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(54) BISPECIFIC ANTIBODIES AGAINST PLASMA KALLIKREIN AND FACTOR XII

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(52) U.S. Cl.

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(57)

ABSTRACT

Described herein are bispecific antibodies that bind to plasma kallikrein (pKal) and Factor XII and methods of producing and using such bi-specific antibodies for treating diseases or disorders associated with the contact system, e.g., hereditary angioedema or thrombosis.

Specification includes a Sequence Listing.

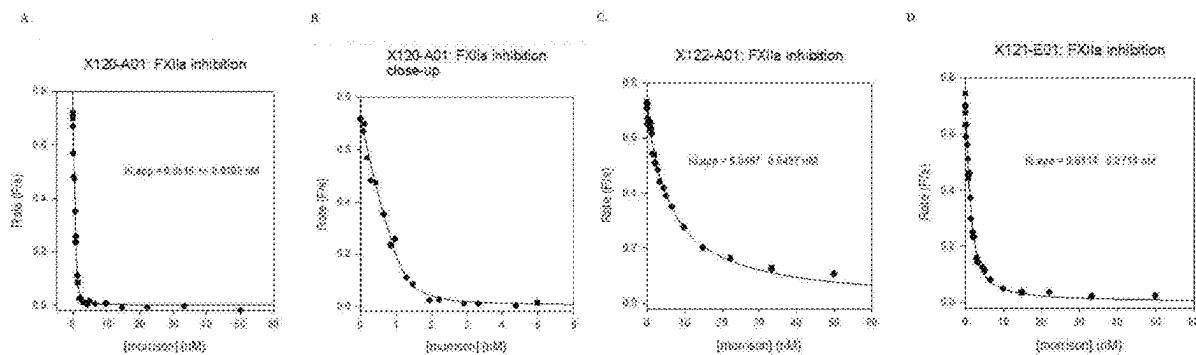
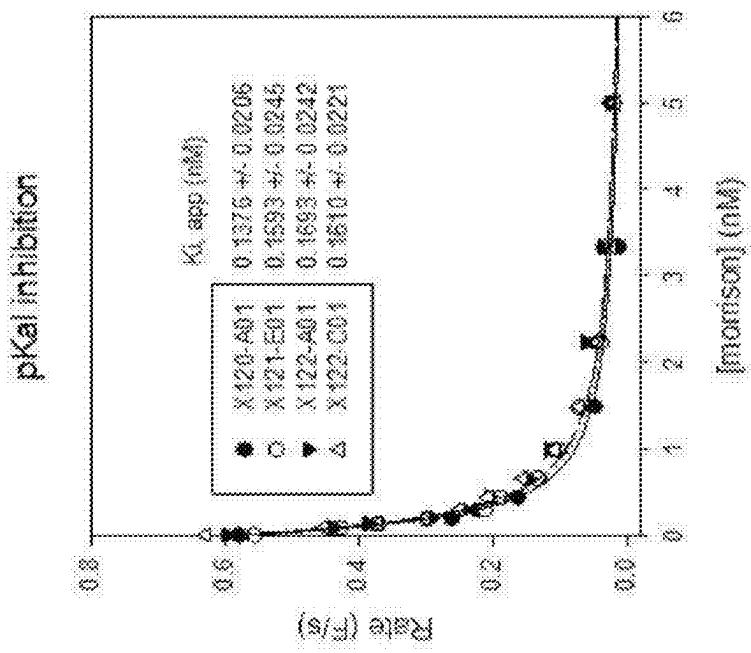


FIG. 1



X120-A01 (scFv = 559C-M184-B04-H41)
X121-E01 (scFv = 559C-M180-G03-H41)
X122-A01 (scFv = 559C-M71-F06-H41)
X122-C01 (scFv = 559C-M71-F06-L4H)

FIG. 2

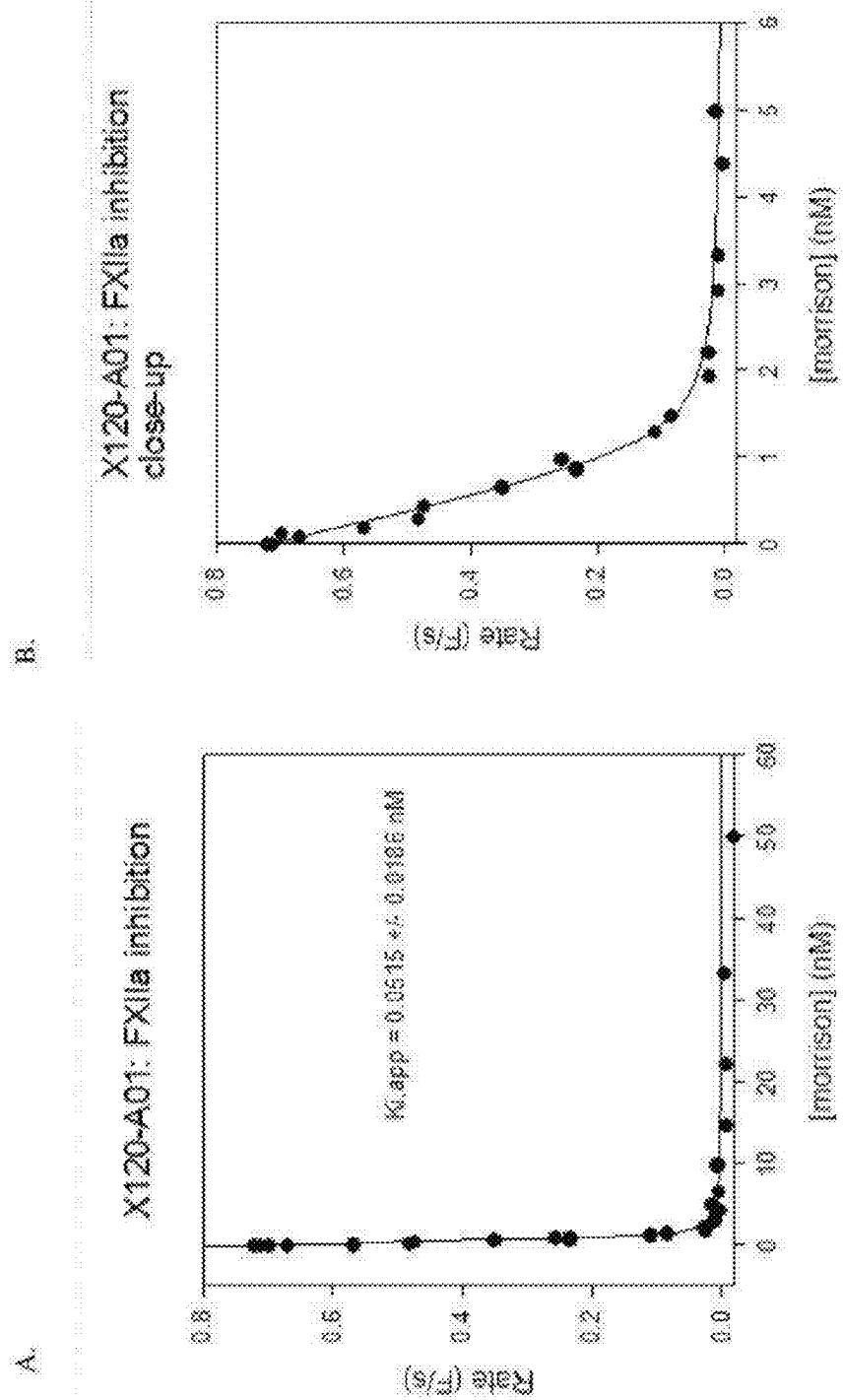
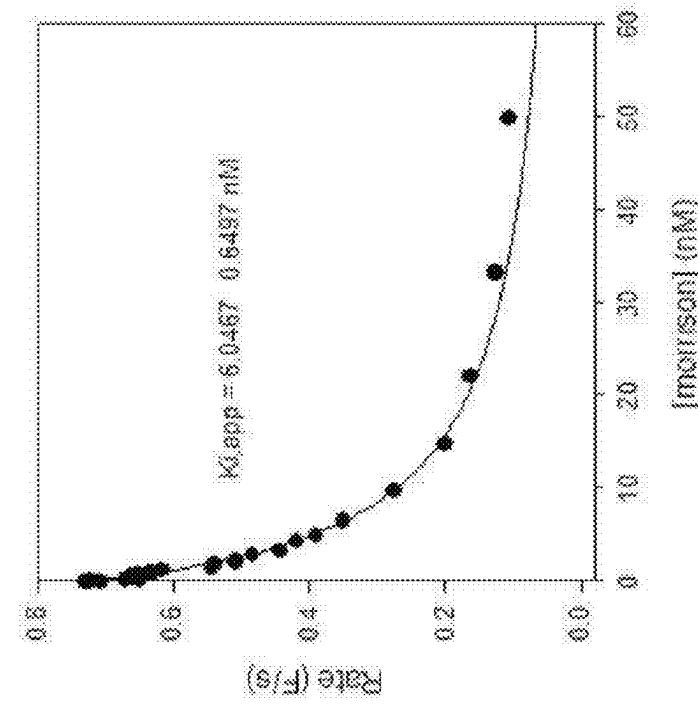


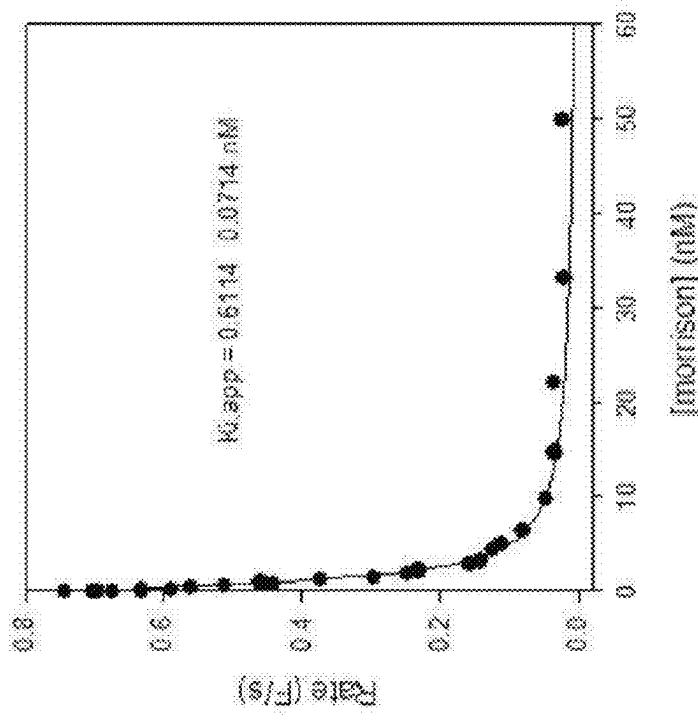
FIG. 2 (CONT'D)

X122-A01: FXIIa inhibition



C.

X121-E01: FXIIa inhibition



D.

FIG. 2 (CONT'D)

X122-CO1: FXIIa inhibition

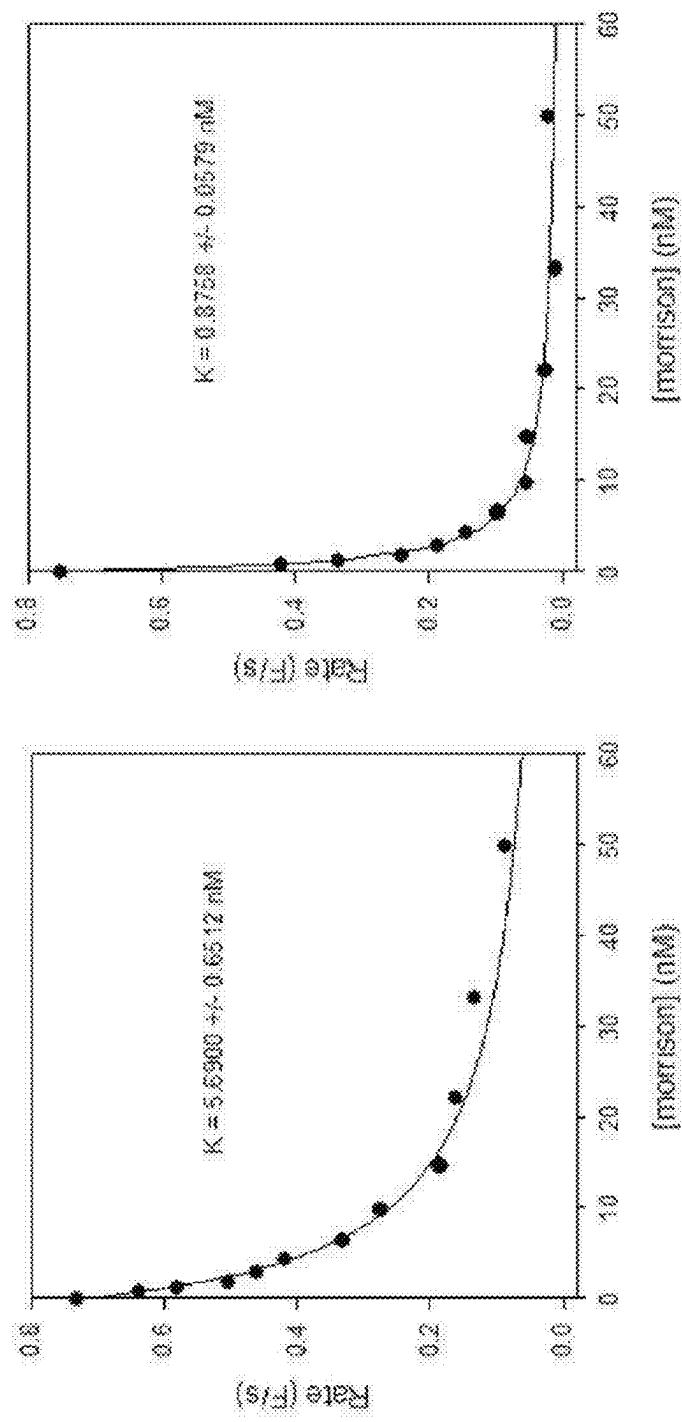


FIG. 3

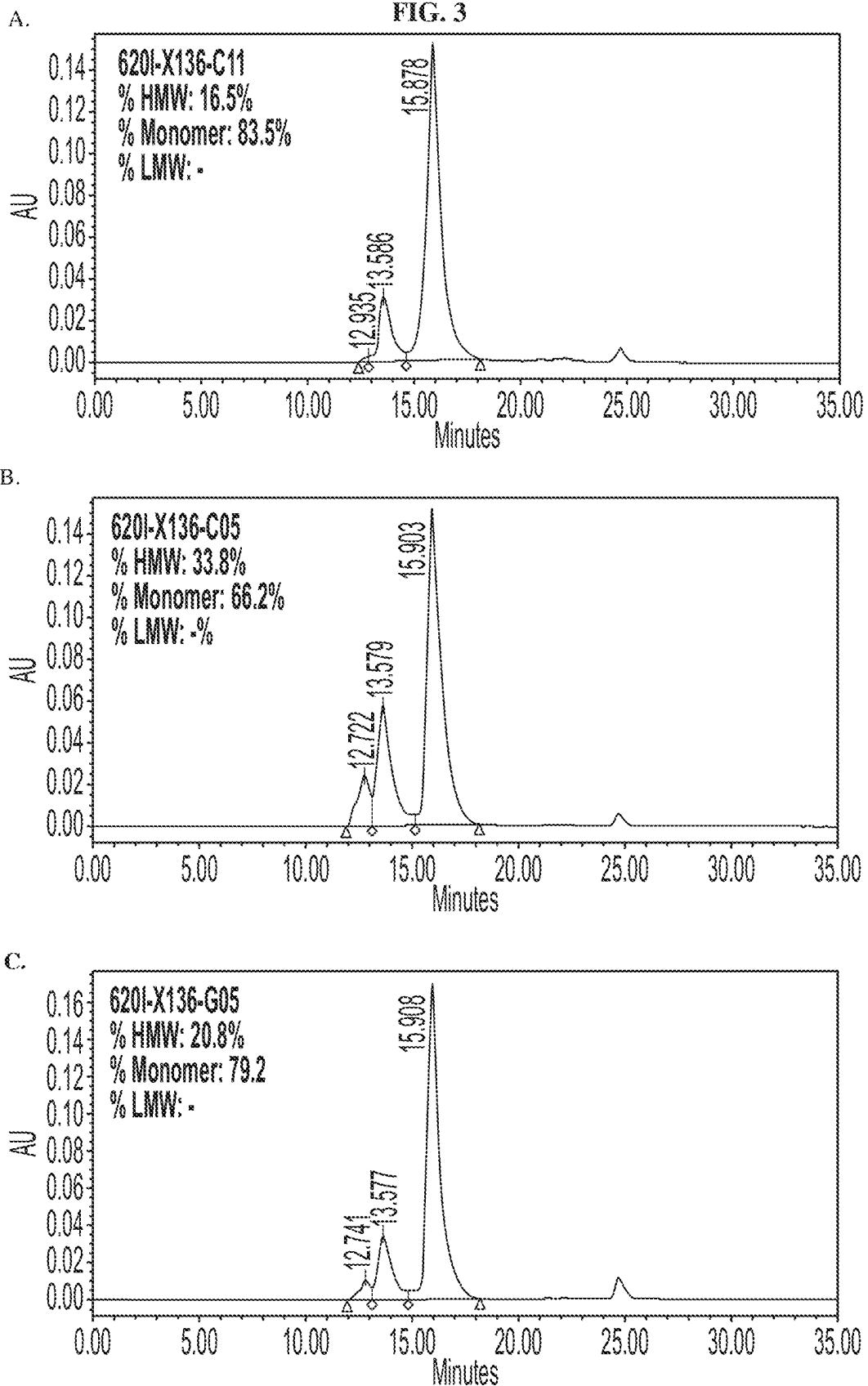
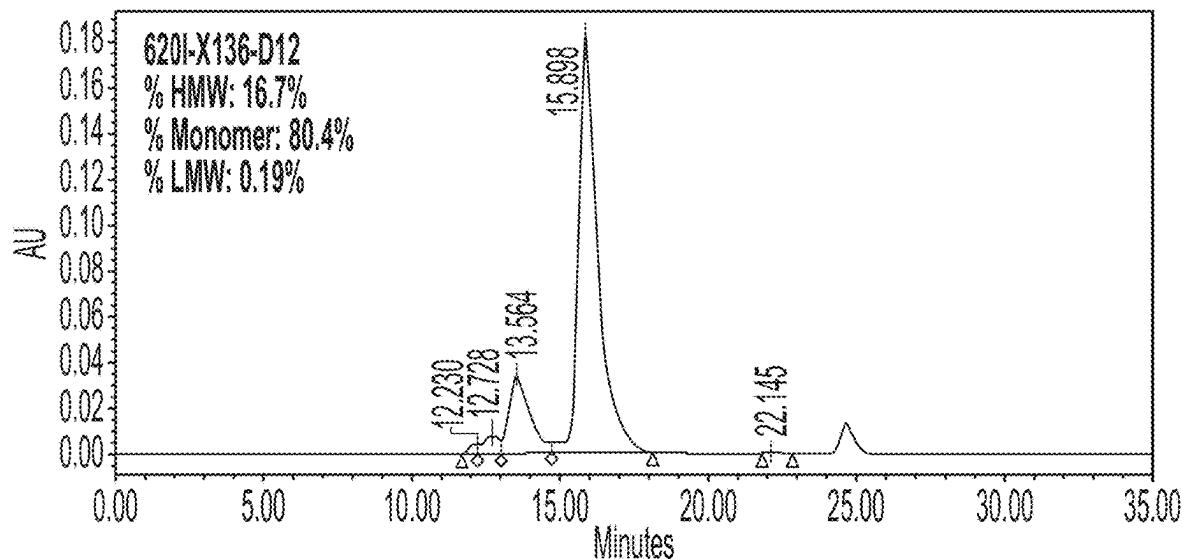


FIG. 3 (CONT'D)

D.



E.

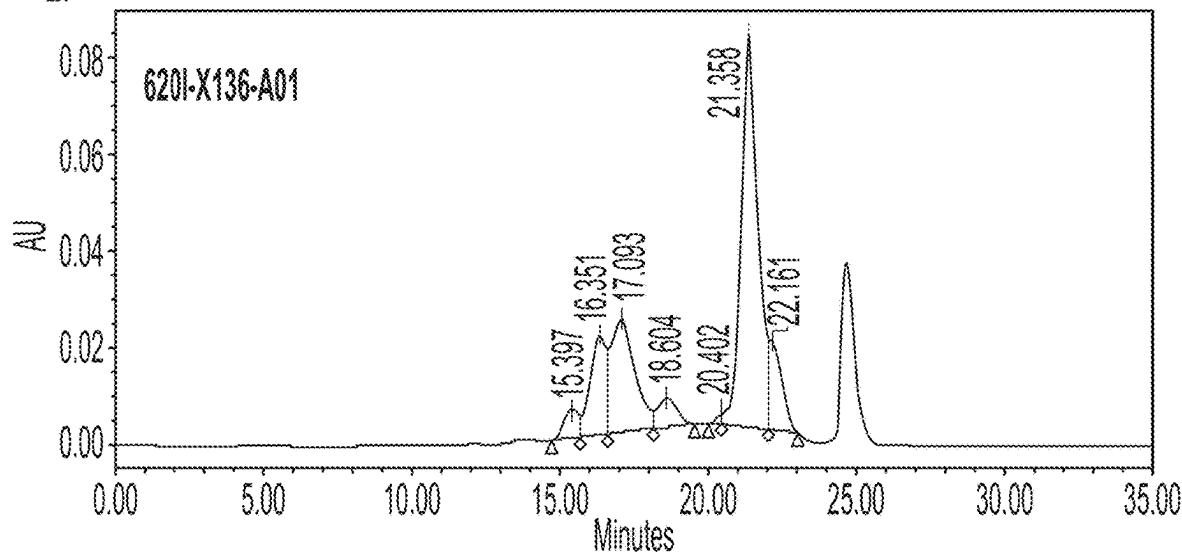
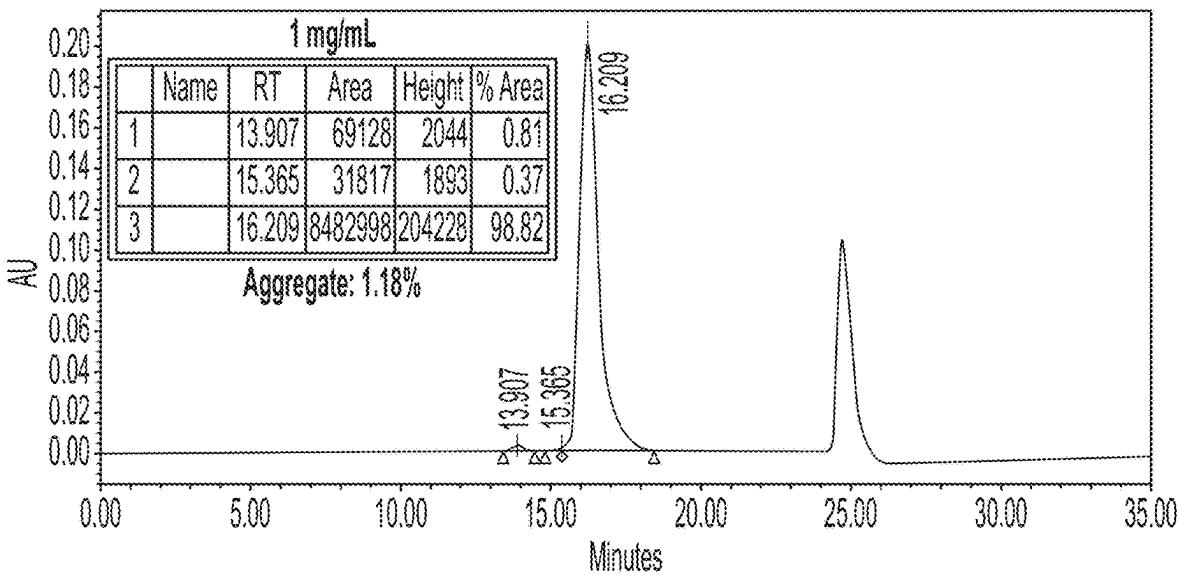


FIG. 4

A.



B.

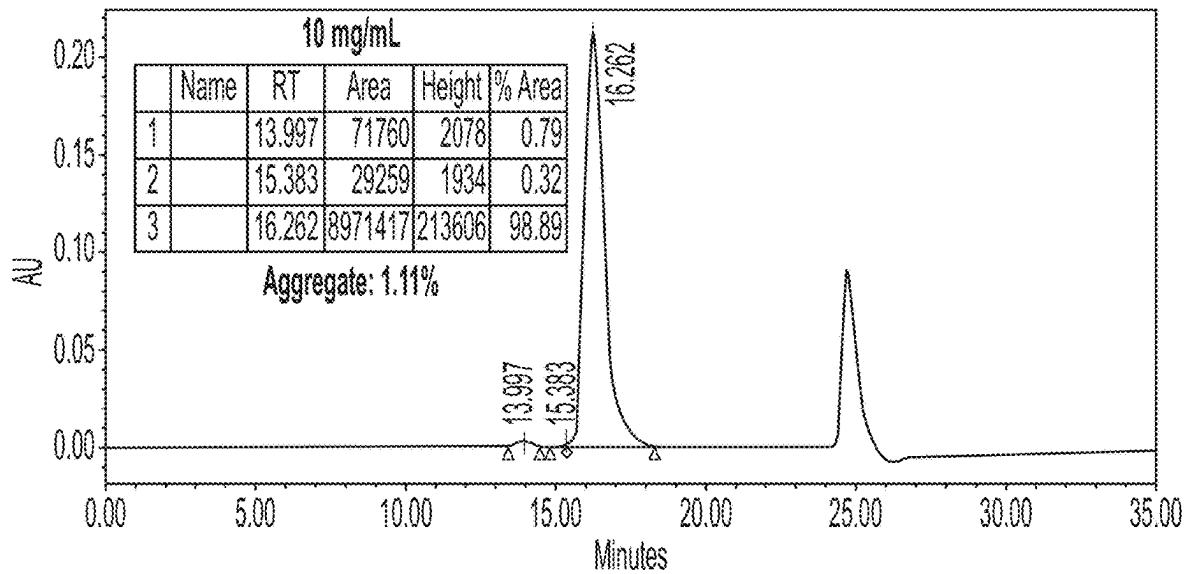


FIG. 4 (CONT'D)

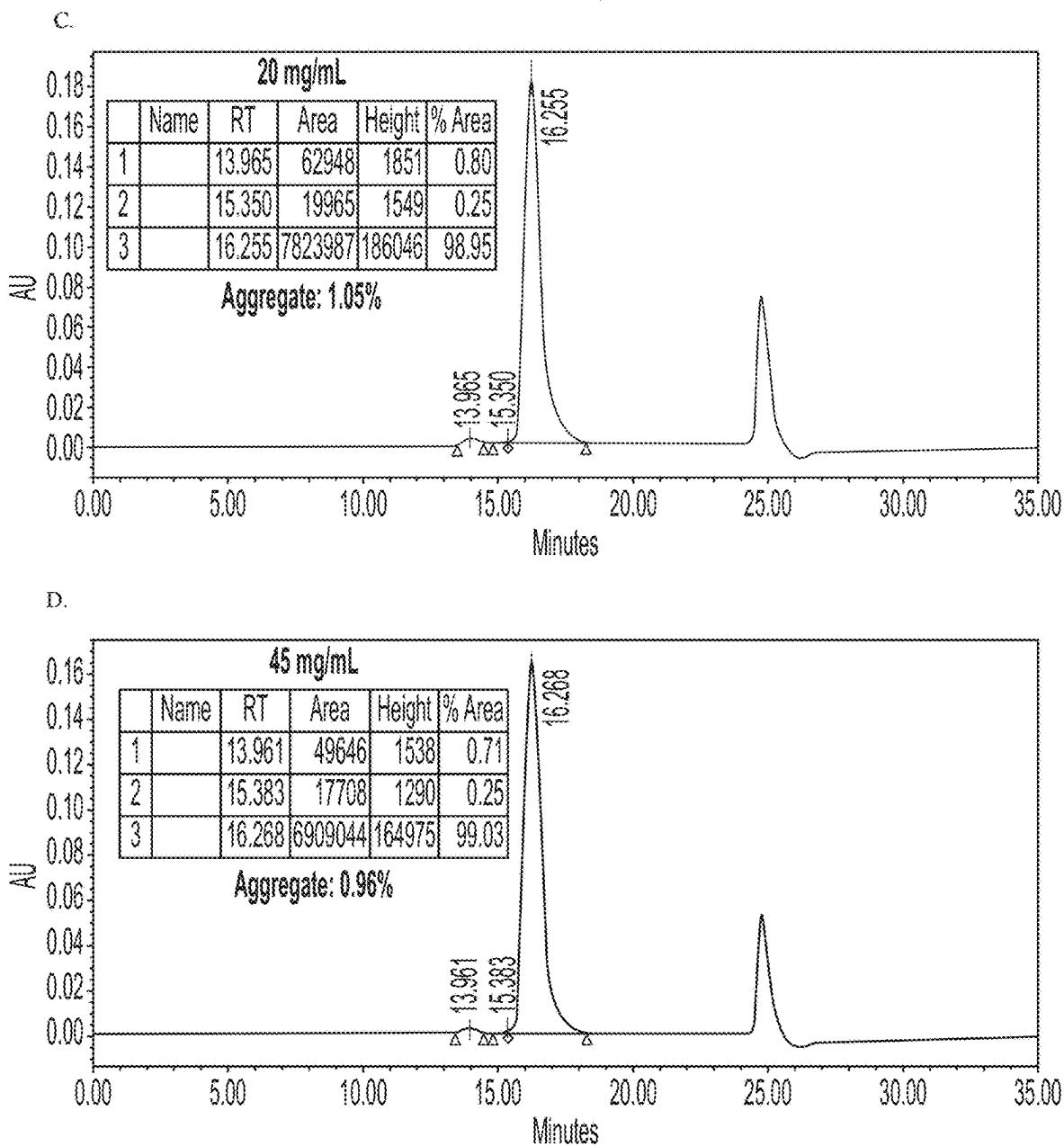


FIG. 5

A.
B.

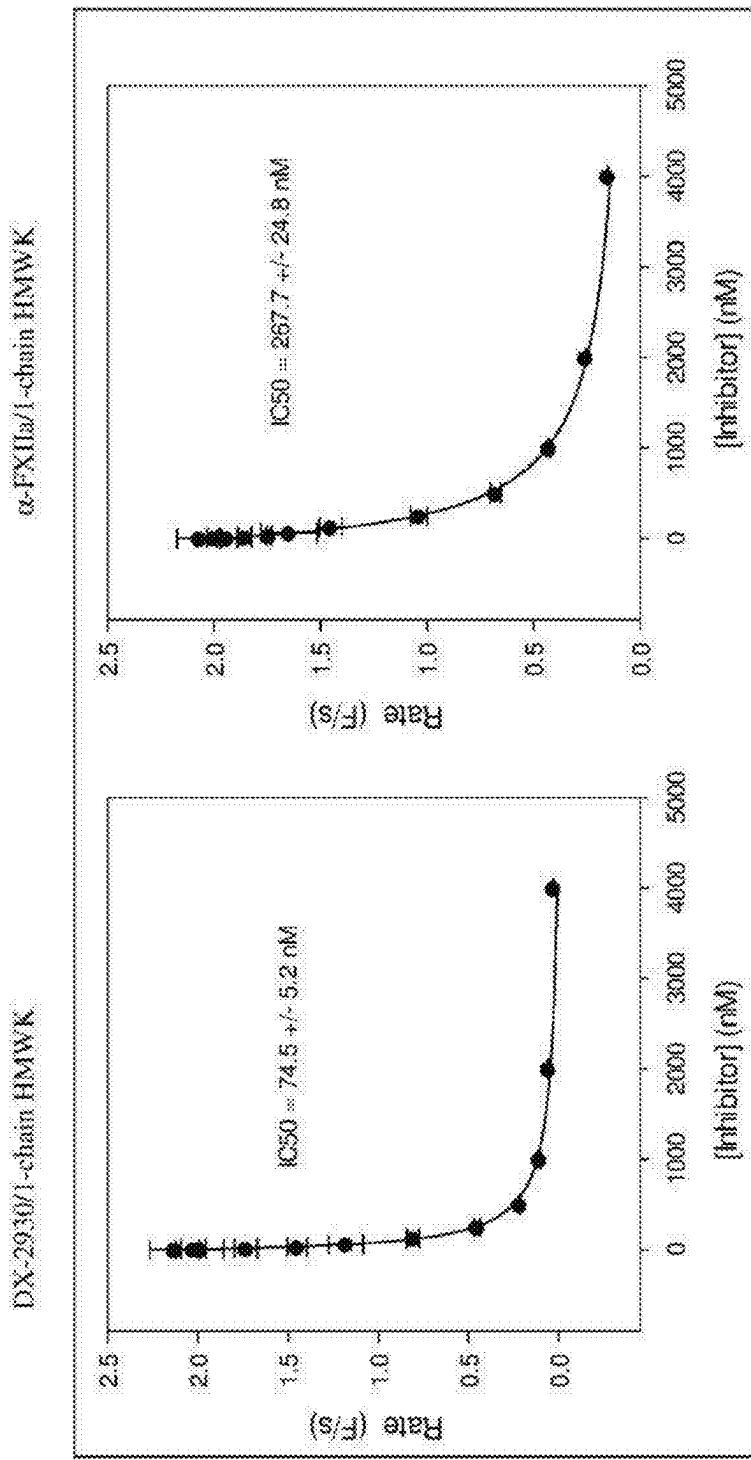


FIG. 5 (CONT'D)

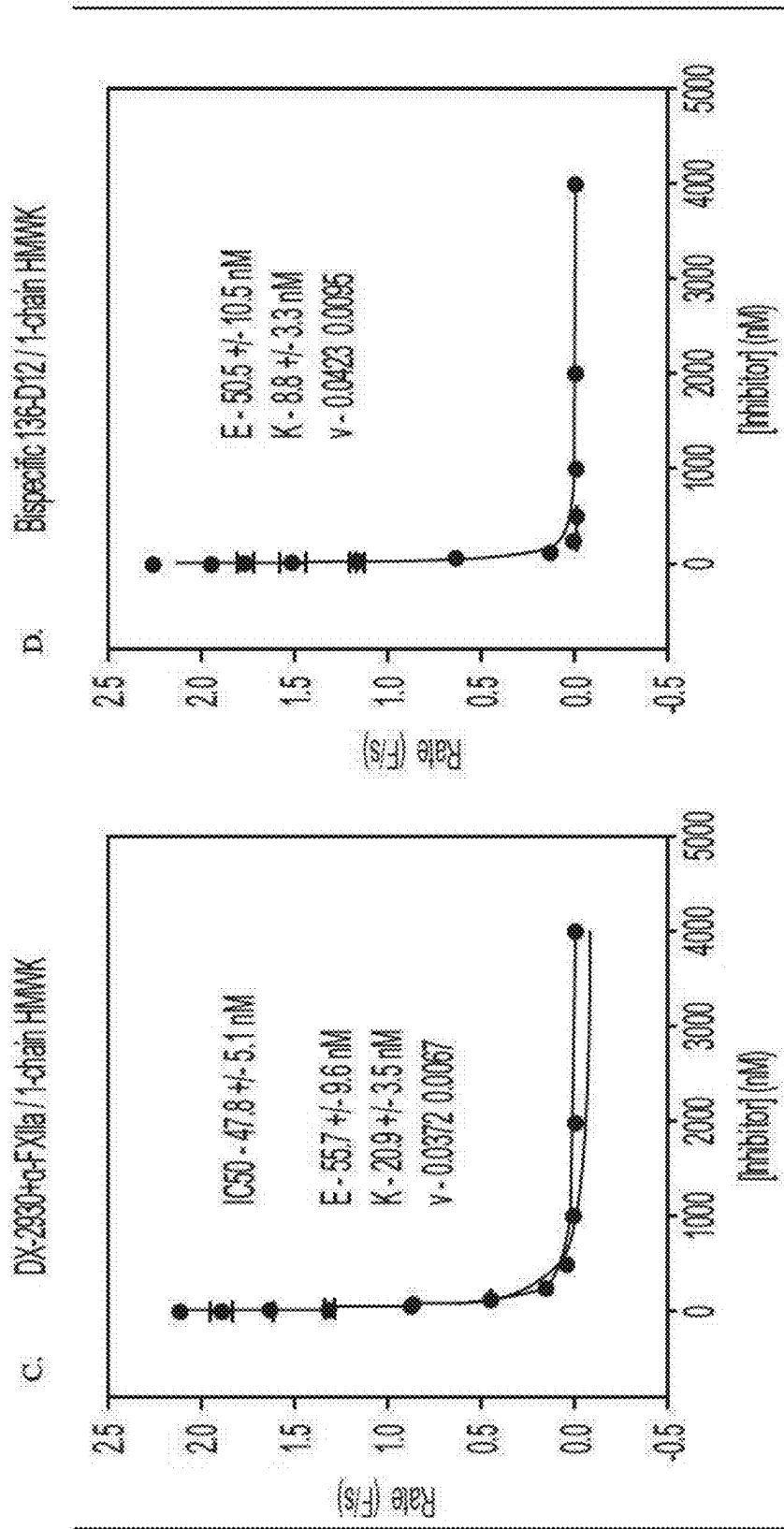
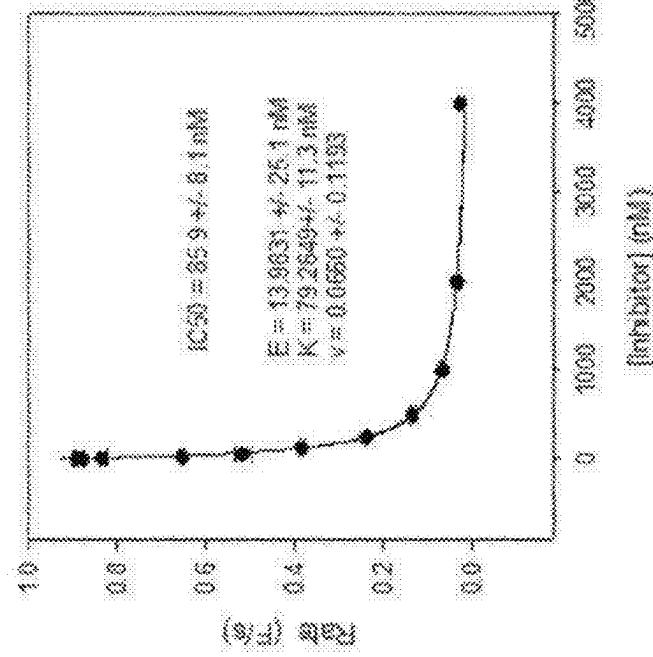


FIG. 6

A.

DX-2930/HMWK



B.

α -PEI/No HMWK

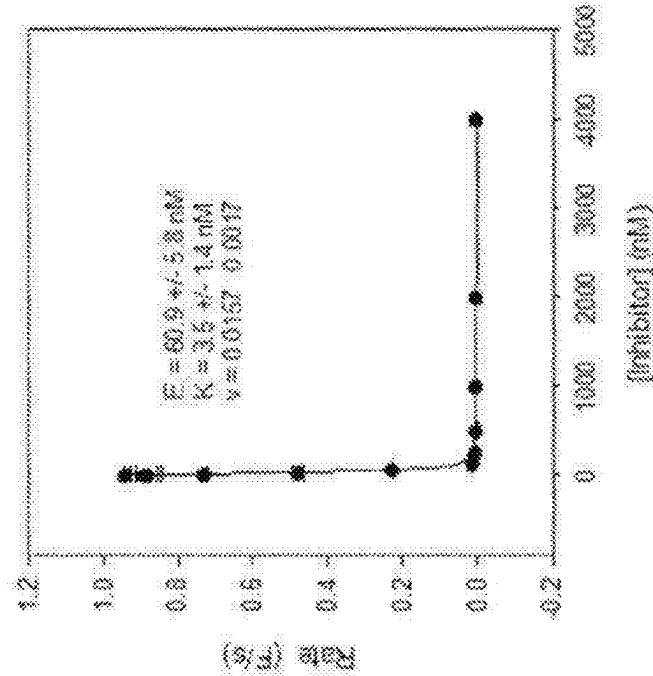


FIG. 6 (CONT'D)

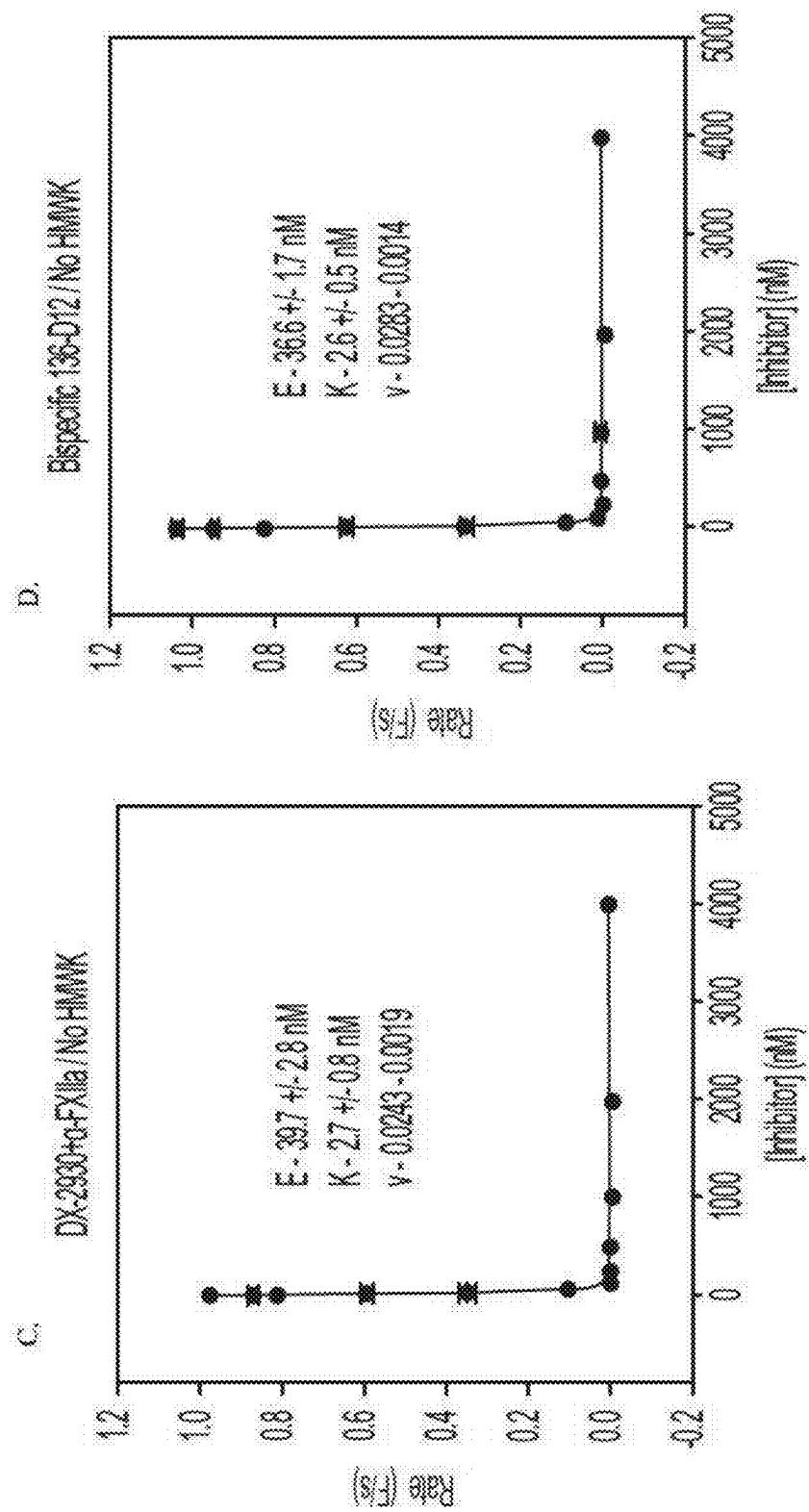


FIG. 7



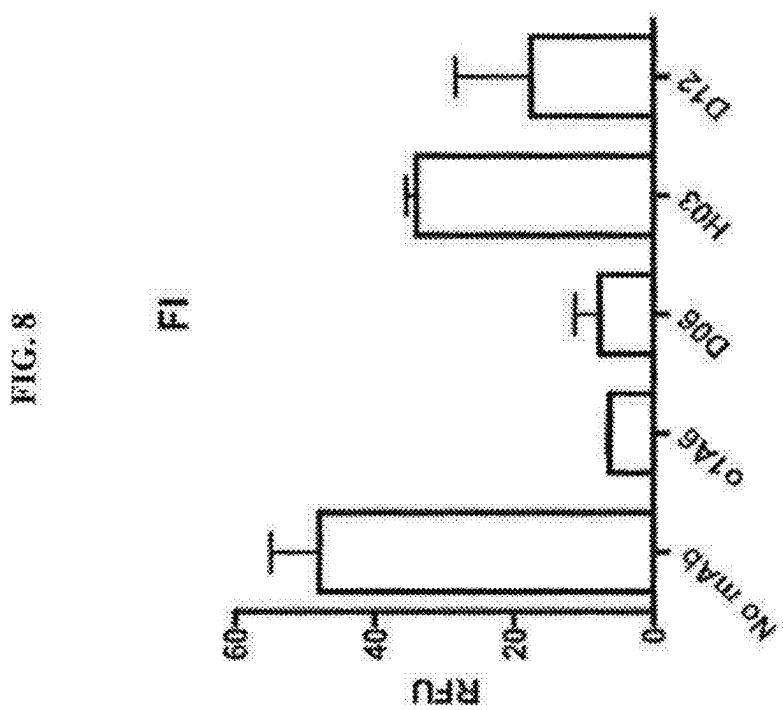


FIG. 9

A.

