID NOs: 269, 270, and 271, respectively; a sequence as set forth in SEQ ID NOs: 500, 501, and 274, respectively; a sequence as set forth in SEQ ID NOs: 275, 276, and 277, respectively; a sequence as set forth in SEQ ID NOs: 281, 282, and 283, respectively; a sequence as set forth in SEQ ID NOs: 278, 279, and 280, respectively; a sequence as set forth in SEQ ID NOs: 488, 489, and 490, respectively; a sequence as set forth in SEQ ID NOs: 491, 492, and 493, respectively; or a sequence as set forth in SEQ ID NOs: 494, 495, and 496, respectively.

73. The binding protein of any one of claims 60-71, wherein V_{L2} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, and 524.

74. The binding protein of any one of claims 60-73, wherein V_{L2} comprises a light chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, and 524.

75. The binding protein of any one of claims 60-74, wherein V_{L3} comprises a CDR-L1, CDR-L2, and CDR-L3 comprising a sequence as set forth in SEQ ID NOs: 266, 267, and 268, respectively; a sequence as set forth in SEQ ID NOs: 269, 270, and 271, respectively; a sequence as set forth in SEQ ID NOs: 500, 501, and 274, respectively; a sequence as set forth in SEQ ID NOs: 275, 276, and 277, respectively; a sequence as set forth in SEQ ID NOs: 281, 282, and 283, respectively; a sequence as set forth in SEQ ID NOs: 278, 279, and 280, respectively; a sequence as set forth in SEQ ID NOs: 488, 489, and 490, respectively; a sequence as set forth in SEQ ID NOs: 491, 492, and 493, respectively; or a sequence as set forth in SEQ ID NOs: 494, 495, and 496, respectively.

76. The binding protein of any one of claims 60-74, wherein V_{L3} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, and 524.

77. The binding protein of any one of claims 60-76, wherein V_{L3} comprises a light chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, and 524.

78. The binding protein of any one of claims 60-77, wherein V_{H1} comprises a CDR-H1, CDR-H2, and CDR-H3 comprising a sequence as set forth in SEQ ID NOs: 248, 497, and 250, respectively; a sequence as set forth in SEQ ID NOs: 251, 252, and 253, respectively; a sequence as set forth in SEQ ID NOs: 254, 255, and 256, respectively; a sequence as set forth in SEQ ID NOs: 254, 255, and 498, respectively; a sequence as set forth in SEQ ID NOs: 257, 258, and 259, respectively; a sequence as set forth in SEQ ID NOs: 263, 264, and 265, respectively; a sequence as set forth in SEQ ID NOs: 499, 261, and 262, respectively; a sequence as set forth in SEQ ID NOs: 479, 480, and 481, respectively; a sequence as set forth in SEQ ID NOs: 482, 483, and 484, respectively; or a sequence as set forth in SEQ ID NOs: 485, 486, and 487, respectively.

79. The binding protein of any one of claims 60-77, wherein V_{H1} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 502, 503, 504, 505, 506, 507, 508, 509, 510, and 511.

80. The binding protein of any one of claims 60-79, wherein V_{H1} comprises a heavy chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 502, 503, 504, 505, 506, 507, 508, 509, 510, and 511.

81. The binding protein of any one of claims 60-80, wherein V_{H2} comprises a CDR-H1, CDR-H2, and CDR-H3 comprising a sequence as set forth in SEQ ID NOs: 248, 497, and 250, respectively; a sequence as set forth in SEQ ID NOs: 251, 252, and 253, respectively; a sequence as set forth in SEQ ID NOs: 254, 255, and 256, respectively; a sequence as set forth in SEQ ID NOs: 254, 255, and 498, respectively; a sequence as set forth in SEQ ID NOs: 257, 258, and 259, respectively; a sequence as set forth in SEQ ID NOs: 263, 264, and 265, respectively; a sequence as set forth in SEQ ID NOs: 499, 261, and 262, respectively; a sequence as set forth in SEQ ID NOs: 479, 480, and 481, respectively; a sequence as set forth in SEQ ID NOs: 482, 483, and 484, respectively; or a sequence as set forth in SEQ ID NOs: 485, 486, and 487, respectively.

82. The binding protein of any one of claims 60-80, wherein V_{H2} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 502, 503, 504, 505, 506, 507, 508, 509, 510, and 511.