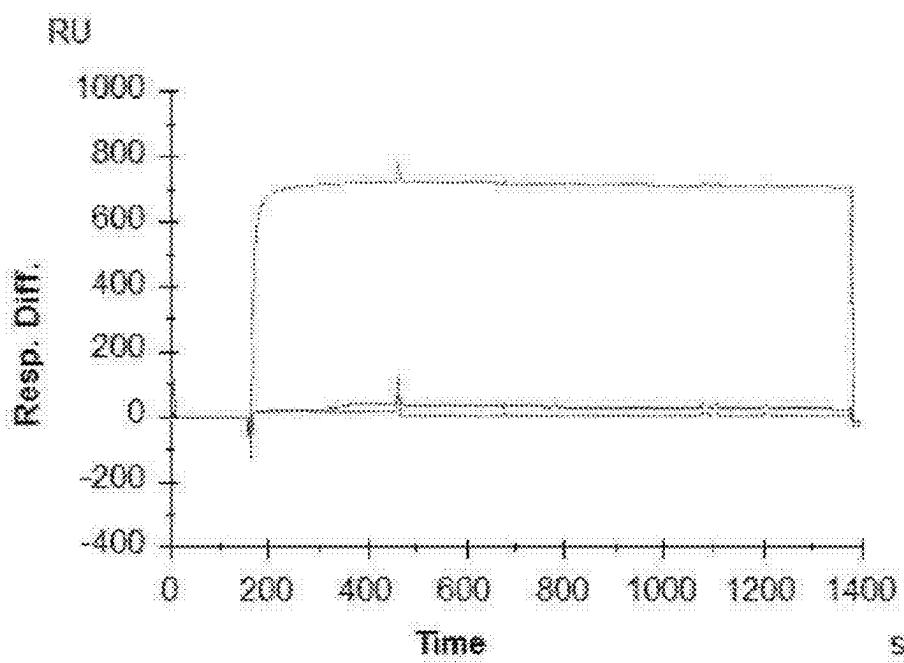
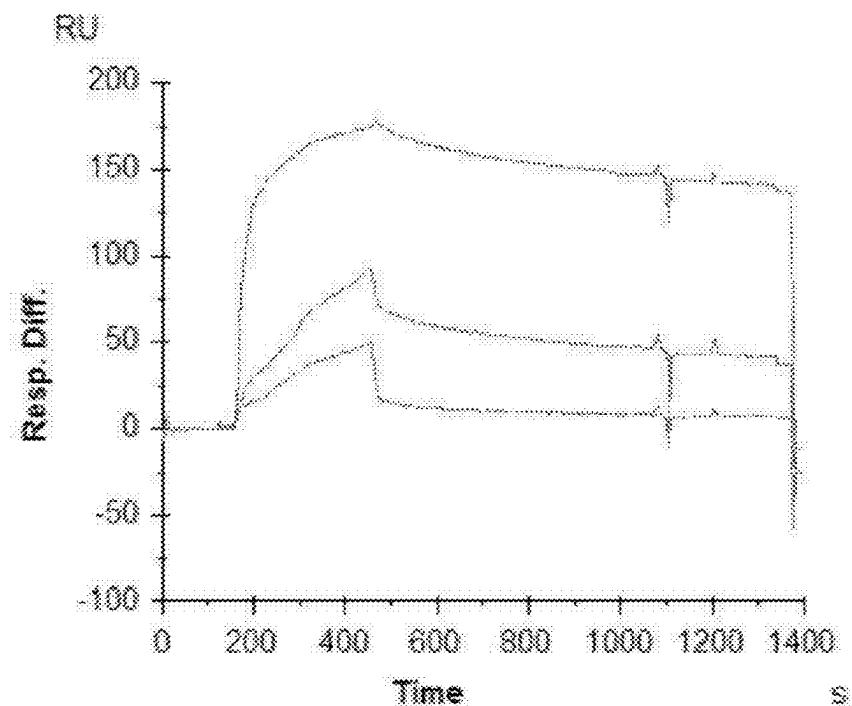


FIG. 10
A.
B.

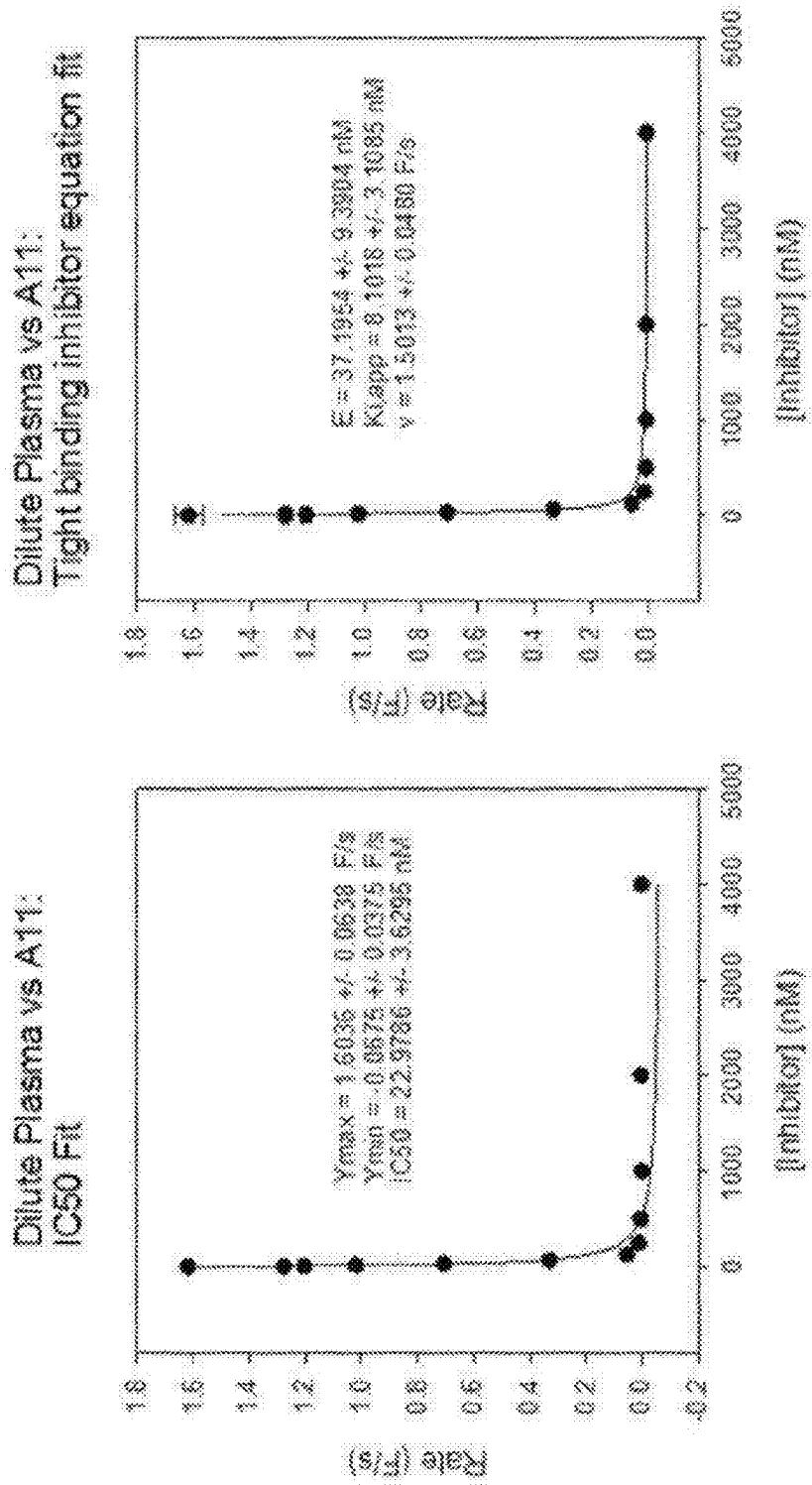


FIG. 10 (CONT'D)

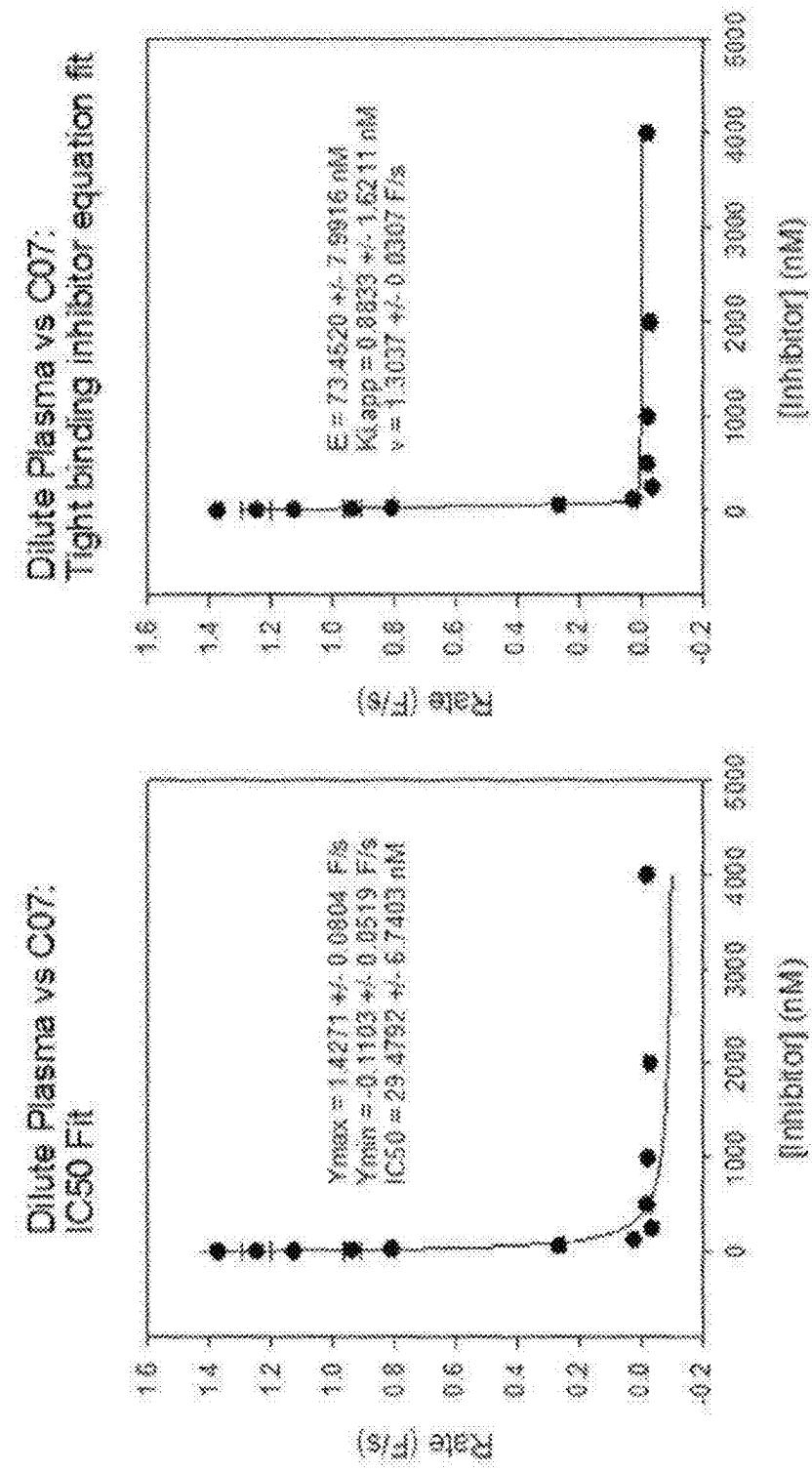
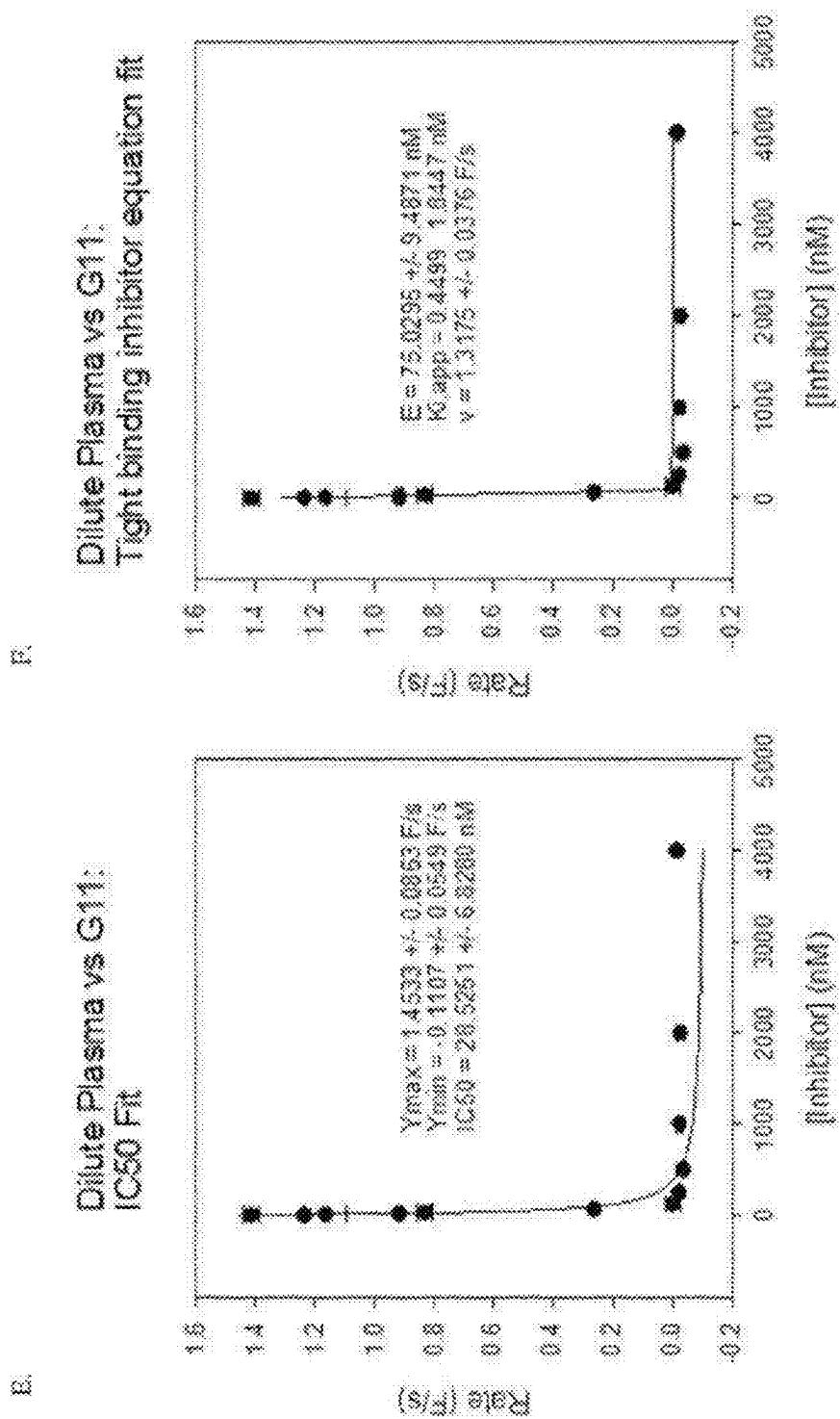
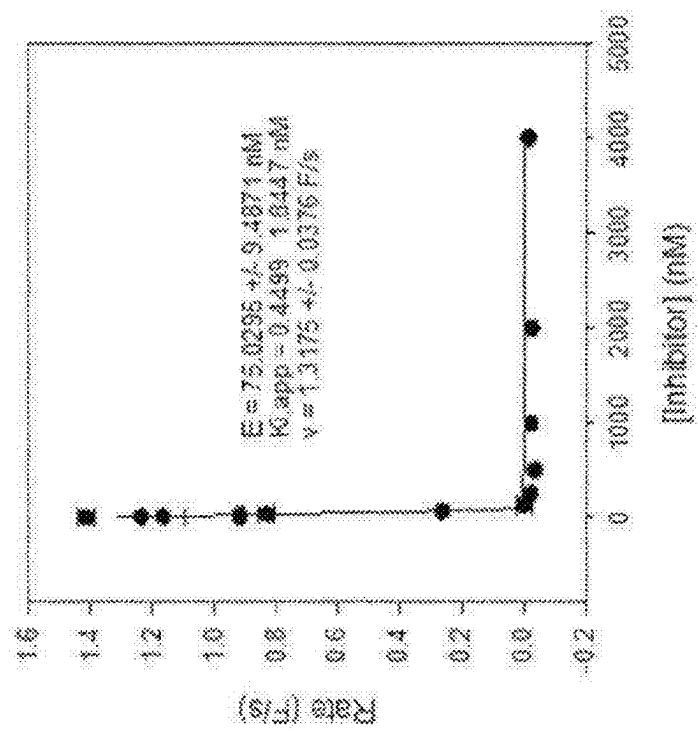


FIG. 10 (CONT'D)

Dilute Plasma vs C11:
IC₅₀ Fit



Dilute Plasma vs C11:
Tight binding inhibitor equation fit



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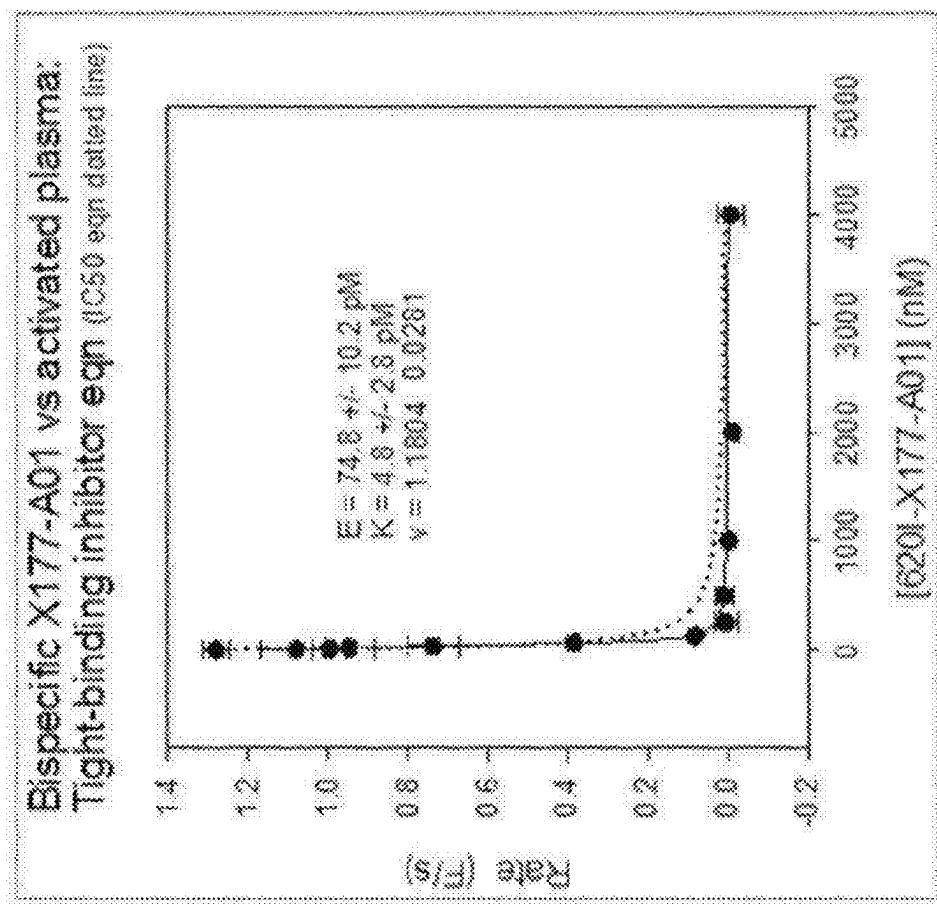
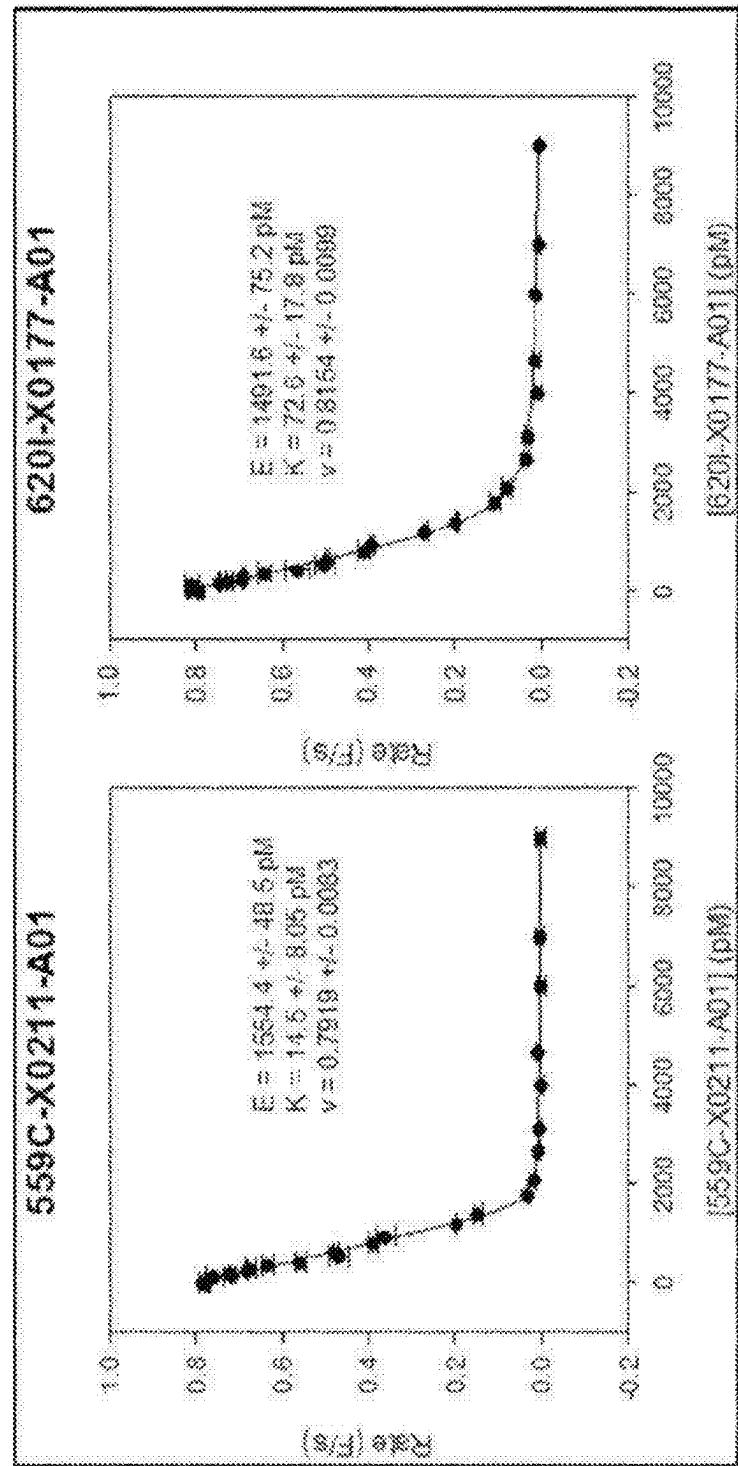


FIG. 12



A.

8.

559C-X0211-A01

$$\text{Bispec } A(0) \text{ vs } h \text{ [K]} \\ C((E+K)+s \operatorname{qr}((E+K)^2+4^*E^K))/2 \\ F=^{\circ}\text{C}$$

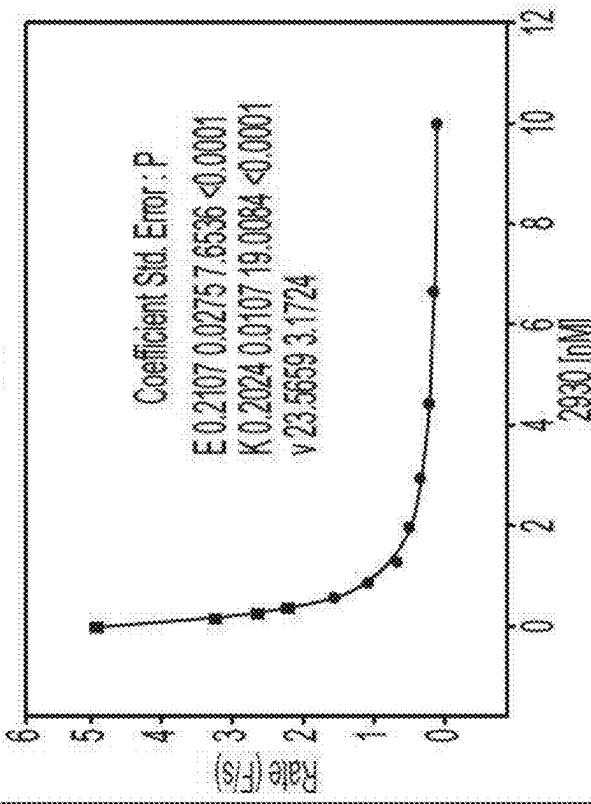


FIG. 12 (CONT'D)

6201-X0177-A01

$$\text{Bispec } A(0) \text{ vs } h \text{ [K]} \\ C((E+K)+s \operatorname{qr}((E+K)^2+4^*E^K))/2 \\ F=^{\circ}\text{C}$$

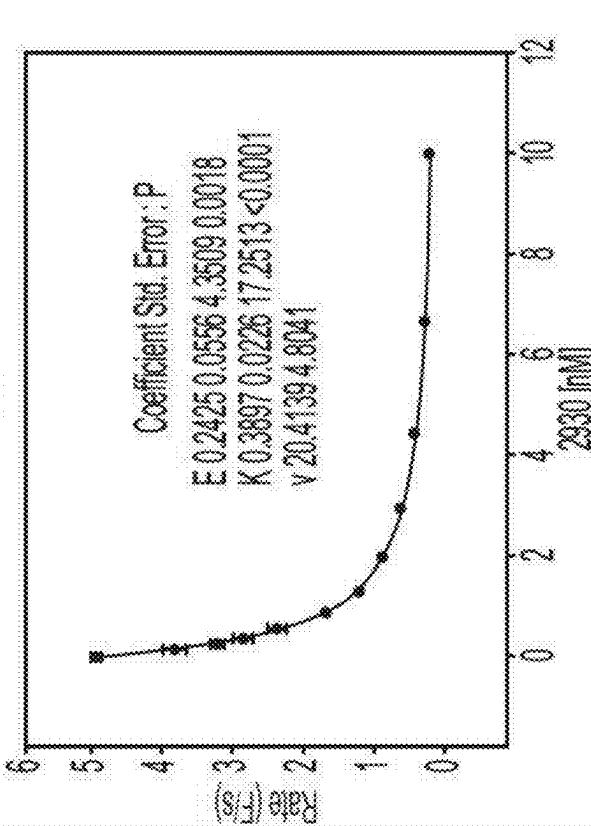


FIG. 13

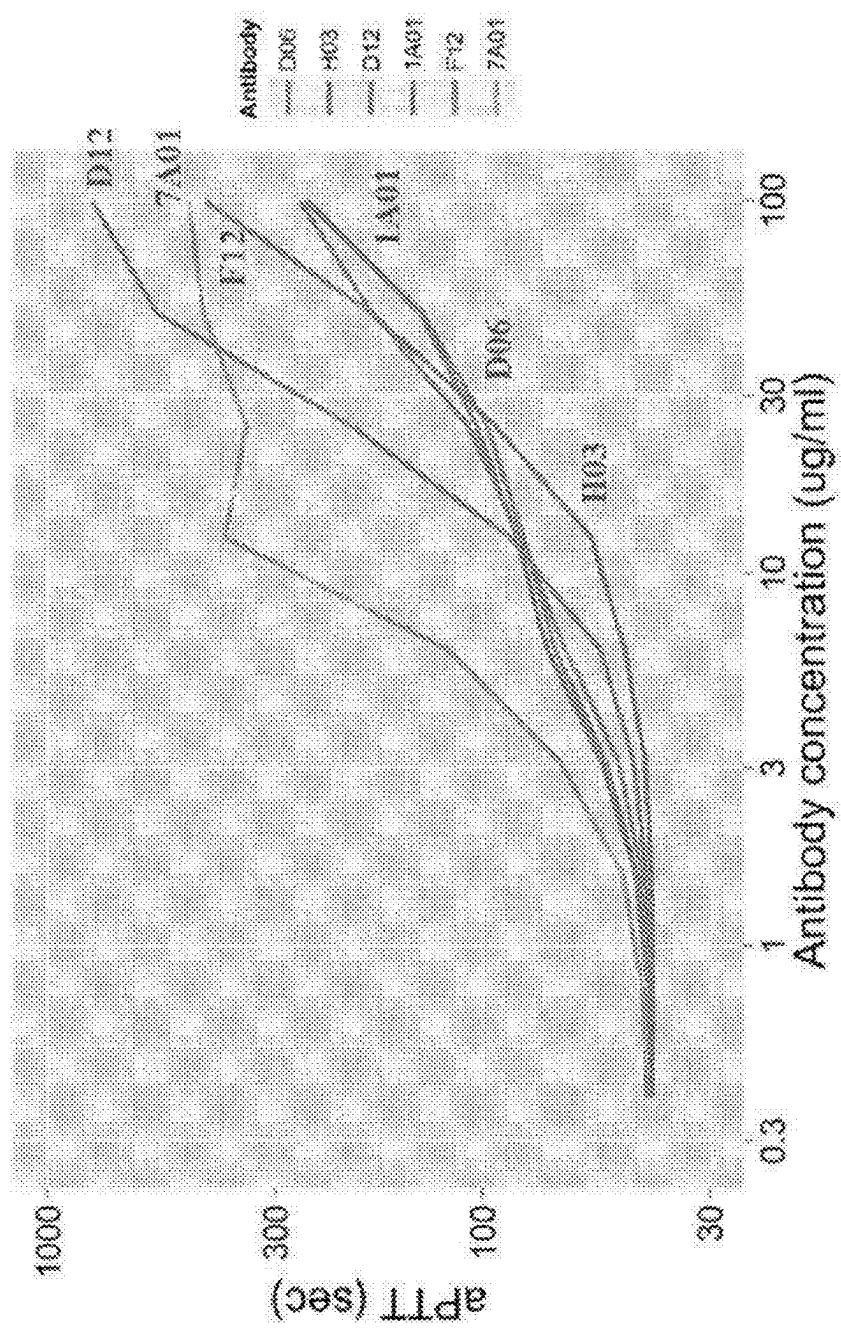


FIG. 14

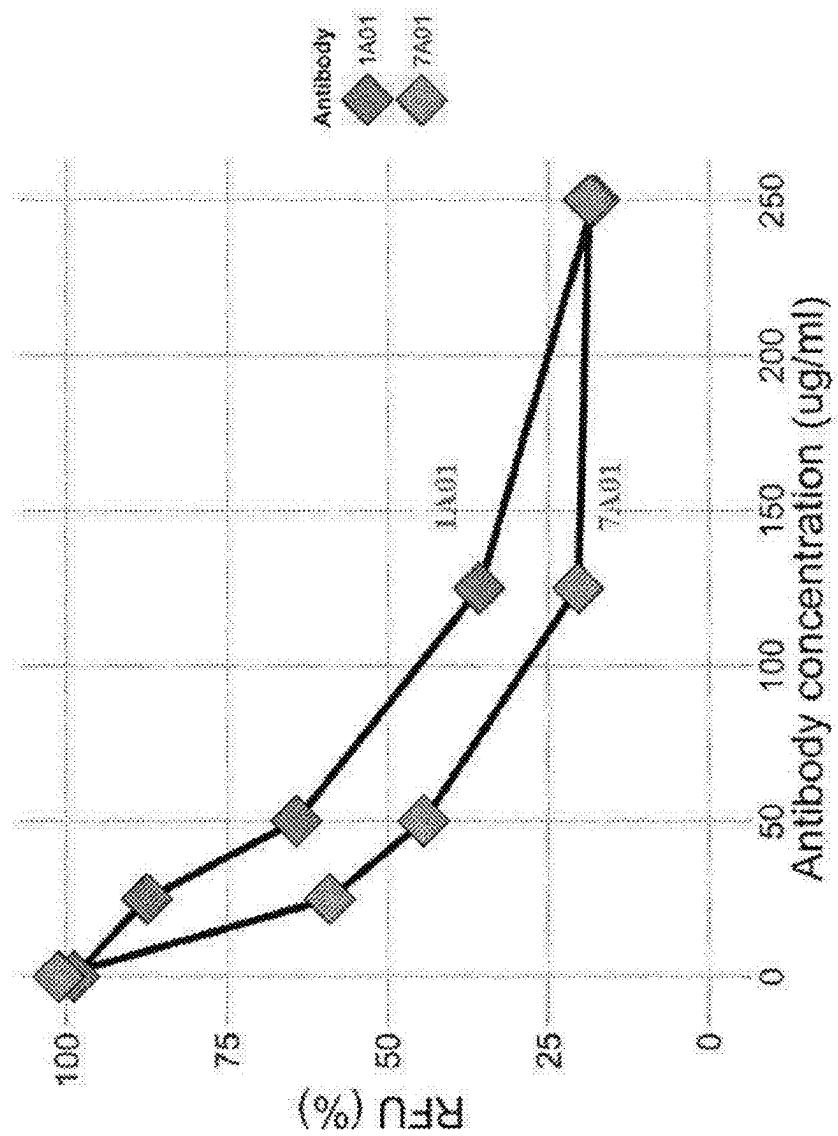


FIG. 15

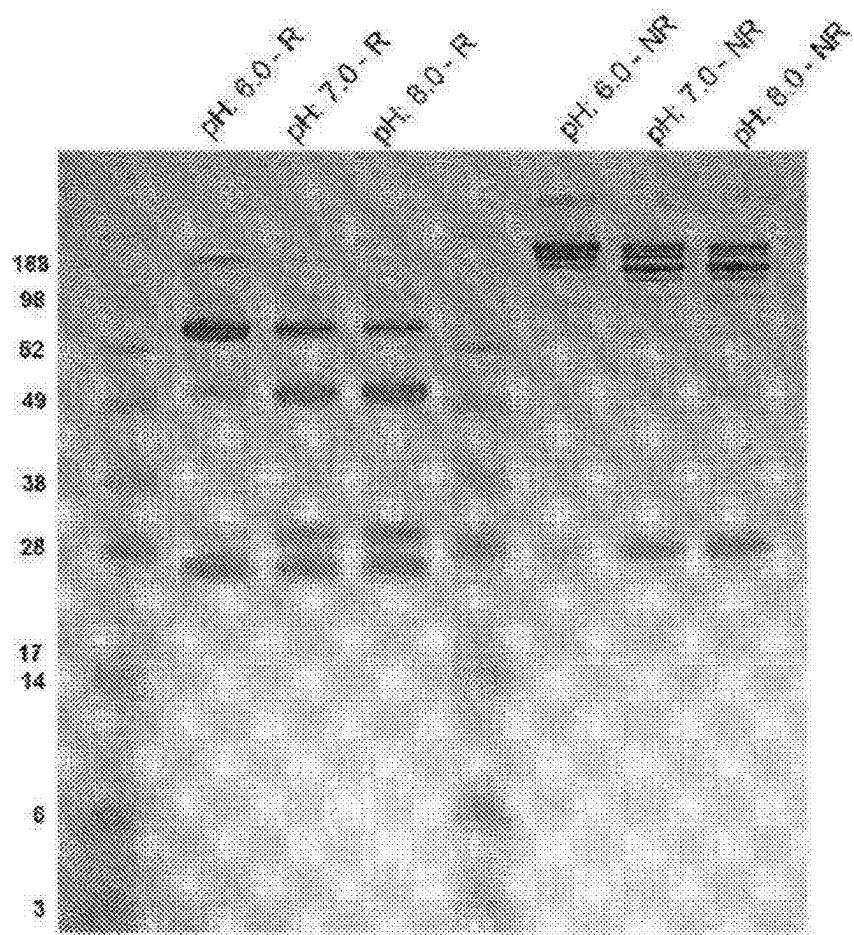
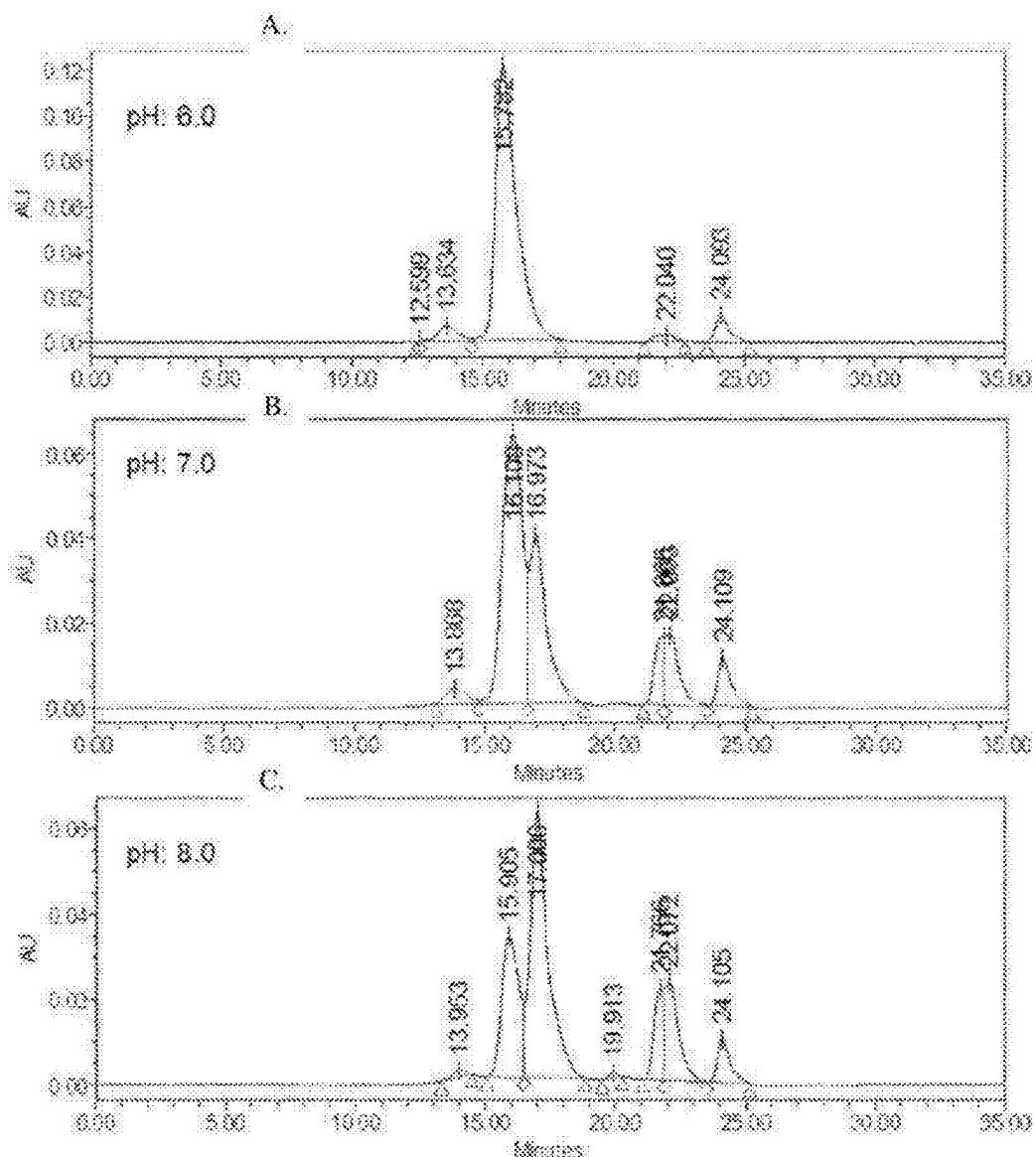
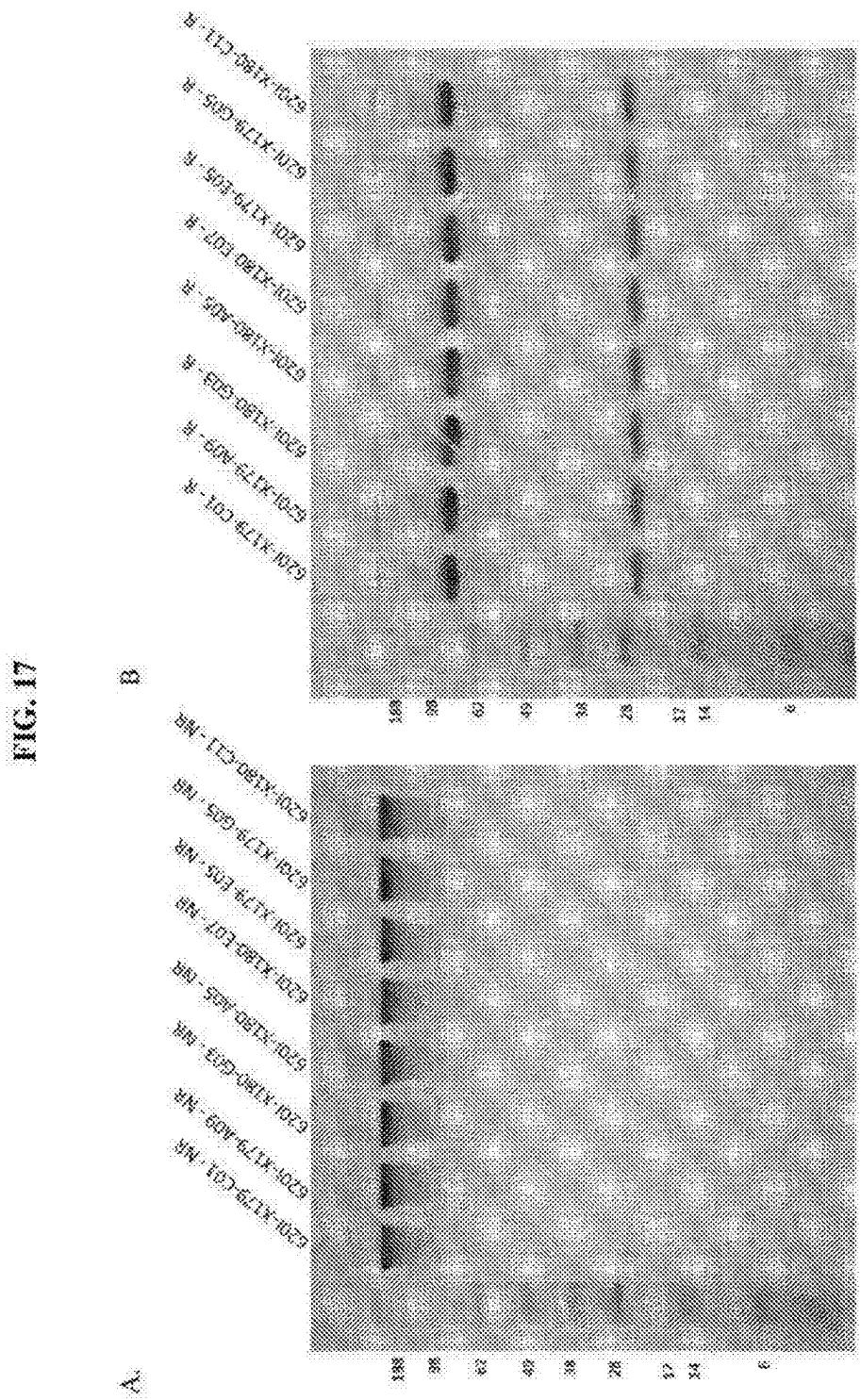


FIG. 16





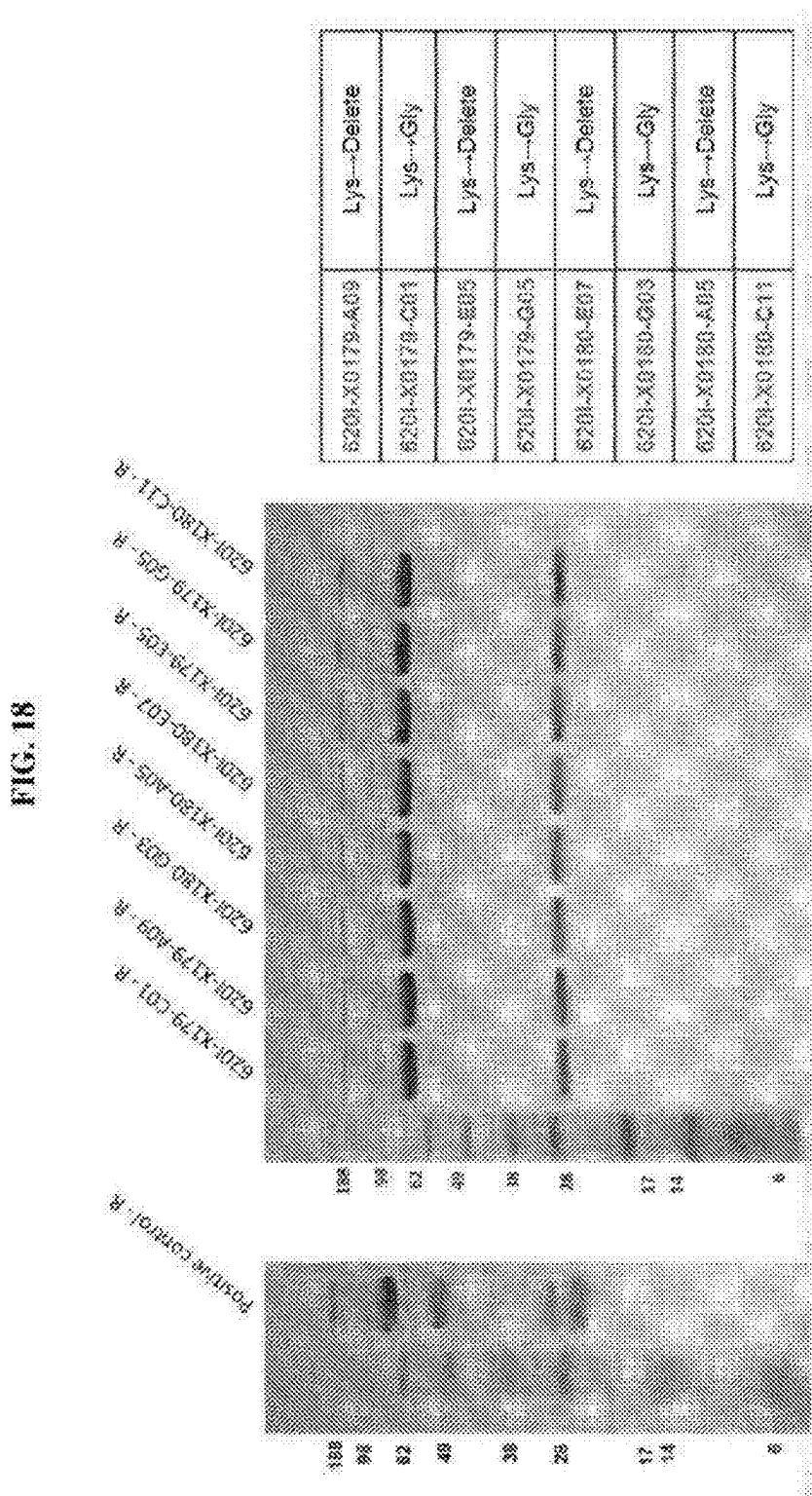


FIG. 19

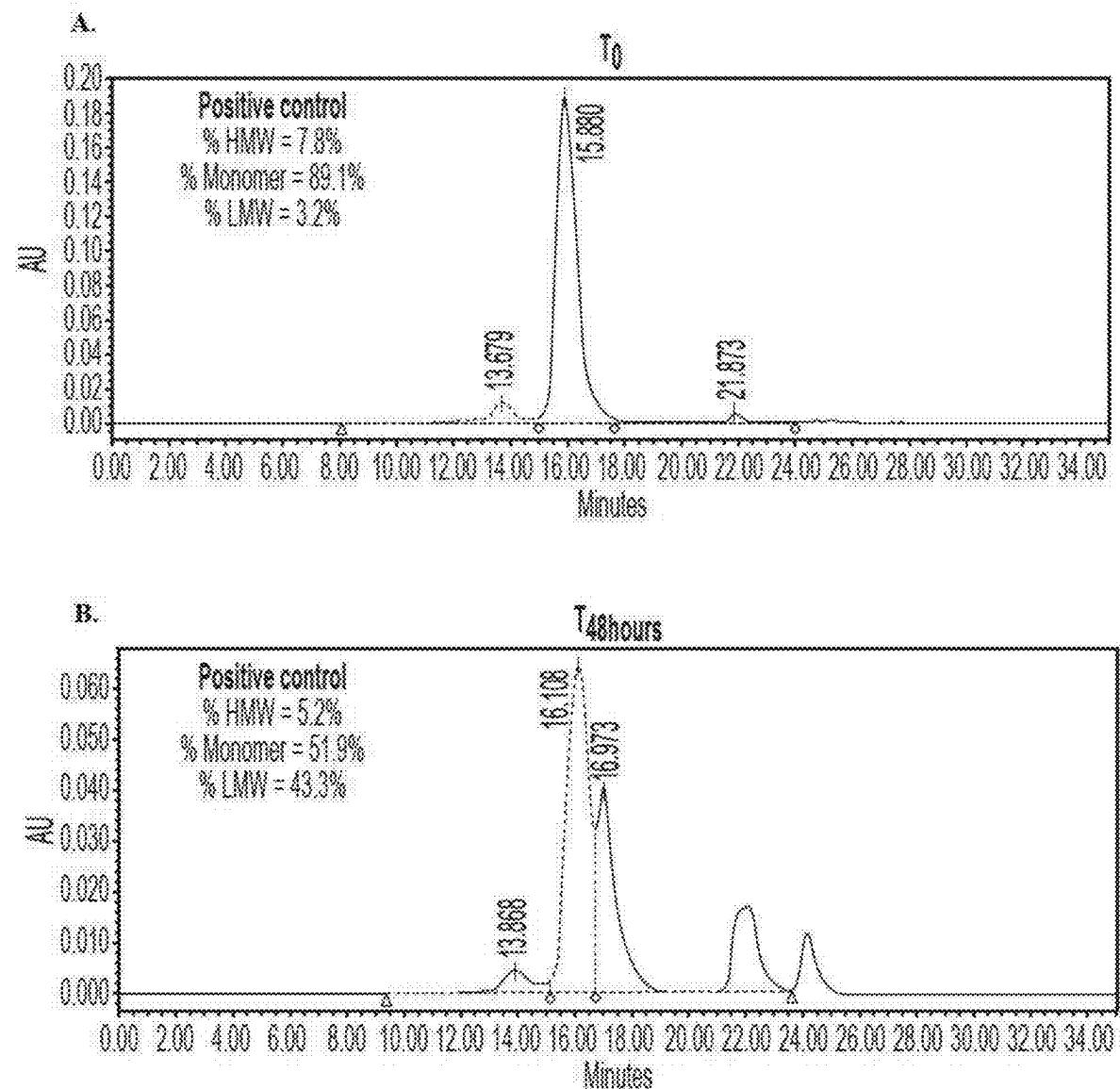
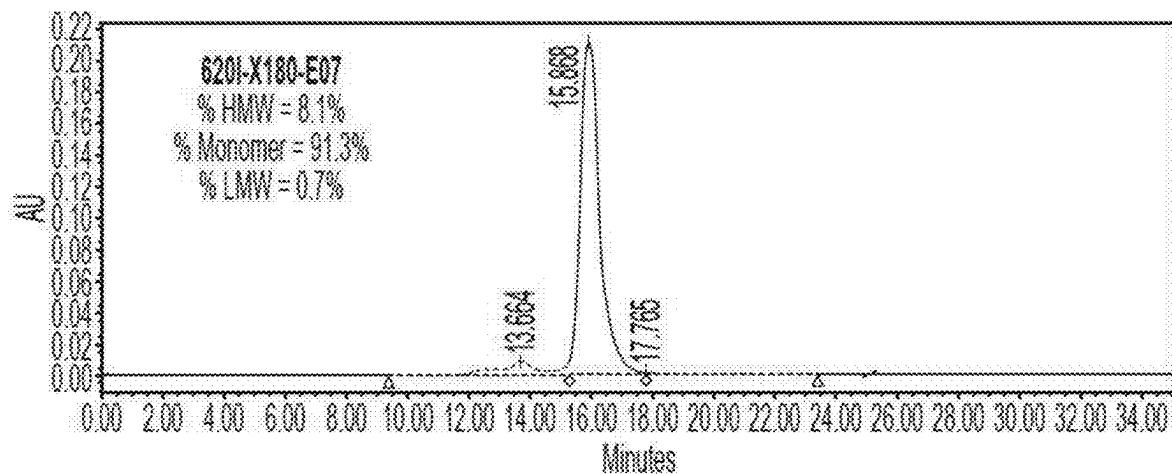


FIG. 20

A.



B

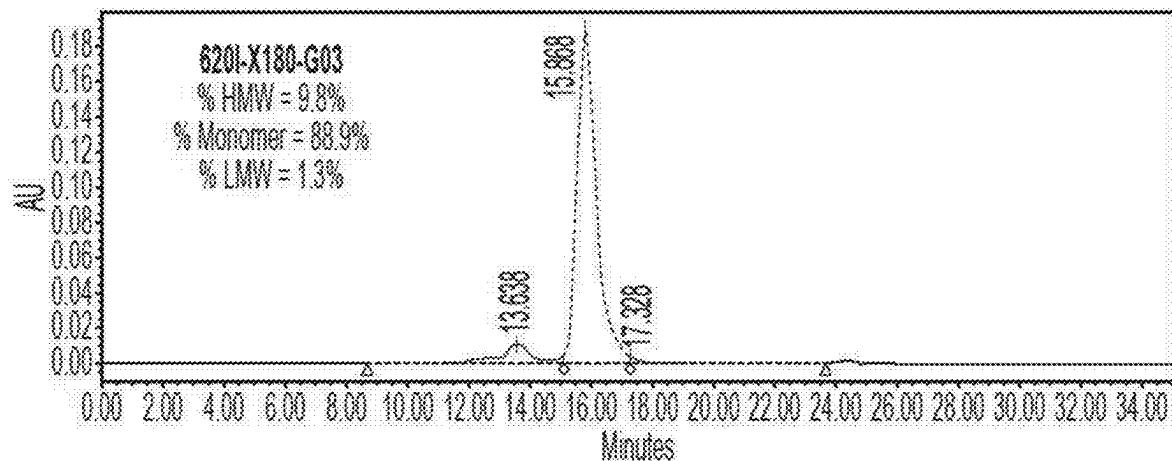


FIG. 20

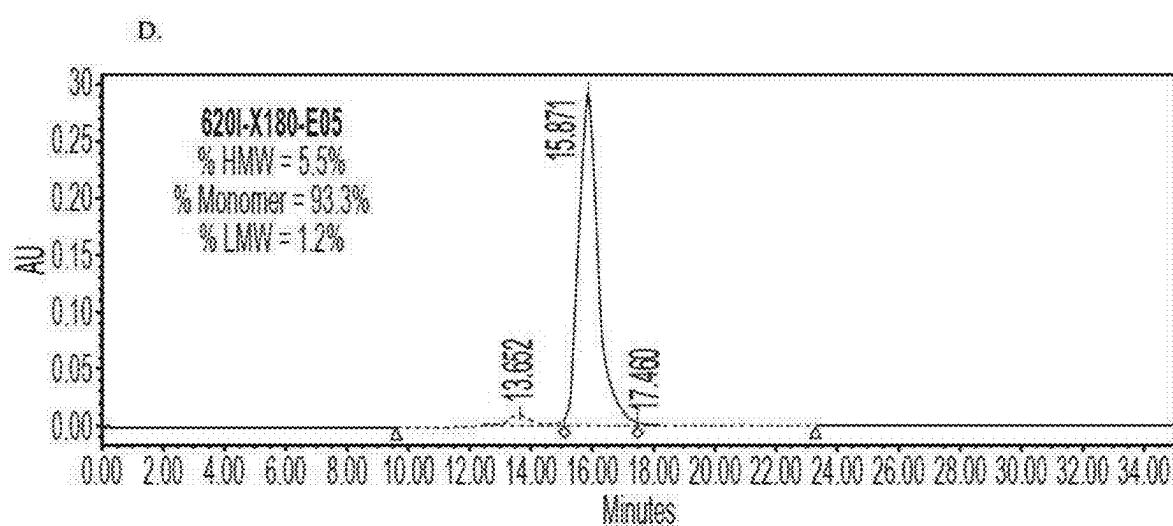
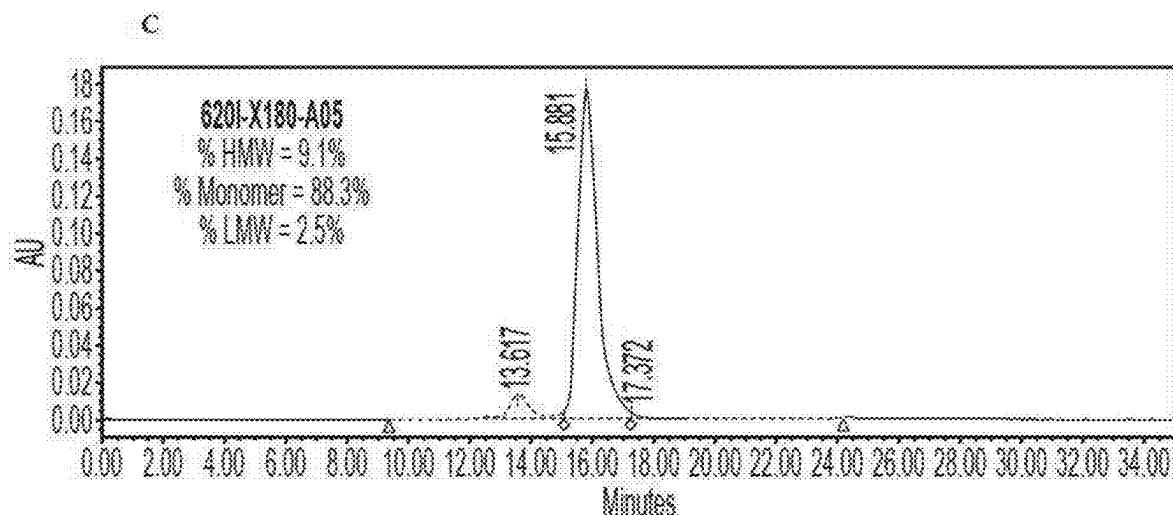


FIG. 20

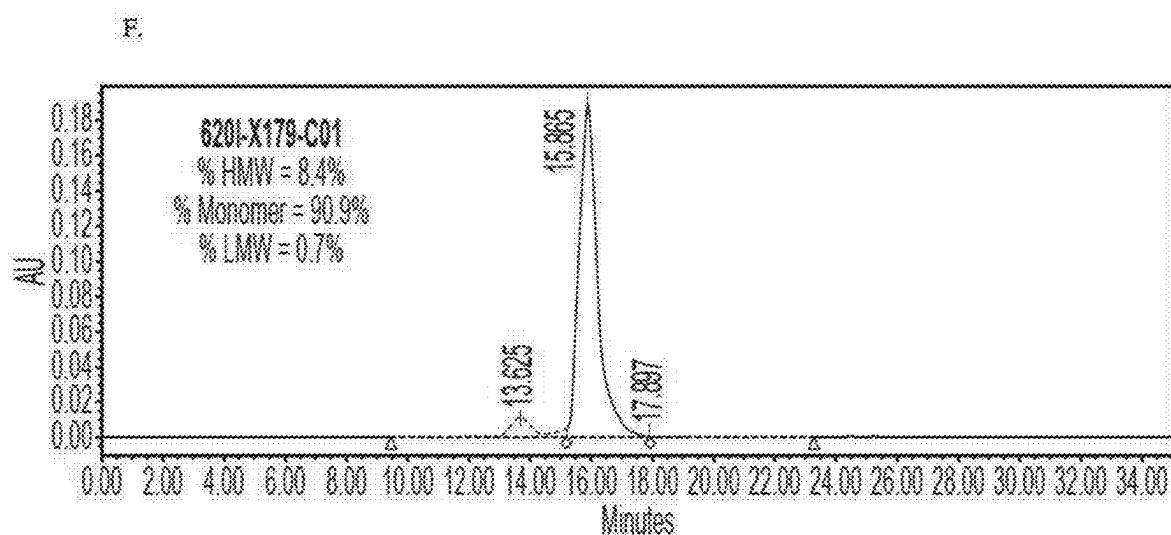
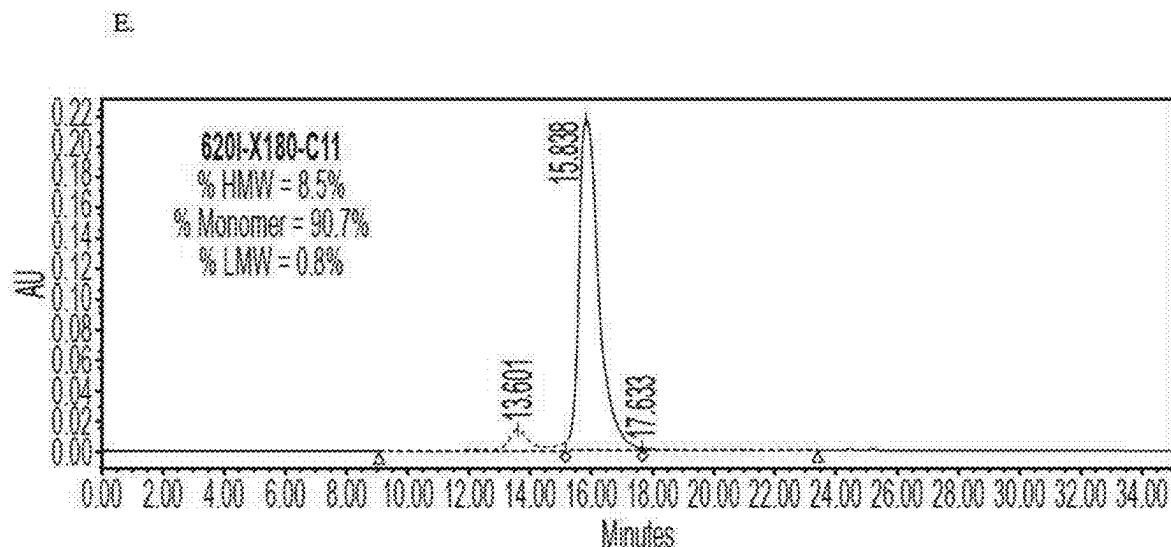


FIG. 20

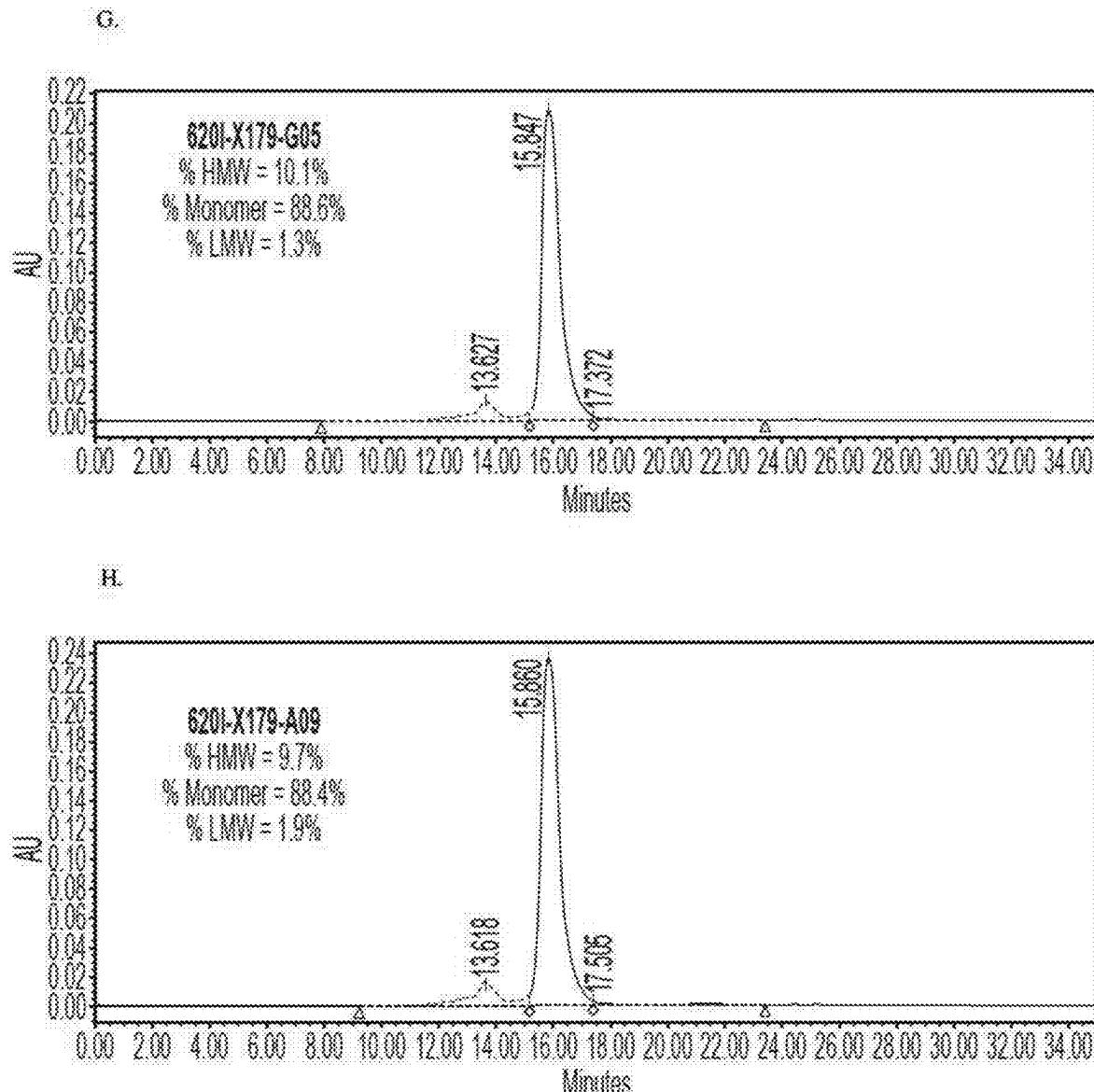


FIG. 21

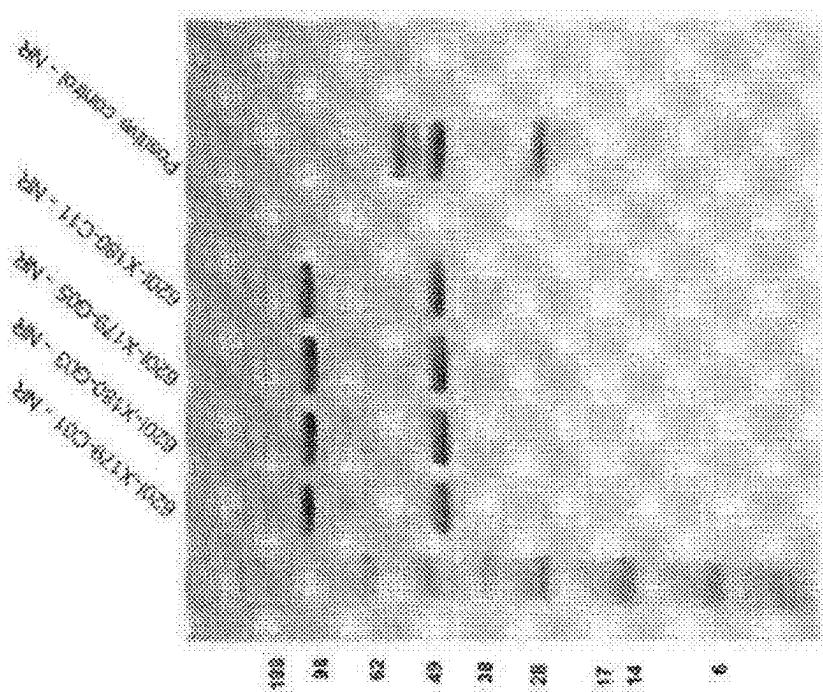


FIG. 22

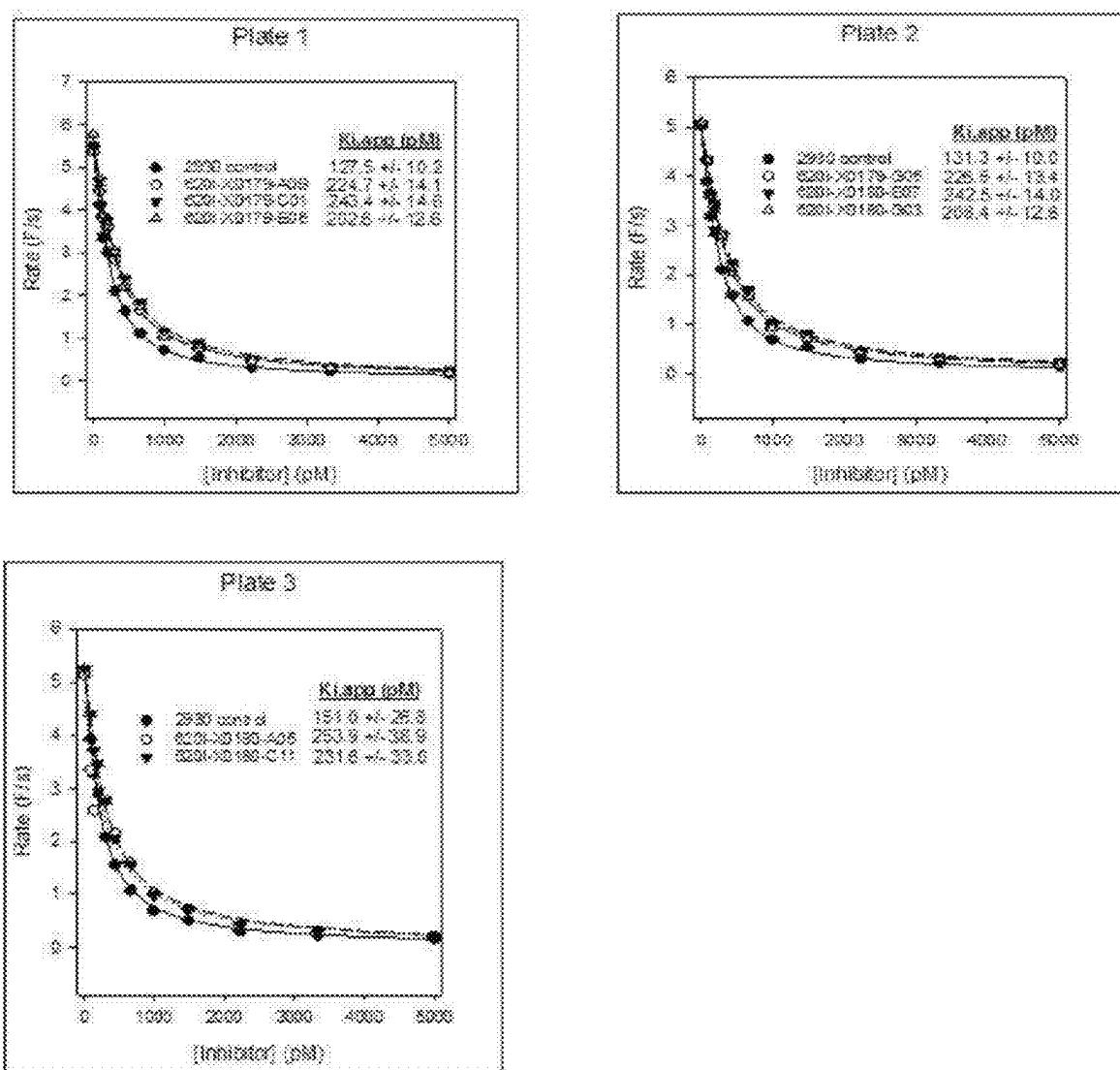


FIG. 23

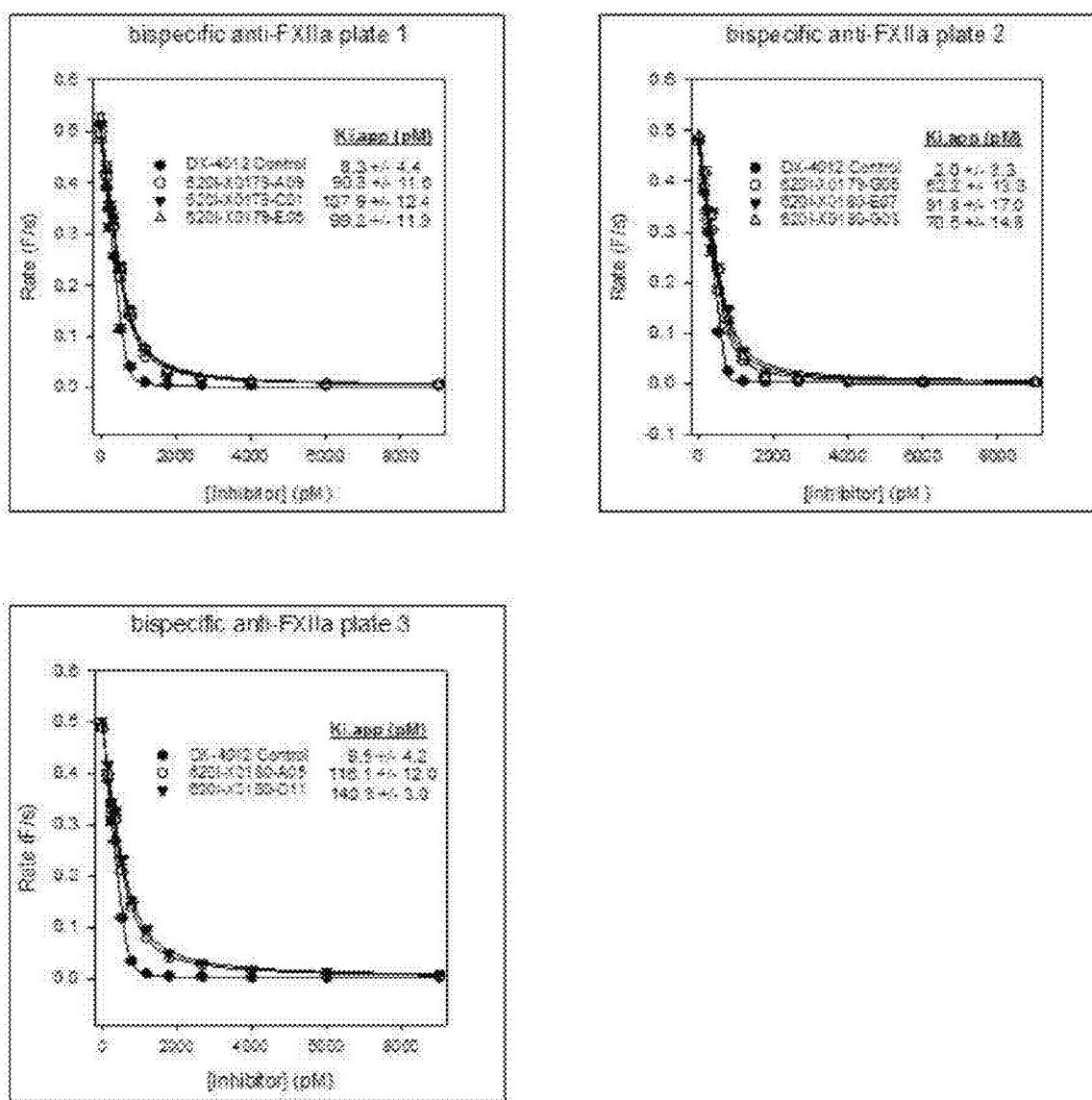
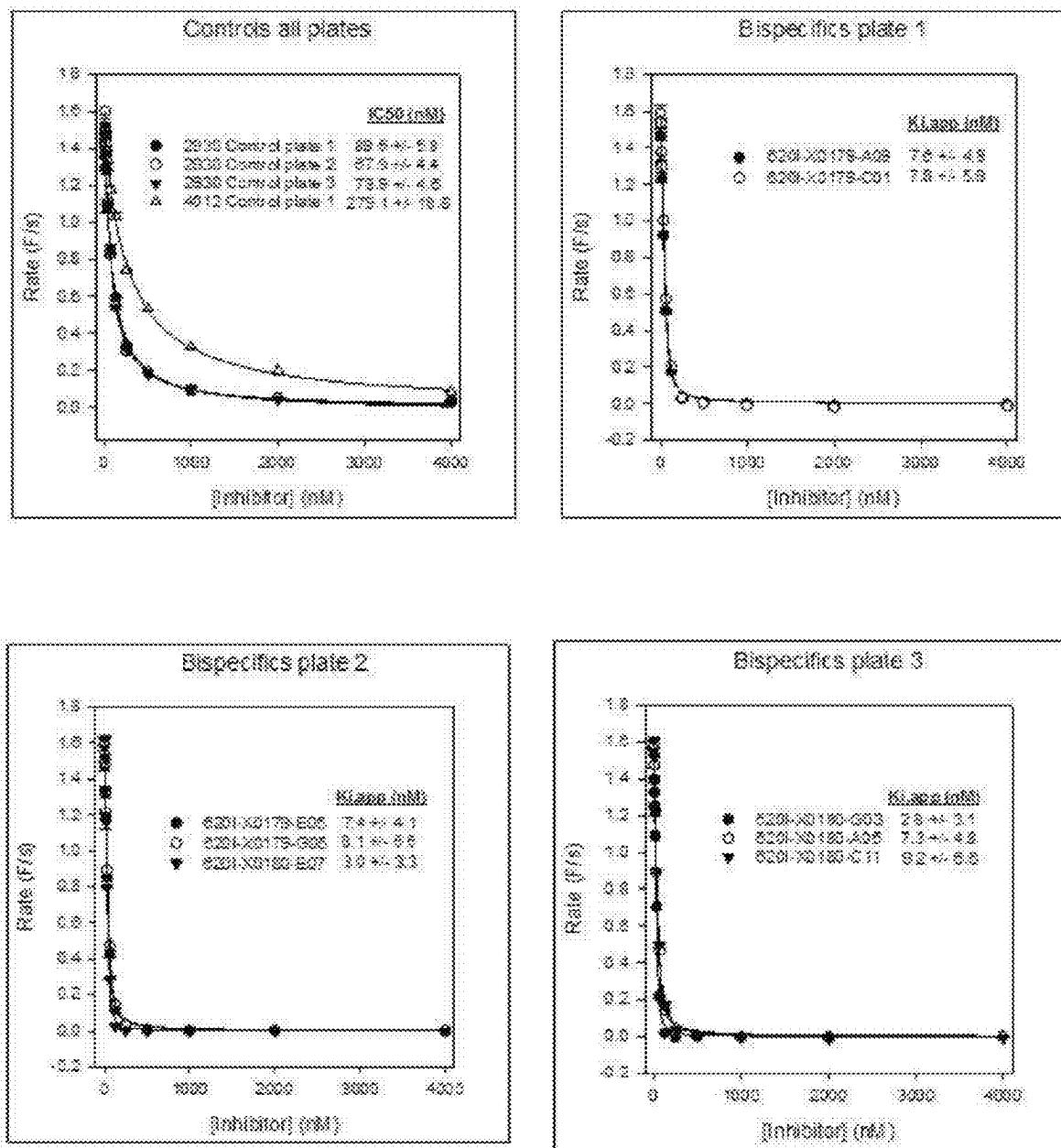


FIG. 24



BISPECIFIC ANTIBODIES AGAINST PLASMA KALLIKREIN AND FACTOR XII

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application is a Division of U.S. application Ser. No. 17/838,769, filed Jun. 13, 2022, which is a continuation of U.S. application Ser. No. 15/541,066, filed Jun. 30, 2017, now issued as U.S. Pat. No. 11,390,687, which is a national stage filing under 35 U.S.C. § 371 of international application number PCT/US2015/068238, filed Dec. 21, 2015, which claims the benefit under 35 U.S.C. § 119(e) of U.S. provisional application Ser. No. 62/261,609, filed Dec. 1, 2015, U.S. provisional application Ser. No. 62/200,363, filed Aug. 3, 2015, and U.S. provisional application Ser. No. 62/099,236, filed Jan. 2, 2015. Each of the prior applications is herein incorporated by reference in its entirety.

REFERENCE TO AN ELECTRONIC SEQUENCE LISTING

[0002] The content of the electronic sequence listing (D061770065US06-SEQ-ACZ.xml; Size: 316,553 bytes; and Date of Creation: Jan. 28, 2025) is herein incorporated by reference in its entirety.

BACKGROUND OF THE INVENTION

[0003] Factor XII (FXII) is the primary activator that converts pre-kallikrein into plasma kallikrein (pKal). Activated plasma kallikrein cleaves high molecular weight kininogen (HMWK) to release bradykinin (BK). pKal can also activate latent Factor XII into active Factor XII (Factor XIIa). In disease states related to aberrant activation of the contact system, such as Hereditary Angioedema, uncontrolled levels of BK can induce patient attacks.

SUMMARY OF THE INVENTION

[0004] One aspect of the present disclosure is a bispecific antibody, comprising: a first polypeptide that comprises a light chain of a first antibody, the light chain comprising a light chain variable region (V_L) and a light chain constant region (C_L) (e.g., a kappa light chain or a lambda light chain); and a second polypeptide that comprises a heavy chain of the first antibody, the heavy chain comprising a heavy chain variable region (V_H) and a heavy chain constant region (C_H). Either the first polypeptide or the second polypeptide of the bispecific antibody further comprises a second antibody, which is a single chain antibody and can be fused to the C-terminus of either the first polypeptide or the second polypeptide. One of the first and second antibodies binds plasma kallikrein (pKal) (e.g., active pKal) and the other antibody binds Factor XII (e.g., active Factor XII or FXIIa), for example, the first antibody binds pKal and the second antibody binds FXIIa, or vice versa.

[0005] In some embodiments, the first antibody is an IgG. In one example, the IgG comprises a mutated heavy chain, which, as compared with the wild-type counterpart, has the C-terminal lysine residue deleted or mutated. For example, the mutated heavy chain of the first antibody may contain a C-terminal glycine residue, instead of a lysine residue as in a wild-type IgG heavy chain. In one example, the bispecific antibody can be tetravalent.

[0006] In some embodiments, the second polypeptide in the bispecific antibody comprises a peptide linker between

the heavy chain of the first antibody and the second antibody. In one example, the peptide linker can be SGGS (SEQ ID NO:22).

[0007] In the second antibody, which is a scFv antibody, the V_H can be fused to the N-terminus of the V_L . Alternatively, the V_H is fused to the C-terminus of the V_L . In some examples, the second antibody comprises a peptide linker between the V_H and V_L regions, e.g., a linker of (G₄S)₄ (SEQ ID NO:23). In some embodiments, the scFc antibody comprises a disulfide bond formed between the V_H and V_L chains. For example, the V_H chain may contain a cysteine residue at position 44 (C44) and the VL chain may contain a cysteine residue at position 100, wherein a disulfide bond can be formed between C₄₄ in the V_H and C₁₀₀ in the V_L . In some examples, the second antibody does not contain a KR motif at its C-terminus.

[0008] In any of the bispecific antibodies described herein, the V_H of the first antibody has the same complementarity determining regions (CDRs) as those in SEQ ID NO:1. In some examples, the V_H of the first antibody comprises the amino acid sequence of SEQ ID NO:1. In one example, the heavy chain of the first antibody comprises the amino acid sequence of residues 20-470 of SEQ ID NO: 9. In one example, the heavy chain of the first antibody comprises the amino acid sequence of SEQ ID NO: 9, 149, or 150. Alternatively or in addition, the V_L of the first antibody has the same CDRs as those in SEQ ID NO:2. In some examples, the V_L of the first antibody comprises the amino acid sequence of SEQ ID NO:2.

[0009] Further, the V_H of the second antibody can have the same CDRs as those in any of SEQ ID NOs:3, 4 and 123-126. In some example, the V_H of the second antibody comprises any of the amino acid sequences of SEQ ID NO:3, 4 and 123-126. Alternatively or in addition, the V_L of the second antibody has the same CDRs as those in any of SEQ ID NOs:5-8 and 127-130. In some examples, the V_L of the second antibody comprises residues 1-111 of any one of the amino acid sequences of SEQ ID NOs:5-8 and 127. In one example, the V_L of the second antibody comprises any one of the amino acid sequences of SEQ ID Nos: 5-8 and 127-130.

[0010] In some examples, the bispecific antibody described herein comprises a first polypeptide that comprises the amino acid sequence of SEQ ID NO:10 and the second polypeptide comprises any of the amino acid sequences of SEQ ID NOs: 11-20, 47-122, 141-148, and 151-158.

[0011] In another aspect, the present disclosure provides a bispecific antibody, which comprises a first antibody binding to plasma kallikrein (pKal) and a second antibody binding to Factor XII, for example, the first antibody binding to active pKal and/or the second antibody binding to active Factor XII (FXIIa). In some embodiments, the first antibody comprises a V_H chain that comprises the same complementarity determining regions (CDRs) as those in SEQ ID NO:1, and/or a V_L chain that comprises the same CDRs as those in SEQ ID NO:2. For example, the V_H of the first antibody comprises the amino acid sequence of SEQ ID NO:1, and/or the V_L of the first antibody comprises the amino acid sequence of SEQ ID NO:2.

[0012] Alternatively or in addition, the second antibody comprises a V_H chain that comprises the same CDRs as those in SEQ ID NO:3 or 4, and/or a V_L chain that comprises the same CDRs as those in SEQ ID NO:5, 6, 7, or 8. For

example, the V_H chain of the second antibody comprises the amino acid sequence of SEQ ID NO:3 or 4; and/or the V_L of the second antibody comprises the amino acid sequence of SEQ ID NO:5, 6, 7, or 8.

[0013] Alternatively or in addition, the second antibody comprises a V_H chain that comprises the same CDRs as those in any of SEQ ID NOs:123-126, and/or a V_L chain that comprises the same CDRs as those in SEQ ID NOs:127. For example, the V_H chain of the second antibody comprises the amino acid sequence of any one of SEQ ID NO: 123-126; and/or the V_L of the second antibody comprises residues 1-111 of any one of the amino acid sequence of SEQ ID NO: 5-8 and 127.

[0014] In yet another aspect, the present disclosure provides an isolated nucleic acid or nucleic acid set, comprising a first nucleotide sequence encoding the first polypeptide or first antibody as described herein and a second nucleotide sequence encoding the second polypeptide or second antibody as described herein. In some embodiments, the first and second nucleotide sequences are located on two separate nucleic acid molecules (e.g., two vectors such as expression vectors). Alternatively, the first and second nucleic nucleotide sequences are located on one nucleic acid molecule (e.g., a vector such as an expression vector).

[0015] The nucleic acid or nucleic acid set described herein can be a vector set comprising a first vector that comprises the first nucleotide sequence and a second vector that comprises the second nucleotide sequence. In some examples, the first and second vectors are expression vectors, in which the first and second nucleotide sequences are in operably linkage to a promoter. In other examples, the nucleic acid described herein is a vector comprising both the first and second nucleotide sequences. Any of the vectors described herein can be an expression vector. For example, the expression vector can comprise the first and second nucleotide sequences are in operably linkage to a promoter. Also within the scope of this disclosure is a host cell comprising the vector or vector set described herein.

[0016] Further, the present disclosure provides compositions comprising any of the bispecific antibodies or the nucleic acid/nucleic acid sets as described herein and a pharmaceutically acceptable carrier. Such a composition can be used to treat a disease associated with the contact activation system (e.g., hereditary angioedema (HAE) or thrombosis). The treatment method described herein comprises administering to a subject in need thereof an effective amount of the pharmaceutical composition described herein. The present disclosure also provides a pharmaceutical composition for use in treating the disease as described herein, wherein the pharmaceutical composition comprises any of the bispecific antibody described herein or a nucleic acid/nucleic acid set that encodes the bispecific antibody, and a pharmaceutical acceptable carrier, and the use of such a pharmaceutical composition in manufacturing a medicament for use in treating such a disease such as HAE or thrombosis. In some embodiments, thrombosis is associated with atrial fibrillation, deep vein thrombosis (DVT), pulmonary embolism, stroke, or an arterial or venous thrombotic event.

[0017] In still another aspect, the present disclosure features a method for preparing a bispecific antibody, the method comprising: (a) culturing the host cell or host cell set as described herein under conditions allowing for expression of the first polypeptide and the second polypeptide; and (b) isolating the bispecific antibody that comprises the first

polypeptide and the second polypeptide. In some examples, the host cell comprises an expression vector comprising a first nucleotide sequence encoding the first polypeptide and a second nucleotide sequence encoding the second polypeptide.

[0018] The details of one or more embodiments of the disclosure are set forth in the description below. Other features or advantages of the present disclosure will be apparent from the following drawings and detailed description of several embodiments, and also from the appended claims.