83. The binding protein of any one of claims 60-82, wherein V_{H2} comprises a heavy chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 502, 503, 504, 505, 506, 507, 508, 509, 510, and 511.

84. The binding protein of any one of claims 60-83, wherein V_{H3} comprises a CDR-H1, CDR-H2, and CDR-H3 comprising a sequence as set forth in SEQ ID NOs: 248, 497, and 250, respectively; a sequence as set forth in SEQ ID NOs: 251, 252, and 253, respectively; a sequence as set forth in SEQ ID NOs: 254, 255, and 256, respectively; a sequence as set forth in SEQ ID NOs: 254, 255, and 498, respectively; a sequence as set forth in SEQ ID NOs: 257, 258, and 259, respectively; a sequence as set forth in SEQ ID NOs: 263, 264, and 265, respectively; a sequence as set forth in SEQ ID NOs: 499, 261, and 262, respectively; a sequence as set forth in SEQ ID NOs: 479, 480, and 481, respectively; a sequence as set forth in SEQ ID NOs: 482, 483, and 484, respectively; or a sequence as set forth in SEQ ID NOs: 485, 486, and 487, respectively.

85. The binding protein of any one of claims 60-83, wherein V_{H3} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 502, 503, 504, 505, 506, 507, 508, 509, 510, and 511.

86. The binding protein of any one of claims 60-85, wherein V_{H3} comprises a heavy chain variable domain comprising a sequence selected from the group consisting of SEQ ID NOs: 502, 503, 504, 505, 506, 507, 508, 509, 510, and 511.

87. The binding protein of any one of claims 60-86, wherein V_{L1} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 488, a CDR-L2 comprising the sequence of SEQ ID NO: 489, and a CDR-L3 comprising the sequence of SEQ ID NO: 490; V_{L2} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 494, a CDR-L2 comprising the sequence of SEQ ID NO: 495, and a CDR-L3 comprising the sequence of SEQ ID NO: 496; V_{L3} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 269, a CDR-L2 comprising the sequence of SEQ ID NO: 270, and a CDR-L3 comprising the sequence of SEQ ID NO: 271; V_{H1} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 479, a CDR-H2 comprising the sequence of SEQ ID NO: 480, and a CDR-H3 comprising the sequence of SEQ ID NO: 481; V_{H2} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 485, a CDR-H2 comprising the sequence of SEQ ID NO: 486, and a CDR-H3 comprising the sequence of SEQ ID NO: 487; and V_{H3} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 251, a CDR-H2 comprising the sequence of SEQ ID NO: 252, and a CDR-H3 comprising the sequence of SEQ ID NO: 253.

88. The binding protein of any one of claims 60-86, wherein V_{L1} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 522; V_{L2} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 524; V_{L3} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 513; V_{H1} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 509; V_{H2} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 511; and V_{H3} comprises a CDR-H1, CDR-H2, and CDR-H3 of a

heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 503.

89. The binding protein of any one of claims 60-88, wherein V_{L1} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 522; V_{L2} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 524; V_{L3} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 513; V_{H1} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 509; V_{H2} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 511; and V_{H3} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 503.

90. The binding protein of any one of claims 60-86, wherein V_{L1} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 494, a CDR-L2 comprising the sequence of SEQ ID NO: 495, and a CDR-L3 comprising the sequence of SEQ ID NO: 496; V_{L2} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 488, a CDR-L2 comprising the sequence of SEQ ID NO: 489, and a CDR-L3 comprising the sequence of SEQ ID NO: 490; V_{L3} comprises a CDR-L1 comprising the sequence of SEQ ID NO: 269, a CDR-L2 comprising the sequence of SEQ ID NO: 270, and a CDR-L3 comprising the sequence of SEQ ID NO: 271; V_{H1} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 485, a CDR-H2 comprising the sequence of SEQ ID NO: 486, and a CDR-H3 comprising the sequence of SEQ ID NO: 487; V_{H2} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 479, a CDR-H2 comprising the sequence of SEQ ID NO: 480, and a CDR-H3 comprising the sequence of SEQ ID NO: 481; and V_{H3} comprises a CDR-H1 comprising the sequence of SEQ ID NO: 251, a CDR-H2 comprising the sequence of SEQ ID NO: 252, and a CDR-H3 comprising the sequence of SEQ ID NO: 253.

91. The binding protein of any one of claims 60-86, wherein V_{L1} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 524; V_{L2} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 522; V_{L3} comprises a CDR-L1, CDR-L2, and CDR-L3 of a light chain variable domain comprising the light chain variable domain sequence of SEQ ID NO: 513; V_{H1} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 511; V_{H2} comprises a CDR-H1, CDR-H2,

and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 509; and V_{H3} comprises a CDR-H1, CDR-H2, and CDR-H3 of a heavy chain variable domain comprising the heavy chain variable domain sequence of SEQ ID NO: 503.

92. The binding protein of any one of claims 60-86 and 90-91, wherein V_{L1} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 524; V_{L2} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 522; V_{L3} comprises a light chain variable domain comprising the sequence of SEQ ID NO: 513; V_{H1} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 511; V_{H2} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 509; and V_{H3} comprises a heavy chain variable domain comprising the sequence of SEQ ID NO: 503.

93. The binding protein of claim 60, wherein the second polypeptide chain further comprises 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.

94. The binding protein of claim 60, wherein the third polypeptide chain further comprises 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.

95. The binding protein of claim 60, wherein 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 first Fc region comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 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 C_{H1}, the second Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} 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 according to EU Index, wherein the amino acid substitutions are Y349C, T366S, L368A, and Y407V.

96. The binding protein of claim 60, wherein 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 first Fc region comprises amino acid substitutions at positions corresponding to positions 349, 366, 368, and 407 of human IgG1 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 C_{H1}, the second Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} 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 according to EU Index, wherein the amino acid substitutions are S354C and T366W.

97. The binding protein of claim 60, wherein 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, and 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 comprise amino acid substitutions at positions corresponding to positions 428 and 434 of human IgG1 according to EU Index, wherein the amino acid substitutions are M428L and N434S.

98. The binding protein of claim 61, wherein the C_{H3} domain of the second polypeptide chain comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 according to EU Index, wherein the amino acid substitutions are S354C and T366W; and wherein the 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 according to EU Index, wherein the amino acid substitutions are Y349C, T366S, L368A, and Y407V.

99. The binding protein of claim 61, wherein the 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 according to EU Index, wherein the amino acid substitutions are Y349C, T366S, L368A, and Y407V; and wherein the C_{H3} domain of the third polypeptide chain comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 according to EU Index, wherein the amino acid substitutions are S354C and T366W.

100. The binding protein of claim 61, wherein the C_{H3} domains of the second and the third polypeptide chains both comprise amino acid substitutions at positions corresponding to positions 428 and 434 of human IgG1 according to EU Index, wherein the amino acid substitutions are M428L and N434S.

101. The binding protein of claim 60 or claim 61, wherein at least one of L_1, L_2, L_3, or L_4 is independently 0 amino acids in length.

102. The binding protein of claim 60 or claim 61, wherein L_1, L_2, L_3, or L_4 are each independently at least one amino acid in length.

103. The binding protein of any one of claims 60-102, wherein L_1 is Gly-Gln-Pro-Lys-Ala-Ala-Pro (SEQ ID NO: 299).

104. A binding protein comprising four polypeptide chains that form three antigen binding sites, 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:

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

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

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

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 the immunoglobulin C_{H1} heavy chain constant domain; 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:

(a) V_{L1}, V_{L2} and V_{L3} are each independently a variable domain derived from an amino acid sequence as set forth in any one of SEQ ID NOs: 303, 305, 311, 313, 319, 321, 327, 329, 335, 337, 343, 345, 351, 353, 359, 361, 367, 369, 375, 377, 383, 385, 391, 393, 399, 401, 407, 409, 415, 417, 423, 425, 431, 433, 439, 441, 447, 449, 455, 457, 463, 465, 471, 473; or

(b) V_{L1}, V_{L2} and V_{L3} each independently comprise light chain complementarity determining regions of a variable domain comprising an amino acid sequence as set forth in any one of SEQ ID NOs: 266-271, 275-277, 488-496; and

wherein:

(a) V_{H1}, V_{H2}, and V_{H3} are each independently a variable domain derived from an amino acid sequence as set forth in any one of SEQ ID NOs: 302, 304, 310, 312, 318, 320, 326, 328, 334, 336, 342, 344, 350, 352, 358, 360, 366, 368, 374, 376, 382, 384, 390, 392, 398, 400, 406, 408, 414, 416, 422, 424, 430, 432, 438, 440, 446, 448, 454, 456, 462, 464, 470, 472; or

(b) V_{H1}, V_{H2}, and V_{H3} each independently comprise heavy chain complementarity determining regions of a variable domain comprising an amino acid sequence as set forth in any one of SEQ ID NOs: 248-253, 257-259, 479-487.