BRIEF DESCRIPTION OF THE DRAWINGS

[0019] The following drawings form part of the present specification and are included to further demonstrate certain aspects of the present disclosure, which can be better understood by reference to one or more of these drawings in combination with the detailed description of specific embodiments presented herein.

[0020] FIG. 1 is a graph showing the activity of various bispecific antibody clones for inhibiting pKal, including clones X120-A01 (scFv=559C-M184-B04 H4L), X121-E01 (scFv=559C-M184-G03 H4L), X122-A01 (scFv=559C-M71-F06 H4L), and X122-C01 (scFv=559C-M71-F06 L4H).

[0021] FIG. 2 includes graphs showing the FXIIa inhibition activity of clones X120-A01 (A and B), X122-A01 (C), X121-E01 (D), X122-C01 (E), and control clone M71-F06 IgG (F).

[0022] FIG. 3 includes graphs showing the analytical size exclusion chromatography (SEC) traces of 5 exemplary bispecific molecules. The front peak shows that these clones have a high molecular weight aggregate, ranging from % HMW 16.5-33.8. A: 620I-X136-C11. B: 620I-X136-C05. C: 620I-X136-G05. D: 620I-X136-D12. E: 620I-X136-A01.

[0023] FIG. 4 includes graphs showing reduction of high molecular weight aggregate for 620I-X0173-A11 (620I-X0136-D12 with H44/L100 engineered disulfide bond) across a range of concentrations. A: 620I-X0173-A11 at 1mg/mL. B: 620I-X0173-A11 at 10 mg/mL. C: 620I-X0173-A11 at 20 mg/ml. D: 620I-X0173-A11 at 45 mg/ml.

[0024] FIG. 5 includes graphs showing the inhibitory activities of an anti-pKal antibody, an anti-FXIIa antibody, a combination of the anti-pKal antibody and the anti-FXIIa antibody, and the bispecific antibody D12, as determined by a reconstituted plasma assay. A: DX-2930 in the presence of one-chain HMWK. B: anti-FXIIa antibody in the presence of one-chain HMWK. C: DX-2930+ anti-FXIIa in the presence of one-chain HMWK. D: bispecific clone 620I-X0136-D12 in the presence of one-chain HMWK.

[0025] FIG. 6 includes graphs showing the inhibitory activities of an anti-pKal antibody, an anti-FXIIa antibody, a combination of the anti-pKal antibody and the anti-FXIIa antibody, and the bispecific antibody D12, as determined by a reconstituted plasma assay. A: DX-2930 in the absence of HMWK. B: anti-FXIIa antibody in the absence of HMWK. C: DX-2930+ anti-FXIIa in the absence of HMWK. D: bispecific clone 620I-X0136-D12 in the absence of HMWK.

[0026] FIG. 7 includes graphs showing the inhibitory activities of an anti-pKal antibody, an anti-FXIIa antibody, a combination of the anti-pKal antibody and the anti-FXIIa antibody, and the bispecific antibody D12, as determined by a plasma assay. A: DX-2930 in the absence of HMWK. B: anti-FXIIa antibody in the absence of HMWK. C:

DX-2930+ anti-FXIIa in the absence of HMWK. D: bispecific clone D12 in the absence of HMWK.

[0027] FIG. 8 is a graph showing the effects of a bispecific antibody (D12) at three concentrations compared to an anti-FXIIa antibody (D06) and an anti-pKal antibody (H03) in an activated partial thromboplastin time (APTT) assay.

[0028] FIG. 9 includes graphs showing biacore binding of 620I-X0173-A11 (620I-X0136-D12 with disulfides) against pKal (Top sensorgram) and FXIIa (Bottom sensorgram). A: pKal binding (top curve) is higher than blank surface (middle) and pre-Kallikrein (bottom). Original FXIIa isolates showed non-specific binding to the biacore chip, which explains the binding signals seen for pre-Kal and blanks. B: FXIIa binding (top curve) is demonstrably higher than FXII (bottom) and blank (middle).

[0029] FIG. 10 includes graphs showing IC₅₀ and Ki, apparent calculations of 3 disulfide-constrained bispecific antibodies in Plasma Inhibition Assay. A and B: clone 620I-X0173-A11. C and D: clone 620I-X0173-C07. E and F: clone 620I-X0173-G11.

[0030] FIG. 11 is a graph showing the inhibitory features of bispecific antibody 620I-X0177-A01 (a.k.a. 620I-X0173-A11) as determined in Plasma Inhibition Assay.

[0031] FIG. 12 includes graphs showing that there are drop-offs in affinity between the parent IgGs and the bispecific antibodies. A: binding features of parent clone 559C-X0211-A01 (left panel) and bispecific antibody 620I-X0177-A01 (right panel). B: binding features of parent clone DX-2930 (left panel) and bispecific antibody A01 (right panel).

[0032] FIG. 13 is a chart showing dose-dependent delay of APTT by various antibodies as indicated. Clones D06, 1A01 and F12 are anti-FXIIa antibodies. Clone H03 is an anti-pKal antibody. Clones D12 and 7A01 are bispecific antibodies without and with disulfide bond, respectively.

[0033] FIG. 14 is a chart showing dose-dependent delay of fibrin deposition by clones 1A01 (559C-X211-A01) and 7A01 (620I-X0177-A01).

[0034] FIG. 15 is a SDS-PAGE protein gel showing samples of the bispecific antibody 620I-X0177-A01 under reduced conditions (lanes 2-4) and non-reduced conditions (lanes 6-8).

[0035] FIG. 16 includes graphs showing the analytical size exclusion chromatography (SEC) traces of the bispecific antibody 620I-X0177-A01 demonstrating pH dependent cleavage. The peaks between 15.7-16.1 minutes represent the correctly formed bispecific antibody. The peaks at 17 minutes represent DX-2930 IgG1. The peaks at 22 minutes represent the cleaved single chain antibody. A: pH 6.0. B: pH 7.0. C: 8.0.

[0036] FIG. 17 includes SDS-PAGE protein gels of the indicated bispecific antibodies, which are engineered to either mutate or delete the IgG C-terminal Lysine at t=0. A: non-reduced conditions. B: reduced conditions.

[0037] FIG. 18 shows a SDS-PAGE protein gel including the indicated bispecific antibodies engineered to either mutate or delete the IgG C-terminal lysine at t=48 hr under reduced conditions. The positive control is bispecific antibody 620I-X0177-A01.

[0038] FIG. 19 includes graphs showing the analytical size exclusion chromatography (SEC) traces of control bispecific antibody 620I-X0177-A01. The peaks between 15.7-16.1 minutes represent the correctly formed bispecific antibody. The peaks at 17 minutes represent DX-2930 IgG1. The

peaks at 22 minutes represent the cleaved single chain antibody. A: t=0. B: t=48 hrs.

[0039] FIG. 20 includes graphs showing the analytical size exclusion chromatography (SEC) traces of re-engineered bispecific antibodies after 48 hours at room temperature at pH=7.5. A: 620I-X180-E07. B: 620I-X180-G03. C: 620I-X180-A05. D: 620I-X180-E06. E: 620I-X180-C11. F: 620I-X179-C01. G: 620I-X179-G05. H: 620I-X179-A09.

[0040] FIG. 21 shows a SDS-PAGE protein gel showing the indicated bispecific antibodies engineered to either mutate or delete the heavy chain IgG C-terminal lysine under non-reduced conditions. The positive control is 620I-X0177-A01. Samples were incubated with Endoproteinase Lys C at 37° C. for 1 hour.

[0041] FIG. 22 includes graphs showing pKal inhibition by example bispecific antibodies. Plate 1 shows inhibition features of bispecific antibodies 620I-X0179-A09 (open circles), 620I-X0179-C01 (closed triangles), and 620I-X0179-E05 (open triangles). Plate 2 shows inhibition features of bispecific antibodies 620I-X0179-G05 (open circles), 620I-X0180-E07 (closed triangles), and 620I-X0180-G03 (open triangles). Plate 3 shows inhibition features of bispecific antibodies 620I-X0180-A05 (open circles) and 620I-X0180-C11 (closed triangles). The antibody DX-2930 was used as a control on each of the plates.

[0042] FIG. 23 includes graphs showing FXIIa inhibition by example bispecific antibodies. Plate 1 shows inhibition features of bispecific antibodies 620I-X0179-A09 (open circles), 620I-X0179-C01 (closed triangles), and 620I-X0179-E05 (open triangles). Plate 2 shows inhibition features of bispecific antibodies 620I-X0179-G05 (open circles), 620I-X0180-E07 (closed triangles), and 620I-X0180-G03 (open triangles). Plate 3 shows inhibition features of bispecific antibodies 620I-X0180-A05 (open circles) and 620I-X0180-C11 (closed triangles). The antibody DX-4012 (559C-M0192-H11) was used as a control on each of the plates.

[0043] FIG. 24 includes graphs showing inhibition of activated plasma by example bispecific antibodies. The top left panel shows inhibition features of DX-2930 from control plates 1, 2, and 3, and DX-4012. The top right panel shows inhibition features of bispecific antibodies 620I-X0179-A09 (closed circles), 620I-X0179-C01 (open circles). The bottom left panel shows inhibition features of bispecific antibodies 620I-X0179-E05 (closed circles), 620I-X0179-G05 (open circles), and 620I-X0180-E07 (closed triangles). The bottom right panel shows inhibition features of bispecific antibodies 620I-X0180-G03 (closed circles), 620I-X0180-A05 (open circles), and 620I-X0180-C11 (closed triangles).

DETAILED DESCRIPTION OF THE INVENTION

[0044] The contact activation system initiates the intrinsic pathway of coagulation through the release of the proinflammatory peptide bradykinin (BK). BK release is facilitated by a series of enzyme activation steps in the contact activation system. Factor XIIa (FXIIa) converts pre-kallikrein to plasma kallikrein (pKal). Activated pKal then cleaves high molecular weight kininogen (HMWK) to release bradykinin (BK). Importantly, pKal can also activate latent Factor XII to produce additional active Factor XIIa. It

is believed that a positive feedback loop is formed, with pKal activating FXII to FXIIa, and FXIIa activating pre-kallikrein to pKal.

[0045] In diseases associated with the contact activation system, such as hereditary angioedema (HAE) or thrombosis, uncontrolled levels of BK can induce inflammatory responses, such as patient HAE attacks. Accordingly, agents for controlling the levels of BK, e.g., inhibitors of pKal and FXII, may have important therapeutic value.

[0046] Described herein are bispecific antibodies that bind to both pKal and FXII, e.g., active pKal and/or FXIIa, and uses thereof in inhibiting both pKal and FXII and treating diseases associated with the contact activation system, such as hereditary angioedema (HAE) and thrombosis. As shown in Examples below, a number of exemplary bispecific antibodies as described herein were shown to inhibit both pKal and FXIIa activities. Without wishing to be bound by theory, the bispecific antibodies described herein are expected to exhibit superior therapeutic effects in treating diseases associated with contact activation system, as compared to agents that can inhibit either pKal or FXII, because the bispecific antibodies can inhibit the activity of both pKal and FXII, thereby reducing the BK levels synergistically via, e.g., blocking the positive feedback loop between pKal and FXII. Bispecific Antibodies Binding to pKal and FXII

[0047] As used herein, an antibody (interchangeably used in plural form) is an immunoglobulin molecule, or a functional fragment thereof, that is capable of binding to a target antigen, such as a carbohydrate, polynucleotide, lipid, or polypeptide, through at least one antigen recognition site located in the variable region of the immunoglobulin molecule. A multispecific antibody, e.g., a bispecific antibody, is an immunoglobulin molecule or a functional fragment/variant thereof, that is capable of binding to multiple target antigens, e.g., two antigens or two epitopes of one antigen. The bispecific antibodies described herein can bind to both plasma kallikrein (pKal) and Factor XII. In some embodiments, the bispecific antibodies can bind to and inhibit both active pKal and FXIIa.

[0048] Antigen, as used herein, refers to any molecule (e.g., protein, nucleic acid, polysaccharide, or lipid) that has the ability to generate antibodies. An epitope is a portion of an antigen (e.g., a portion of pKal or FXII) to which an antibody binds. Epitopes usually consist of chemically active (such as polar, non-polar or hydrophobic) surface groupings of moieties such as amino acids or polysaccharide side chains and can have specific three-dimensional structural characteristics, as well as specific charge characteristics. An epitope can be linear in nature or can be a discontinuous epitope, e.g., a conformational epitope, which is formed by a spatial relationship between non-contiguous amino acids of an antigen rather than a linear series of amino acids. A conformational epitope includes epitopes resulting from folding of an antigen, where amino acids from differing portions of the linear sequence of the antigen come in close proximity in 3-dimensional space.

[0049] The bispecific antibody described herein comprises two antibody portions, a first antibody portion binding to pKal (e.g., active pKal) and a second antibody portion binding to FXII (e.g., FXIIa). The first and second antibodies portions can be derived from two parent antibodies capable of binding to the desired antigens, i.e., pKal (e.g., active pKal) and FXII (e.g., FXIIa). One or both of the parent antibodies for constructing the bispecific antibodies as

described herein can be naturally occurring antibodies (e.g., an antibody derived from a suitable donor such as human, mouse, rat, rabbit, horse, or sheep), genetically engineered antibodies (e.g., humanized antibodies, chimeric antibodies), or antibodies derived from a natural or synthetic antibody library. In some embodiments, one parent antibody is an IgG antibody, e.g., an IgG antibody binding to pKal such as DX-2930 or an IgG antibody binding to FXIIa, and the other parent antibody is a scFv antibody, e.g., a scFv antibody binding to FXIIa such as the anti-FXIIa clones described herein or an scFv antibody binding to pKal.

[0050] The heavy chain of a naturally occurring IgG molecule typically contains a lysine residue at the C-terminus. In some embodiments, this C-terminal lysine residue can be either deleted or mutated, e.g., to a glycine residue, in the bispecific antibodies disclosed herein. Alternatively or in addition, the KR motif, which typically presents at the junction of a light chain variable region and a light chain constant region, can be deleted from the light chain of the first antibody, the second antibody, or both, in the bispecific antibodies described herein. In some examples, the KR motif is deleted from the scFv portion (e.g., at the C-terminus of the scFv) of any of the bispecific antibodies described herein. These mutations may reduce proteolytic cleavage and/or improve expression, production, and/or manufacture of the bispecific antibody.

[0051] In some examples, at least one parent antibody can be an affinity matured antibody, which refers to an antibody having one or more modifications in one or more CDRs or framework regions (FRs) as compared to the unmodified parent antibody, leading to an improvement in the affinity of the antibody for the target antigen. Preferred affinity matured antibodies may have nanomolar or even picomolar affinities for the target antigen. Affinity maturation of an antibody can be performed by various methods known in the art, including by variable domain shuffling (see, e.g., Marks et al., 1992, Bio/Technology 10:779-783), random mutagenesis of CDR and/or FR residues (see, e.g., Barbas et al., 1994, Proc Natl. Acad. Sci., USA 91:3809-3813; Schier et al., 1995, Gene 169:147-155; Yelton et al., 1995, J. Immunol. 155: 1994-2004; Jackson et al., 1995, J. Immunol. 154(7):3310⁻⁹; and Hawkins et al., 1992, J. Mol. Biol. 226:889-896). The parent antibodies can be of any class, such as IgD, IgE, IgG, IgA, or IgM, or a sub-class thereof, or a single chain antibody, such as a scFv.

[0052] Each antibody portion in the bispecific antibody as described herein can be an antibody in any form, including, but not limited to, intact (i.e., full-length) antibodies, antigen-binding fragments thereof (such as Fab, Fab', F(ab')₂, Fv), single chain antibodies (scFv antibodies), and tetravalent antibodies. In some embodiments, the bispecific antibody is tetravalent, which comprises two binding sites for pKal and two binding sites for FXII.

[0053] In some embodiments, the anti-pKal portion, the anti-FXII portion, or both in the bispecific antibodies described herein specifically bind to the corresponding target antigen or an epitope thereof. An antibody that "specifically binds" to an antigen or an epitope is a term well understood in the art, and methods to determine such specific binding are also well known in the art. A molecule is said to exhibit "specific binding" if it reacts or associates more frequently, more rapidly, with greater duration and/or with greater affinity with a particular target antigen than it does with alternative targets. An antibody "specifically

binds" to a target antigen or epitope if it binds with greater affinity, avidity, more readily, and/or with greater duration than it binds to other substances. For example, an antibody that specifically (or preferentially) binds to an antigen (e.g., human pKal or FXII) or an antigenic epitope therein is an antibody that binds this target antigen with greater affinity, avidity, more readily, and/or with greater duration than it binds to other antigens or other epitopes in the same antigen. It is also understood by reading this definition that, for example, an antibody that specifically binds to a first target antigen may or may not specifically or preferentially bind to a second target antigen. As such, "specific binding" or "preferential binding" does not necessarily require (although it can include) exclusive binding. Generally, but not necessarily, reference to binding means preferential binding. In some examples, an antibody that "specifically binds" to a target antigen or an epitope thereof may not bind to other antigens or other epitopes in the same antigen. In some embodiments, the bispecific antibody described herein specifically binds to both active pKal and FXIIa.

[0054] In some embodiments, a bispecific antibody as described herein has a suitable binding affinity for one or both of the target antigens (e.g., pKal or FXIIa) or antigenic epitopes thereof. As used herein, "binding affinity" refers to the apparent association constant or K_A . The K_A is the reciprocal of the dissociation constant (K_D). The bispecific antibody described herein may have a binding affinity (K_D) of at least 10^{-5} , 10^{-6} , 10^{-7} , 10^{-8} , 10^{-9} , 10^{-10} M, or lower for one or both of the target antigens or antigenic epitopes. An increased binding affinity corresponds to a decreased K_D . Higher affinity binding of an antibody for a first antigen and a second antigen relative to a third antigen can be indicated by a higher K_A (or a smaller numerical value K_D) for binding the first antigen and second antigen than the K_A (or numerical value K_D) for binding the third antigen. In such cases, the antibody has specificity for the first antigen and second antigen (e.g., a first protein in a first conformation or mimic thereof and a second protein in a first conformation or mimic thereof) relative to the third antigen (e.g., the same first or second protein in a second conformation or mimic thereof; or a third protein). Differences in binding affinity (e.g., for specificity or other comparisons) can be at least 1.5, 2, 3, 4, 5, 10, 15, 20, 37.5, 50, 70, 80, 91, 100, 500, 1000, 10,000 or 10^5 fold.

[0055] Binding affinity (or binding specificity) can be determined by a variety of methods including equilibrium dialysis, equilibrium binding, gel filtration, ELISA, surface plasmon resonance, or spectroscopy (e.g., using a fluorescence assay). Exemplary conditions for evaluating binding affinity are in HBS-P buffer (10 mM HEPES pH7.4, 150 mM NaCl, 0.005% (v/v) Surfactant P20). These techniques can be used to measure the concentration of bound binding protein as a function of target protein concentration. The concentration of bound binding protein ([Bound]) is related to the concentration of free target protein ([Free]) and the concentration of binding sites for the binding protein on the target where (N) is the number of binding sites per target molecule by the following equation:

$$[\text{Bound}] = [N][\text{Free}]/(Kd + [\text{Free}])$$

[0056] It is not always necessary to make an exact determination of KA, though, since sometimes it is sufficient to obtain a quantitative measurement of affinity, e.g., determined using a method such as ELISA or FACS analysis, is proportional to KA, and thus can be used for comparisons, such as determining whether a higher affinity is, e.g., 2-fold higher, to obtain a qualitative measurement of affinity, or to obtain an inference of affinity, e.g., by activity in a functional assay, e.g., an *in vitro* or *in vivo* assay.

(i) Anti-pKal Portion

[0057] Any antibody capable of binding to pKal, such as active pKal, can be used in constructing the bispecific antibodies described herein. In some examples, the anti-pKal antibody portion in the bispecific antibody can bind to human pKal and inhibits its activity by at least 50% (e.g., 60%, 70%, 80%, 90%, 95% or greater). The inhibition constant (Ki) provides a measure of inhibitor potency; it is the concentration of inhibitor required to reduce enzyme activity by half and is not dependent on enzyme or substrate concentrations. The inhibitory activity of an anti-pKal antibody portion in the bispecific antibody described herein can be determined by routine methods. In some examples, the bispecific antibody as described herein has an anti-pKal $K_{i,app}$ value lower than 1 nM, e.g., 0.5 nM, 0.2 nM, 0.1 nM, 0.09 nM, 0.08 nM, 0.07 nM, 0.06 nM, 0.05 nM, 0.04 nM, 0.03 nM, 0.02 nM, 0.01 nM, or lower. The $K_{i,app}$ value of an antibody can be estimated following the methods known in the art.

[0058] In some embodiments, the anti-pKal portion of the bispecific antibody can interact with one or more of the following residues: V410, L412, T413, A414, Q415, R416, L418, C419, H434, C435, F436, D437, G438, L439, W445, Y475, K476, V477, S478, E479, G480, D483, F524, E527, K528, Y552, D554, Y555, A564, D572, A573, C574, K575, G576, S578, T596, 5597, W598, G599, E600, G601, C602, A603, R604, Q607, P608, G609, V610, and Y611 in human pKal. The amino acid sequence of the C-terminal fragment of human pKal that encompasses the involved amino acid residues (boldfaced and underlined) is shown below (SEQ ID NO:21):

391-IVGGTNSSWG EWPWQVSLQV **KLT**AQR**H**L**C**G GSLIGHQWVL
TAA**HCFDGLP** LQDVWRIYSG ILNLSDITKD TPFSQIKEII
IHQN**YKVSEG** NH**DIALIKLQ** APLNYTEFQK PISLPSKGDT
STIYIINCWTI **GWGFSKEKGE** IQNIILQKVNI PLVTNEECQK
RY**QDYK**ITQR MVCAGYKEGG **KDACKGDS**GG PLVCKHNGMW
RLVGIT**TSGE** **GCARRE****QPGV** YTKVAEYMDW ILEKTQSSDG
KAQMOSPA-638

[0059] In some examples, the anti-pKal antibody portion can bind an epitope of the pKal, the epitope comprising one of the following segments in SEQ ID NO:21 shown above: V410-C419, H434-L439, Y475-G480, F524-K528, Y552-Y555, D572-S578, T596-R604, or Q607-Y611.

[0060] In one example, the anti-pKal portion of the bispecific antibody described herein is derived from antibody DX-2930, which is described in US 20120201756 (incorporated by reference herein). The heavy chain variable region and light chain variable region of DX-2930, as well

as the full-length heavy chain and light chain of this antibody, are provided below (CDR regions: boldfaced and underlined; signal sequences: italic). The heavy chain CDR1-3 sequences correspond to SEQ ID NOs: 159-161, respectively, and the light chain CDR1-3 sequences correspond to SEQ ID NOs: 162-164.

```

Heavy chain variable region of DX-2930
(SEQ ID NO: 1):
EVOLLESGGGLVQPGGSLRLSCAASGFTFS
HYIMMWVRQAPGKGLEWVSGIYSSGGITVYADSVVKGRF
TISRDN SKNTLYLQMNSLRAEDTAVYYCAY
RIGVPRRDEFDIWGQGTMVTVSS

Light chain variable region of DX-2930
(SEQ ID NO: 2):
DIQMTQSPSTLSASVGDRV TITCRASQSISSWLA
WYQQKPGKAPKLLIYKASTLESGVPSRFSGSGSG
TEFTLTISLQPDDFATYYCQQYNTYWTFQGQTKVEIK

DX-2930 heavy chain (SEQ ID NO: 9)
MGWS CIIILFLVATATGAHSEVOLLESGGGLVQPGGSLRLSCAASGFTFSH
YIMMWVRQAPGKGLEWVSGIYSSGGITVYADSVKGRT TISRDN SKNTLYL
QMNSLRAEDTAVYYCAYRRIGVPRRDEF D IWI GQGT MVT VSSA STKGPSVF
PLAPSSKSTSGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP AVLQS
SGLYSLSSVTVTPSSSLGTQTYICVN HKSNTKVDKRVEPKSCDKTHTC
PPCPAPELLGGPSVFLFPPKP KDTLMISRPEVTCVVVDVSHEDPEVKFN
WYVDGVEVHNAKTKPREEQYN STYRVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPIEKTIKAKGQPREPVYTLPPSREEMTKNQVSLTCLVKGFYPSD
IAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS
VMHEALHNHYTQKSLSLSPGK

DX-2930 light chain (SEQ ID NO: 10)
MGWS CIIILFLVATATGVHSDI QM TQSPSTLSASVGDRV TITCRASQSISS
WLAWYQQKPGKAPKLLIYKASTLESGVPSRFSGSGSGTEFTLTISLQP D
DFATYYCQQYNTYWTFGQGT KVEIKRTVAAPS VFI FPPSDEQLKSGTASV
VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSSLSTTLS
KADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

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[0061] In some examples, the anti-pKal portion of the bispecific antibody comprises a heavy chain variable region that comprises an amino acid sequence at least 80% (e.g., 85%, 90%, 95%, or 98%) identical to SEQ ID NO:1 and/or a light chain variable region that comprises an amino acid sequence at least 80% (e.g., 85%, 90%, 95%, or 98%) identical to SEQ ID NO:2. The “percent identity” of two amino acid sequences is determined using the algorithm of Karlin and Altschul *Proc. Natl. Acad. Sci. USA* 87:2264-68, 1990, modified as in Karlin and Altschul *Proc. Natl. Acad. Sci. USA* 90:5873-77, 1993. Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) of Altschul, et al. *J. Mol. Biol.* 215:403-10, 1990. BLAST protein searches can be performed with the XBLAST program, score=50, wordlength=3 to obtain amino acid sequences homologous to the protein molecules

of interest. Where gaps exist between two sequences, Gapped BLAST can be utilized as described in Altschul et al., *Nucleic Acids Res.* 25(17):3389-3402, 1997. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used.

[0062] In other examples, the anti-pKal portion in the bispecific antibody as described herein comprises a heavy chain variable region that comprises the same three CDRs as those in SEQ ID NO:1, and/or the same three CDRs as those in SEQ ID NO:2. Two heavy chain variable regions (or two light chain variable regions) having the same CDRs means that the CDRs in the two heavy chain variable regions (or light chain variable regions) as determined by the same numbering scheme are identical. Exemplary numbering schemes for determining antibody CDRs include the “Kabat” numbering scheme (Kabat et al. (1991), 5th Ed. Public Health Service, National Institutes of Health, Bethesda, Md.), the “Chothia” numbering scheme (Al-Lazikani et al., (1997) JMB 273,927-948), the “Contact” numbering scheme (MacCallum et al., *J. Mol. Biol.* 262: 732-745 (1996)), the “IMGT” numbering scheme (Lefranc MP et al., *Dev Comp Immunol*, 2003 January; 27(1):55-77), and the “AHo” numbering scheme (Honegger A and Pluckthun A, *J Mol Biol*, 2001 Jun. 8; 309(3):657-70). As known to those skilled in the art, the CDR regions of the exemplary anti-pKal and anti-FXII antibodies identified herein are determined by the “Chothia” numbering scheme, which is used as an example.

[0063] Alternatively, the anti-pKal portion can include one or more (e.g., up to 2, 3, 4, 5, 6, 7, or 8) mutations in one or more of the CDRs as compared to SEQ ID NO:1 and/or SEQ ID NO:2. Such mutations can be conservative amino acid substitutions. As used herein, a “conservative amino acid substitution” refers to an amino acid substitution that does not alter the relative charge or size characteristics of the protein in which the amino acid substitution is made. Conservative substitutions of amino acids include substitutions made amongst amino acids within the following groups: (a) M, I, L, V; (b) F, Y, W; (c) K, R, H; (d) A, G; (e) S, T; (f) Q, N; and (g) E, D.

[0064] In any of the examples described herein, the anti-pKal portion of the bispecific antibody may comprise one or more (e.g., 1, 2, 3, 4, 5, or more) mutations or deletions as compared with a reference antibody. Such mutations may be introduced, for example to reduce proteolytic cleavage of the bispecific antibody, and/or to improve expression, production, and/or manufacture of the bispecific antibody. In some embodiments, the anti-pKal portion of the bispecific antibody is an IgG and the heavy chain of the IgG has the C-terminal lysine residue removed or mutated as compared with its wild-type counterpart. In some embodiments, the IgG heavy chain C-terminal lysine is mutated to a neutral amino acid residue, for example, a glycine residue or an alanine residue.

[0065] Example sequences of such mutated heavy chains of the anti-pKal portion of a bispecific antibody are provided below (using the heavy chain of DX-2930 as an example).

DX-2930 heavy chain including deletion of C-terminal lysine residue

(SEQ ID NO: 149)

```
MGWSCIILFLVATATGAHSEVOLLESGGGLVQPGGSLRLSCAASGFTFSH
YIMMWVRQAPGKGLEWVSGIYSSGGITVYADSVKGRFTISRDNSKNTLYL
QMNSLRAEDTAVYYCAYRRIGVPRRDEFDIWGQGTMVTVSSASTKGPSVF
PLAPSSKSTSGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ
SGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTC
PPCPAPELLGGPSVFLFPPKPKDTLMISRTPETCVVVVDVSHEDPEVKFN
WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPIEKTIKAKGQPREPQVTLPSSREEMTKNQVSLTCLVKGFYPSPD
IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS
VMHEALHNHYTQKSLSLSPG
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DX-2930 heavy chain including mutation of C-terminal lysine to glycine

(SEQ ID NO: 150)

```
MGWSCIILFLVATATGAHSEVOLLESGGGLVQPGGSLRLSCAASGFTFSH
YIMMWVRQAPGKGLEWVSGIYSSGGITVYADSVKGRFTISRDNSKNTLYL
QMNSLRAEDTAVYYCAYRRIGVPRRDEFDIWGQGTMVTVSSASTKGPSVF
PLAPSSKSTSGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ
SGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTC
PPCPAPELLGGPSVFLFPPKPKDTLMISRTPETCVVVVDVSHEDPEVKFN
WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPIEKTIKAKGQPREPQVTLPSSREEMTKNQVSLTCLVKGFYPSPD
IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS
VMHEALHNHYTQKSLSLSPGG
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[0066] The italicized portions of the sequences provided above refer to the signal peptides. The anti-pKal portion of the bispecific antibody disclosed herein may include the same signal peptides, may have the signal peptides removed or replaced with a different signal peptide. Signal peptides for use in producing secretory proteins are well known in the art.

[0067] The anti-pKal portion in the bispecific antibody can be in any antibody form, including, but not limited to, intact (i.e., full-length) antibodies, antigen-binding fragments thereof (such as Fab, Fab', F(ab')₂, Fv), and single chain antibodies. In some examples, the heavy chain variable region of the anti-pKal portion as described herein is linked to a heavy chain constant region (C_H), which can be the full-length of a heavy chain constant region or a portion thereof (e.g., C_{H1} , C_{H2} , C_{H3} , or a combination thereof). The heavy chain constant region can be derived from any C_H known in the art. In some embodiments, the C_H is a gamma heavy chain. Alternatively or in addition, the light chain variable region of the anti-pKal portion is linked to a light chain constant region (C_L), which can be any C_L known in the art. In some examples, the C_L is a kappa light chain. In other examples, the C_L is a lambda light chain. Antibody heavy and light chain constant regions are well known in the art, e.g., those provided in the IMGT database (www.imgt.org) or at www.vbase2.org/vbstat.php, both of which are

incorporated by reference herein. In some examples, the anti-pKal portion is an IgG, which can comprise the same heavy chain as DX-2930 (SEQ ID NO:9) and/or the same light chain as DX-2930 (SEQ ID NO:10).

[0068] Alternatively, the anti-pKal portion in the bispecific antibody as described herein can be a single-chain antibody (ScFv), in which a heavy chain variable region and light chain variable region are fused, e.g., via a peptide linker such as the linker of (GGGGS)₄ (SEQ ID NO:23). In one example, the heavy chain variable region and light chain variable region are fused in an H→L orientation. In another example, the heavy chain variable region and light chain variable region are fused in an L→H orientation. In some embodiments, the light chain portion of the ScFv does not contain a Lys-Arg (KR) motif at its C-terminus.

[0069] In one example, the anti-pKal portion in the bispecific antibody described herein is DX-2930 (an IgG antibody) described herein, which comprises a heavy chain of SEQ ID NO:9 and a light chain of SEQ ID NO:10, or an antigen-binding fragment thereof.

(ii) Anti-FXII Portion

[0070] Any antibody capable of binding to FXII, such as active FXII (FXIIa), can be used in constructing the bispecific antibodies described herein. In some examples, the anti-FXII antibody portion in the bispecific antibody can bind to human FXIIa and inhibits its activity by at least 50% (e.g., 60%, 70%, 80%, 90%, 95% or greater). The inhibitory activity of the anti-FXII antibody portion in the bispecific antibody described herein can be determined by routine methods. In some examples, the bispecific antibody as described herein has an anti-FXIIa $K_{i,app}$ value lower than 1 nM, e.g., 0.5 nM, 0.2 nM, 0.1 nM, 0.09 nM, 0.08 nM, 0.07 nM, 0.06 nM, 0.05 nM, 0.04 nM, 0.03 nM, 0.02 nM, 0.01 nM, or lower. The $K_{i,app}$ value of an antibody can be estimated following the methods known in the art.

[0071] In some example, the anti-FXII portion of the bispecific antibody described herein is derived from anti-FXII clones 559C-M0071-F06, 559C-M0179-D04, 559C-M0181-C02, 559C-M0180-G03, and 559C-M0184-B04. The heavy chain variable regions and light chain variable regions of these clones are provided below (CDRs in bold-face and underlined):

Heavy chain variable region of clones 559C-M0071-F06, 559C-M0179-D04, 559C-M0181-C02, and 559C-M0180-G03 (SEQ ID NO: 3):
EVQLLESGGGLVQPGGSLRLSCAASGFTFSGYIMA

WVRQAPGKGLEWVSYIYPSSGGITVYADSVKGRF

TISRDNSKNTLYLQMNSLRAEDTAVYYCTR

ORYRGPKYYYYMDVWGKGTTVTVSS

Heavy chain variable region of clone 559C-M0184-B04 (SEQ ID NO: 4):
EVQLLESGGGLVQPGGSLRLSCAASGFTFSFYSMH

WVRQAPGKGLEWVSRIYPSSGGVTKYADSVKGRF

TISRDNSKNTLYLQMNSLRAEDTAVYYCTR

ORYRGPKYYYYMDVWGKGTTVTVSS

-continued

Light chain variable region of clones 559C-M0071-F06 and 559C-M0184-B04 (SEQ ID NO: 5):
DIQMTQSPLSLPVTPGEPASISCRSSQSLLHSNGNYLD

WYLQKPGQSPQQLIYLGSNRASGVPDFRS

GSGSGTDFTLKISRVEAEDVGVYYC

MQALQTPWTFGQGTKVEIKR

Light chain variable region of clone 559C-M0179-D04 (SEQ ID NO: 6):
DIQMTQSPLSLSVAPGEPASISCRSSQSLLHRNGHNYLD

WYLQKPGQSPQQLIYLGSNRASGVPERFS

GSGSGTDFTLRISRVEAEDVGVYYC

MQALQARTFGQGTKVEIKR

Light chain variable region of clone 559C-M0181-C02 (SEQ ID NO: 7):
DIQMTQSPLSLPVTPGEPASISCRSSQSLLHSNGNYLD

WYLQKPGQSPQQLIYLGSNRASGVPDFRS

GSGSGTDFTLKISRVEAEDVGVYYC

MQALQTRTFGQGTKVEIKR

Light chain variable region of clone 559C-M0180-G03 (SEQ ID NO: 8):
DIQMTQSPLSLPVTPGEPASISCRSSQSLLHSNGNYLD

WYLQKPGQSPQIMIYLGSNRASGVPDFRS

GSGSGTDFTLKISRVEAEDVGVYYC

MQALQTPRTFGQGTKVEIKR

Heavy chain variable region of clone 620I-X0173-A11 (620I-X0177-A01) (SEQ ID NO: 123):
EVQLLESGGLVQPGGSLRLSCAASGFTFSSQYVMH

WVRQAPGKCLEWVSSIWPSGGHTRYADSVKGFR

TISRDNSKNTLYLQMNSLRAEDTAVYYCAR

ORYRGPKYVVYMDVWGQGTTVTVSS

Heavy chain variable region of clone 620I-X0173-C07 (620I-X0177-C01) (SEQ ID NO: 124):
EVQLLESGGLVQPGGSLRLSCAASGFTFSWYVMH

WVRQAPGKCLEWVSSIWPSGGKTSYADSVKGFR

TISRDNSKNTLYLQMNSLRAEDTAVYYCAR

ORYRGPKYVVYMDVWGQGTTVTVSS

Heavy chain variable region of clone 620I-X0173-E07 (620I-X0177-E01) (SEQ ID NO: 125):
EVQLLESGGLVQPGGSLRLSCAASGFTFSWYSMH

WVRQAPGKCLEWVSSIWPSGGKTRYADSVKGFR

TISRDNSKNTLYLQMNSLRAEDTAVYYCAR

ORYRGPKYVVYMDVWGQGTTVTVSS

-continued

Heavy chain variable region of clone 620I-X0173-G11 (620I-X0177-G01) (SEQ ID NO: 126):
EVQLLESGGLVQPGGSLRLSCAASGFTFSHYVMH

WVRQAPGKCLEWVSSIWPSGGLTKYADSVKGFR

TISRDNSKNTLYLQMNSLRAEDTAVYYCAR

ORYRGPKYVVYMDVWGQGTTVTVSS

Light chain variable region of clone 620I-X0173-A11 (SEQ ID NO: 127):
DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGNYLD

WYLQKPGQSPQQLIYLGSNRASGVPDFRS

GSGSGTDFTLKISRVEAEDVGVYYC

MQALQTPWTFGCGTKVEIKR

Light chain variable region of clone 620I-X0173-C07 (SEQ ID NO: 128):
DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGNYLD

WYLQKPGQSPQQLIYLGSNRASGVPDFRS

GSGSGTDFTLKISRVEAEDVGVYYC

MQALQTPWTFGCGTKVEIKR

Light chain variable region of clone 620I-X0173-E07 (SEQ ID NO: 129):
DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGNYLD

WYLQKPGQSPQQLIYLGSNRASGVPDFRS

GSGSGTDFTLKISRVEAEDVGVYYC

MQALQTPWTFGCGTKVEIKR

Light chain variable region of clone 620I-X0173-G11 (SEQ ID NO: 130):
DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGNYLD

WYLQKPGQSPQQLIYLGSNRASGVPDFRS

GSGSGTDFTLKISRVEAEDVGVYYC

MQALQTPWTFGCGTKVEIKR

[0072] The light chain variable regions of clones 620I-X0173-A11 (SEQ ID No:127), 620I-X0173-C07 (SEQ ID NO: 128), 620I-X0173-E07 (SEQ ID NO: 129), and 620I-X0173-G11 (SEQ ID NO: 130) are identical.

[0073] In some examples, the anti-FXIIa portion of the bispecific antibody comprises a heavy chain variable region that comprises an amino acid sequence at least 80% (e.g., 85%, 90%, 95%, or 98%) identical to SEQ ID NO:3 or SEQ ID NO:4, and/or a light chain variable region that comprises an amino acid sequence at least 80% (e.g., 85%, 90%, 95%, or 98%) identical to any of SEQ ID NOs:5-8. For example, the heavy chain variable region can comprise an amino acid sequence at least 80% (e.g., 85%, 90%, 95%, or 98%) identical to SEQ ID NO:3 and the light chain variable region can comprise an amino acid sequence at least 80% (e.g., 85%, 90%, 95%, or 98%) identical to any of SEQ ID NOs:5-8. Alternatively, the heavy chain variable region can comprise an amino acid sequence at least 80% (e.g., 85%, 90%, 95%, or 98%) identical to SEQ ID NO:4 and the light chain variable region can comprise an amino acid sequence at least 80% (e.g., 85%, 90%, 95%, or 98%) identical to SEQ ID NO:5.

[0074] In some examples, the anti-FXIIa portion of the bispecific antibody comprises a heavy chain variable region that comprises an amino acid sequence at least 80% (e.g., 85%, 90%, 95%, or 98%) identical to any of SEQ ID NOs: 123-126, and/or a light chain variable region that comprises an amino acid sequence at least 80% (e.g., 85%, 90%, 95%, or 98%) identical to any of SEQ ID NOs:127-130. For example, the heavy chain variable region can comprise an amino acid sequence at least 80% (e.g., 85%, 90%, 95%, or 98%) identical to SEQ ID NO:123 and the light chain variable region can comprise an amino acid sequence at least 80% (e.g., 85%, 90%, 95%, or 98%) identical to SEQ ID NO: 127. Alternatively, the heavy chain variable region can comprise an amino acid sequence at least 80% (e.g., 85%, 90%, 95%, or 98%) identical to SEQ ID NO:124 and the light chain variable region can comprise an amino acid sequence at least 80% (e.g., 85%, 90%, 95%, or 98%) identical to SEQ ID NO: 128. Alternatively, the heavy chain

variable region can comprise an amino acid sequence at least 80% (e.g., 85%, 90%, 95%, or 98%) identical to SEQ ID NO:125 and the light chain variable region can comprise an amino acid sequence at least 80% (e.g., 85%, 90%, 95%, or 98%) identical to SEQ ID NO: 129. Alternatively, the heavy chain variable region can comprise an amino acid sequence at least 80% (e.g., 85%, 90%, 95%, or 98%) identical to SEQ ID NO:126 and the light chain variable region can comprise an amino acid sequence at least 80% (e.g., 85%, 90%, 95%, or 98%) identical to SEQ ID NO: 130.

[0075] In other examples, the anti-FXIIa portion in the bispecific antibody as described herein comprises a heavy chain variable region and/or a light chain variable region that comprises the same three CDRs as those in clones 559C-M0071-F06, 559C-M0179-D04, 559C-M0181-C02, 559C-M0180-G03, 559C-M0184-B04, 620I-X0173-A11, 620I-X0173-C07, 620I-X0173-E07, or 620I-X0173-G11, and/or the same three CDRs as those in these clones. See Table 1 below:

TABLE 1

CDR Sequences of Anti-FXIIa Clones:						
Clones	LCDR1	LCDR2	LCDR3	HCDR1	HCDR2	HCDR3
559C-M0071-F06	RSSQSLLHSN GY NYLD (SEQ ID NO: 36) NO: 34) SEQ ID NO: 5	LGSNRAS (SEQ ID WT (SEQ ID NO: 36)	MQALQTP WT (SEQ ID NO: 37)	GYIMA (SEQ ID NO: 41)	YIYPSGGITV YA DSVKG (SEQ ID NO: 43) NO: 3	QRYRGPKY YYMDV (SEQ ID NO: 45)
559C-M0179-D04	RSSQSLLHRN GH NYLD (SEQ ID NO: 36) NO: 35) SEQ ID NO: 6	LGSNRAS (SEQ ID (SEQ ID NO: 36)	MQALQART (SEQ ID NO: 38)	GYIMA (SEQ ID NO: 41)	YIYPSGGITV YA DSVKG (SEQ ID NO: 43) NO: 3	QRYRGPKY YYMDV (SEQ ID NO: 45)
559C-M0181-C02	RSSQSLLHSN GY NYLD (SEQ ID NO: 36) NO: 34) SEQ ID NO: 7	LGSNRAS (SEQ ID (SEQ ID NO: 36)	MQALQTRT (SEQ ID NO: 39)	GYIMA (SEQ ID NO: 41)	YIYPSGGITV YA DSVKG (SEQ ID NO: 43) NO: 3	QRYRGPKY YYMDV (SEQ ID NO: 45)
559C-M0180-G03	RSSQSLLHSN GY NYLD (SEQ ID NO: 36) NO: 34) SEQ ID NO: 8	LGSNRAS (SEQ ID T (SEQ ID NO: 40)	MQALQTPR (SEQ ID NO: 40)	GYIMA (SEQ ID NO: 41)	YIYPSGGITV YA DSVKG (SEQ ID NO: 43) NO: 3	QRYRGPKY YYMDV (SEQ ID NO: 45)
559C-M0184-B04	RSSQSLLHSN GY NYLD (SEQ ID NO: 36) NO: 34) SEQ ID NO: 8	LGSNRAS (SEQ ID WT (SEQ ID NO: 37)	MQALQTP WT (SEQ ID NO: 37)	FYSMH (SEQ ID NO: 42)	RIYPSGGVTK YA DSVKG (SEQ ID NO: 44) NO: 4	QRYRGPKY YYMDV (SEQ ID NO: 45)
620I-X0173-A11	RSSQSLLHSN GYNLYD (SEQ ID NO: 131) SEQ ID NO: 123	LGSNRAS (SEQ ID WT (SEQ ID NO: 36)	MQALQTP WT (SEQ ID NO: 37)	QYVMH (SEQ ID NO: 132)	SIWPSGGHTR YADSVKG (SEQ ID NO: 133) NO: 127	QRYRGPKYYYY MDV (SEQ ID NO: 134)
620I-X0173-C07	RSSQSLLHSN GYNLYD (SEQ ID NO: 131) SEQ ID NO: 124	LGSNRAS (SEQ ID WT (SEQ ID NO: 36)	MQALQTP WT (SEQ ID NO: 37)	WYVMH (SEQ ID NO: 135)	SIYPSGGKTS YADSVKG (SEQ ID NO: 136) NO: 128	QRYRGPKYYYY MDV (SEQ ID NO: 134)
620I-X0173-E07	RSSQSLLHSN GYNLYD (SEQ ID NO: 131)	LGSNRAS (SEQ ID WT (SEQ ID NO: 36)	MQALQTP WT (SEQ ID NO: 37)	WYSMH (SEQ ID NO: 137)	VIYPSGGKTR YADSVKG (SEQ ID NO: 138)	QRYRGPKYYYY MDV (SEQ ID NO: 134)

TABLE 1-continued

CDR Sequences of Anti-FXIIa Clones:						
Clones	LCDR1	LCDR2	LCDR3	HCDR1	HCDR2	HCDR3
620I-X0173-G11	RSSQSLLHSN (SEQ ID NO: 131)	LGSNRAS (SEQ ID NO: 36)	MQALQTP (SEQ ID NO: 37)	HYVMH (SEQ ID NO: 139)	SIYPSGGLTK YADSVKG (SEQ ID NO: 140)	QRYRGPKYYYY MDV (SEQ ID NO: 134)

[0076] Alternatively, the anti-FXIIa portion can include one or more (e.g., up to 2, 3, 4, 5, 6, 7, or 8) mutations in one or more of the heavy chain and/or light chain CDRs listed in Table 1 above, as compared to any of the clones 559C-M0071-F06, 559C-M0179-D04, 559C-M0181-C02, 559C-M0180-G03, 559C-M0184-B04, 620I-X0173-A11, 620I-X0173-C07, 620I-X0173-E07, or 620I-X0173-G11. Such mutations can be conservative amino acid substitutions as described herein.

[0077] In some embodiments, the anti-FXIIa portion in the bispecific antibody described herein is an IgG molecule, which can be a naturally-occurring IgG or a mutant, e.g., comprising one or more (e.g., 1, 2, 3, 4, 5, or more) mutations or deletions, for example to reduce proteolytic cleavage of the bispecific antibody, to reduce charge heterogeneity of the bispecific antibody, and/or to improve expression, production, and/or manufacture of the bispecific antibody. In some embodiments, the heavy chain of the IgG has the C-terminal lysine residue removed or mutated as compared with its wild-type counterpart. In some embodiments, the IgG heavy chain C-terminal lysine is mutated to a neutral amino acid residue, for example, a glycine residue or an alanine residue.

[0078] The anti-FXIIa portion in the bispecific antibody can be in any antibody form, including, but not limited to intact (i.e., full-length) antibodies, antigen-binding fragments thereof (such as Fab, Fab', F(ab')₂, Fv), and single chain antibodies. In some examples, the heavy chain variable region of the anti-pKal portion as described herein is linked to a heavy chain constant region (C_H), which may be the full-length of a heavy chain constant region or a portion thereof (e.g., C_H1, C_H2, C_H3, or a combination thereof). The heavy chain constant region can be derived from any C_H known in the art. In some embodiments, the C_H is a gamma heavy chain. Alternatively or in addition, the light chain variable region of the anti-pKal portion is linked to a light chain constant region (C_L), which can be any C_L known in the art. In some examples, the C_L is a kappa light chain. In other examples, the C_L is a lambda light chain. Antibody heavy and light chain constant regions are well known in the art, e.g., described herein.

[0079] Alternatively, the anti-FXIIa portion in the bispecific antibody as described herein can be a single-chain antibody, in which a heavy chain variable region and light chain variable region are fused, e.g., via a flexible peptide linker such as the linker of (GGGGS)₄ (SEQ ID NO:23). The heavy chain variable region and light chain variable region can be fused in an H→L orientation, or fused in an L→H orientation. In some embodiments, the light chain portion of the ScFv does not contain a KR motif at its C-terminus.

[0080] In some embodiments, the anti-FXIIa portion is a scFv comprising a heavy chain variable region of SEQ ID NO:3 or SEQ ID NO:4, and/or a light chain variable region

of any of SEQ ID NOs:5-8. In one example, the anti-FXIIa portion is a scFv antibody comprising a heavy chain variable region of SEQ ID NO:3 and a light chain variable region of any of SEQ ID NOs:5-8 in either H→L or L→H orientation. In another example, the anti-FXIIa portion is a scFv antibody comprising a heavy chain variable region of SEQ ID NO:4 and a light chain variable region of SEQ ID NO:5 in either H→L or L→H orientation. In some embodiments, the anti-FXIIa portion is a scFv comprising a heavy chain variable region of any of SEQ ID NOs:123-126, and/or a light chain variable region of any of SEQ ID NOs:127-130. In one example, the anti-FXIIa portion is a scFv antibody comprising a heavy chain variable region of SEQ ID NO:123 and a light chain variable region of SEQ ID NO:127 in either H→L or L→H orientation. In one example, the anti-FXIIa portion is a scFv antibody comprising a heavy chain variable region of SEQ ID NO:124 and a light chain variable region of SEQ ID NO:128 in either H→L or L→H orientation. In another example, the anti-FXIIa portion is a scFv antibody comprising a heavy chain variable region of SEQ ID NO:125 and a light chain variable region of SEQ ID NO:129 in either H→L or L→H orientation. In another example, the anti-FXIIa portion is a scFv antibody comprising a heavy chain variable region of SEQ ID NO:126 and a light chain variable region of SEQ ID NO:130 in either H→L or L→H orientation.

[0081] In some embodiments, the heavy chain and light chain variable region of any of the scFv antibodies described herein are further connected, e.g., via disulfide bond, such as between a V_H residue 44 and a V_L 100 residue. (iii) Format of the Anti-pKal/Anti-FXII Bispecific Antibodies

[0082] The anti-pKal/anti-FXIIa bispecific antibodies as described herein can be in any format of bispecific antibodies as known in the art, e.g., those described in Klein et al., mAbs 4(6):653-663, 2012; Kontermann et al., mAbs 4(2): 182-197, 2012; and Coloma et al., Nature Biotechnology 15:159-163, 1997. In some examples, the bispecific antibody can be a hybrid full-length antibody (also known as a quadroma or trifunctional antibody) comprising one arm (a heavy chain/light chain complex) binding to pKal and another arm (a heavy chain/light chain complex) binding to FXII. In some examples, the bispecific antibody is a bispecific Fab'₂, which comprises one Fab fragment binding to pKal and another Fab fragment binding to FXII, or a tri-Fab molecule comprising two copies of a Fab fragment binding to one target antigen (e.g., pKal or FXIIa) and one copy of a Fab fragment binding to the other target antigen (e.g., FXIIa or pKal). Alternatively, the bispecific antibody is a

tandem scFv molecule, which comprises at least one copy of a scFv binding to pKal and one copy of another scFv binding to FXIIa. The bispecific antibody described herein can also be a diabody or a single chain diabody as known in the art. Other examples include, but are not limited to, IgG₂, F(ab')₂, CovX-body, scFv₄-Ig, IgG-scFv, scFv-IgG, DVD-Ig, IgG-sVD, sVD-IgG, 2-in-1-IgG, mAb², Tandemab common LC, kih IgG, kih IgG common LC, CrossMab, kih IgG-scFab, mAb-Fv, charge pairs, SEED-body, Diabody (Db), dsDd, scDb, tandAbs, tandem scFv, triple body, Fab-scFv, and F(ab')₂-scFv₂. See, e.g., FIG. 2 of Kontermann et al., *mAbs* 4(2):182-197, 2012.

[0083] In some embodiments, the scaffold of the bispecific antibodies described herein is designed to comprise an IgG antibody portion and a scFv portion, which is fused to the C-terminus of either a heavy chain or a light chain of the IgG portion (e.g., the C-terminus of the heavy chain of the IgG, see, e.g., Coloma, M. J. & Morrison, S.L. Design and production of novel tetravalent bispecific antibodies. *Nature Biotechnology*. 15(2): 159-163. 1997). The IgG heavy or light chain can be fused with the scFv via a short peptide linker, such as a peptide that is rich in Gly and Ser residues. In one example, the peptide linker comprises the amino acid sequence of SGGS (SEQ ID NO:22).

[0084] Such a bispecific antibody can comprise a first polypeptide that comprises a light chain of a first antibody, which comprises a light chain variable region (V_L) and a light chain constant region (C_L); and a second polypeptide that comprises a fusion protein comprising, from the N-terminus to the C-terminus, a heavy chain of the first antibody, which comprises a heavy chain variable region (V_H), a heavy chain constant region (C_H) and a second antibody, which can be a single chain antibody. Alternatively, the bispecific antibody can comprise a first polypeptide that comprises a heavy chain of a first antibody, the heavy chain comprising a heavy chain variable region (V_H) and a heavy chain constant region (C_H) or a portion thereof; and a second polypeptide that comprises a fusion protein comprising, from N-terminus to C-terminus, a light chain of the first antibody, which comprises a light chain variable region (V_L) and a light chain constant region (C_L), and a second antibody, which is a single chain antibody. In some examples, the first antibody can bind to pKal (e.g., active pKal) and the second antibody can bind to FXII (e.g., FXIIa). In other examples, the first antibody can bind to FXIIa and the second antibody can bind to pKal.

[0085] The C_L of the light chain of the first antibody may be any C_L known in the art. In some embodiments, the C_L is a kappa light chain. In some embodiments, the C_L is a lambda light chain. The C_H of the heavy chain of the first antibody may be any C_H known in the art. In some embodiments, the C_H is a gamma heavy chain. Such heavy and light chain constant regions are well known in the art, e.g., as described herein.

[0086] In one example, the bispecific comprises an IgG antibody derived from DX-2930 and a scFv antibody derived from clone 559C-M0071-F06, 559C-M0179-D04, 559C-M0181-C02, 559C-M0180-G03, 559C-M0184-B04, 620I-X0173-A11, 620I-X0173-C07, 620I-X0173-E07, or 620I-X0173-G11, in either H→L or L→H orientation. See above disclosures. An antibody derived from a parent antibody may comprise heavy chain and light chain substantially similar to those of the parent antibody (share at least 80%, 85%, 90%, 95%, or 98% sequence identity). In some

examples, such an antibody comprises the same heavy chain and light chain CDRs as the parent antibody. In other examples, such an antibody comprises heavy chain and/or light chain CDRs that are substantially identical to those of the parent antibody, e.g., comprises up to 5, 4, 3, 2, or 1 amino acid residue variations such as conservative amino acid residue substitutions as compared to the CDRs of the parent antibody.

[0087] In some embodiments, the scFv antibody in the bispecific antibody comprises a V_H fused to the N-terminus of the V_L. In other embodiments, the scFv antibody comprises a V_H fused to the C-terminus of the V_L. In any of the scFv antibodies described herein, the V_H and V_L regions can be fused via a linker, such as a peptide linker.

[0088] A peptide linker as described herein can comprise, for example, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more amino acid residues. In some embodiments, the peptide linker can comprise 2-50, 5-25, or 5-20 amino acids. In some embodiments, the peptide linker is SGGS. In some embodiments, the peptide linker is (G_xS)_x, wherein x can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more. In some embodiments, x is 4.

[0089] Any of the peptide linkers described herein, e.g., the SGGS (SEQ ID NO:22) linker or the (GGGS)₄ (SEQ ID NO:23) linker, can comprise naturally occurring amino acids and/or non-naturally occurring amino acids. Naturally occurring amino acids include alanine (Ala), arginine (Arg), asparagine (Asn), aspartic acid (Asp), cysteine (Cys), glutamic acid (Glu), glutamine (Gln), glycine (Gly), histidine (His), isoleucine (He), leucine (Leu), lysine (Lys) methionine (Met), ornithine (Orn), phenylalanine (Phe), proline (Pro), serine (Ser), threonine (Thr), tryptophan (Trp), tyrosine (Tyr), and valine (Val). Non-naturally occurring amino acids can include protected amino acids such as naturally occurring amino acids protected with groups such as acetyl, formyl, tosyl, nitro and the like. Non-limiting examples of non-naturally occurring amino acids include azidohomoalanine, homopropargylglycine, homoallylglycine, p-bromophenylalanine, p-iodophenylalanine, azidophenylalanine, acetylphenylalanine or ethynylephenylalanine, amino acids containing an internal alkene such as trans-crotylalkene, serine allyl ether, allyl glycine, propargyl glycine, vinyl glycine, pyrrolsine, N-sigma-o-azidobenzylloxycarbonyl-L-Lysine (AzZLys), N-sigma-propargyloxycarbonyl-L-Lysine, N-sigma-2-azidoethoxycarbonyl-L-Lysine, N-sigma-tert-butyloxycarbonyl-L-Lysine (BocLys), N-sigma-allyloxy carbonyl-L-Lysine (AlocLys), N-sigma-acetyl-L-Lysine (AcLys), N-sigma-benzylloxycarbonyl-L-Lysine (ZLys), N-sigma-cyclopentyloxycarbonyl-L-Lysine (CycLys), N-sigma-D-prolyl-L-Lysine, N-sigma-nicotinoyl-L-Lysine (NicLys), N-sigma-N-Me-anthraniloyl-L-Lysine (NmaLys), N-sigma-biotinyl-L-Lysine, N-sigma-9-fluorenylmethoxycarbonyl-L-Lysine, N-sigma-methyl-L-Lysine, N-sigma-dimethyl-L-Lysine, N-sigma-trimethyl-L-Lysine, N-sigma-isopropyl-L-Lysine, N-sigma-dansyl-L-Lysine, N-sigma-o,p-dinitrophenyl-L-Lysine, N-sigma-p-toluene-sulfonyl-L-Lysine, N-sigma-DL-2-amino-2carboxyethyl-L-Lysine, N-sigma-phenylpyruvamide-L-Lysine, N-sigma-pyruvamide-L-Lysine, azidohomoalanine, homopropargylglycine, homoallylglycine, p-bromophenylalanine, p-iodophenylalanine, azidophenylalanine, acetylphenylalanine or ethynylephenylalanine, amino acids containing an internal alkene such as trans-crotylalkene, serine allyl ether, allyl glycine, propargyl glycine, and vinyl glycine.

[0090] In some embodiments, the scFv portion of the bispecific antibodies described herein may be engineered to introduce cysteine residues in both the V_H and V_L chains for formation of one or more disulfide bonds, which may reduce the formation of high molecular weight aggregates. In some examples, a cysteine residue may be introduced into residue 44 of the V_H chain. Alternatively or in addition, a cysteine residue may be introduced into residue 100 of the V_L chain.

[0091] Exemplary anti-pKal/anti-FXIIa bispecific antibodies include clones X0120-A01, X0120-C01, X0120-E01, X0120-G01, X0121-A03, X0121-C01, X0121-E01, X0121-G01, X0122-A01, X0122-C01, 620I-X0173-A11, 620I-X0173-C07, 620I-X0173-E07, and 620I-X0173-G11 described in Examples below. Other exemplary anti-pKal/anti-FXIIa bispecific antibodies include clones 620I-X138-A08, 620I-X136-B02, 620I-X139-A12, 620I-X137-B08, 620I-X142-A04, 620I-X142-B11, 620I-X138-B01, 620I-X136-C01, 620I-X138-A12, 620I-X136-A12, 620I-X138-A02, 620I-X136-A05, 620I-X138-C07, 620I-X136-E07, 620I-X142-B02, 620I-X136-F11, 620I-X142-A05, 620I-X136-C09, 620I-X138-B10, 620I-X136-C08, 620I-X139-A11, 620I-X136-D05, 620I-X138-D04, 620I-X136-G08, 620I-X142-B07, 620I-X142-A11, 620I-X138-G12, 620I-X142-A10, 620I-X138-D03, 620I-X137-C08, 620I-X142-E02, 620I-X136-E05, 620I-X138-B06, 620I-X136-A09, 620I-X138-A06, 620I-X137-A10, 620I-X139-B10, 620I-X136-A04, 620I-X138-D06, 620I-X136-C11, 620I-X138-B07, 620I-X136-A02, 620I-X139-G02, 620I-X136-B07, 620I-X138-E03, 620I-X136-G05, 620I-X139-D12, 620I-X136-A01, 620I-X138-C12, 620I-X136-G10, 620I-X138-D05, 620I-X136-F07, 620I-X138-A01, 620I-X142-E09, 620I-X138-D11, 620I-X136-C05, 620I-X142-A02, 620I-X136-C04, 620I-X138-F02, 620I-X136-G04, 620I-X139-G12, 620I-X136-B11, 620I-X142-D04, 620I-X136-D06, 620I-X139-A01, 620I-X136-D12, 620I-X138-F05, 620I-X136-A11, 620I-X139-E05, 620I-X136-C12, and 620I-X138-E05 described in the Examples below.

Preparation of Bispecific Antibodies

[0092] Any suitable methods known in the art, e.g., the standard recombinant technology, can be used for preparing the bispecific antibodies described herein. Examples are provided below.

[0093] Heavy chain and light chain genes of suitable parent antibodies can be obtained via routine technology, e.g., PCR amplification from a suitable source. In one example, DNA encoding a monoclonal antibody specific to a target antigen can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of the monoclonal antibodies). A cell, such as a hybridoma cell, may serve as a source of such DNA. In another example, the sequence of DNA encoding a monoclonal antibody specific for a target antigen may be obtained, e.g., from a database or other publically available source, and the DNA can be synthesized. The parent antibody genes can also be obtained from screening a suitable antibody library with an antigen of interest.

[0094] The antibody heavy and light chain genes thus obtained can be analyzed to identify the complementarity determining regions (CDR) regions following routine technology. Any of the polypeptides in the bispecific antibodies as described herein can be prepared via conventional recom-

binant technology and inserted into suitable expression vectors for production in suitable host cells.

[0095] The nucleotide sequences encoding one or more of the polypeptides of a bispecific antibody as described herein can be cloned into one expression vector, each nucleotide sequence being in operable linkage to a suitable promoter. Alternatively, the nucleotides sequences can be in operable linkage with a single promoter, such that both sequences are expressed from the same promoter. In some examples, the expression of the two polypeptides is controlled by a common promoter. In other examples, the expression of each of the two polypeptides is under the control of a distinct promoter. In another alternative, the nucleotide sequences encoding the two polypeptides are cloned into two vectors, which can be introduced into the same or different cells. When the two polypeptides are expressed in different cells, each of them can be isolated from the host cells expressing such and the two isolated heavy chains can be mixed and incubated under suitable conditions allowing for the formation of the bispecific antibody.

[0096] Generally, a nucleic acid sequence encoding one or all chains of a bispecific antibody can be cloned into a suitable expression vector in operable linkage with a suitable promoter using methods known in the art. For example, the nucleotide sequence and vector can be contacted, under suitable conditions, with a restriction enzyme to create complementary ends on each molecule that can pair with each other and be joined together with a ligase. Alternatively, synthetic nucleic acid linkers can be ligated to the termini of a gene. These synthetic linkers contain nucleic acid sequences that correspond to a particular restriction site in the vector. The selection of expression vectors/promoter would depend on the type of host cells for use in producing the antibodies.

[0097] A variety of promoters can be used for expression of the bispecific antibodies described herein, including, but not limited to, cytomegalovirus (CMV) intermediate early promoter, a viral LTR such as the Rous sarcoma virus LTR, HIV-LTR, HTLV-1 LTR, the simian virus 40 (SV40) early promoter, *E. coli* lac UV5 promoter, and the herpes simplex tk virus promoter.

[0098] Regulatable promoters can also be used. Such regulatable promoters include those using the lac repressor from *E. coli* as a transcription modulator to regulate transcription from lac operator-bearing mammalian cell promoters [Brown, M. et al., *Cell*, 49:603-612 (1987)], those using the tetracycline repressor (tetR) [Gossen, M., and Bujard, H., *Proc. Natl. Acad. Sci. USA* 89:5547-5551 (1992); Yao, F. et al., *Human Gene Therapy*, 9:1939-1950 (1998); Shockelt, P., et al., *Proc. Natl. Acad. Sci. USA*, 92:6522-6526 (1995)]. Other systems include FK506 dimer, VP16 or p65 using astradiol, RU486, diphenol murislerone, or rapamycin. Inducible systems are available from Invitrogen, Clontech and Ariad.

[0099] Regulatable promoters that include a repressor with the operon can be used. In one embodiment, the lac repressor from *E. coli* can function as a transcriptional modulator to regulate transcription from lac operator-bearing mammalian cell promoters [M. Brown et al., *Cell*, 49:603-612 (1987)]; Gossen and Bujard (1992); [M. Gossen et al., *Nat. Acad. Sci. USA*, 89:5547-5551 (1992)] combined the tetracycline repressor (tetR) with the transcription activator (VP 16) to create a tetR-mammalian cell transcription activator fusion protein, tTa (tetR-VP 16), with the tetO-

bearing minimal promoter derived from the human cytomegalovirus (hCMV) major immediate-early promoter to create a tetR-tet operator system to control gene expression in mammalian cells. In one embodiment, a tetracycline inducible switch is used. The tetracycline repressor (tetR) alone, rather than the tetR-mammalian cell transcription factor fusion derivatives can function as potent trans-modulator to regulate gene expression in mammalian cells when the tetracycline operator is properly positioned downstream for the TATA element of the CMVIE promoter (Yao et al., Human Gene Therapy). One particular advantage of this tetracycline inducible switch is that it does not require the use of a tetracycline repressor-mammalian cells transactivator or repressor fusion protein, which in some instances can be toxic to cells (Gossen et al., *Natl. Acad. Sci. USA*, 89:5547-5551 (1992); Shockett et al., *Proc. Natl. Acad. Sci. USA*, 92:6522-6526 (1995)), to achieve its regulatable effects.

[0100] Additionally, the vector can contain, for example, some or all of the following: a selectable marker gene, such as the neomycin gene for selection of stable or transient transfectants in mammalian cells; enhancer/promoter sequences from the immediate early gene of human CMV for high levels of transcription; transcription termination and RNA processing signals from SV40 for mRNA stability; SV40 polyoma origins of replication and ColE1 for proper episomal replication; internal ribosome binding sites (IRE-Ses), versatile multiple cloning sites; and T7 and SP6 RNA promoters for in vitro transcription of sense and antisense RNA. Suitable vectors and methods for producing vectors containing transgenes are well known and available in the art.

[0101] Examples of polyadenylation signals useful to practice the methods described herein include, but are not limited to, human collagen I polyadenylation signal, human collagen II polyadenylation signal, and SV40 polyadenylation signal.

[0102] Other aspects of the disclosure relate to a method for preparing a bispecific antibody, comprising: culturing a host cell or host cell set described herein under conditions allowing for expression of the first polypeptide and the second polypeptide; and isolating the bispecific antibody that comprises the first polypeptide and the second polypeptide. In some embodiments, the host cell comprises an expression vector comprising a first nucleotide sequence encoding a first polypeptide as described herein and a second nucleotide sequence encoding a second polypeptide as described herein.

[0103] Suitable host cells for use in preparing the bispecific antibodies described herein can be any host cells known in the art that can be used for protein production, including, but not limited to, bacterial cells, yeast cells, insect cells, plant cells, or mammalian cells. The bispecific antibodies described herein can be produced in bacterial cells, e.g., *E. coli* cells. Alternatively, the bispecific antibodies can be produced in eukaryotic cells. In one embodiment, the antibodies are expressed in a yeast cell such as *Pichia* (see, e.g., Powers et al., 2001, *J. Immunol. Methods*. 251:123-35), *Hansenula*, or *Saccharomyces*. In another embodiment, the bispecific antibodies can be produced in mammalian cells. Mammalian host cells for expressing the antibodies include, but are not limited to, 293 cells (see, e.g., ATCC CRL-1573, American Type Culture Collection®, and Expi293F™ cells, Life Technologies™), Chinese Hamster Ovary (CHO cells)

(including dhfr-CHO cells, described in Urlaub and Chasin, 1980, *Proc. Natl. Acad. Sci. USA* 77:4216-4220, used with a DHFR selectable marker, e.g., as described in Kaufman and Sharp, 1982, *Mol. Biol.* 159:601 621), lymphocytic cell lines, e.g., NS0 myeloma cells and SP2 cells, COS cells, and a cell from a transgenic animal, e.g., a transgenic mammal. For example, the cell is a mammary epithelial cell.

[0104] In an exemplary system for recombinant expression of a bispecific antibody as described herein, a recombinant expression vector encoding both of the polypeptides in the bispecific antibody is introduced into dhfr CHO cells by calcium phosphate-mediated transfection. Within the recombinant expression vector, the nucleic acids encoding the two polypeptides are operatively linked to enhancer/promoter regulatory elements (e.g., derived from SV40, CMV, adenovirus and the like, such as a CMV enhancer/AdMLP promoter regulatory element or an SV40 enhancer/AdMLP promoter regulatory element) to drive high levels of transcription of the genes. The recombinant expression vector also carries a DHFR gene, which allows for selection of CHO cells that have been transfected with the vector using methotrexate selection/amplification. The selected transformant host cells are cultured to allow for expression of the two polypeptides. The tetrameric molecule formed thereby can be recovered from the culture medium. Another exemplary system for recombinant expression is described in Example 2.

[0105] Standard molecular biology techniques are used to prepare the recombinant expression vector, transfet the host cells, select for transformants, culture the host cells and recover the antibody from the culture medium. For example, some antibodies can be isolated by affinity chromatography with a Protein A or Protein G coupled matrix.

Utilities of the Bispecific Antibodies

[0106] The bispecific antibodies or the encoding nucleic acids or nucleic acid sets described herein can be used for diagnostic and therapeutic purposes. They also can be used as research tools in basic researches and therapeutic researches.

(i) Pharmaceutical Compositions

[0107] The bispecific antibody (or the encoding nucleic acids or nucleic acid sets) as described herein can be mixed with a pharmaceutically acceptable carrier (excipient), including buffer, to form a pharmaceutical composition for use in treating a target disease. "Acceptable" means that the carrier must be compatible with the active ingredient of the composition (and preferably, capable of stabilizing the active ingredient) and not deleterious to the subject to be treated. Pharmaceutically acceptable excipients (carriers) including buffers, which are well known in the art. See, e.g., Remington: The Science and Practice of Pharmacy 20th Ed. (2000) Lippincott Williams and Wilkins, Ed. K. E. Hoover.

[0108] The pharmaceutical compositions to be used in the present methods can comprise pharmaceutically acceptable carriers, excipients, or stabilizers in the form of lyophilized formulations or aqueous solutions. (Remington: The Science and Practice of Pharmacy 20th Ed. (2000) Lippincott Williams and Wilkins, Ed. K. E. Hoover). Acceptable carriers, excipients, or stabilizers are nontoxic to recipients at the dosages and concentrations used, and may comprise buffers such as phosphate, citrate, and other organic acids; antioxi-

dants including ascorbic acid and methionine; preservatives (such as octadecyltrimethylbenzyl ammonium chloride; hexamethonium chloride; benzalkonium chloride, benzethonium chloride; phenol, butyl or benzyl alcohol; alkyl parabens such as methyl or propyl paraben; catechol; resorcinol; cyclohexanol; 3-pentanol; and m-cresol); low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, histidine, arginine, or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugars such as sucrose, mannitol, trehalose or sorbitol; salt-forming counter-ions such as sodium; metal complexes (e.g. Zn-protein complexes); and/or non-ionic surfactants such as TWEEN™, PLURONIC™ or polyethylene glycol (PEG).

[0109] In some examples, the pharmaceutical composition described herein comprises liposomes containing the bispecific antibody, which can be prepared by methods known in the art, such as described in Epstein, et al., Proc. Natl. Acad. Sci. USA 82:3688 (1985); Hwang, et al., Proc. Natl. Acad. Sci. USA 77:4030 (1980); and U.S. Pat. Nos. 4,485,045 and 4,544,545. Liposomes with enhanced circulation time are disclosed in U.S. Pat. No. 5,013,556. Particularly useful liposomes can be generated by the reverse phase evaporation method with a lipid composition comprising phosphatidylcholine, cholesterol and PEG-derivatized phosphatidylethanolamine (PEG-PE). Liposomes are extruded through filters of defined pore size to yield liposomes with the desired diameter.

[0110] The bispecific antibody, or the encoding nucleic acid(s), may also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacrylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles and nanocapsules) or in macroemulsions. Such techniques are known in the art, see, e.g., Remington, The Science and Practice of Pharmacy 20th Ed. Mack Publishing (2000).

[0111] In other examples, the pharmaceutical composition described herein can be formulated in sustained-release format. Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in the form of shaped articles, e.g. films, or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinyl alcohol)), poly(lactides) (U.S. Pat. No. 3,773,919), copolymers of L-glutamic acid and D,L-ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOT™ (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), sucrose acetate isobutyrate, and poly-D-(+)-3-hydroxybutyric acid.

[0112] The pharmaceutical compositions to be used for in vivo administration must be sterile. This is readily accomplished by, for example, filtration through sterile filtration membranes. Therapeutic antibody compositions are generally placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

[0113] The pharmaceutical compositions described herein can be in unit dosage forms such as tablets, pills, capsules, powders, granules, solutions or suspensions, or suppositories, for oral, parenteral or rectal administration, or administration by inhalation or insufflation. For preparing solid compositions such as tablets, the principal active ingredient can be mixed with a pharmaceutical carrier, e.g. conventional tabletting ingredients such as corn starch, lactose, sucrose, sorbitol, talc, stearic acid, magnesium stearate, dicalcium phosphate or gums, and other pharmaceutical diluents, e.g. water, to form a solid preformulation composition containing a homogeneous mixture of a compound of the present invention, or a non-toxic pharmaceutically acceptable salt thereof. When referring to these preformulation compositions as homogeneous, it is meant that the active ingredient is dispersed evenly throughout the composition so that the composition may be readily subdivided into equally effective unit dosage forms such as tablets, pills and capsules. This solid preformulation composition is then subdivided into unit dosage forms of the type described above containing from 0.1 to about 500 mg of the active ingredient of the present invention. The tablets or pills of the novel composition can be coated or otherwise compounded to provide a dosage form affording the advantage of prolonged action. For example, the tablet or pill can comprise an inner dosage and an outer dosage component, the latter being in the form of an envelope over the former. The two components can be separated by an enteric layer that serves to resist disintegration in the stomach and permits the inner component to pass intact into the duodenum or to be delayed in release. A variety of materials can be used for such enteric layers or coatings, such materials including a number of polymeric acids and mixtures of polymeric acids with such materials as shellac, cetyl alcohol and cellulose acetate.

[0114] Suitable surface-active agents include, in particular, non-ionic agents, such as polyoxyethylenesorbitans (e.g. Tween™ 20, 40, 60, 80 or 85) and other sorbitans (e.g. Span™ 20, 40, 60, 80 or 85). Compositions with a surface-active agent will conveniently comprise between 0.05 and 5% surface-active agent, and can be between 0.1 and 2.5%. It will be appreciated that other ingredients may be added, for example mannitol or other pharmaceutically acceptable vehicles, if necessary.

[0115] Suitable emulsions may be prepared using commercially available fat emulsions, such as Intralipid™, Liposyn™, Infonutrol™, Lipofundin™ and Lipophysan™. The active ingredient may be either dissolved in a pre-mixed emulsion composition or alternatively it may be dissolved in an oil (e.g. soybean oil, safflower oil, cottonseed oil, sesame oil, corn oil or almond oil) and an emulsion formed upon mixing with a phospholipid (e.g. egg phospholipids, soybean phospholipids or soybean lecithin) and water. It will be appreciated that other ingredients may be added, for example glycerol or glucose, to adjust the tonicity of the emulsion. Suitable emulsions will typically contain up to 20% oil, for example, between 5 and 20%. The fat emulsion can comprise fat droplets between 0.1 and 1.0 μm, particularly 0.1 and 0.5 μm, and have a pH in the range of 5.5 to 8.0.

[0116] The emulsion compositions can be those prepared by mixing a bispecific antibody with Intralipid™ or the components thereof (soybean oil, egg phospholipids, glycerol and water).

[0117] Pharmaceutical compositions for inhalation or insufflation include solutions and suspensions in pharma-

aceutically acceptable, aqueous or organic solvents, or mixtures thereof, and powders. The liquid or solid compositions may contain suitable pharmaceutically acceptable excipients as set out above. In some embodiments, the compositions are administered by the oral or nasal respiratory route for local or systemic effect.

[0118] Compositions in preferably sterile pharmaceutically acceptable solvents may be nebulised by use of gases. Nebulised solutions may be breathed directly from the nebulising device or the nebulising device may be attached to a face mask, tent or intermittent positive pressure breathing machine. Solution, suspension or powder compositions may be administered, preferably orally or nasally, from devices which deliver the formulation in an appropriate manner.

(ii) Disease Treatment

[0119] The bispecific antibodies (or the encoding nucleic acids or nucleic acid sets) described herein are useful for treating a disease or disorder associated one or both of the antigens to which the bispecific antibody binds. For example, if the bispecific antibody is capable of binding to and blocking the activity of pKal and FXIIa, it can be used for treating diseases associated with dysregulation of the contact activation system, e.g., HAE and thrombosis.

[0120] HAE (including Type I, Type II, and Type III HAE) is a disorder characterized by recurrent episodes of severe swelling at, e.g., the limbs, face, intestinal tract, and airway. HAE attack may be triggered by minor trauma or stress. Swelling the intestinal tract due to HAE attack can cause severe abdominal pain, nausea, and vomiting. Swelling in the airway can restrict breathing and lead to life-threatening obstruction of the airway.

[0121] Thrombosis (e.g., venous thrombosis or arterial thrombosis) refers to the formation of blood clots inside a blood vessel, which may obstruct the flow of blood through the circulation system. Thrombosis may include thrombosis associated with atrial fibrillation, DVT, pulmonary embolism, stroke, or other arterial or venous thrombotic events.

[0122] To practice the method disclosed herein, an effective amount of the pharmaceutical composition described above can be administered to a subject (e.g., a human) in need of the treatment via a suitable route, such as intravenous administration, e.g., as a bolus or by continuous infusion over a period of time, by intramuscular, intraperitoneal, intracerebrospinal, subcutaneous, intra-articular, intrasynovial, intrathecal, oral, inhalation or topical routes. Commercially available nebulizers for liquid formulations, including jet nebulizers and ultrasonic nebulizers are useful for administration. Liquid formulations can be directly nebulized and lyophilized powder can be nebulized after reconstitution. Alternatively, the bispecific antibodies as described herein can be aerosolized using a fluorocarbon formulation and a metered dose inhaler, or inhaled as a lyophilized and milled powder.

[0123] The subject to be treated by the methods described herein can be a mammal, more preferably a human. Mammals include, but are not limited to, farm animals, sport animals, pets, primates, horses, dogs, cats, mice and rats. A human subject who needs the treatment may be a human patient having, at risk for, or suspected of having a target disease/disorder, such as HAE or thrombosis. In some embodiments, thrombosis is associated with atrial fibrillation, deep vein thrombosis (DVT), pulmonary embolism,

stroke, or an arterial or venous thrombotic event. A subject having a target disease or disorder can be identified by routine medical examination, e.g., laboratory tests, organ functional tests, CT scans, or ultrasounds. A subject suspected of having any of such target disease/disorder might show one or more symptoms of the disease/disorder. A subject at risk for the disease/disorder can be a subject having one or more of the risk factors for that disease/disorder.

[0124] "An effective amount" as used herein refers to the amount of each active agent required to confer therapeutic effect on the subject, either alone or in combination with one or more other active agents. Effective amounts vary, as recognized by those skilled in the art, depending on the particular condition being treated, the severity of the condition, the individual patient parameters including age, physical condition, size, gender and weight, the duration of the treatment, the nature of concurrent therapy (if any), the specific route of administration and like factors within the knowledge and expertise of the health practitioner. These factors are well known to those of ordinary skill in the art and can be addressed with no more than routine experimentation. It is generally preferred that a maximum dose of the individual components or combinations thereof be used, that is, the highest safe dose according to sound medical judgment. It will be understood by those of ordinary skill in the art, however, that a patient may insist upon a lower dose or tolerable dose for medical reasons, psychological reasons or for virtually any other reasons.