105. A binding protein comprising four polypeptide chains that form three antigen binding sites, 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 the 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:

(a) V_{L1}, V_{L2} and V_{L3} are each independently a variable domain derived from an amino acid sequence as set forth in any one of SEQ ID NOs: 303, 305, 311, 313, 319, 321, 327, 329, 335, 337, 343, 345, 351, 353, 359, 361, 367, 369, 375, 377, 383, 385, 391, 393, 399, 401, 407, 409, 415, 417, 423, 425, 431, 433, 439, 441, 447, 449, 455, 457, 463, 465, 471, 473; or

(b) V_{L1}, V_{L2} and V_{L3} each independently comprise light chain complementarity determining regions of a variable domain comprising an amino acid sequence as set forth in any one of SEQ ID NOs: 266-271, 275-277, 488-496; and
wherein:

(a) V_{H1}, V_{H2}, and V_{H3} are each independently a variable domain derived from an amino acid sequence as set forth in any one of SEQ ID NOs: 302, 304, 310, 312, 318, 320, 326, 328, 334, 336, 342, 344, 350, 352, 358, 360, 366, 368, 374, 376, 382, 384, 390, 392, 398, 400, 406, 408, 414, 416, 422, 424, 430, 432, 438, 440, 446, 448, 454, 456, 462, 464, 470, 472; or

(b) V_{H1}, V_{H2}, and V_{H3} each independently comprise heavy chain complementarity determining regions of a variable domain comprising an amino acid sequence as set forth in any one of SEQ ID NOs: 248-253, 257-259, 479-487.

106. The binding protein of claim 104, wherein the second polypeptide chain further comprises 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.

107. The binding protein of claim 104, wherein the third polypeptide chain further comprises 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.

108. The binding protein of claim 104, wherein 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 first Fc region comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 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 C_{H1}, the second Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} 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 according to EU Index, wherein the amino acid substitutions are Y349C, T366S, L368A, and Y407V.

109. The binding protein of claim 104, wherein 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 first Fc region comprises amino acid substitutions at positions corresponding to positions 349, 366, 368, and 407 of human IgG1 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 C_{H1}, the second Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} 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 according to EU Index, wherein the amino acid substitutions are S354C and T366W.

110. The binding protein of claim 104, wherein 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, and 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 comprise amino acid

substitutions at positions corresponding to positions 428 and 434 of human IgG1 according to EU Index, wherein the amino acid substitutions are M428L and N434S.

111. The binding protein of claim 105, wherein the C_{H3} domain of the second polypeptide chain comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 according to EU Index, wherein the amino acid substitutions are S354C and T366W; and wherein the 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 according to EU Index, wherein the amino acid substitutions are Y349C, T366S, L368A, and Y407V.

112. The binding protein of claim 105, wherein the 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 according to EU Index, wherein the amino acid substitutions are Y349C, T366S, L368A, and Y407V; and wherein the C_{H3} domain of the third polypeptide chain comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 according to EU Index, wherein the amino acid substitutions are S354C and T366W.

113. The binding protein of claim 105, wherein the C_{H3} domains of the second and the third polypeptide chains both comprise amino acid substitutions at positions corresponding to positions 428 and 434 of human IgG1 according to EU Index, wherein the amino acid substitutions are M428L and N434S.

114. The binding protein of claim 104 or claim 105, wherein at least one of L_1, L_2, L_3, or L_4 is independently 0 amino acids in length.

115. The binding protein of claim 104 or claim 105, wherein L_1, L_2, L_3, or L_4 are each independently at least one amino acid in length.