[0125] Empirical considerations, such as the half-life, generally will contribute to the determination of the dosage. For example, antibodies that are compatible with the human immune system, such as humanized antibodies or fully human antibodies, may be used to prolong half-life of the antibody and to prevent the antibody being attacked by the host's immune system. Frequency of administration may be determined and adjusted over the course of therapy, and is generally, but not necessarily, based on treatment and/or suppression and/or amelioration and/or delay of a target disease/disorder. Alternatively, sustained continuous release formulations of a bispecific antibody may be appropriate. Various formulations and devices for achieving sustained release are known in the art.

[0126] In one example, dosages for a bispecific antibody as described herein may be determined empirically in individuals who have been given one or more administration(s) of the antibody. Individuals are given incremental dosages of the antagonist. To assess efficacy of the antagonist, an indicator of the disease/disorder can be followed.

[0127] Generally, for administration of any of the antibodies described herein, an initial candidate dosage can be about 2 mg/kg. For the purpose of the present disclosure, a typical daily dosage might range from about any of 0.1 g/kg to 3 g/kg to 30 g/kg to 300 g/kg to 3 mg/kg, to 30 mg/kg to 100 mg/kg or more, depending on the factors mentioned above. For repeated administrations over several days or longer, depending on the condition, the treatment is sustained until a desired suppression of symptoms occurs or until sufficient therapeutic levels are achieved to alleviate a target disease or disorder, or a symptom thereof. An exemplary dosing regimen comprises administering an initial dose of about 2 mg/kg, followed by a weekly maintenance dose of about 1 mg/kg of the antibody, or followed by a maintenance dose of about 1 mg/kg every other week. However, other dosage

regimens may be useful, depending on the pattern of pharmacokinetic decay that the practitioner wishes to achieve. For example, dosing from one-four times a week is contemplated. In some embodiments, dosing ranging from about 3 g/mg to about 2 mg/kg (such as about 3 g/mg, about 10 g/mg, about 30 g/mg, about 100 g/mg, about 300 g/mg, about 1 mg/kg, and about 2 mg/kg) may be used. In some embodiments, dosing frequency is once every week, every 2 weeks, every 4 weeks, every 5 weeks, every 6 weeks, every 7 weeks, every 8 weeks, every 9 weeks, or every 10 weeks; or once every month, every 2 months, or every 3 months, or longer. The progress of this therapy is easily monitored by conventional techniques and assays. The dosing regimen (including the antibody used) can vary over time.

[0128] In some embodiments, for an adult patient of normal weight, doses ranging from about 0.3 to 5.00 mg/kg may be administered. The particular dosage regimen, i.e., dose, timing and repetition, will depend on the particular individual and that individual's medical history, as well as the properties of the individual agents (such as the half-life of the agent, and other considerations well known in the art).

[0129] For the purpose of the present disclosure, the appropriate dosage of a bispecific antibody as described herein will depend on the specific antibody (or compositions thereof) employed, the type and severity of the disease/disorder, whether the antibody is administered for preventive or therapeutic purposes, previous therapy, the patient's clinical history and response to the antagonist, and the discretion of the attending physician. Typically the clinician will administer a bispecific antibody, until a dosage is reached that achieves the desired result. Administration of one or more bispecific antibody can be continuous or intermittent, depending, for example, upon the recipient's physiological condition, whether the purpose of the administration is therapeutic or prophylactic, and other factors known to skilled practitioners. The administration of a bispecific antibody may be essentially continuous over a preselected period of time or may be in a series of spaced dose, e.g., either before, during, or after developing a target disease or disorder.

[0130] As used herein, the term "treating" refers to the application or administration of a composition including one or more active agents to a subject, who has a target disease or disorder, a symptom of the disease/disorder, or a predisposition toward the disease/disorder, with the purpose to cure, heal, alleviate, relieve, alter, remedy, ameliorate, improve, or affect the disorder, the symptom of the disease, or the predisposition toward the disease or disorder.

[0131] Alleviating a target disease/disorder includes delaying the development or progression of the disease, or reducing disease severity. Alleviating the disease does not necessarily require curative results. As used therein, "delaying" the development of a target disease or disorder means to defer, hinder, slow, retard, stabilize, and/or postpone progression of the disease. This delay can be of varying lengths of time, depending on the history of the disease and/or individuals being treated. A method that "delays" or alleviates the development of a disease, or delays the onset of the disease, is a method that reduces probability of developing one or more symptoms of the disease in a given time frame and/or reduces extent of the symptoms in a given time frame, when compared to not using the method. Such

comparisons are typically based on clinical studies, using a number of subjects sufficient to give a statistically significant result.

[0132] "Development" or "progression" of a disease means initial manifestations and/or ensuing progression of the disease. Development of the disease can be detectable and assessed using standard clinical techniques as well known in the art. However, development also refers to progression that may be undetectable. For purpose of this disclosure, development or progression refers to the biological course of the symptoms. "Development" includes occurrence, recurrence, and onset. As used herein "onset" or "occurrence" of a target disease or disorder includes initial onset and/or recurrence.

[0133] In some embodiments, the bispecific antibody described herein is administered to a subject in need of the treatment at an amount sufficient to inhibit the activity of one or both of the target antigen by at least 20% (e.g., 30%, 40%, 50%, 60%, 70%, 80%, 90% or greater) in vivo. In other embodiments, the antibody is administered in an amount effective in reducing the level of one or both target antigens by at least 20% (e.g., 30%, 40%, 50%, 60%, 70%, 80%, 90% or greater).

[0134] Conventional methods, known to those of ordinary skill in the art of medicine, can be used to administer the pharmaceutical composition to the subject, depending upon the type of disease to be treated or the site of the disease. This composition can also be administered via other conventional routes, e.g., administered orally, parenterally, by inhalation spray, topically, rectally, nasally, buccally, vaginally or via an implanted reservoir. The term "parenteral" as used herein includes subcutaneous, intracutaneous, intravenous, intramuscular, intraarticular, intraarterial, intrasynovial, intrasternal, intrathecal, intralesional, and intracranial injection or infusion techniques. In addition, it can be administered to the subject via injectable depot routes of administration such as using 1-, 3-, or 6-month depot injectable or biodegradable materials and methods.

[0135] Injectable compositions may contain various carriers such as vegetable oils, dimethylactamide, dimethylformamide, ethyl lactate, ethyl carbonate, isopropyl myristate, ethanol, and polyols (glycerol, propylene glycol, liquid polyethylene glycol, and the like). For intravenous injection, water soluble antibodies can be administered by the drip method, whereby a pharmaceutical formulation containing the antibody and a physiologically acceptable excipients is infused. Physiologically acceptable excipients may include, for example, 5% dextrose, 0.9% saline, Ringer's solution or other suitable excipients. Intramuscular preparations, e.g., a sterile formulation of a suitable soluble salt form of the antibody, can be dissolved and administered in a pharmaceutical excipient such as Water-for-Injection, 0.9% saline, or 5% glucose solution.

[0136] In one embodiment, a bispecific antibody is administered via site-specific or targeted local delivery techniques. Examples of site-specific or targeted local delivery techniques include various implantable depot sources of the bispecific antibody or local delivery catheters, such as infusion catheters, an indwelling catheter, or a needle catheter, synthetic grafts, adventitial wraps, shunts and stents or other implantable devices, site specific carriers, direct injection, or direct application. See, e.g., PCT Publication No. WO 00/53211 and U.S. Pat. No. 5,981,568.

[0137] Targeted delivery of therapeutic compositions containing an antisense polynucleotide, expression vector, or subgenomic polynucleotides can also be used. Receptor-mediated DNA delivery techniques are described in, for example, Findeis et al., Trends Biotechnol. (1993) 11:202; Chiou et al., Gene Therapeutics: Methods And Applications Of Direct Gene Transfer (J. A. Wolff, ed.) (1994); Wu et al., J. Biol. Chem. (1988) 263:621; Wu et al., J. Biol. Chem. (1994) 269:542; Zenke et al., Proc. Natl. Acad. Sci. USA (1990) 87:3655; Wu et al., J. Biol. Chem. (1991) 266:338.

[0138] Therapeutic compositions containing a polynucleotide (e.g., those encoding the bispecific antibodies described herein) are administered in a range of about 100 ng to about 200 mg of DNA for local administration in a gene therapy protocol. In some embodiments, concentration ranges of about 500 ng to about 50 mg, about 1 g to about 2 mg, about 5 g to about 500 g, and about 20 g to about 100 g of DNA or more can also be used during a gene therapy protocol.

[0139] The therapeutic polynucleotides and polypeptides described herein can be delivered using gene delivery vehicles. The gene delivery vehicle can be of viral or non-viral origin (see generally, Jolly, Cancer Gene Therapy (1994) 1:51; Kimura, Human Gene Therapy (1994) 5:845; Connelly, Human Gene Therapy (1995) 1:185; and Kaplitt, Nature Genetics (1994) 6:148). Expression of such coding sequences can be induced using endogenous mammalian or heterologous promoters and/or enhancers. Expression of the coding sequence can be either constitutive or regulated.

[0140] Viral-based vectors for delivery of a desired polynucleotide and expression in a desired cell are well known in the art. Exemplary viral-based vehicles include, but are not limited to, recombinant retroviruses (see, e.g., PCT Publication Nos. WO 90/07936; WO 94/03622; WO 93/25698; WO 93/25234; WO 93/11230; WO 93/10218; WO 91/02805; U.S. Pat. Nos. 5,219,740 and 4,777,127; GB Patent No. 2,200,651; and EP Patent No. 0 345 242), alphavirus-based vectors (e.g., Sindbis virus vectors, Semliki forest virus (ATCC VR-67; ATCC VR-1247), Ross River virus (ATCC VR-373; ATCC VR-1246) and Venezuelan equine encephalitis virus (ATCC VR-923; ATCC VR-1250; ATCC VR 1249; ATCC VR-532)), and adenovirus-associated virus (AAV) vectors (see, e.g., PCT Publication Nos. WO 94/12649, WO 93/03769; WO 93/19191; WO 94/28938; WO 95/11984 and WO 95/00655). Administration of DNA linked to killed adenovirus as described in Curiel, Hum. Gene Ther. (1992) 3:147 can also be employed.

[0141] Non-viral delivery vehicles and methods can also be employed, including, but not limited to, polycationic condensed DNA linked or unlinked to killed adenovirus alone (see, e.g., Curiel, Hum. Gene Ther. (1992) 3:147); ligand-linked DNA (see, e.g., Wu, J. Biol. Chem. (1989) 264:16985); eukaryotic cell delivery vehicles (see, e.g., U.S. Pat. No. 5,814,482; PCT Publication Nos. WO 95/07994; WO 96/17072; WO 95/30763; and WO 97/42338) and nucleic charge neutralization or fusion with cell membranes. Naked DNA can also be employed. Exemplary naked DNA introduction methods are described in PCT Publication No. WO 90/11092 and U.S. Pat. No. 5,580,859. Liposomes that can act as gene delivery vehicles are described in U.S. Pat. No. 5,422,120; PCT Publication Nos. WO 95/13796; WO 94/23697; WO 91/14445; and EP Patent No. 0524968. Additional approaches are described in

Philip, Mol. Cell. Biol. (1994) 14:2411, and in Woffendin, Proc. Natl. Acad. Sci. (1994) 91:1581.

[0142] The particular dosage regimen, i.e., dose, timing and repetition, used in the method described herein will depend on the particular subject and that subject's medical history. In some embodiments, more than one bispecific antibodies, or a combination of a bispecific antibody and another suitable therapeutic agent, may be administered to a subject in need of the treatment. The bispecific antibody can also be used in conjunction with other agents that serve to enhance and/or complement the effectiveness of the agents.

[0143] Treatment efficacy for a target disease/disorder can be assessed by methods well-known in the art.

Kits for Use in Treating Target Diseases

[0144] The present disclosure also provides kits for use in alleviating target diseases or disorders. Such kits can include one or more containers comprising one or more of the bispecific antibodies and/or one or more the isolated nucleic acids or nucleic acid sets described herein.

[0145] In some embodiments, the kit can comprise instructions for use in accordance with any of the methods described herein. The included instructions can comprise a description of administration of the bispecific antibody to treat, delay the onset, or alleviate a target disease such as HAE or thrombosis. The kit may further comprise a description of selecting an individual suitable for treatment based on identifying whether that individual has the target disease. In still other embodiments, the instructions comprise a description of administering an antibody to an individual at risk of the target disease.

[0146] The instructions relating to the use of a bispecific antibody as described herein generally include information as to dosage, dosing schedule, and route of administration for the intended treatment. The containers may be unit doses, bulk packages (e.g., multi-dose packages) or sub-unit doses. Instructions supplied in the kits of the invention are typically written instructions on a label or package insert (e.g., a paper sheet included in the kit), but machine-readable instructions (e.g., instructions carried on a magnetic or optical storage disk) are also acceptable.

[0147] The label or package insert indicates that the composition is used for treating, delaying the onset and/or alleviating a target disease or disorder. Instructions may be provided for practicing any of the methods described herein.

[0148] The kits of this invention are in suitable packaging. Suitable packaging includes, but is not limited to, vials, bottles, jars, flexible packaging (e.g., sealed Mylar or plastic bags), and the like. Also contemplated are packages for use in combination with a specific device, such as an inhaler, nasal administration device (e.g., an atomizer) or an infusion device such as a minipump. A kit 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). The container may also 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). At least one active agent in the composition is a bispecific antibody as those described herein.

[0149] Kits may optionally provide additional components such as buffers and interpretive information. Normally, the kit comprises a container and a label or package insert(s) on or associated with the container. In some embodiments, the

invention provides articles of manufacture comprising contents of the kits described above.

General Techniques

[0150] The practice of the present invention will employ, unless otherwise indicated, conventional techniques of molecular biology (including recombinant techniques), microbiology, cell biology, biochemistry and immunology, which are within the skill of the art. Such techniques are explained fully in the literature, such as, Molecular Cloning: A Laboratory Manual, second edition (Sambrook, et al., 1989) Cold Spring Harbor Press; Oligonucleotide Synthesis (M. J. Gait, ed., 1984); Methods in Molecular Biology, Humana Press; Cell Biology: A Laboratory Notebook (J. E. Cellis, ed., 1998) Academic Press; Animal Cell Culture (R. I. Freshney, ed., 1987); Introduction to Cell and Tissue Culture (J. P. Mather and P. E. Roberts, 1998) Plenum Press; Cell and Tissue Culture: Laboratory Procedures (A. Doyle, J. B. Griffiths, and D. G. Newell, eds., 1993-8) J. Wiley and Sons; Methods in Enzymology (Academic Press, Inc.); Handbook of Experimental Immunology (D. M. Weir and C. C. Blackwell, eds.); Gene Transfer Vectors for Mammalian Cells (J. M. Miller and M. P. Calos, eds., 1987); Current Protocols in Molecular Biology (F. M. Ausubel, et al., eds., 1987); PCR: The Polymerase Chain Reaction, (Mullis, et al., eds., 1994); Current Protocols in Immunology (J. E. Coligan et al., eds., 1991); Short Protocols in Molecular Biology (Wiley and Sons, 1999); Immunobiology (C. A. Janeway and P. Travers, 1997); Antibodies (P. Finch, 1997); Antibodies: a practical approach (D. Catty., ed., IRL Press, 1988-1989); Monoclonal antibodies: a practical approach (P. Shepherd and C. Dean, eds., Oxford University Press, 2000); Using antibodies: a laboratory manual (E. Harlow and D. Lane (Cold Spring Harbor Laboratory Press, 1999); The Antibodies (M. Zanetti and J. D. Capra, eds., Harwood Academic Publishers, 1995).

[0151] Without further elaboration, it is believed that one skilled in the art can, based on the above description, utilize the present invention to its fullest extent. The following specific embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever. All publications cited herein are incorporated by reference for the purposes or subject matter referenced herein.

Example 1: Construction and Characterization of Exemplary Bispecific Antibodies that Bind pKal and Factor XIIa

[0152] A number of exemplary anti-pKal/anti-FXIIa bispecific antibodies, including clones X0120-A01, X0120-C01, X0120-E01, X0120-G01, X0121-A03, X0121-C01, X0121-E01, X0121-G01, X0122-A01, and X0122-C01, were constructed, using DX-2930 and one of anti-FXIIa clones 559C-M0071-F06, 559C-M0184-B04, 559C-M0179-D04, 559C-M0181-C02 and 559C-M0180-G03 as the parent antibodies. See Table 2 below:

TABLE 2

Components of Exemplary Bispecific Antibodies		
Bispecific Antibody Clones	Anti-pKal portion	Anti-FXIIa portion
X0120-A01	DX-2930 (IgG)	scFv of clone 559C-M0184-B04 (H→L) fused to the C-terminus of the heavy chain of DX-2930
X0120-C01	DX-2930 (IgG)	scFv of clone 559C-M0184-B04 (L→H) fused to the C-terminus of the heavy chain of DX-2930
X0120-E01	DX-2930 (IgG)	scFv of clone 559C-M0179-D04 (H→L) fused to the C-terminus of the heavy chain of DX-2930
X0120-G01,	DX-2930 (IgG)	scFv of clone 559C-M0179-D04 (L→H) fused to the C-terminus of the heavy chain of DX-2930
X0121-A03	DX-2930 (IgG)	scFv of clone 559C-M0181-C02 (H→L) fused to the C-terminus of the heavy chain of DX-2930
X0121-C01	DX-2930 (IgG)	scFv of clone 559C-M0181-C02 (L→H) fused to the C-terminus of the heavy chain of DX-2930
X0121-E01	DX-2930 (IgG)	scFv of clone 559C-M0180-G03 (H→L) fused to the C-terminus of the heavy chain of DX-2930
X0121-G01	DX-2930 (IgG)	scFv of clone 559C-M0180-G03 (L→H) fused to the C-terminus of the heavy chain of DX-2930
X0122-A01,	DX-2930 (IgG)	scFv of clone 559C-M0071-F06 (H→L) fused to the C-terminus of the heavy chain of DX-2930
X0122-C01	DX-2930 (IgG)	scFv of clone 559C-M0071-F06 (L→H) fused to the C-terminus of the heavy chain of DX-2930

[0153] Among the anti-FXIIa clones, 559C-M0071-F06 is a parental clone, 559C-M0184-B04 is obtained from HCDR1+2 Affinity maturation, and 559C-M0179-D04, 559C-M0181-C02, and 559C-M0180-G03 are clones obtained from light chain affinity maturation.

[0154] All of the exemplary bispecific antibodies clones listed in Table 2 above are tetravalent molecules comprising four polypeptide chains, including two polypeptide chains of the light chain of DX-2930 (SEQ ID NO:10 provided above), and two fusion polypeptide chains of the heavy chain of DX-2930 (excluding a Lysine residue in the hinge domain of the constant chain) fused to a scFv chain of one of the FXIIa clones. The scFv chain of each of the 5 anti-FXIIa clones was synthesized in both the Heavy-Light (H→L) orientation and Light-Heavy orientation (L→H). In all examples of the scFv chains, an internal (GGGGS)₄ linker (SEQ ID NO:23) was used. The scFvs were constructed such that clones in the Light-Heavy orientation contained the initial two amino acids (RT) that initiate the constant region before the linker sequence begins. The clones in the Heavy-Light orientation contained only the first amino acid (R) from the light constant region before the stop codons.

[0155] The amino acid sequences of the fusion polypeptides of each of the exemplary bispecific antibodies are provided below:

Bispecific antibody clone X0120-A01 Heavy Chain-ScFv Fusion (SEQ ID NO: 11) :
MGWSCIILFLVATATGAHSEVQLESAGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSGIYSSGG
ITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRRIGVPRRDEFDIWGQGTMVTVSSASTKGPSVF
PLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPALQSSGLYSLSSVTVPSSSLGTQTYICN
VNHKPSNTKVDKRVEPKSCDTHCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPVYTL
PSREEMTKNQVSLTCLVKGFYPSDIAVEWESEGQOPENNYKTPVLDSDGSFFLYSKLTVDKSRWQOGNVFSCSV
MHEALHNHYTQKSLSLSPGKSGGGSEVQLLESAGGGLVQPGGSLRLSCAASGFTFSFYSMHWVRQAPGKGLEWVSR
IYPSGGVTKYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRQRYRGPKYYYYMDVWGKTTTVSSGG
GGSGGGGGGGGGGGGGGGSDIQMTQSPSLPVTGEPASISCRSSQSLHSNGNYLDWYLQKPGQSPQLIYLG
NRASGVPERFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPWTFQGQTKVEIKR

Bispecific antibody clone X0120-C01 Heavy Chain-ScFv Fusion (SEQ ID NO: 12) :
MGWSCIILFLVATATGAHSEVQLESAGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSGIYSSGG
ITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRRIGVPRRDEFDIWGQGTMVTVSSASTKGPSVF
PLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPALQSSGLYSLSSVTVPSSSLGTQTYICN
VNHKPSNTKVDKRVEPKSCDTHCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPVYTL
PSREEMTKNQVSLTCLVKGFYPSDIAVEWESEGQOPENNYKTPVLDSDGSFFLYSKLTVDKSRWQOGNVFSCSV
MHEALHNHYTQKSLSLSPGKSGGGSDIQMTQSPSLPVTGEPASISCRSSQSLHSNGNYLDWYLQKPGQSPQ
LIYLGSNRASGVPERFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPWTFQGQTKVEIKRTGGGGGGGGSG
GGGGGGGGSEVQLLESAGGGLVQPGGSLRLSCAASGFTFSFYSMHWVRQAPGKGLEWVSR IYPSGGVTKYADSVKG
RFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRQRYRGPKYYYYMDVWGKTTTVSSGG

Bispecific antibody clone X0120-E01 Heavy Chain-ScFv Fusion (SEQ ID NO: 13) :
MGWSCIILFLVATATGAHSEVQLESAGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSGIYSSGG
ITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRRIGVPRRDEFDIWGQGTMVTVSSASTKGPSVF
PLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPALQSSGLYSLSSVTVPSSSLGTQTYICN
VNHKPSNTKVDKRVEPKSCDTHCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPVYTL
PSREEMTKNQVSLTCLVKGFYPSDIAVEWESEGQOPENNYKTPVLDSDGSFFLYSKLTVDKSRWQOGNVFSCSV
MHEALHNHYTQKSLSLSPGKSGGGSEVQLLESAGGGLVQPGGSLRLSCAASGFTFSGYIMAWVRQAPGKGLEWVSY
IYPSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRQRYRGPKYYYYMDVWGKTTTVSSGG
GGSGGGGGGGGGGGGGGGSDIQMTQSPSLSVAPGEPASISCRSSQSLHRNGHNYLDWYLQKPGQSPQLIYLG
NRASGVPERFSGSGSGTDFTLRISRVEAEDVGVYYCMQALQARTFGQGQTKVEIKR

Bispecific antibody clone X0120-G01 Heavy Chain-ScFv Fusion (SEQ ID NO: 14) :
MGWSCIILFLVATATGAHSEVQLESAGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSGIYSSGG
ITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRRIGVPRRDEFDIWGQGTMVTVSSASTKGPSVF
PLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPALQSSGLYSLSSVTVPSSSLGTQTYICN
VNHKPSNTKVDKRVEPKSCDTHCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPVYTL
PSREEMTKNQVSLTCLVKGFYPSDIAVEWESEGQOPENNYKTPVLDSDGSFFLYSKLTVDKSRWQOGNVFSCSV
MHEALHNHYTQKSLSLSPGKSGGGSDIQMTQSPSLSVAPGEPASISCRSSQSLHRNGHNYLDWYLQKPGQSPQ

- continued

LLIYLGSNRASGVPERSGSGSGTDFTLRISRVEAEDVGVYYCMQALQARTFGQGTKVEIKRTGGGSGGGSGG
GGSGGGSEVQLLESGGLVQPGGLRLSCAASGFTFSGYIMAWVRQAPGKGLEWVSYIYPGGITVYADSVKGR
FTISRDNSKNTLYLQMNSLRAEDTAVYYCTRQYRGPKYYYYMDVWGKGTTVTVSS

Bispecific antibody clone X0121-A03 Heavy Chain-ScFv Fusion (SEQ ID NO: 15) :
MGWSCIILFLVATATGAHSEVQLLESGGLVQPGGLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSGIYSSGG

ITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRRIGVPRRDEFDIWGQGTMVTVSSASTKGPSVF
PLAPSSKSTSGGTAALGCLVKDYFPEPVTWSWNSGALTSGVHTFPALQSSGLYSLSSVTPSSSLGTQTYICN
VNHKPSNTKVDKRVEPKSCDHTCPPCPAPEELLGGPSVFLFPPKPDKTLMSRTPEVTCVVVDVSHDPEVFKNW
YVDGVEVHNNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPVYTL
PSREEMTKNQVSLTCLVKGFYPSDIAVEWESENQGPENNYKTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGKSGGGSEVQLLESGGLVQPGGLRLSCAASGFTFSGYIMAWVRQAPGKGLEWVSY
IYPGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRQYRGPKYYYYMDVWGKGTTVTVSSGG
GGSGGGGGGGGGGGGGSDIQMTQSPLSLPVTPGEPAISCRSSQSLLSNGNYLDWYLQKPGQSPQLIYLGS
NRASGVPDFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTRTFGQGTKEIKR

Bispecific antibody clone X0121-C01 Heavy Chain-ScFv Fusion (SEQ ID NO: 16) :
MGWSCIILFLVATATGAHSEVQLLESGGLVQPGGLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSGIYSSGG

ITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRRIGVPRRDEFDIWGQGTMVTVSSASTKGPSVF
PLAPSSKSTSGGTAALGCLVKDYFPEPVTWSWNSGALTSGVHTFPALQSSGLYSLSSVTPSSSLGTQTYICN
VNHKPSNTKVDKRVEPKSCDHTCPPCPAPEELLGGPSVFLFPPKPDKTLMSRTPEVTCVVVDVSHDPEVFKNW
YVDGVEVHNNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPVYTL
PSREEMTKNQVSLTCLVKGFYPSDIAVEWESENQGPENNYKTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGKSGGGSDIQMTQSPLSLPVTPGEPAISCRSSQSLLSNGNYLDWYLQKPGQSPQ
LLIYLGSNRASGVPDFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTRTFGQGTKEIKRRTGGGSGGGSGG
GGSGGGGGSEVQLLESGGLVQPGGLRLSCAASGFTFSGYIMAWVRQAPGKGLEWVSYIYPGGITVYADSVKGR
FTISRDNSKNTLYLQMNSLRAEDTAVYYCTRQYRGPKYYYYMDVWGKGTTVTVSS

Bispecific antibody clone X0121-E01 Heavy Chain-ScFv Fusion (SEQ ID NO: 17) :
MGWSCIILFLVATATGAHSEVQLLESGGLVQPGGLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSGIYSSGG

ITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRRIGVPRRDEFDIWGQGTMVTVSSASTKGPSVF
PLAPSSKSTSGGTAALGCLVKDYFPEPVTWSWNSGALTSGVHTFPALQSSGLYSLSSVTPSSSLGTQTYICN
VNHKPSNTKVDKRVEPKSCDHTCPPCPAPEELLGGPSVFLFPPKPDKTLMSRTPEVTCVVVDVSHDPEVFKNW
YVDGVEVHNNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPVYTL
PSREEMTKNQVSLTCLVKGFYPSDIAVEWESENQGPENNYKTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGKSGGGSEVQLLESGGLVQPGGLRLSCAASGFTFSGYIMAWVRQAPGKGLEWVSY
IYPGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRQYRGPKYYYYMDVWGKGTTVTVSSGG
GGSGGGGGGGGGGGGGSDIQMTQSPLSLPVTPGEPAISCRSSQSLLSNGNYLDWYLQKPGQSPQIMIYLGS
NRASGVPDFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTRTFGQGTKEIKR

Bispecific antibody clone X0121-G01 Heavy Chain-ScFv Fusion (SEQ ID NO: 18) :
MGWSCIILFLVATATGAHSEVQLLESGGLVQPGGLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSGIYSSGG

ITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRRIGVPRRDEFDIWGQGTMVTVSSASTKGPSVF
PLAPSSKSTSGGTAALGCLVKDYFPEPVTWSWNSGALTSGVHTFPALQSSGLYSLSSVTPSSSLGTQTYICN
VNHKPSNTKVDKRVEPKSCDHTCPPCPAPEELLGGPSVFLFPPKPDKTLMSRTPEVTCVVVDVSHDPEVFKNW

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YVDGVEVHNNAKTKPREEQYNSTYRvvSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREGQVYTL
PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGKSGGGSDIQMTQSPSLPVTGEPASCRSSQSLLSNGNYLDWYLQKPGQSPQ
IMIYLGSNRASGVPDFRGSGSGTDFTLKISRVEAEDVGYYCMQALQTPTFGQGKVEIKRTGGGSGGGSG
GGGGGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSGYIMAWVRQAPGKGLEWVSYIYPGGITVYADSVKG
RFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRQYRGPKYMMMDVWGKGT TVVSS

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Bispecific antibody clone X0122-A01 Heavy Chain-ScFv Fusion (SEQ ID NO: 19) :
MGWSCIILFLVATATGAHSEVQLLESGGGLVQPGGSLRLSCAASGFTFSGYIMAWVRQAPGKGLEWVSGIYSSGG

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ITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRIGVPRRDEFDIWGQGTMVTVSSASTKGPSVF
PLAPSSKSTSGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPALQSSGLYSLSSVTPSSSLGTQTYICN
VNHKPSNTKVDKRVEPKSCDTHCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNNAKTKPREEQYNSTYRvvSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREGQVYTL
PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGKSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSGYIMAWVRQAPGKGLEWVSY
IYPGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRQYRGPKYMMMDVWGKGT TVVSS
GGGGGGGGGGGGGGGGSDIQMTQSPSLPVTGEPASCRSSQSLLSNGNYLDWYLQKPGQSPQLIYLGS
NRASGVPDFRGSGSGTDFTLKISRVEAEDVGYYCMQALQTPTFGQGKVEIKR

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Bispecific antibody clone X0122-C01 Heavy Chain-ScFv Fusion (SEQ ID NO: 20) :
MGWSCIILFLVATATGAHSEVQLLESGGGLVQPGGSLRLSCAASGFTFSGYIMAWVRQAPGKGLEWVSGIYSSGG

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ITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRIGVPRRDEFDIWGQGTMVTVSSASTKGPSVF
PLAPSSKSTSGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPALQSSGLYSLSSVTPSSSLGTQTYICN
VNHKPSNTKVDKRVEPKSCDTHCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNNAKTKPREEQYNSTYRvvSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREGQVYTL
PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGKSGGGSDIQMTQSPSLPVTGEPASCRSSQSLLSNGNYLDWYLQKPGQSPQ
LIYLGSNRASGVPDFRGSGSGTDFTLKISRVEAEDVGYYCMQALQTPTFGQGKVEIKRTGGGSGGGSG
GGGGGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSGYIMAWVRQAPGKGLEWVSYIYPGGITVYADSVKG
RFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRQYRGPKYMMMDVWGKGT TVVSS

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[0156] To construct the expression cassette for the exemplary bispecific antibodies described above, the coding sequences for the heavy and light chains of DX-2930 were cloned into a pH1-CHO vector, modified with a C-terminal SGGGS linker that connects to the scFv coding sequence. The linker region contained a BamHI restriction site for efficient cloning of the scFvs. Five anti-Factor XIIa clones were selected for insertion into the construct via Bam-HIXbaI restriction sites.

[0157] The italicized portions of the sequences provided above refer to the signal peptides. The anti-pKal portion of the bispecific antibody disclosed herein may include the same signal peptides, or may have the signal peptides removed or replaced with a different signal peptide. Signal peptides for use in producing secretory proteins are well known in the art.

[0158] The nucleotide sequences encoding the bispecific antibodies (in cis-tronic operon format) are provided below:

X0120-A01

(SEQ ID NO: 24)

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ATGGGATGGCTCTGCATCATCTGTTCTGGTGCTACAGCCACAGCGTGCACTCCGACATCCAGAT
GACCCAGTCCCCCTCCACCCCTGTCCGCCCTGTGGCGACAGAGTGACCATCACCTGTCGGCCTCCC
AGTCCATCTCCAGCTGGCTGGCTGGTATCAGCAGAAGGCCGGAAAGGCCCAAGCTGCTGATCTAC
AAGGCCAGCACCCCTGGAATCCGGCTGCCCTCCAGATTCTCCGGCTCTGGCTCCGGCACCGAGTCAC

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CCTGACCATCAGCTCCCTGCAGCCCCGACGACTCGCCACCTACTACTGCCAGCAGTACAACACCTACT
GGACCTTCGGCCAGGGCACCAAGGTGGAAATCAAGCGGACCGTGCCGCTCCCTCCGTGTTCATCTTC
CCACCCCTCCGACGAGCAGCTGAAGTCCGGCACCGCCTCCGTGGTCTGCCTGCTGAACAACCTCTACCC
CCCGCAGGCCAAGGTGCAGTGGAAAGGTGGACAACGCCCTGCAGTCGGCAACTCCCAGGAATCCGTGA
CCGAGCAGGACTCCAAGGACAGCACCTACTCCCTGTCCTACCCCTGACCCTGTCCAAGGCCGACTAC
GAGAAGCACAAGGTGACGCCCTGCAGGTGACCCACCAGGGCTGTCCAGCCCCGTGACCAAGTCCTT
CAACCGGGCGAGTGTGATGAGGCGCGCTTCGCGTCGAGCATGCATCTAGGGCGGCAATTCCGCC
CCTCTCCCCCCCCCCCCCTAACGTTACTGGCGAAGCCGTTGGATAAGGCCGGTGTGCGTTGTCT
ATATGTTATTTCCACCATATTCCGTCTTGGCAATGTGAGGGCCGGAAACCTGGCCCTGTCTTC
TTGACGAGCATTCTAGGGTCTTCCCTCTCGCCAAGGAATGCAAGGTCTGTTGAATGTCGTGAA
GGAAGCAGTCTCTGGAAGCTTCTGAAGACAAACAACGTCTGTAGCGACCCCTTGCAAGGCCG
ACCCCCCACCTGGCAGGGTGCCTCTGCCGAAAAGCCACGTGTATAAGATAACACCTGCAAAGGCG
GCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCAGGCTCTCTCAAGCGT
ATTCAACAAGGGCTGAGGATGCCAGAAGGTACCCATTGATGGGATCTGATCTGGGCTCGGT
GCAGATGCTTACATGTGTTAGTCGAGGTTAAAAAAACGTCTAGGCCCGGAACACGGGAGCTG
GTTTCCCTTGAAAAACACGATGATAATATGCCACAACCAGGGATGGCTGCACTCATCTGTTTC
TGGTGGCACAGGCCACAGCGCTCACTCGAGGTGCAATTGCTGGAATCCGGCGAGGACTGGTGCAG
CCTGGCGCTCCCTGAGACTGCTTGCGCCGCTCCGGCTCACCTCTCCACTACATCATGATGTG
GGTGCAGAGGCTCCGGCAAGGGGCTGGAATGGGTGTCGGCATCTACTCTCCGGCGCATACCG
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CAGATGAACTCCCTGCCGCGAGGACACCGCCGTGACTACTGCCCTACCGCGGATCGCGTGCC
CACACGGGACGAGTCGACATCTGGGGCAGGGCACCATGGTACAGTGTCTCCGCTCCACCAAGG
GCCCTCTGTGTTCCCGTAGCACCTCCAGCAAGTCCACCTCCGGCGACCGCTGCTGGCTGC
CTCGTAAGGACTACTTCCCAGGCCGTGACCGTGTCTGGAACTCTGGCCCTGACCAGGGAGT
GCATACCTCCCTGCCGTGCTCAGTCTCCGCCGTACAGCCTGCTCTGTGACCGTGCCT
CCAGCTCCCTGGCACCCAGACCTACATCTGCAACGTGAACCAAGCCCTCCAACACCAAAGTGGAC
AAGCGGGTGGAAACCAAGTCCTGCGACACCCACACCTGCCCCCTGCCCTGCCCTGAACTGCTGG
CGGACCCAGCGTGTCTGTTCCCCAAAGCCAAGGACACCCGTATGATCTCCGGACCCCGAAG
TGACCTCGTGGTGGAGCTGCTCCACGAGGACCCGTGAAAGTGAAGTTAAATTGGTACGTGGACGGC
GTGGAAGTGCATAACGCCAAGACCAAGCCCAGAGAGGAACAGTACAACCTACCGCTACCGGGTGGTGC
CGTGTGACCGTGTGACCCAGGACTGGCTGAAACGGCAAGAGTACAAGTGCAGGTGTCAGAAG
CCCTGCCCTGCCCTGAAAGACCATCAGCAAGGCCAAGGGCCAGCCTCGCAGCCCCAGGTGTAC
ACCTGCCCTAGCGGGAAAGAGATGACCAAGAACCGGTGCTCTGACCTGTGGTCAAGGGCTT
CTACCCCTCCGATATGCCGTGGAATGGGAGTCCAACGGCCAGCCCAGAACAACACTACAAGACCA
CCCTGTGCTGGACAGCGACGGCTCATTCTCTGTACTCCAAGTGACCGTGGACAAGTCCCGGT
CAGCAGGGCAACGTGTTCTCTGCTCCGTATGACGAGGCCCTGCACAACCAACTACACCCAGAGTC
CCTGCTCCCTGTCTCCCGCAAGTCTGGCGAGGATCCGAAGTGCAGCTGCTGGAAAGCGGGAGGCC
TGGTGCAGCCTGGAGGGAGCCTGAGACTGTTGCGCTGCCAGCGGCTTCACCTTCAGCTTACAGC
ATGCACTGGTCCGACAGGCTCAGGCCAAGGGCTGGAATGGGTGTCGGGATCTACCCCTGCGG

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CGTGACCAAATACGCCGACAGCGTGAAGGGCGGTTCACCATCAGCCGGACAACAGCAAGAACACCC
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AGAGGCCCAAGTACTACTACATGGACGTGTGGGCAAGGGACAACCGTGACCGTGTCTAGCGG
AGCGGGAGGATCTGGCGGAGGTGGAAGTGGTGGTGGCGGAAGTGGCGGAGGCCGGCAGCGACATCCAGA
TGACCCAGAGCCCCCTGAGCCTGCCGTGACACCTGGCGAGCCTGCCAGCATCAGCTGCAGAAGCAGC
CAGAGCCTGCTCACAGCAACGGCTACAACCTACCTGGACTGGTATCTGCAGAAGGCCGGCAGTCCCC
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CCGGCACCGACTTCACCCCTGAAGATCAGCCGGTGGAAAGCCGAGGACGTGGCGTGTACTATTGCATG
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X0120-C01
(SEQ ID NO: 25)
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CGTGCTGACCGTGTGCAACAGGACTGGCTGAACGGCAAAGAGTACAAGTGAAGGTGTCAAACAAGG
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GA

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X0120-E01

(SEQ ID NO: 26)

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 X0120-G01
 (SEQ ID NO: 27)
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X0121-A03
(SEQ ID NO: 28)
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X0121-C01

(SEQ ID NO: 29)

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X0121-E01
(SEQ ID NO: 30)
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X0121-G01

(SEQ ID NO: 31)

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CCGGCACCGACTTCACCCCTGAAGATCAGCCGGTGGAGCCAGGACGTGGCGTGTACTATTGCATG
CAGGCCCTGCAGACCCCCCTGGACCTTCGGCCAGGGACCAAGGTGGAAATCAAGAGATGAATCTAGA

X0122-C01

(SEQ ID NO: 33)

ATGGGATGGTCTGCATCATCTGTTCTGGTGGTACAGCCACAGCGTGCACCGACATCCAGAT
GACCCAGTCCCCCTCCACCCCTGCGCTCTGAGGACAGAGTGCACCATCACCTGTCGGCCTCCC
AGTCCATCTCCAGCTGGCTGGCTGGTATCAGCAGAAGCCGGCAAGGCCCAAGCTGCTGATCTAC
AAGGCCAGCACCCCTGGAATCCGGCGTGCCTCCAGATTCTCCGGCTGGCTCCGGCACCGAGTTCAC
CCTGACCATCAGCTCCCTGCAGCCGACGACTCGCCACCTACTACTGCCAGCAGTACAACACCTACT
GGACCTTCGGCCAGGGACCAAGGTGGAAATCAAGCGGACCGTGGCGCTCCCTCCGTGTTCATCTTC
CCACCCCTCCGAGGAGCAGCTGAAGTCCGGCACCGCCTCCGTGGTCTGCCTGCTGAACAACCTTACCC
CCCGGAGGCCAGGTGCAGTGGAGGTGGACAACGCCCTGCAGTCCGGCAACTCCAGGAATCCGTGA
CCGAGCAGGACTCCAAGGACAGCACCTACTCCCTGCTCTACCCCTGACCCGTCCAAGGCCACTAC
GAGAACACAAGGTGTACGCTGCGAAGTGACCCACCAGGGCTGTCCAGCCCGTGAACAGTCCTT
CAACCGGGCGAGTGTGATGAGGCGCGCTCGCGTCGAGCATGCATCTAGGGCGGCAATTCCGCC
CCTCTCCCCCCCCCCCCCTAACGTTACTGGCGAAGCCGTTGGATAAGGCCGGTGTGCGTTGTCT
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TTGACGAGCATTCTAGGGTCTTCCCCTCTGCCAAAGGAATGCAAGGTCTGTTGAATGTCGTGAA
GGAAGCAGTCTGGAGCTTGAAGACAACACGCTGTAGCGACCCCTTGCAAGCGGA
ACCCCCCACCTGGCGACAGGTGCCTCTGCCAAAAGCCACGTGTATAAGATAACACCTGCAAAGCG
GCACAACCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCAGGCTCTCTCAAGCGT
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GCAGATGCTTACATGTGTTAGTCGAGGTTAAAAAAACGTCTAGGCCCGAACCACGGGACGTG
GTTTCCCTTGAACACGATGATAATATGCCACAACCATGGATGGCTGCATCATCTGTTTC
TGGTGGCACAGCCACAGGCCTCACTCGAGGTGCAATTGCTGGAATCCGGGGAGGACTGGTGCAG
CCTGGCGCTCCCTGAGACTGTCTGCGCCCTCGGCTCACCTCTCCACTACATCATGATGTG
GGTGCACAGGCTCTGGCAAGGGCTGGAATGGGTGTCGGCATCTACTCCCTGGCGCATACCG
TGTACCGGACTCGTGAGGGCGGTCACCATCTCGGACAACCTCAAGAACACCTGTACCTG
CAGATGAACTCCCTGCGGCCGAGGACACCGCGTGTACTACTGCGCCTACCGGGATCGCGTGC
CAGACGGGACGAGTCGACATCTGGGGCAGGGCACCATGGTGACAGTGTCTCCGCTCAGG
GCCCTCTGTGTTCCCGTAGCACCTCCAGCAAGTCCACCTCGGCGGACCGCTGCTGGCTGC
CTCGTCAAGGACTACTCCCCGAGCCGTGACCGTGTGAACTCTGGCCCTGACCAGGGAGT
GCATACCTCCCTGCCGTGCTCCAGCTCGCCTGTACAGCCTGCTCTGTCGTGACCGTGC
CCAGCTCCCTGGCACCCAGACCTACATCTGCAACGTGAACCACAAGCCCTCCAACACCAAAGTGGAC
AAGCGGGTGGACCCAAGTCTCGACACCCACACCTGCCCCCTGCCCTGCCCTGAACTGCTGG
CGGACCCAGCGTGTCCCTGTTCCCCAAAGCCAAGGACACCCCTGATGATCTCCGGACCCCGAAG
TGACCTGCGTGGTGGACGTGCCCACGAGGACCCCTGAAAGTTAATTGGTACGTGGAC
GTGGAAGTGCATAACGCCAAGACCAAGCCCAGAGAGGAACAGTACAACCTCCACCTACGGGTTGTC
CGTGCTACCGTGTGCAACAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTC
CCCTGCCTGCCCATCGAAAAGACCATCAGCAAGGCCAAGGCCAGCCTGCGAGCCCCAGGTGTAC
ACCCCTGCCCTAGCCGGAAAGAGATGACCAAGAACAGGTGCCCCGACCTGTCGTCAAGGGCT
CTACCCCTCCGATATGCCGTGGAATGGGAGTCCAACGCCAGCCGAGAACAACTACAAGAC
CCCGCTGTGCTGGACAGCAGGCTCATTCTCCTGACTCCAAGCTGACCGTGGACAAGTCCGGTGG
CAGCAGGGCAACGTGTTCTCTGCTCCGTATGCACGAGGCCCTGCACAACCAACTACACCCAGAGTC
CCTGCTCCCTGTCCTCCGGCAAGTCTGGCGAGGATCCGACATCCAGATGACCCAGAGCCCCCTGAGCC
TGCCCGTGCACACCTGGCAGGCCAGCATCAGCTGCAGAAGCAGCCAGAGCCTGTCACAGCAAC
GGCTACAACACTGGACTGGTATCTGCAGAACGCCGCCAGTCCCCCAGCTGCTGATCACCTGG
CAGCAACAGAGCCAGCGCGTGCCGACAGATTAGCGAGGCCAGCAGGCTCCGGACCGACTTCACCC
AGATCAGCCGGTCAAGCCAGGGACGTGGCGTGTACTACTGCTGCAGGCCAGAGCCTGTCACAGCAAC
ACCTTCGGCCAGGGACCAAGGTGAAATCAAGCGGACAGGCCGGAGGCTCTGGCGGAGGTGGAAG
CGGAGGGAGGAAGTGGCGAGGCCGCTCTGAGGTGACGCTGCTGGAATCTGGCGGCGACTGGTGC
AGCCTGGCGCAGGCCCTGAGACTGTCTGCGCCGCCAGCGGCTCACCTCAGCGGCTACATCATGCC
TGGGTCCGACAGGCCCTGGCAAGGGCTGGAATGGGTGTCCTACATCTACCCAGCGGCGCATCAC
CGTGTACGCCGACAGCGTGAAGGGCGGTTACCATCAGCGGGACAACAGCAAGAACACCC
TGCAGATGAAACGCCCTGCGGGCGAGGACACCGCCGTGTACTATTGCAACCCGGCAGCGGTACAGAGGC
CCCAAGTACTACTACATGGACGTGTTGGGCAAGGGCACCCAGTGCACCGTGTCCAGCTGAATCTA
GA

[0159] pRh1 expression plasmids encoding the above-noted bispecific antibodies were generated. Following 0.2 µm sterile filtration, the plasmids were transfected into 60 mL dl cultures of Expi293F™ cells, cultured in Expi293™ expression medium, using ExpiFectamine™ as a transfection reagent, as described by the LifeTech protocol (Life Technologies™, Carlsbad, CA). ExpiFectamine™ transfection enhancers 1 and 2 were added on day 2 of culture as described in LifeTech protocol. Cultures were incubated at 37 °C, 8% CO₂, 140 rpm through day 7. Cultures were harvested by centrifugation followed by 0.2 µm sterile filtration and stored at 4° C. Clones were batch purified using a protein A column.

[0160] Varying concentrations of the bispecific antibodies were incubated with individual FXIIa and pKal samples, and the ability of these proteases to cleave a peptide substrate was monitored over time by measuring changes in the fluorescence of a chemical moiety covalently attached to the peptide substrate. Slopes of this kinetic data are equivalent to enzymatic proteolytic rates, which are then plotted against the concentration of the inhibitor. The resulting plots are then fit to a tight binding inhibitor equation (Equation 1) by nonlinear regression to obtain apparent inhibition constants (K_i^{app}).

$$v = V_0 \cdot \frac{\frac{([E] - [I] - K_i^{app}) +}{\sqrt{([E] - [I] - K_i^{app})^2 - 4[E] \cdot K_i^{app}}}}{2} \quad [\text{Equation 1}]$$

[0161] FIGS. 1 and 2 show the plots of pKal and FXIIa inhibition activities for each bispecific antibody tested. All clones tested were able to inhibit both pKal and FXIIa. The K_i^{app} pKal and FXIIa for each bispecific antibody is listed below in Table 3.

TABLE 3

Apparent inhibition constants for bispecific antibodies		
Bispecific antibody	K _i ^{app} pKal (nM)	K _i ^{app} FXIIa (nM)
X120-A01	0.1376 +/- 0.0206	0.0515 +/- 0.0186
X121-E01	0.1593 +/- 0.0245	0.6114 +/- 0.0714
X122-A01	0.1693 +/- 0.0242	6.0467 +/- 0.6497
X122-C01	0.1610 +/- 0.0221	5.6900 +/- 0.6512
Control M71-F06 IgG	N/A	0.8758 +/- 0.0579

Example 2: Construction and Characterization of Exemplary Bispecific Antibodies that Bind pKal and Factor XIIa

[0162] Another exemplary set of anti-pKal/anti-FXIIa bispecific antibodies was constructed as follows. The IgG portion of the molecule was the same as used in Example 1, i.e., DX-2930. For the anti-FXIIa component, 36 isolates were chosen and were converted to scFvs in both the Light/Heavy and Heavy/Light orientations. The scFvs were fused to the DX-2930 IgG using an SGGS (SEQ ID NO: 22) linker. When constructing the scFvs, a (G₄S)₄ linker was used to fuse the anti-FXIIa variable heavy and variable light domains to each other. The sequences of the bi-specific antibodies are provided below.

[0163] The constructed bispecific molecules showed anti-pKal activity generally consistent with values previously

determined for DX-2930 (Table 4). Some values showed less potency against pKal, possibly due to errors in calculating concentration, or possibly due to aggregation. The anti-FXIIa activity of the scFv component was typically lower than the previously determined values, possibly due to inherent instability associated with scFvs (Table 4). The activity of the bispecific molecules in the plasma assay showed marked improvement over DX-2930 and the anti-FXIIa IgGs. DX-2930 showed a range between 70-100 nM in this assay, while the anti-FXIIa parent antibody showed inhibition in the ~100 nM range. A panel of the bispecific molecules tested show inhibition in the 1-10 nM range (Table 5).

TABLE 4

Ki, apparent of 72 bispecific anti-pKal + anti-FXIIa antibodies against the respective targets. DX-2930 and a FXIIa lead candidate (559C-M0292-D07) were used as controls.					
	ScFv Orientation	Bispecific Isolate	FXII-name	Anti-pKal Corrected Ki, app (pM)	Anti-FXIIa Corrected Ki, app (pM)
1	H→L	620L-X136-C07	559C-M0177-B11	182	699
	L→H	620L-X138-A08	559C-M0177-B11	920	357
2	H→L	620L-X136-B02	559C-M0177-C12	210	2857
	L→H	620L-X139-A12	559C-M0177-C12	2053	4084
3	H→L	620L-X137-B08	559C-M0178-A08	312	409
	L→H	620L-X142-A04	559C-M0178-A08	162	1233
4	H→L	620L-X142-B11	559C-M0179-A03	622	7719
	L→H	620L-X138-B01	559C-M0179-A03	169	6628
5	H→L	620L-X136-C01	559C-M0182-B04	173	957
	L→H	620L-X138-A12	559C-M0182-B04	405	1925
6	H→L	620L-X136-A12	559C-M0182-D04	234	304
	L→H	620L-X138-A02	559C-M0182-D04	206	288
7	H→L	620L-X136-A05	559C-M0182-H01	179	111
	L→H	620L-X138-C07	559C-M0182-H01	196	314
8	H→L	620L-X136-E07	559C-M0182-H04	190	312
	L→H	620L-X142-B02	559C-M0182-H04	156	955
9	H→L	620L-X136-F11	559C-M0183-B12	201	235
	L→H	620L-X142-A05	559C-M0183-B12	160	2140
10	H→L	620L-X136-C09	559C-M0183-C03	173	90
	L→H	620L-X138-B10	559C-M0183-C03	75	58
11	H→L	620L-X136-C08	559C-M0183-D08	216	1231
	L→H	620L-X139-A11	559C-M0183-D08	235	3835
12	H→L	620L-X136-D05	559C-M0183-H08	55	13
	L→H	620L-X138-D04	559C-M0183-H08	215	79

TABLE 4-continued

K_i, apparent of 72 bispecific anti-pKal + anti-FXIIa antibodies against the respective targets. DX-2930 and a FXIIa lead candidate (559C-M0292-D07) were used as controls.

	ScFv Orientation	Bispecific Isolate	FXII-name	Anti-pKal Corrected Ki, app (pM)	Anti-FXIIa Corrected Ki, app (pM)
13	H→L	620I-X136-G08	559C-M0184-B04	176	28
	L→H	620I-X142-B07	559C-M0184-B04	224	775
14	H→L	620I-X142-A11	559C-M0184-D01	158	195
	L→H	620I-X138-G12	559C-M0184-D01	186	766
15	H→L	620I-X142-A10	559C-M0184-E06	175	389
	L→H	620I-X138-D03	559C-M0184-E06	79	344
16	H→L	620I-X137-C08	559C-M0184-F12	153	34
	L→H	620I-X142-E02	559C-M0184-F12	162	186
17	H→L	620I-X136-E05	559C-M0191-A03	158	172
	L→H	620I-X138-B06	559C-M0191-A03	330	405
18	H→L	620I-X136-A09	559C-M0191-B11	190	X
	L→H	620I-X138-A06	559C-M0191-B11	145	X
19	H→L	620I-X137-A10	559C-M0191-C09	195	205
	L→H	620I-X139-B10	559C-M0191-C09	247	189
20	H→L	620I-X136-A04	559C-M0191-E04	171	230
	L→H	620I-X138-D06	559C-M0191-E04	199	132
21	H→L	620I-X136-C11	559C-M0191-E09	154	38
	L→H	620I-X138-B07	559C-M0191-E09	246	135
22	H→L	620I-X136-A02	559C-M0191-H09	176	136
	L→H	620I-X139-G02	559C-M0191-H09	171	161
23	H→L	620I-X136-B07	559C-M0191-H10	168	99
	L→H	620I-X138-E03	559C-M0191-H10	178	122
24	H→L	620I-X136-G05	559C-M0192-A01	179	100
	L→H	620I-X139-D12	559C-M0192-A01	428	383
25	H→L	620I-X136-A01	559C-M0192-A03	135	224
	L→H	620I-X138-C12	559C-M0192-A03	267	697
26	H→L	620I-X136-G10	559C-M0192-D02	171	28
	L→H	620I-X138-D05	559C-M0192-D02	519	139
27	H→L	620I-X136-F07	559C-M0192-D12	183	167
	L→H	620I-X138-A01	559C-M0192-D12	154	465
28	H→L	620I-X142-E09	559C-M0192-F01	174	163
	L→H	620I-X138-D11	559C-M0192-F01	178	443
29	H→L	620I-X136-C05	559C-M0192-F06	150	58
	L→H	620I-X142-A02	559C-M0192-F06	152	63

TABLE 4-continued

K_i, apparent of 72 bispecific anti-pKal + anti-FXIIa antibodies against the respective targets. DX-2930 and a FXIIa lead candidate (559C-M0292-D07) were used as controls.

	ScFv Orientation	Bispecific Isolate	FXII-name	Anti-pKal Corrected Ki, app (pM)	Anti-FXIIa Corrected Ki, app (pM)
30	H→L	620I-X136-C04	559C-M0192-F07	205	189
	L→H	620I-X138-F02	559C-M0192-F07	464	794
31	H→L	620I-X136-G04	559C-M0192-G03	179	107
	L→H	620I-X139-G12	559C-M0192-G03	276	252
32	H→L	620I-X136-B11	559C-M0192-G05	172	184
	L→H	620I-X142-D04	559C-M0192-G05	170	414
33	H→L	620I-X136-D06	559C-M0192-H04	176	84
	L→H	620I-X139-A01	559C-M0192-H04	146	53
34	H→L	620I-X136-D12	559C-M0192-H11	179	63
	L→H	620I-X138-F05	559C-M0192-H11	214	147
35	H→L	620I-X136-A11	559C-M0292-D07	199	193
	L→H	620I-X139-E05	559C-M0292-D07	196	172
36	H→L	620I-X136-C12	559C-M0177-A06	217	1567
	L→H	620I-X138-E05	559C-M0177-A06	186	245
37	Plate 1		DX-2930	160	X
	Plate 2		DX-2930	138	X
38	Plate 1		559C-M292-D07	X	36
	Plate 2		559C-M292-D07	X	38

TABLE 5

Comparison of parental anti-FXIIa isolates and anti-pKal/anti-FXIIa bispecific molecules in plasma activation assay. Plasma was diluted 1:40. Inhibitors added to dilute plasma. 2.5% Ellagic Acid added to plasma. After 2 minutes, activation was quenched by addition of Cohn Trypsin Inhibitor. pKal activity was measured by the addition of a profluorescent substrate.

FXII IgG isolate name	Bispecific Iso name	Plasma Inhibition	
		IgG IC50 (nM)	bispecific IC50/Ki (nM)
559C-M0192-A03	620I-X0136-A01	514	52
559C-M0192-F06	620I-X0136-C05	304	2.6
559C-M0191-E09	620I-X0136-C11	31	1.8
559C-M0192-H11	620I-X0136-D12	101	3
559C-M0192-A01	620I-X0136-G05	198	8

[0164] Five exemplary candidates (620I-X0136-D12, 620I-X0136-C05, 620I-X0136-C11, 620I-X0136-G05, and 620I-X0136-A01) were selected for further analysis. Of these 5 lead candidates, 620I-X0136-A01 was eliminated due to low expression values and multiple species in the size exclusion chromatography (SEC) traces. Of the remaining 4 lead candidates, each isolate contained a varying degree of High Molecular Weight aggregate (16-35%) (FIG. 3). This

aggregate was determined to be concentration-dependent and was hypothesized to be dimeric structures interacting through the scFv domains.

[0165] An exemplary bispecific antibody, 620I-X0136-D12 (D12) was assessed for its ability to inhibit plasma pKal activity by the plasma inhibition assay. Briefly, reconstituted plasma containing quantities of pre-pKal and FXII in the presence or absence of HMWK was diluted 1:40 in an assay buffer (20 mM Tris-HCl pH 7.5, 150 mM NaCl, 1 mM EDTA, 0.1% PEG-8000 and 0.1% Triton X-100). The concentrations of pre-pKal, FXII, and HMWK are equivalent to their normal concentrations in plasma. Inhibitors were added to the reconstituted plasma at varying concentrations in a 96-well microplate at room temperature. Contact activation was then initiated by the addition of 25% (2.5% final) of a dilute ellagic acid solution, the microplate was mixed by gentle shaking, and allowed to proceed for 2 minutes at room temperature, whereby 100 nM of CTI was added. 10 µl of this mixture was then removed to a replicate microplate containing 80 µl of assay buffer at pre-equilibrated at 30 C. This dilution plate was then incubated a further 5 minutes at 30 C, and proteolysis of PFR-AMC assessed as above, but with back-calculated concentrations of inhibitor used in the X-axis for curve-fitting to a modified Morrison equation for tight binding inhibitors (plasma was diluted 1:400 in final assay read). The results of this study are shown in FIG. 5 (in the presence of one-chain HMWK) and FIG. 6 (in the absence of HMWK). The bispecific antibody performed better than the sum of the parent IgGs, particularly in the presence of HMWK. Using the tight binding inhibitor equation, the apparent Ki values of D12 were determined to be 8.8 nM in the presence of HMWK and 2.6 nM in the absence of HMWK.

[0166] The bispecific antibody candidate 620I-X0136-D12 (D12) was also assessed for its ability to delay activated partial thromboplastin time (APTT) in an APTT assay compared to an anti-FXIIa antibody (D06) and an anti-pKal antibody (H03) (FIG. 7). Briefly, inhibitors molecules (or control dilution buffer=25 mM HEPES, pH 7.5, 125 mM NaCl) were added at three concentrations (25, 50, 100) to neat plasma in a 1:1 mixture, and pre-equilibrated at 37° C. for 5 minutes. 2×50 µl of this mix was dispensed to 2 separate KC4 Delta assay cuvettes (with metal ball). After 60 seconds, 50 µl of aPTT reagent (activator, Pacific Hemostasis APTT-XL) was added to the rotating cuvettes, and 180 seconds after aPTT addition (at t=0 secs), 50 µl of CaCl₂ was added. The KC4 Delta instrument recorded the time of coagulation in seconds.

[0167] The bispecific antibody candidate 620I-X0136-D12 (D12) was also assessed for its ability to inhibit fibrin formation (FIG. 8).

[0168] Antibody sequences: All bispecific molecules described in this Example contained a first polypeptide comprising the DX-2930 Heavy Chain, a SGGS linker, and an anti-FXIIa scFv in either the Heavy/Light or Light/Heavy orientations. The DX-2930 Light Chain was also expressed using the same vector. Only the Heavy Chain+scFv sequences are listed for each isolate.

```
>DX-2930 Light Chain (without signal sequence)
(SEQ ID NO: 46)
DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYK
ASTLESGVPSRSGSGTEFTLTISSLQPDDFATYYCQQYNTYWTFGQG
TKVEIKRTVAAPSVFIPPPSDEQLKSGTASVVCLNNFYPREAKVQWKVD
NALQSGNSQESVTEQDSKDSTYSLSSTLTSKADYEKHKVYACEVTHQGL
SSPVTKSFNRGEC
```

```
Bispecifics derived from 36 exemplary anti-FXIIa
IgGs:
>620I-X0136-C07 = DX2930 Heavy Chain +
559C-M0177-B11 L4H scFv
(SEQ ID NO: 51)
```

```
EVQLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
IGVPRRDEFDIWGQGTMTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPALQSSGLYSLSSVVTVPSSSLGT
QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVPLFPP
KPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAAKTPREEQ
YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP
PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVHEALHNHTQKSLSLSP
GKSGGGSEVQLESGGGLVQPGGSLRLSCAASGFTFSRYIMMWVRQAPGK
GLEWVSRIYPSGGYTRYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
YYCTQRQYRGPKYYYYMDVWGKTTVTSSGGGGGGGGGGGGGGGGGGGS
DIQMTQSPSLPVTGPGEPASISCRSSQSLHSNGNYLDWYLQKPGQSPQ
LLIYLGSNRASGVPDFRSGSGSGTDFTLKISRVEAEVGYYYCMQALQTP
WTPGQGTKVEIKR
```

```
>620I-X0138-A08 = DX2930 Heavy Chain +
559C-M0177-B11 H4L scFv
(SEQ ID NO: 52)
```

```
EVQLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
IGVPRRDEFDIWGQGTMTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPALQSSGLYSLSSVVTVPSSSLGT
QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVPLFPP
KPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAAKTPREEQ
YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP
PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVHEALHNHTQKSLSLSP
GKSGGGSDIQMTQSPSLPVTGPGEPASISCRSSQSLHSNGNYLDWYLQ
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KPGQSPQLIYLGSNRASGVPDFSGSGSTDFTLKISRVEAEDVGVYYC
 MQALQTPWTFGQGTKVEIKRTGGGGGGGGGGGGGGGGSEVQLLESGG
 GLVQPGGSLRLSCAASGFTFSRYIMVVVRQAPGKGLEWVSRIYPSGGYTR
 YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRQRYRGPKYYYY
 MDVWGKGTTVTVSS
 >620I-X0136-B02 = DX2930 Heavy Chain +
 559C-M0177-C12 L4H scFv
 (SEQ ID NO: 53)
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWWVRQAPGKGLEWVG
 IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
 IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
 VKDYFPEPVTVWNNGALTSGVHTFPABLQSSGLYSLSSVVTVPSSSLGT
 QTYICNVNHPKSNTVKDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPP
 KPKDTLMISRTPETCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSP
 GKSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSFYIMMWWVRQAPGK
 GLEWWSRIVPSGGMTRYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
 YYCTRQYRGPKYYYYMDVWGKGTTVTVSSGGGGGGGGGGGGGGGGGG
 DIQMTQSPLSLPVTGEPASIICRSSQSLLHSNGNYLDWYLQKPGQSPQ
 LLIYLGSNRASGVPDFRGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP
 WTPGQGTKVEIKR

>620I-X0139-A12 = DX2930 Heavy Chain +
 559C-M0177-C12 H4L scFv
 (SEQ ID NO: 54)
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWWVRQAPGKGLEWVG
 IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
 IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
 VKDYFPEPVTVWNNGALTSGVHTFPABLQSSGLYSLSSVVTVPSSSLGT
 QTYICNVNHPKSNTVKDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPP
 KPKDTLMISRTPETCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSP
 GKSGGGSDIQMTQSPLSLPVTGEPASIICRSSQSLLHSNGNYLDWYLQ
 KPGQSPQLIYLGSNRASGVPDFRGSGSGTDFTLKISRVEAEDVGVYYC

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MQALQTPWTFGQGTKVEIKRTGGGGGGGGGGGGGGGGSEVQLLESGG
 GLVQPGGSLRLSCAASGFTFSFYIMMWWVRQAPGKGLEWVSRIVPSGMTR
 YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRQRYRGPKYYYY
 MDVWGKGTTVTVSS
 >620I-X0137-B08 = DX2930 Heavy Chain +
 559C-M0178-A08 L4H scFv
 (SEQ ID NO: 55)
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWWVRQAPGKGLEWVG
 IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
 IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
 VKDYFPEPVTVWNNGALTSGVHTFPABLQSSGLYSLSSVVTVPSSSLGT
 QTYICNVNHPKSNTVKDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPP
 KPKDTLMISRTPETCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSP
 GKSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSFYIMMWWVRQAPGK
 GLEWWSRIVPSGGATQYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
 YYCTRQYRGPKYYYYMDVWGKGTTVTVSSGGGGGGGGGGGGGGGG
 DIQMTQSPLSLPVTGEPASIICRSSQSLLHSNGNYLDWYLQKPGQSPQ
 LLIYLGSNRASGVPDFRGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP
 WTPGQGTKVEIKR
 >620I-X0142-A04 = DX2930 Heavy Chain +
 559C-M0178-A08 H4L scFv
 (SEQ ID NO: 56)
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWWVRQAPGKGLEWVG
 IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
 IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
 VKDYFPEPVTVWNNGALTSGVHTFPABLQSSGLYSLSSVVTVPSSSLGT
 QTYICNVNHPKSNTVKDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPP
 KPKDTLMISRTPETCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSP
 GKSGGGSDIQMTQSPLSLPVTGEPASIICRSSQSLLHSNGNYLDWYLQ
 KPGQSPQLIYLGSNRASGVPDFRGSGSGTDFTLKISRVEAEDVGVYYC

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MQALQTPWTFQGQTKVEIKRTGGGGSGGGGGGGGGSEVQLLESGG
GLVQPGGSLRLSCAASGFTFSFYIMGVVRQAPGKGLEWVSRIYPSGGATQ
YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRQYRGPKEYYY
MDVWGKGTTVTVSS

>620I-X0142-B11 = DX2930 Heavy Chain +
559C-M0179-A03 L4H scFv
(SEQ ID NO: 57)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVG
IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT
QTYICNVNHPKSNTKVDKRVEPKSCDKTHTCPPCPAPEELLGGPSVLFPP
KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVEVHNAAKTKPREEQ
YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP
PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GKSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTPSGYIMAWVRQAPGK
GLEWVSYIYPSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
YYCTRQYRGPKEYYYMDVWGKGTTVTSSGGGSGGGSGGGSGGG
DIQMTQSPLSLPVTGPGEPASISCRSSQSLHSNGYNYLDWYLQKPGQSPQ
LLIYLGSNRASGVPDFRGSGSGTDFTLKISRVEAEDIVYYCMQGRHRP
YTFGQGTRLEIKR

>620I-X0138-B01 = DX2930 Heavy Chain +
559C-M0179-A03 H4L scFv
(SEQ ID NO: 58)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVG
IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT
QTYICNVNHPKSNTKVDKRVEPKSCDKTHTCPPCPAPEELLGGPSVLFPP
KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVEVHNAAKTKPREEQ
YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP
PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GKSGGGSDIQMTQSPLSLPVTGPGEPASISCRSSQSLHSNGYNYLDWYLQ
KPGQSPQLLIYLGSNRASGVPDFRGSGSGTDFTLKISRVEAEDIVYYC
MQALQTPWTFQGQTKVEIKRTGGGGGGGGGGGGGGSEVQLLESGG
GLVQPGGSLRLSCAASGFTPSGYIMAWVRQAPGKGLEWVSYIYPSGGHTK
YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRQYRGPKEYYY
MDVWGKGTTVTVSS

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>620I-X0136-C01 = DX2930 Heavy Chain +
559C-M0182-B04 L4H scFv
(SEQ ID NO: 59)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVG
IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT
QTYICNVNHPKSNTKVDKRVEPKSCDKTHTCPPCPAPEELLGGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVEVHNAAKTKPREEQ
YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP
PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GKSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSWYVMQWVRQAPGK
GLEWVSYIYPSGGHTKYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
YYCTRQYRGPKEYYYMDVWGKGTTVTSSGGGSGGGSGGGSGGG
DIQMTQSPLSLPVTGPGEPASISCRSSQSLHSNGYNYLDWYLQKPGQSPQ
LLIYLGSNRASGVPDFRGSGSGTDFTLKISRVEAEDIVYYCMQALQTP
WTFQGQTKVEIKR

>620I-X0138-A12 = DX2930 Heavy Chain +
559C-M0182-B04 H4L scFv
(SEQ ID NO: 60)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVG
IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT
QTYICNVNHPKSNTKVDKRVEPKSCDKTHTCPPCPAPEELLGGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVEVHNAAKTKPREEQ
YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP
PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GKSGGGSDIQMTQSPLSLPVTGPGEPASISCRSSQSLHSNGYNYLDWYLQ
KPGQSPQLLIYLGSNRASGVPDFRGSGSGTDFTLKISRVEAEDIVYYC
MQALQTPWTFQGQTKVEIKRTGGGGGGGGGGGGGGSEVQLLESGG
GLVQPGGSLRLSCAASGFTFSWYVMQWVRQAPGKGLEWVSYIYPSGGHTK
YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRQYRGPKEYYY
MDVWGKGTTVTVSS

>620I-X0136-A12 = DX2930 Heavy Chain +
559C-M0182-D04 L4H scFv
(SEQ ID NO: 61)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVG
IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT

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 QTYICNVNHPNSNTKVDKRVEPKSCDKTHTCPCPAPELLGGPSVLFPP
 KPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQP
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTT
 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
 GKSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSMYTMNWVRQAPGK
 GLEWWSRIVYPSGGKTLYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
 YYCTRQYRGPKYYYYMDVWGKGTTVTSSGGGSGGGSGGGSGGG
 DIQMTQSPLSLPVTGPGEPASISCRSSQSLHSNGNYLDWYLQKPGQSPQ
 LLIYLGSNRASGVPDFRSQSGSGTDFTLKISRVEAEDVGVYYCMQALQTP
 WTFGQGTKVEIKR

>620I-X0138-A02 = DX2930 Heavy Chain +
 559C-M0182-D04 H4L scFv
 (SEQ ID NO: 62)

EVQLESGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
 IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
 IGVPRRDEFDIWQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
 VKDYFPEPVTVWNSGALTSGVHTFPABLQSSGLYSLSSVTVPSSLGT
 QTYICNVNHPNSNTKVDKRVEPKSCDKTHTCPCPAPELLGGPSVLFPP
 KPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQP
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTT
 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
 GKSGGGSDIQMTQSPLSLPVTGPGEPASISCRSSQSLHSNGNYLDWYLQ
 KPGQSPQPLLIYLGSNRASGVPDFRSQSGSGTDFTLKISRVEAEDVGVYYC
 MQALQTPWTFGQGTKVEIKRTGGGGGGGGGGGGGGSEVQLLESGG
 GLVQPGGSLRLSCAASGFTFSRYVMHWVRQAPGKGLEWSSIWPSSGM
 YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRQYRGPKYYYY
 MDVWGKGTTVTSS

>620I-X0136-A05 = DX2930 Heavy Chain +
 559C-M0182-H01 L4H scFv
 (SEQ ID NO: 63)

EVQLESGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
 IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
 IGVPRRDEFDIWQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
 VKDYFPEPVTVWNSGALTSGVHTFPABLQSSGLYSLSSVTVPSSLGT
 QTYICNVNHPNSNTKVDKRVEPKSCDKTHTCPCPAPELLGGPSVLFPP
 KPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQP
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTT
 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
 GKSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSWYIMGWVRQAPGK
 GLEWWSRIVYPSGGTTFYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
 YYCTRQYRGPKYYYYMDVWGKGTTVTSSGGGSGGGSGGGSGGG
 DIQMTQSPLSLPVTGPGEPASISCRSSQSLHSNGNYLDWYLQKPGQSPQ
 LLIYLGSNRASGVPDFRSQSGSGTDFTLKISRVEAEDVGVYYCMQALQTP
 WTFGQGTKVEIKR

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 GLEWVSSIWPSGGMTKYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
 YYCTRQYRGPKYYYYMDVWGKGTTVTSSGGGSGGGSGGGSGGG
 DIQMTQSPLSLPVTGPGEPASISCRSSQSLHSNGNYLDWYLQKPGQSPQ
 LLIYLGSNRASGVPDFRSQSGSGTDFTLKISRVEAEDVGVYYCMQALQTP
 WTFGQGTKVEIKR

>620I-X0138-C07 = DX2930 Heavy Chain +
 559C-M0182-H01 H4L scFv
 (SEQ ID NO: 64)

EVQLESGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
 IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
 IGVPRRDEFDIWQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
 VKDYFPEPVTVWNSGALTSGVHTFPABLQSSGLYSLSSVTVPSSLGT
 QTYICNVNHPNSNTKVDKRVEPKSCDKTHTCPCPAPELLGGPSVLFPP
 KPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQP
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTT
 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
 GKSGGGSDIQMTQSPLSLPVTGPGEPASISCRSSQSLHSNGNYLDWYLQ
 KPGQSPQPLLIYLGSNRASGVPDFRSQSGSGTDFTLKISRVEAEDVGVYYC
 MQALQTPWTFGQGTKVEIKRTGGGGGGGGGGGGGGSEVQLLESGG
 GLVQPGGSLRLSCAASGFTFSRYVMHWVRQAPGKGLEWSSIWPSSGM
 YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRQYRGPKYYYY
 MDVWGKGTTVTSS

>620I-X0136-E07 = DX2930 Heavy Chain +
 559C-M0182-H04 L4H scFv
 (SEQ ID NO: 65)

EVQLESGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
 IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
 IGVPRRDEFDIWQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
 VKDYFPEPVTVWNSGALTSGVHTFPABLQSSGLYSLSSVTVPSSLGT
 QTYICNVNHPNSNTKVDKRVEPKSCDKTHTCPCPAPELLGGPSVLFPP
 KPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQP
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTT
 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
 GKSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSWYIMGWVRQAPGK
 GLEWWSRIVYPSGGTTFYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
 YYCTRQYRGPKYYYYMDVWGKGTTVTSSGGGSGGGSGGGSGGG
 DIQMTQSPLSLPVTGPGEPASISCRSSQSLHSNGNYLDWYLQKPGQSPQ
 LLIYLGSNRASGVPDFRSQSGSGTDFTLKISRVEAEDVGVYYCMQALQTP
 WTFGQGTKVEIKR

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>620I-X0142-B02 = DX2930 Heavy Chain +
559C-M0182-H04 H4L scFv
(SEQ ID NO: 66)
EVQLLESGGLVQPGGSLRLSCAASGFTFSHYIMMWRQAPGKGLEWVSG
IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVWNSGALTSGVHTFPABLQSSGLYLSLSSVVTVPSSSLGT
QTYICNVNHPKPSNTKVDKRVEPKSCDKTHCPCPAPELLGGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVEVHNAKTKPREEQ
YNSTYRVVSLVTLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP
PVLDSDGSFFLYSKLTVKSRWQQGNVFSCSVMVHEALHNHYTQKSLSLSP
GKSGGGSDIQMTQSPLSLPVTGPAPASCRSSQSLHSNGYNYLDWYLQ
KPGQSPQLIYLGSNRASGVPDFRGSGSGTDFTLKISRVEAEDVGVYYC
MQALQTWPWTFGQGKVEIKRTGGGGGGGGGGGGGGSEVQLLESGG
GLVQPGGSLRLSCAASGFTFSWYIMGWVRQAPGKGLEWVSRIYPSGGTF
YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRQYRGPKEYYY
MDVWGKGTIVTWS

>620I-X0136-C09 = DX2930 Heavy Chain +
559C-M0183-C03 L4H scFv
(SEQ ID NO: 69)
EVQLLESGGLVQPGGSLRLSCAASGFTFSHYIMMWRQAPGKGLEWVSG
IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVWNSGALTSGVHTFPABLQSSGLYLSLSSVVTVPSSSLGT
QTYICNVNHPKPSNTKVDKRVEPKSCDKTHCPCPAPELLGGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVEVHNAKTKPREEQ
YNSTYRVVSLVTLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP
PVLDSDGSFFLYSKLTVKSRWQQGNVFSCSVMVHEALHNHYTQKSLSLSP
GKSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSWYIMWVRQAPGK
GLEWWSRIYPSGGITHYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
YYCTRQYRGPKEYYYMDVWGKTTVTSSGGGGGGGGGGGGGGGG
DIQMTQSPLSLPVTGPAPASCRSSQSLHSNGYNYLDWYLQKPGQSPQ
LLIYLGSNRASGVPDFRGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP
WTFGQGKVEIKR

>620I-X0136-F11 = DX2930 Heavy Chain +
559C-M0183-B12 L4H scFv
(SEQ ID NO: 67)
EVQLLESGGLVQPGGSLRLSCAASGFTFSHYIMMWRQAPGKGLEWVSG
IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVWNSGALTSGVHTFPABLQSSGLYLSLSSVVTVPSSSLGT
QTYICNVNHPKPSNTKVDKRVEPKSCDKTHCPCPAPELLGGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVEVHNAKTKPREEQ
YNSTYRVVSLVTLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP
PVLDSDGSFFLYSKLTVKSRWQQGNVFSCSVMVHEALHNHYTQKSLSLSP
GKSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSWYIMWVRQAPGK
GLEWWSRIYPSGGITHYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
YYCTRQYRGPKEYYYMDVWGKTTVTSSGGGGGGGGGGGGGGGG
DIQMTQSPLSLPVTGPAPASCRSSQSLHSNGYNYLDWYLQKPGQSPQ
LLIYLGSNRASGVPDFRGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP
WTFGQGKVEIKR

>620I-X0142-A05 = DX2930 Heavy Chain +
559C-M0183-B12 H4L scFv
(SEQ ID NO: 68)
EVQLLESGGLVQPGGSLRLSCAASGFTFSHYIMMWRQAPGKGLEWVSG
IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVWNSGALTSGVHTFPABLQSSGLYLSLSSVVTVPSSSLGT

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QTYICNVNHPKPSNTKVDKRVEPKSCDKTHCPCPAPELLGGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVEVHNAKTKPREEQ
YNSTYRVVSLVTLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP
PVLDSDGSFFLYSKLTVKSRWQQGNVFSCSVMVHEALHNHYTQKSLSLSP
GKSGGGSDIQMTQSPLSLPVTGPAPASCRSSQSLHSNGYNYLDWYLQ
KPGQSPQLIYLGSNRASGVPDFRGSGSGTDFTLKISRVEAEDVGVYYC
MQALQTWPWTFGQGKVEIKRTGGGGGGGGGGGGGGSEVQLLESGG
GLVQPGGSLRLSCAASGFTFSWYIMWVRQAPGKGLEWVSRIYPSGGITH
YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRQYRGPKEYYY
MDVWGKGTIVTWS

>620I-X0136-C09 = DX2930 Heavy Chain +
559C-M0183-C03 L4H scFv
(SEQ ID NO: 69)
EVQLLESGGLVQPGGSLRLSCAASGFTFSHYIMMWRQAPGKGLEWVSG
IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVWNSGALTSGVHTFPABLQSSGLYLSLSSVVTVPSSSLGT
QTYICNVNHPKPSNTKVDKRVEPKSCDKTHCPCPAPELLGGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVEVHNAKTKPREEQ
YNSTYRVVSLVTLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP
PVLDSDGSFFLYSKLTVKSRWQQGNVFSCSVMVHEALHNHYTQKSLSLSP
GKSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSWYIMWVRQAPGK
GLEWWSRIYPSGGITHYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
YYCTRQYRGPKEYYYMDVWGKTTVTSSGGGGGGGGGGGGGGGG
DIQMTQSPLSLPVTGPAPASCRSSQSLHSNGYNYLDWYLQKPGQSPQ
LLIYLGSNRASGVPDFRGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP
WTFGQGKVEIKR

>620I-X0138-B10 = DX2930 Heavy Chain +
559C-M0183-C03 H4L scFv
(SEQ ID NO: 70)
EVQLLESGGLVQPGGSLRLSCAASGFTFSHYIMMWRQAPGKGLEWVSG
IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVWNSGALTSGVHTFPABLQSSGLYLSLSSVVTVPSSSLGT
QTYICNVNHPKPSNTKVDKRVEPKSCDKTHCPCPAPELLGGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVEVHNAKTKPREEQ
YNSTYRVVSLVTLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP
PVLDSDGSFFLYSKLTVKSRWQQGNVFSCSVMVHEALHNHYTQKSLSLSP
GKSGGGSDIQMTQSPLSLPVTGPAPASCRSSQSLHSNGYNYLDWYLQ

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KPGQSPQLLIYLGSNRASGVPDFSGSGSGTDFTLKISRVEAEDVGVYYC
MQALQTPTFGQGTKVEIKRTGGGGGGGGGGGGGGGGSEVQLLESGG
GLVQPGGSLRLSCAASGFTFSWYNMWVRQAPGKGLEWVSYIISPSGGKTK
YTDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYCTRQRYRGPKYYYY
MDVWGKGTTVTVSS

>620I-X0136-C08 = DX2930 Heavy Chain +
559C-M0183-H08 L4H scFv
(SEQ ID NO: 71)

EVQLLESGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYCCAYRR
IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVWNSGALTSGVHTFPABLQSSGLYSLSVVTPVSSSLGT
QTYICNVNHPKSNKVDKRVPKSCDKTHTCPCPAPELLGGPSVLFPP
KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVEVHNAKTKPREEQ
YNSTYRVVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP
PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GKSGGGSEVQLLESGGLVQPGGSLRLSCAASGFTFSRYIMGVWRQAPGK
GLEWVSSIYPGGVTRYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
YYCTRQYRGPKYYYYMDVWGKGTTVTVSSGGGGGGGGGGGGGGGG
DIQMTQSPLSLPVTGEPASISCRSSQSLHSNGYNYLDWYLQKPGQSPQ
LLIYLGSNRASGVPDFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP
WTFGQGTKVEIKR

>620I-X0139-A11 = DX2930 Heavy Chain +
559C-M0183-D08 H4L scFv
(SEQ ID NO: 72)

EVQLLESGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYCCAYRR
IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVWNSGALTSGVHTFPABLQSSGLYSLSVVTPVSSSLGT
QTYICNVNHPKSNKVDKRVPKSCDKTHTCPCPAPELLGGPSVLFPP
KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVEVHNAKTKPREEQ
YNSTYRVVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP
PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GKSGGGSDIQMTQSPLSLPVTGEPASISCRSSQSLHSNGYNYLDWYLQ
KPGQSPQLLIYLGSNRASGVPDFSGSGSGTDFTLKISRVEAEDVGVYYC
MQALQTPTFGQGTKVEIKRTGGGGGGGGGGGGGGSEVQLLESGG
GLVQPGGSLRLSCAASGFTFSRYIMGVWRQAPGKGLEWVSSIYPGGVTK
YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYCTRQRYRGPKYYYY
MDVWGKGTTVTVSS

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>620I-X0136-D05 = DX2930 Heavy Chain +
559C-M0183-H08 L4H scFv

(SEQ ID NO: 73)

EVQLLESGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYCCAYRR
IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVWNSGALTSGVHTFPABLQSSGLYSLSVVTPVSSSLGT
QTYICNVNHPKSNKVDKRVPKSCDKTHTCPCPAPELLGGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVEVHNAKTKPREEQ
YNSTYRVVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP
PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GKSGGGSEVQLLESGGLVQPGGSLRLSCAASGFTFSRYIMGVWRQAPGK
GLEWVSSIYPGGVTRYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
YYCTRQYRGPKYYYYMDVWGKGTTVTVSSGGGGGGGGGGGGGG
DIQMTQSPLSLPVTGEPASISCRSSQSLHSNGYNYLDWYLQKPGQSPQ
LLIYLGSNRASGVPDFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP
WTFGQGTKVEIKR

>620I-X0138-D04 = DX2930 Heavy Chain +
559C-M0183-H08 H4L scFv
(SEQ ID NO: 74)

EVQLLESGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYCCAYRR
IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVWNSGALTSGVHTFPABLQSSGLYSLSVVTPVSSSLGT
QTYICNVNHPKSNKVDKRVPKSCDKTHTCPCPAPELLGGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVEVHNAKTKPREEQ
YNSTYRVVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP
PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GKSGGGSDIQMTQSPLSLPVTGEPASISCRSSQSLHSNGYNYLDWYLQ
KPGQSPQLLIYLGSNRASGVPDFSGSGSGTDFTLKISRVEAEDVGVYYC
MQALQTPTFGQGTKVEIKRTGGGGGGGGGGGGGGSEVQLLESGG
GLVQPGGSLRLSCAASGFTFSRYIMGVWRQAPGKGLEWVSSIYPGGVTK
YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYCTRQYRGPKYYYY
MDVWGKGTTVTVSS

>620I-X0136-G08 = DX2930 Heavy Chain +
559C-M0184-B04 L4H scFv
(SEQ ID NO: 75)

EVQLLESGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYCCAYRR
IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVWNSGALTSGVHTFPABLQSSGLYSLSVVTPVSSSLGT

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QTYICNVNHPNSNTKVDKRVEPKSCDKTHTCPCPAPELLGGPSVLFPP
 KPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQP
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTP
 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
 GKSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSYMSMWVRQAPGK
 GLEWVSRIYPSSGGVTKYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
 YYCTRQYRGPKYYYYMDVWGKGTTVTSSGGGSGGGSGGGSGGG
 DIQMTQSPLSLPVTGPGEPASISCRSSQSLHSNGNYLDWYLQKPGQSPQ
 LLIYLGSNRASGVPDFRSGSGSGTDFTLKISRVEAEVGVYYCMQALQTP
 WTFGQGKTVEIKR
 >620I-X0142-B07 = DX2930 Heavy Chain +
 559C-M0184-B04 H4L scFv
 (SEQ ID NO: 76)
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVG
 IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
 IGVPDRDEFDIWQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
 VKDYFPEPVTVWNSGALTSGVHTFPABLQSSGLYSLSSVTVPSSSLGT
 QTYICNVNHPNSNTKVDKRVEPKSCDKTHTCPCPAPELLGGPSVLFPP
 KPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQP
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTP
 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
 GKSGGGSDIQMTQSPLSLPVTGPGEPASISCRSSQSLHSNGNYLDWYLQ
 KPGQSPQQLIYLGSNRASGVPDFRSGSGSGTDFTLKISRVEAEVGVYYC
 MQALQTPWTFGQGKTVEIKRTGGGGGGGGGGGGGGSEVQLLESGG
 GLVQPGGSLRLSCAASGFTFSYVMGWVRQAPGKGLEWVSRIYPSSGG
 YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRQYRGPKYYYY
 MDVWGKGTTVTSS
 >620I-X0142-A10 = DX2930 Heavy Chain +
 559C-M0184-E06 L4H scFv
 (SEQ ID NO: 77)
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVG
 IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
 IGVPDRDEFDIWQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
 VKDYFPEPVTVWNSGALTSGVHTFPABLQSSGLYSLSSVTVPSSSLGT
 QTYICNVNHPNSNTKVDKRVEPKSCDKTHTCPCPAPELLGGPSVLFPP
 KPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQP
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTP
 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
 GKSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSYVMQWVRQAPGK
 GLEWVSSIWPSGGKTVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
 YYCTRQYRGPKYYYYMDVWGKGTTVTSSGGGSGGGSGGGSGGG
 DIQMTQSPLSLPVTGPGEPASISCRSSQSLHSNGNYLDWYLQKPGQSPQ
 LLIYLGSNRASGVPDFRSGSGSGTDFTLKISRVEAEVGVYYCMQALQTP
 WTFGQGKTVEIKR

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GLEWVSRIYPSSGGLTQYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
 YYCTRQYRGPKYYYYMDVWGKGTTVTSSGGGSGGGSGGGSGGG
 DIQMTQSPLSLPVTGPGEPASISCRSSQSLHSNGNYLDWYLQKPGQSPQ
 LLIYLGSNRASGVPDFRSGSGSGTDFTLKISRVEAEVGVYYCMQALQTP
 WTFGQGKTVEIKR
 >620I-X0138-G12 = DX2930 Heavy Chain +
 559C-M0184-D01 H4L scFv
 (SEQ ID NO: 78)
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVG
 IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
 IGVPDRDEFDIWQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
 VKDYFPEPVTVWNSGALTSGVHTFPABLQSSGLYSLSSVTVPSSSLGT
 QTYICNVNHPNSNTKVDKRVEPKSCDKTHTCPCPAPELLGGPSVLFPP
 KPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQP
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTP
 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
 GKSGGGSDIQMTQSPLSLPVTGPGEPASISCRSSQSLHSNGNYLDWYLQ
 KPGQSPQQLIYLGSNRASGVPDFRSGSGSGTDFTLKISRVEAEVGVYYC
 MQALQTPWTFGQGKTVEIKRTGGGGGGGGGGGGGGSEVQLLESGG
 GLVQPGGSLRLSCAASGFTFSYVMGWVRQAPGKGLEWVSRIYPSSGG
 YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRQYRGPKYYYY
 MDVWGKGTTVTSS
 >620I-X0142-A10 = DX2930 Heavy Chain +
 559C-M0184-E06 L4H scFv
 (SEQ ID NO: 79)
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVG
 IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
 IGVPDRDEFDIWQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
 VKDYFPEPVTVWNSGALTSGVHTFPABLQSSGLYSLSSVTVPSSSLGT
 QTYICNVNHPNSNTKVDKRVEPKSCDKTHTCPCPAPELLGGPSVLFPP
 KPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQP
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTP
 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
 GKSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSYVMQWVRQAPGK
 GLEWVSSIWPSGGKTVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
 YYCTRQYRGPKYYYYMDVWGKGTTVTSSGGGSGGGSGGGSGGG
 DIQMTQSPLSLPVTGPGEPASISCRSSQSLHSNGNYLDWYLQKPGQSPQ
 LLIYLGSNRASGVPDFRSGSGSGTDFTLKISRVEAEVGVYYCMQALQTP
 WTFGQGKTVEIKR

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>620I-X0138-D03 = DX2930 Heavy Chain +
559C-M0184-E06 H4L scFv
(SEQ ID NO: 80)
EVQLLESGGLVQPGGSLRLSCAASGFTFSHYIMMWRQAPGKGLEWVG
IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVWNSGALTSGVHTFPABLQSSGLYLSLSSVVTVPSSSLGT
QTYICNVNHPKPSNTKVDKRVEPKSCDKTHCPCPAPELLGGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVSHDPEVKFNWYDGVEVHNNAKTKPREEQ
YNSTYRVVSLVTLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP
PVLDSDGSFFLYSKLTVKSRWQQGNVFSCVMHEALHNHYTQKSLSLSP
GKSGGGSDIQMTQSPLSLPVTGPAPASCRSSQSLHSNGYNYLDWYLQ
KPGQSPQLLIYLGSNRASGVPDFRGSGSGTDFTLKISRVEAEDGVVY
MQALQTWPWTFGQGKVEIKRTGGGGGGGGGGGGGGSEVQLLES
GLVQPGGSLRLSCAASGFTFSWYVMQWVRQAPGKGLEWVSSIWPSGGKTV
YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRQYRGPKYYYY
MDVWGKGTTVTVSS
>620I-X0136-E05 = DX2930 Heavy Chain +
559C-M0191-A03 L4H scFv
(SEQ ID NO: 83)
EVQLLESGGLVQPGGSLRLSCAASGFTFSHYIMMWRQAPGKGLEWVG
IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVWNSGALTSGVHTFPABLQSSGLYLSLSSVVTVPSSSLGT
QTYICNVNHPKPSNTKVDKRVEPKSCDKTHCPCPAPELLGGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVSHDPEVKFNWYDGVEVHNNAKTKPREEQ
YNSTYRVVSLVTLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP
PVLDSDGSFFLYSKLTVKSRWQQGNVFSCVMHEALHNHYTQKSLSLSP
GKSGGGSEVQLLESGLVQPGGSLRLSCAASGFTFSWYVMHWRQAPGK
GLEWVSSIYPSGGNTKYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
YYCTRQYRGPKYYYYMDVWGKGTIVTSSGGGGGGGGGGGGGG
DIQMTQSPLSLPVTGPAPASCRSSQSLHSNGYNYLDWYLQKPGQSPQ
LLIYLGSNRASGVPDFRGSGSGTDFTLKISRVEAEDGVVYCMQALQP
WTFGQGKVEIKR
>620I-X0138-B06 = DX2930 Heavy Chain +
559C-M0191-A03 H4L scFv
(SEQ ID NO: 84)
EVQLLESGGLVQPGGSLRLSCAASGFTFSHYIMMWRQAPGKGLEWVG
IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVWNSGALTSGVHTFPABLQSSGLYLSLSSVVTVPSSSLGT
QTYICNVNHPKPSNTKVDKRVEPKSCDKTHCPCPAPELLGGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVSHDPEVKFNWYDGVEVHNNAKTKPREEQ
YNSTYRVVSLVTLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP
PVLDSDGSFFLYSKLTVKSRWQQGNVFSCVMHEALHNHYTQKSLSLSP
GKSGGGSDIQMTQSPLSLPVTGPAPASCRSSQSLHSNGYNYLDWYLQ

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KPGQSPQLIYLGSNRASGVPDFSGSGSTDFTLKISRVEAEDVGVYYC
 MQALQTPTFGQGTKVEIKRTGGGGGGGGGGGGGGGGSEVQLLESGG
 GLVQPGGSLRLSCAASGFTFSQYIMHWVRQAPGKGLEWVSSYIYPSSGGNTK
 YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRQRYRGPKEYYY
 MDVWGKGTTVTVSS

>620I-X0136-A09 = DX2930 Heavy Chain +
 559C-M0191-B11 H4L scFv

(SEQ ID NO: 85)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
 IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
 IGVPRRDEFDIWGQGTMVTSSASTKGPSVFPLAPSSKSTSGGTAALGCL
 VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSVVTPSSSLGT
 QTYICNVNHPKSNTKVDKRVPKSCDKTHTCPPCPAPEELLGGPSVFLFPP
 KPKDTLMISRTPETCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCVMHEALHNHTQKSLSLSP
 GKSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFS

>620I-X0138-A06 = DX2930 Heavy Chain +
 559C-M0191-B11 H4L scFv

(SEQ ID NO: 86)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
 IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
 IGVPRRDEFDIWGQGTMVTSSASTKGPSVFPLAPSSKSTSGGTAALGCL
 VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSVVTPSSSLGT
 QTYICNVNHPKSNTKVDKRVPKSCDKTHTCPPCPAPEELLGGPSVFLFPP
 KPKDTLMISRTPETCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCVMHEALHNHTQKSLSLSP
 GKSGGGSDIQMTQSPLSLPVTGEPASISCRSSQSLLHSNGNYLDWYLQ
 KPGQSPQLIYLGSNRASGVPDFSGSGSTDFTLKISRVEAEDVGVYYC
 MQALQTPTFGQGTKVEIKRTGGGGGGGGGGGGGGGGSEVQLLESGG
 GLVQPGGSLRLSCAASGFTFSPYIMHWVRQAPGKGLEWVSRIPSSGGATV
 YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRQRYRGPKEYYY
 MDVWGKGTTVTVSS

>620I-X0136-A04 = DX2930 Heavy Chain +
 559C-M0191-E04 L4H scFv

(SEQ ID NO: 89)

(SEQ ID NO: 87)
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
 IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
 IGVPRRDEFDIWGQGTMVTSSASTKGPSVFPLAPSSKSTSGGTAALGCL
 VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSVVTPSSSLGT
 QTYICNVNHPKSNTKVDKRVPKSCDKTHTCPPCPAPEELLGGPSVFLFPP
 KPKDTLMISRTPETCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCVMHEALHNHTQKSLSLSP
 GKSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSMYIMHWVRQAPGK
 GLEWVSSIIYPSSGMTKYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
 YYCTRQRYRGPKEYYYMDVWGKTTTVSSGGGGGGGGGGGGGGGGGG
 DIQMTQSPLSLPVTGEPASISCRSSQSLLHSNGNYLDWYLQKPGQSPQ

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PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCVMHEALHNHTQKSLSLSP
 GKSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSPYIMHWVRQAPGK
 GLEWVSSIIYPSSGMTKYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
 YYCTRQRYRGPKEYYYMDVWGKTTTVSSGGGGGGGGGGGGGGGG
 DIQMTQSPLSLPVTGEPASISCRSSQSLLHSNGNYLDWYLQKPGQSPQ
 LLIYLGSNRASGVPDFSGSGSTDFTLKISRVEAEDVGVYYCMQALQTP
 WTPGQGTKVEIKR

>620I-X0139-B10 = DX2930 Heavy Chain +
 559C-M0191-C09 H4L scFv

(SEQ ID NO: 88)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
 IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
 IGVPRRDEFDIWGQGTMVTSSASTKGPSVFPLAPSSKSTSGGTAALGCL
 VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSVVTPSSSLGT
 QTYICNVNHPKSNTKVDKRVPKSCDKTHTCPPCPAPEELLGGPSVFLFPP
 KPKDTLMISRTPETCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCVMHEALHNHTQKSLSLSP
 GKSGGGSDIQMTQSPLSLPVTGEPASISCRSSQSLLHSNGNYLDWYLQ
 KPGQSPQLIYLGSNRASGVPDFSGSGSTDFTLKISRVEAEDVGVYYC
 MQALQTPTFGQGTKVEIKRTGGGGGGGGGGGGGGGGGGSEVQLLESGG
 GLVQPGGSLRLSCAASGFTFSPYIMHWVRQAPGKGLEWVSRIPSSGGATV
 YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRQRYRGPKEYYY
 MDVWGKGTTVTVSS