116. The binding protein of any one of claims 104-115, wherein L_1 is Gly-Gln-Pro-Lys-Ala-Ala-Pro (SEQ ID NO: 299).

117. A binding protein comprising a first polypeptide chain, a second polypeptide chain, a third polypeptide chain and a fourth polypeptide chain wherein:

(a) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 305 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 305; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 304 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 304; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 302 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 302; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 303 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 303;

(b) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 313 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 313; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 312 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 312; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 310 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 310; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 311 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 311;

(c) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 321 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 321; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 320 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 320; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 318 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 318; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 319 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 319;

(d) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 329 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 329; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 328 or an amino acid sequence that is at least 95% identical to the amino acid sequence

of SEQ ID NO: 328; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 326 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 326; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 327 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 327;

(e) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 337 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 337; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 336 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 336; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 334 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 334; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 335 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 335;

(f) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 345 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 345; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 344 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 344; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 342 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 342; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 343 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 343;

(g) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 353 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 353; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 352 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:352; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 350 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 350; and the fourth polypeptide chain comprises the amino acid

sequence of SEQ ID NO: 351 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 351;

(h) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 361 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 361; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 360 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 360; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 358 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 358; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 359 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 359;

(i) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 369 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 369; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 368 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 368; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 366 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 366; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 367 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 367;

(j) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 377 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 377; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 376 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 376; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 374 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 374; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 375 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 375;

(k) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 385 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ

ID NO: 385; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 384 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 384; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 382 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 382; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 383 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 383;

(l) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 393 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 393; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 392 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 392; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 390 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 390; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 391 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 391;

(m) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 401 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 401; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 400 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 400; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 398 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 398; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 399 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 399;

(n) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 409 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 409; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 408 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 408; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 406 or an amino acid sequence that is at least 95% identical to the amino acid

sequence of SEQ ID NO: 406; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 407 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 407;

(p) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 417 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 417; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 416 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 416; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 414 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 414; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 415 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 415;

(q) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 425 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 425; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 424 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 424; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 422 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 422; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 423 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 423;

(r) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 433 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:433; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 432 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 432; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 430 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 430; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 431 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 431;

(s) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 441 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 441; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 440 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 440; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 438 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 438; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 439 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 439;

(t) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 449 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 449; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 448 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 448; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 446 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 446; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 447 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 447;

(u) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 457 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 457; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 456 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 456; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 454 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 454; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 455 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 455;

(v) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 465 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 465; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 464 or an amino acid sequence that is at least 95% identical to the amino acid sequence

of SEQ ID NO: 464; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 462 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 462; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 463 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 463; or

(w) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 473 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 473; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 472 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 472; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO: 470 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 470; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO: 471 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 471.

118. An isolated nucleic acid molecule comprising a nucleotide sequence encoding the binding protein of any one of claims 1-117.

119. An expression vector comprising the nucleic acid molecule of claim 118.

120. An isolated host cell comprising the nucleic acid molecule of claim 118.

121. An isolated host cell comprising the expression vector of claim 119.

122. The isolated host cell of claim 120 or claim 121, wherein the host cell is a mammalian cell or an insect cell.

123. 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 1-117.

124. The vector system of claim 123, 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.

125. The vector system of claim 123, wherein 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.

126. The vector system of any one of claims 123-125, wherein the one or more vectors are expression vectors.

127. An isolated host cell comprising the vector system of any one of claims 123-126.

128. The isolated host cell of claim 127, wherein the host cell is a mammalian cell or an insect cell.

129. A method of producing a binding protein, the method comprising:

a) culturing a host cell of any one of claims 120-122 and claims 127-128 under conditions such that the host cell expresses the binding protein; and

b) isolating the binding protein from the host cell.

130. 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 1-117.

131. The method of claim 130, wherein the binding protein is co-administered with standard anti-retroviral therapy.

132. The method of claim 130 or claim 131, wherein administration of the at least one binding protein results in the neutralization of one or more HIV virions.

133. The method of any one of claims 130-132, 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.

134. The method of any one of claims 130-133, wherein the patient is a human.

135. The binding protein of any one of claims 1-117 for the prevention or treatment of an HIV infection in a patient.

136. The binding protein of claim 135, wherein the binding protein is co-administered with standard anti-retroviral therapy.

137. The binding protein of claim 135 or claim 136, wherein the binding protein causes the neutralization of one or more HIV virions in the patient.

138. The binding protein of any one of claims 135-137, wherein the binding protein causes the elimination of one or more latently and/or chronically HIV-infected cells in the patient.

139. The binding protein of any one of claims 135-138, wherein the patient is a human.