>620I-X0136-A04 = DX2930 Heavy Chain +
 559C-M0191-E04 L4H scFv

(SEQ ID NO: 89)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
 IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
 IGVPRRDEFDIWGQGTMVTSSASTKGPSVFPLAPSSKSTSGGTAALGCL
 VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSVVTPSSSLGT
 QTYICNVNHPKSNTKVDKRVPKSCDKTHTCPPCPAPEELLGGPSVFLFPP
 KPKDTLMISRTPETCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCVMHEALHNHTQKSLSLSP
 GKSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSMYIMHWVRQAPGK
 GLEWVSSIIYPSSGMTKYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
 YYCTRQRYRGPKEYYYMDVWGKTTTVSSGGGGGGGGGGGGGGGG
 DIQMTQSPLSLPVTGEPASISCRSSQSLLHSNGNYLDWYLQKPGQSPQ

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LLIYLGSNRASGVPDFRGSGSGTDFTLKISRVEAEDVGVYCMQALQTP
WTFGQGTKVEIKR

>620I-X0138-D06 = DX2930 Heavy Chain +
559C-M0191-E04 H4L scFv
(SEQ ID NO: 90)
EVQLLESGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVWSNMGALTSGVHTFPABLQSSGLYSLSSVVTVPSSSLGT
QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPCPAPELLGGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVSHDPEVFKFNWYDGVEVHNNAKTKPREEQ
YNSTYRVVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWQQGNVFCVSMHEALHNHYTQKSLSLSP
GKSGGGSDIQMTQSPLSLPVTGEPASISCRSSQSLHSNGNYLDWYLQ
KPGQSPQLLIYLGNSNRASGVPDFRGSGSGTDFTLKISRVEAEDVGVYCC
MQALQTWPWTFGQGTKVEIKRTGGGGGGGGGGGGGGSEVQLLESQGG
GLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSVIYPSGGKTR
YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRQYRGPKYZZY
MDVWGKTTTVSS

>620I-X0136-A02 = DX2930 Heavy Chain +
559C-M0191-H09 L4H scFv
(SEQ ID NO: 93)

EVQLLESGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVWSNMGALTSGVHTFPABLQSSGLYSLSSVVTVPSSSLGT
QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPCPAPELLGGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVSHDPEVFKFNWYDGVEVHNNAKTKPREEQ
YNSTYRVVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWQQGNVFCVSMHEALHNHYTQKSLSLSP
GKSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSMYVMHWVRQAPGK
GLEWVSSIYPSGGLTKYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
YYCTRQYRGPKYZZYMDVWGKTTTVSSGGGGGGGGGGGGGGGGGG
DIQMTQSPLSLPVTGEPASISCRSSQSLHSNGNYLDWYLQKPGQSPQ
LLIYLGSNRASGVPDFRGSGSGTDFTLKISRVEAEDVGVYCMQALQTP
WTFGQGTKVEIKR

>620I-X0138-B07 = DX2930 Heavy Chain +
559C-M0191-E09 H4L scFv
(SEQ ID NO: 92)

EVQLLESGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR

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IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL

VKDYFPEPVTVWSNMGALTSGVHTFPABLQSSGLYSLSSVVTVPSSSLGT
QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPCPAPELLGGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVSHDPEVFKFNWYDGVEVHNNAKTKPREEQ
YNSTYRVVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWQQGNVFCVSMHEALHNHYTQKSLSLSP
GKSGGGSDIQMTQSPLSLPVTGEPASISCRSSQSLHSNGNYLDWYLQ
KPGQSPQLLIYLGNSNRASGVPDFRGSGSGTDFTLKISRVEAEDVGVYCC
MQALQTWPWTFGQGTKVEIKRTGGGGGGGGGGGGGGSEVQLLESQGG
GLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSVIYPSGGKTR
YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRQYRGPKYZZY
MDVWGKTTTVSS

>620I-X0136-C11 = DX2930 Heavy Chain +
559C-M0191-E09 L4H scFv
(SEQ ID NO: 91)

EVQLLESGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVWSNMGALTSGVHTFPABLQSSGLYSLSSVVTVPSSSLGT
QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPCPAPELLGGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVSHDPEVFKFNWYDGVEVHNNAKTKPREEQ
YNSTYRVVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWQQGNVFCVSMHEALHNHYTQKSLSLSP
GKSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSMYVMHWVRQAPGK
GLEWVSSIYPSGGLTKYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
YYCTRQYRGPKYZZYMDVWGKTTTVSSGGGGGGGGGGGGGGGG
DIQMTQSPLSLPVTGEPASISCRSSQSLHSNGNYLDWYLQKPGQSPQ
LLIYLGSNRASGVPDFRGSGSGTDFTLKISRVEAEDVGVYCMQALQTP
WTFGQGTKVEIKR

>620I-X0139-G02 = DX2930 Heavy Chain +
559C-M0191-H09 H4L scFv
(SEQ ID NO: 94)

EVQLLESGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVWSNMGALTSGVHTFPABLQSSGLYSLSSVVTVPSSSLGT
QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPCPAPELLGGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVSHDPEVFKFNWYDGVEVHNNAKTKPREEQ
YNSTYRVVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP

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PVLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GKSGGGSDIQMTQSPLSLPVTPEGEPASISCRSSQSLHSNGNYLDWYLQ
KPGQSPQLLIYLGSNRASGVPDFRGSGSGTDFTLKISRVEAEDVGVYYC
MQALQTPWTFGQGTKVEIKRTGGGGGGGGGGGGGGGGSEVQLLESGG
GLVQPGGSLRLSCAASGFTFSMYVMHWVRQAPGKGLEWVSSIYPSSGLTK
YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRQRYRGPKEYYY
MDVWGKGTTVTVSS

>620I-X0136-B07 = DX2930 Heavy Chain +
559C-M0191-H10 L4H scFv
(SEQ ID NO: 95)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPVSSSLGT
QTYICNVNHPKSNTKVDKRVEPKSCDKTHTCPPCPAPEELLGGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GKSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSWYTMHWVRQAPGK
GLEWVSSIYPSSGLTRYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
YYCTRQRYRGPKEYYYMDVWGKGTTVTSSGGGGGGGGGGGGGGGG
DIQMTQSPLSLPVTPEGEPASISCRSSQSLHSNGNYLDWYLQKPGQSPQ
LLIYLGSNRASGVPDFRGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP
WTFGQGTKVEIKR

>620I-X0138-E03 = DX2930 Heavy Chain +
559C-M0191-H10 H4L scFv
(SEQ ID NO: 96)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPVSSSLGT
QTYICNVNHPKSNTKVDKRVEPKSCDKTHTCPPCPAPEELLGGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GKSGGGSDIQMTQSPLSLPVTPEGEPASISCRSSQSLHSNGNYLDWYLQ
KPGQSPQLLIYLGSNRASGVPDFRGSGSGTDFTLKISRVEAEDVGVYYC
MQALQTPWTFGQGTKVEIKRTGGGGGGGGGGGGGGGGSEVQLLESGG

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GLVQPGGSLRLSCAASGFTFSWYTMHWVRQAPGKGLEWVSSIYPSSGGFTR

YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRQRYRGPKEYYY
MDVWGKGTTVTVSS

>620I-X0136-G05 = DX2930 Heavy Chain +
559C-M0192-A01 L4H scFv

(SEQ ID NO: 97)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPVSSSLGT
QTYICNVNHPKSNTKVDKRVEPKSCDKTHTCPPCPAPEELLGGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GKSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGK
GLEWVSSIYPSSGLTKYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
YYCTRQRYRGPKEYYYMDVWGKGTTVTSSGGGGGGGGGGGGGGGG
DIQMTQSPLSLPVTPEGEPASISCRSSQSLHSNGNYLDWYLQKPGQSPQ
LLIYLGSNRASGVPDFRGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP
WTFGQGTKVEIKR

>620I-X0139-D12 = DX2930 Heavy Chain +
559C-M0192-A01 H4L scFv

(SEQ ID NO: 98)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPVSSSLGT
QTYICNVNHPKSNTKVDKRVEPKSCDKTHTCPPCPAPEELLGGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GKSGGGSDIQMTQSPLSLPVTPEGEPASISCRSSQSLHSNGNYLDWYLQ
KPGQSPQLLIYLGSNRASGVPDFRGSGSGTDFTLKISRVEAEDVGVYYC
MQALQTPWTFGQGTKVEIKRTGGGGGGGGGGGGGGGGSEVQLLESGG

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GLVQPGGSLRLSCAASGFTFSHYVMHWVRQAPGKGLEWVSSIYPSGGLTK
 YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRQRYRGPKEYYY
 MDVWGKGTTVTVSS
 >620I-X0136-A01 = DX2930 Heavy Chain +
 559C-M0192-A03 L4H scFv
 (SEQ ID NO: 99)
 EVQLLESGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
 IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
 IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
 VKDYFPEPVTVWSNNSALTSVGHTFPAVLQSSGLYSLSSVVTVPSSSLGT
 QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCAPELLGGPSVFLFPP
 KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP
 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
 GKSGGGSEVQLLESGGLVQPGGSLRLSCAASGFTFSWYVMQWVRQAPGK
 GLEWVSSIYPSGGMTKYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
 YYCTQRQYRGPKEYYMDVWGKTTVTVSSGGGGSGGGSGGGSGGGSGGG
 DIQMTQSPLSLPVTPGEPASIICRSSQSLLHSNGNYLDWYLQKPGQSPQ
 LLIYLGSNRASGVPDFRGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP
 WTFGQGKVEIKR
 >620I-X0138-C12 = DX2930 Heavy Chain +
 559C-M0192-A03 H4L scFv
 (SEQ ID NO: 100)
 EVQLLESGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
 IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
 IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
 VKDYFPEPVTVWSNNSALTSVGHTFPAVLQSSGLYSLSSVVTVPSSSLGT
 QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCAPELLGGPSVFLFPP
 KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP
 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
 GKSGGGSDIQMTQSPLSLPVTPGEPASIICRSSQSLLHSNGNYLDWYLQ
 KPGQSPQLIYLGSNRASGVPDFRGSGSGTDFTLKISRVEAEDVGVYYC
 MQALQTPWTFGQGKVEIKRTGGGGGGGGGGGGGGSEVQLLESGG
 GLVQPGGSLRLSCAASGFTFSWYVMQWVRQAPGKGLEWVSSIYPSGGMTK
 YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRQRYRGPKEYYY
 MDVWGKGTTVTVSS

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>620I-X0136-G10 = DX2930 Heavy Chain +
 559C-M0192-D02 L4H scFv
 (SEQ ID NO: 101)
 EVQLLESGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
 IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
 IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
 VKDYFPEPVTVWSNNSALTSVGHTFPAVLQSSGLYSLSSVVTVPSSSLGT
 QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCAPELLGGPSVFLFPP
 KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP
 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
 GKSGGGSEVQLLESGGLVQPGGSLRLSCAASGFTFSQYVMHWVRQAPGK
 GLEWVSSIWPSGGFTKYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
 YYCTQRQYRGPKEYYMDVWGKTTVTVSSGGGGSGGGSGGGSGGGSGGG
 DIQMTQSPLSLPVTPGEPASIICRSSQSLLHSNGNYLDWYLQKPGQSPQ
 LLIYLGSNRASGVPDFRGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP
 WTFGQGKVEIKR
 >620I-X0138-D05 = DX2930 Heavy Chain +
 559C-M0192-D02 H4L scFv
 (SEQ ID NO: 102)
 EVQLLESGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
 IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
 IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
 VKDYFPEPVTVWSNNSALTSVGHTFPAVLQSSGLYSLSSVVTVPSSSLGT
 QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCAPELLGGPSVFLFPP
 KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP
 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
 GKSGGGSDIQMTQSPLSLPVTPGEPASIICRSSQSLLHSNGNYLDWYLQ
 KPGQSPQLIYLGSNRASGVPDFRGSGSGTDFTLKISRVEAEDVGVYYC
 MQALQTPWTFGQGKVEIKRTGGGGGGGGGGGGGGSEVQLLESGG
 GLVQPGGSLRLSCAASGFTFSWYVMQWVRQAPGKGLEWVSSIWPSGGFTK
 YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRQRYRGPKEYYY
 MDVWGKGTTVTVSS
 >620I-X0136-F07 = DX2930 Heavy Chain +
 559C-M0192-D12 L4H scFv
 (SEQ ID NO: 103)
 EVQLLESGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
 IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
 IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
 VKDYFPEPVTVWSNNSALTSVGHTFPAVLQSSGLYSLSSVVTVPSSSLGT

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 QTYICNVNHPNSNTKVDKRVEPKSCDKTHTCPCPAPELLGGPSVLFPP
 KPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQP
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTT
 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
 GKSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSWYIMQWVRQAPGK
 GLEWVSSIIYPSSGRTKYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
 YYCTRQYRGPKYYYYMDVWGKGTTVTSSGGGSGGGSGGGSGGG
 DIQMTQSPLSLPVTPGEPASISCRSSQSLHNSNGYNYLDWYLQKPGQSPQ
 LLIYLGSNRASGVPDFSGSGSTDFTLKISRVEAEDVGVYYCMQALQTP
 WTPFGQGTKVEIKR

>620I-X0138-A01 = DX2930 Heavy Chain +
 559C-M0192-D12 H4L scFv
 (SEQ ID NO: 104)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWRQAPGKGLEWVSG
 IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
 IGVPRRDEFDIWGQGTMVTSSASTKGPSVFP LAPSSKSTSGGTAALGCL
 VKDYFPEPVTVWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSLGT
 QTYICNVNHPNSNTKVDKRVEPKSCDKTHTCPCPAPELLGGPSVLFPP
 KPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQP
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTT
 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
 GKSGGGSDIQMTQSPLSLPVTPGEPASISCRSSQSLHNSNGYNYLDWYLQ
 KPGQSPQPLIYLGSNRASGVPDFSGSGSTDFTLKISRVEAEDVGVYYC
 MQALQTPWTFGQGTKVEIKRTGGGGGGGGGGGGGGSEVQLLES
 GLVQPGGSLRLSCAASGFTFSWYIMQWVRQAPGKGLEWVSSRIYPSSG
 YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRQYRGPKYYYY
 MDVWGKGTTVTSS

>620I-X0142-E09 = DX2930 Heavy Chain +
 559C-M0192-F01 L4H scFv
 (SEQ ID NO: 105)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWRQAPGKGLEWVSG
 IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
 IGVPRRDEFDIWGQGTMVTSSASTKGPSVFP LAPSSKSTSGGTAALGCL
 VKDYFPEPVTVWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSLGT
 QTYICNVNHPNSNTKVDKRVEPKSCDKTHTCPCPAPELLGGPSVLFPP
 KPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQP
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTT
 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
 GKSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSWYIMMWRQAPGK
 GLEWVSSIIYPSSGKTSYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
 YYCTRQYRGPKYYYYMDVWGKGTTVTSSGGGSGGGSGGGSGGG
 DIQMTQSPLSLPVTPGEPASISCRSSQSLHNSNGYNYLDWYLQKPGQSPQ
 LLIYLGSNRASGVPDFSGSGSTDFTLKISRVEAEDVGVYYCMQALQTP
 WTPFGQGTKVEIKR

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 GLEWVSSRIYPSSGMMTQYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
 YYCTRQYRGPKYYYYMDVWGKGTTVTSSGGGSGGGSGGGSGGG
 DIQMTQSPLSLPVTPGEPASISCRSSQSLHNSNGYNYLDWYLQKPGQSPQ
 LLIYLGSNRASGVPDFSGSGSTDFTLKISRVEAEDVGVYYCMQALQTP
 WTPFGQGTKVEIKR

>620I-X0138-D11 = DX2930 Heavy Chain +
 559C-M0192-F01 H4L scFv
 (SEQ ID NO: 106)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWRQAPGKGLEWVSG
 IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
 IGVPRRDEFDIWGQGTMVTSSASTKGPSVFP LAPSSKSTSGGTAALGCL
 VKDYFPEPVTVWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSLGT
 QTYICNVNHPNSNTKVDKRVEPKSCDKTHTCPCPAPELLGGPSVLFPP
 KPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQP
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTT
 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
 GKSGGGSDIQMTQSPLSLPVTPGEPASISCRSSQSLHNSNGYNYLDWYLQ
 KPGQSPQPLIYLGSNRASGVPDFSGSGSTDFTLKISRVEAEDVGVYYC
 MQALQTPWTFGQGTKVEIKRTGGGGGGGGGGGGGGSEVQLLES
 GLVQPGGSLRLSCAASGFTFSWYIMQWVRQAPGKGLEWVSSRIYPSSG
 YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRQYRGPKYYYY
 MDVWGKGTTVTSS

>620I-X0136-C05 = DX2930 Heavy Chain +
 559C-M0192-F06 L4H scFv
 (SEQ ID NO: 107)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWRQAPGKGLEWVSG
 IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
 IGVPRRDEFDIWGQGTMVTSSASTKGPSVFP LAPSSKSTSGGTAALGCL
 VKDYFPEPVTVWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSLGT
 QTYICNVNHPNSNTKVDKRVEPKSCDKTHTCPCPAPELLGGPSVLFPP
 KPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQP
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTT
 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
 GKSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSWYIMMWRQAPGK
 GLEWVSSIIYPSSGKTSYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
 YYCTRQYRGPKYYYYMDVWGKGTTVTSSGGGSGGGSGGGSGGG
 DIQMTQSPLSLPVTPGEPASISCRSSQSLHNSNGYNYLDWYLQKPGQSPQ
 LLIYLGSNRASGVPDFSGSGSTDFTLKISRVEAEDVGVYYCMQALQTP
 WTPFGQGTKVEIKR

>620I-X0142-A02 = DX2930 Heavy Chain +
 559C-M0192-F06 H4L scFv

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(SEQ ID NO: 108)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
 IYSSGGITVYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAYRR
 IGVPRRDEFDIWGQGMVTVSSASTKGPSVPLAPSSKSTSGGTAA LGCL
 VKDYFPEPVTVWSNNSGALTSGVHTFP AVLQSSGLYLSVSVTVPSSSLGT
 QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVLFPP
 KPKDTLMISRTPEVTCVV DVSHDPEVKFNWYVGVEVHNAKTKPREEQ
 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTP
 PVLDSDGSFFFLYSKLTVDKSRWQQGNVFSCVMHEALHNHYTQKSLSLSP
 GKSGGGSDIQMTQSPLSLPVTGP E P ASI CRSSQSLHSNGNYLDWYLQ
 KPGQSPQ LLIYLGSNRASGV PDR FSGSGSGTDF TLKISRVEAEDVG VYYC
 MQALQT PWT FGQGT KVEIKRTGGGSGGGSGGGSGGGSEVQ LLE SGG
 GLVQPGGSLRLSCAASGFTFSQYVMSWVRQAPGKGLEWVSRIVPSGGVTK
 YADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTRQYRGPKYYYY
 MDVWGKGT TVTVSS

>620I-X0136-C04 = DX2930 Heavy Chain +
 559C-M0192-F07 L4H scFv

(SEQ ID NO: 109)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
 IYSSGGITVYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAYRR
 IGVPRRDEFDIWGQGMVTVSSASTKGPSVPLAPSSKSTSGGTAA LGCL
 VKDYFPEPVTVWSNNSGALTSGVHTFP AVLQSSGLYLSVSVTVPSSSLGT
 QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVLFPP
 KPKDTLMISRTPEVTCVV DVSHDPEVKFNWYVGVEVHNAKTKPREEQ
 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTP
 PVLDSDGSFFFLYSKLTVDKSRWQQGNVFSCVMHEALHNHYTQKSLSLSP
 GKSGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSQYVMSWVRQAPGK
 GLEWVSRIWPSGGKTTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAV
 YYCTRQYRGPKYYYYMDVWGKTTVTVSSGGGGSGGGSGGGSGGG
 DIQMTQSPLSLPVTGP E P ASI CRSSQSLHSNGNYLDWYLQKPGQSPQ
 LLIYLGSNRASGV PDR FSGSGSGTDF TLKISRVEAEDVG VYYC MQALQT
 WTPGQGT KVEIKR

>620I-X0138-F02 = DX2930 Heavy Chain +
 559C-M0192-F07 H4L scFv

(SEQ ID NO: 110)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
 IYSSGGITVYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAYRR
 IGVPRRDEFDIWGQGMVTVSSASTKGPSVPLAPSSKSTSGGTAA LGCL
 VKDYFPEPVTVWSNNSGALTSGVHTFP AVLQSSGLYLSVSVTVPSSSLGT
 QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVLFPP
 KPKDTLMISRTPEVTCVV DVSHDPEVKFNWYVGVEVHNAKTKPREEQ

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YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTP
 PVLDSDGSFFFLYSKLTVDKSRWQQGNVFSCVMHEALHNHYTQKSLSLSP
 GKSGGGSDIQMTQSPLSLPVTGP E P ASI CRSSQSLHSNGNYLDWYLQ
 KPGQSPQ LLIYLGSNRASGV PDR FSGSGSGTDF TLKISRVEAEDVG VYYC
 MQALQT PWT FGQGT KVEIKRTGGGSGGGSGGGSGGGSEVQ LLE SGG
 GLVQPGGSLRLSCAASGFTFSQYVMSWVRQAPGKGLEWVSRIVPSGGVTK
 YADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTRQYRGPKYYYY
 MDVWGKGT TVTVSS

>620I-X0136-G04 = DX2930 Heavy Chain +
 559C-M0192-G03 L4H scFv

(SEQ ID NO: 111)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
 IYSSGGITVYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAYRR
 IGVPRRDEFDIWGQGMVTVSSASTKGPSVPLAPSSKSTSGGTAA LGCL
 VKDYFPEPVTVWSNNSGALTSGVHTFP AVLQSSGLYLSVSVTVPSSSLGT
 QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVLFPP
 KPKDTLMISRTPEVTCVV DVSHDPEVKFNWYVGVEVHNAKTKPREEQ
 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTP
 PVLDSDGSFFFLYSKLTVDKSRWQQGNVFSCVMHEALHNHYTQKSLSLSP
 GKSGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSQYNMVWVRQAPGK
 GLEWVSRIWPSGGKTTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAV
 YYCTRQYRGPKYYYYMDVWGKTTVTVSSGGGGSGGGSGGGSGGG
 DIQMTQSPLSLPVTGP E P ASI CRSSQSLHSNGNYLDWYLQKPGQSPQ
 LLIYLGSNRASGV PDR FSGSGSGTDF TLKISRVEAEDVG VYYC MQALQT
 WTPGQGT KVEIKR

>620I-X0139-G12 = DX2930 Heavy Chain +
 559C-M0192-G03 H4L scFv

(SEQ ID NO: 112)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
 IYSSGGITVYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAYRR
 IGVPRRDEFDIWGQGMVTVSSASTKGPSVPLAPSSKSTSGGTAA LGCL
 VKDYFPEPVTVWSNNSGALTSGVHTFP AVLQSSGLYLSVSVTVPSSSLGT
 QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVLFPP
 KPKDTLMISRTPEVTCVV DVSHDPEVKFNWYVGVEVHNAKTKPREEQ
 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTP
 PVLDSDGSFFFLYSKLTVDKSRWQQGNVFSCVMHEALHNHYTQKSLSLSP
 GKSGGGSDIQMTQSPLSLPVTGP E P ASI CRSSQSLHSNGNYLDWYLQ
 KPGQSPQ LLIYLGSNRASGV PDR FSGSGSGTDF TLKISRVEAEDVG VYYC
 MQALQT PWT FGQGT KVEIKRTGGGSGGGSGGGSGGGSEVQ LLE SGG

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GLVQPGGSLRLSCAASGFTFSQYNMVWVRQAPGKGLEWVSRIWPSGGKTT
 YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRQRYRGPKEYYY
 MDVWGKGTTVTVSS

>620I-X0136-B11 = DX2930 Heavy Chain +
 559C-M0192-G05 L4H scFv
 (SEQ ID NO: 113)
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
 IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
 IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
 VKDYFPEPVTVWSNNSALTSVGHTFPAVLQSSGLYSLSSVVTVPSSSLGT
 QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCAPELLGGPSVFLFPP
 KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP
 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
 GKSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSQYTMVWVRQAPGK
 GLEWWSRIYPSGGVTOYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
 YYCTQRQYRGPKEYYMDVWGKTTVTVSSGGGGSGGGSGGGSGGGSGGG
 DIQMTQSPLSLPVTPGEPASIICRSSQSLLHSNGNYLDWYLQKPGQSPQ
 LLIYLGSNRASGVPDFRGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP
 WTFGQGKVEIKR

>620I-X0142-D04 = DX2930 Heavy Chain +
 559C-M0192-G05 H4L scFv
 (SEQ ID NO: 114)
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
 IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
 IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
 VKDYFPEPVTVWSNNSALTSVGHTFPAVLQSSGLYSLSSVVTVPSSSLGT
 QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCAPELLGGPSVFLFPP
 KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP
 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
 GKSGGGSDIQMTQSPLSLPVTPGEPASIICRSSQSLLHSNGNYLDWYLQ
 KPGQSPQLIYLGSNRASGVPDFRGSGSGTDFTLKISRVEAEDVGVYYC
 MQALQTPWTFGQGKVEIKRTGGGGGGGGGGGGGGSEVQLLESGG
 GLVQPGGSLRLSCAASGFTFSQYTMVWVRQAPGKGLEWVSRIYPSGGVTQ
 YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRQRYRGPKEYYY
 MDVWGKGTTVTVSS

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>620I-X0136-D06 = DX2930 Heavy Chain +
 559C-M0192-H04 L4H scFv
 (SEQ ID NO: 115)
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
 IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
 IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
 VKDYFPEPVTVWSNNSALTSVGHTFPAVLQSSGLYSLSSVVTVPSSSLGT
 QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCAPELLGGPSVFLFPP
 KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP
 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
 GKSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSQYVMWVRQAPGK
 GLEWWSRIYPSGGLTYNADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
 YYCTQRQYRGPKEYYMDVWGKTTVTVSSGGGGSGGGSGGGSGGG
 DIQMTQSPLSLPVTPGEPASIICRSSQSLLHSNGNYLDWYLQKPGQSPQ
 LLIYLGSNRASGVPDFRGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP
 WTFGQGKVEIKR

>620I-X0139-A01 = DX2930 Heavy Chain +
 559C-M0192-H04 H4L scFv
 (SEQ ID NO: 116)
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
 IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
 IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
 VKDYFPEPVTVWSNNSALTSVGHTFPAVLQSSGLYSLSSVVTVPSSSLGT
 QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCAPELLGGPSVFLFPP
 KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP
 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
 GKSGGGSDIQMTQSPLSLPVTPGEPASIICRSSQSLLHSNGNYLDWYLQ
 KPGQSPQLIYLGSNRASGVPDFRGSGSGTDFTLKISRVEAEDVGVYYC
 MQALQTPWTFGQGKVEIKRTGGGGGGGGGGGGGGSEVQLLESGG
 GLVQPGGSLRLSCAASGFTFSQYVMWVRQAPGKGLEWVSRIYPSGGLTN
 YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRQYRGPKEYYY
 MDVWGKGTTVTVSS

>620I-X0136-D12 = DX2930 Heavy Chain +
 559C-M0192-H11 L4H scFv
 (SEQ ID NO: 117)
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
 IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
 IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
 VKDYFPEPVTVWSNNSALTSVGHTFPAVLQSSGLYSLSSVVTVPSSSLGT

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QTYICNVNHPNSNTKVDKRVEPKSCDKTHTCPCPAPELLGGPSVLFPP
 KPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQP
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTP
 PVLDSDGSFFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
 GKSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSQYVMHWVRQAPGK
 GLEWVSSIWPSSGGHTRYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
 YYCTRQYRGPKYYYYMDWGQGTTVTSSGGGSGGGSGGGSGGG
 DIQMTQSPLSLPVTGPGEPASISCRSSQSLHSNGNYLDWYLQKPGQSPQ
 LLIYLGSNRASGVPDFRSGSGSGTDFTLKISRVEAEVGVYYCMQALQTP
 WTFGQGKTVEIKR
 >620I-X0139-F05 = DX2930 Heavy Chain +
 559C-M0192-H11 H4L scFv
 (SEQ ID NO: 118)
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
 IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
 IGVPDRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
 VKDYFPEPVTVWNSGALTSGVHTFPABLQSSGLYLSLSSVTVPSSLGT
 QTYICNVNHPNSNTKVDKRVEPKSCDKTHTCPCPAPELLGGPSVLFPP
 KPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQP
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTP
 PVLDSDGSFFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
 GKSGGGSDIQMTQSPLSLPVTGPGEPASISCRSSQSLHSNGNYLDWYLQ
 KPGQSPQPLIYLGSNRASGVPDFRSGSGSGTDFTLKISRVEAEVGVYYC
 MQALQTPWTFGQGKTVEIKRTGGGGGGGGGGGGGGSEVQLLESGG
 GLVQPGGSLRLSCAASGFTFSQYVMHWVRQAPGKGLEWVSSIWPSSGGTK
 YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRQYRGPKYYYY
 MDWVGKGTTVTVSS
 >620I-X0136-A11 = DX2930 Heavy Chain +
 559C-M0292-D07 L4H scFv
 (SEQ ID NO: 119)
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
 IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
 IGVPDRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
 VKDYFPEPVTVWNSGALTSGVHTFPABLQSSGLYLSLSSVTVPSSLGT
 QTYICNVNHPNSNTKVDKRVEPKSCDKTHTCPCPAPELLGGPSVLFPP
 KPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQP
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTP
 PVLDSDGSFFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
 GKSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSYFYSMHWVRQAPGK
 GLEWVSRIVPSGGITSYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
 YYCTRQYRGPKYYYYMDWGQGTTVTSSGGGSGGGSGGGSGGG
 DIQMTQSPLSLPVTGPGEPASISCRSSQSLHSNGNYLDWYLQKPGQSPQ
 LLIYLGSNRASGVPDFRSGSGSGTDFTLKISRVEAEVGVYYCMQALQTP
 WTFGQGKTVEIKR

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GLEWVSSIWPSSGGKTKYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
 YYCTRQYRGPKYYYYMDWGQGTTVTSSGGGSGGGSGGGSGGG
 DIQMTQSPLSLPVTGPGEPASISCRSSQSLHSNGNYLDWYLQKPGQSPQ
 LLIYLGSNRASGVPDFRSGSGSGTDFTLKISRVEAEVGVYYCMQALQTP
 WTFGQGKTVEIKR
 >620I-X0139-E05 = DX2930 Heavy Chain +
 559C-M0292-D07 H4L scFv
 (SEQ ID NO: 120)
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
 IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
 IGVPDRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
 VKDYFPEPVTVWNSGALTSGVHTFPABLQSSGLYLSLSSVTVPSSLGT
 QTYICNVNHPNSNTKVDKRVEPKSCDKTHTCPCPAPELLGGPSVLFPP
 KPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQP
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTP
 PVLDSDGSFFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
 GKSGGGSDIQMTQSPLSLPVTGPGEPASISCRSSQSLHSNGNYLDWYLQ
 KPGQSPQPLIYLGSNRASGVPDFRSGSGSGTDFTLKISRVEAEVGVYYC
 MQALQTPWTFGQGKTVEIKRTGGGGGGGGGGGGGGSEVQLLESGG
 GLVQPGGSLRLSCAASGFTFSQYVMHWVRQAPGKGLEWVSSIWPSSGGTK
 YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRQYRGPKYYYY
 MDWVGKGTTVTVSS
 >620I-X0136-C12 = DX2930 Heavy Chain +
 559C-M0177-A06 L4H scFv
 (SEQ ID NO: 121)
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
 IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
 IGVPDRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
 VKDYFPEPVTVWNSGALTSGVHTFPABLQSSGLYLSLSSVTVPSSLGT
 QTYICNVNHPNSNTKVDKRVEPKSCDKTHTCPCPAPELLGGPSVLFPP
 KPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQP
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTP
 PVLDSDGSFFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
 GKSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSYFYSMHWVRQAPGK
 GLEWVSRIVPSGGITSYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
 YYCTRQYRGPKYYYYMDWGQGTTVTSSGGGSGGGSGGGSGGG
 DIQMTQSPLSLPVTGPGEPASISCRSSQSLHSNGNYLDWYLQKPGQSPQ
 LLIYLGSNRASGVPDFRSGSGSGTDFTLKISRVEAEVGVYYCMQALQTP
 WTFGQGKTVEIKR

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```
>620I-X0138-E05 = DX2930 Heavy Chain +
559C-M0177-A06 H4L scFv
(SEQ ID NO: 122)
EVQLLESGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
IYSSGGITVYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAYRR
IGVPRRDEFDIWGQGTMTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVWSN S GALTSGVHTFP AVLQSSGLYLSLSSVTV PSSLGT
QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEELLGGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVSHEDPEVFKFNWYVDGVEVHNAKTKPREEQ
YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP
PVLDSDGSFFLYSKLTVDKSRWQQGNVFC S VHM EALHNHYTQKSLSLSP
GKSGGGSDIQMTQSPLSLPVT PGEPA SICRSSQSLLHSNGNYLDWYLQ
KPGQSPQ LLIY LGSNRASGV PDRFSGSGTDF TLKISRVEA DVG VYYC
MQALQT PWT FGQ GTKVEIKRTGGGGGGGGGGGGGGGGSEVQLLES GG
GLVQPGGSLRLSCAASGFTFSFYSMHW VRQAPGKGLEWV SRI YPSGGITS
YADSVKGRFTISR DN SKNTLYLQMNSLRAEDTAVYYCTRQRYRGPKYYYY
MDVWGK GTT VTVSS
```

Example 3: Construction and Characterization of Exemplary Bispecific Antibodies that Contain Disulfide Bond

[0169] To combat these aggregates, a disulfide bond between the V_H residue 44 (C_{44}) and V_L residue 100 (C_{100}) was engineered into the scFv region for 4 clones, 620I-X0177-A01 (620I-X0173-A11), 620I-X0177-C01 (620I-X0173-C07), 620I-X0177-E01 (620I-X0173-E07), and 620I-X0177-G01 (620I-X0173-G11). SEC analysis of the bispecifics containing scFvs with disulfides showed dramatic reduction of the high molecular weight peaks, bringing the ranges down to 1-2%. FIG. 4. This reduction of aggregation applied across all concentrations tested. Biacore of these bispecific clones showed tight, specific binding to pKal and FXIIa (FIG. 9). The plasma inhibition of these isolates ranged from the 0.5 to 8 nM range (FIG. 10).

[0170] The plasma inhibition assay as described herein was performed to determine the inhibitory activity of bispecific antibody 620I-X0177-A01. The plasma was diluted 1:40 and the inhibitors were added to the diluted plasma. 2.5% (final concentration) of a dilute Ellagic Acid solution was added to the plasma. Around 2 minutes later, activation of plasma was quenched by addition of CTI. The pKal activity in the plasma was measured by addition of a profluorescent substrate as described herein. The results thus obtained were shown in FIG. 11.

[0171] The inhibitory activity of clone 620I-X0177-A01 was compared with that of the parent antibodies, either alone or in combination. Drop-offs in affinity were observed between the parental IgGs and the bispecific antibody. FIG. 12.

[0172] Further, the abilities of various bispecific antibodies on APTT were assessed following the methods described herein. All tested antibodies showed dose-dependent delay of APTT. FIG. 13.

[0173] The abilities of antibody clones 1A01 (anti-FXIIa) and 7A01 (bispecific against both pKal and FXII) to inhibit fibrin deposition were also examined and the results are shown in FIG. 14. A dose-dependent inhibition of fibrin deposition was observed.

[0174] Overall, enzyme inhibition assays determined that the apparent K_i values of the individual anti-pKal and anti-FXIIa components of the exemplary bispecific antibody 620I-X0177-A01 were similar to the parental molecules, with apparent K_i values of 389 pM and 73 pM, respectively. Surprisingly, additional experiments in contact-activated dilute plasma reveal that this bispecific antibody was >5 times more effective at preventing pKal generation than a 1:1 combination of the parent antibodies, and >20-fold more effective than either of the parent antibodies alone. These data suggest that a bispecific antibody would be uniquely potent in its ability to shut down the positive feedback loop of contact system activation.

[0175] The sequences of the bispecific antibodies with disulfide constrained scFvs are provided below:

```
> 620I-X0173-A11 (620I-X0177-A01) =
620I-X0136-D12 Germlined + Gene
optimized scFv + disulfide stabilization
(SEQ ID NO: 47)
EVQLLESGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
IYSSGGITVYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAYRR
IGVPRRDEFDIWGQGTMTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVWSN S GALTSGVHTFP AVLQSSGLYLSLSSVTV PSSLGT
QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEELLGGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVSHEDPEVFKFNWYVDGVEVHNAKTKPREEQ
YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP
PVLDSDGSFFLYSKLTVDKSRWQQGNVFC S VHM EALHNHYTQKSLSLSP
GKSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSQYVMWVRQAPGK
CLEWVSSI WPSGGHTRYADSVKGRFTISR DN SKNTLYLQMNSLRAEDTAV
YYCARQRYRGPKYYYYMDVWGQGTTVTVSSGGGGGGGGGGGGGGGGGG
DIVMTQSPLSLPVT PGEPA SICRSSQSLLHSNGNYLDWYLQKPGQSPQ
LLIY LGSNRASGV PDRFSGSGTDF TLKISRVEA DVG VYYCMQALQTP
WTFPGCGT KVEIKR

>620I-X0173-C07 (620I-X0177-C01) =
620I-X0136-C05 Germlined + Gene optimized
scFv + disulfide stabilization
(SEQ ID NO: 48)
EVQLLESGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
IYSSGGITVYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAYRR
IGVPRRDEFDIWGQGTMTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVWSN S GALTSGVHTFP AVLQSSGLYLSLSSVTV PSSLGT
QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEELLGGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVSHEDPEVFKFNWYVDGVEVHNAKTKPREEQ
YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
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```
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GKSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSWYVMHWRQAPGK
CLEWVSSIYPSGGKTSYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
YYCARQRYRGPKYYYYMDVWGQGTTVTVSSGGGSGGGSGGGSGGGSGGG
DIVMTQSPLSLPVTPGEPASISCRSSQSLHSNGNYLDWYLQKPGQSPQ
LIYLGSNRASGVPDFRSGSGSTDFTLKISRVEAEDVGVYYCMQALQTP
WTFGCGTKVEIKR
```

>620I-X0173-E07 (620I-X0177-E01) =
620I-X0136-C11 Germlined + Gene optimized
scFv + disulfide stabilization

(SEQ ID NO: 49)

```
EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
IGVPRRDEFEDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSVVTPSSSLGT
QTYICNVNHKPSNTKVDKRVPKSCDKTHTCPPCAPEELLGGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVGVEVHNAKTKPREEQ
YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GKSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSHYVMHWRQAPGK
CLEWVSSIYPSGGKTRYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
YYCARQRYRGPKYYYYMDVWGQGTTVTVSSGGGSGGGSGGGSGGGSGGG
DIVMTQSPLSLPVTPGEPASISCRSSQSLHSNGNYLDWYLQKPGQSPQ
LIYLGSNRASGVPDFRSGSGSTDFTLKISRVEAEDVGVYYCMQALQTP
WTFGCGTKVEIKR
```

>620I-X0173-G11 (620I-X0177-G01) =
620I-X0136-G05 Germlined + Gene optimized
scFv + disulfide stabilization

(SEQ ID NO: 50)

```
EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
IGVPRRDEFEDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSVVTPSSSLGT
QTYICNVNHKPSNTKVDKRVPKSCDKTHTCPPCAPEELLGGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVGVEVHNAKTKPREEQ
YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GKSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSHYVMHWRQAPGK
CLEWVSSIYPSGGLTKYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
YYCARQRYRGPKYYYYMDVWGQGTTVTVSSGGGSGGGSGGGSGGGSGGG
```

- continued

```
DIVMTQSPLSLPVTPGEPASISCRSSQSLHSNGNYLDWYLQKPGQSPQ
LIYLGSNRASGVPDFRSGSGSTDFTLKISRVEAEDVGVYYCMQALQTP
WTFGCGTKVEIKR
```

Example 4: Construction and Characterization of Exemplary Bispecific Antibodies with C-Terminal Mutations and/or Deletions

[0176] Exemplary bispecific antibodies (620I-X0177-A01, 620I-X0177-C01, 620I-X0177-E01, 620I-X0177-G01) were assessed for production and manufacturability. Samples of the bispecific antibodies were incubated at room temperature for 48 hours at various pH prior to analysis. The samples were then separated on a SDS-PAGE protein gel, as shown, for example, for bispecific antibody 620I-X0177-A01 in FIG. 15, or analyzed by size exclusion chromatography (FIG. 16A-16C). A pH-dependent increase of the 30 kDa and 50 kDa bands and a decrease of the 80 kDa bands were observed under reducing conditions (FIG. 15, lanes 2-6). The appearance of these unexpected bands indicating that the bispecific antibodies were undergoing unanticipated proteolytic cleavage. The appearance of the same 30 kDa species under non-reducing conditions indicated the cleaved species was monomeric (FIG. 15, lanes 6-8). By SEC analysis, peaks were observed at 15.7-16.1 minutes representing the correctly formed bispecific antibodies, at 17 minutes representing DX-2930, and at 22 minutes representing the cleaved single chain antibody (FIG. 16).

[0177] Exemplary bispecific antibodies were designed to remove the IgG1 heavy chain C-terminal lysine residue or mutate the lysine to a glycine residue.

[0178] Provided below are the amino acid sequences of the first polypeptides of the bispecific antibodies including a deletion of the C-terminal lysine residue or a mutation of the C-terminal lysine to a glycine residue of the heavy chain of the first antibody. These first polypeptides may be paired with the light chain of DX-2930.

>620I-X0179-A09 (620I-X0177-A01 with IgG-C-term Lys deletion)

(SEQ ID NO: 141)

```
EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
IGVPRRDEFEDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSVVTPSSSLGT
QTYICNVNHKPSNTKVDKRVPKSCDKTHTCPPCAPEELLGGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVGVEVHNAKTKPREEQ
YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSQYVMHWRQAPGKC
LEWVSSIWPSGGHTRYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVY
YYCARQRYRGPKYYYYMDVWGQGTTVTVSSGGGSGGGSGGGSGGGSGGGSD
IVMTQSPLSLPVTPGEPASISCRSSQSLHSNGNYLDWYLQKPGQSPQ
```

- continued

L1YLGSNRASGVPDFRGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPW

TFGCGTKVEIKR

>620I-X0179-C01 (620I-X0177-A01 with IgG-C-term Lys mutation to Gly)

(SEQ ID NO: 142)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVWNSGALTSGVHTFPABLQSSGLYSLSSVVTVPSSSLGT
QTYICNVNKHPSNTKVDKRVEPKSCDKTHTCPPCPAPEELLGGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVEVHNAAKTKPREEQ
YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP
PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSQYVMHWVRQAPGK
CLEWVSSIWPSSGGHTRYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV
YYCARQRYRGPKYYYYMDVWGQGTTTVSSGGGGSGGGSGGGSGGGSGGG
DIVMTQSPLSLPVTPGEPASISCRSSQSLHSNGNYLDWYLQKPGQSPQ
LIYLGSNRASGVPDFRGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP
WTFGCGTKVEIKR

>620I-X0179-E05 (620I-X0177-C01 with IgG-C-term Lys deletion)

(SEQ ID NO: 143)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR
IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVWNSGALTSGVHTFPABLQSSGLYSLSSVVTVPSSSLGT
QTYICNVNKHPSNTKVDKRVEPKSCDKTHTCPPCPAPEELLGGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVEVHNAAKTKPREEQ
YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP
PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSWYVMHWVRQAPGK
LEWVSSIYPSSGGKTSYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVY
YCARQRYRGPKYYYYMDVWGQGTTTVSSGGGGSGGGSGGGSGGGSD
IVMTQSPLSLPVTPGEPASISCRSSQSLHSNGNYLDWYLQKPGQSPQ
LIYLGSNRASGVPDFRGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPW
TFGCGTKVEIKR

>620I-X0179-G05 (620I-X0177-C01 with IgG-C-term Lys mutation to Gly)

(SEQ ID NO: 144)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG
IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR

- continued

IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL

VKDYFPEPVTVWNSGALTSGVHTFPABLQSSGLYSLSSVVTVPSSSLGT

QTYICNVNKHPSNTKVDKRVEPKSCDKTHTCPPCPAPEELLGGPSVFLFPP

KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVEVHNAAKTKPREEQ

YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE

PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP

PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP

GGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSWYVMHWVRQAPGK

CLEWVSSIYPSSGGKTSYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV

YYCARQRYRGPKYYYYMDVWGQGTTTVSSGGGGSGGGSGGGSGGGSGGG

DIVMTQSPLSLPVTPGEPASISCRSSQSLHSNGNYLDWYLQKPGQSPQ

LLIYLGSNRASGVPDFRGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP

WTFGCGTKVEIKR

>620I-X0180-A05 (620I-X0177-G01 with IgG-C-term Lys deletion)

(SEQ ID NO: 145)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSG

IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR

IGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL

VKDYFPEPVTVWNSGALTSGVHTFPABLQSSGLYSLSSVVTVPSSSLGT

QTYICNVNKHPSNTKVDKRVEPKSCDKTHTCPPCPAPEELLGGPSVFLFPP

KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVEVHNAAKTKPREEQ

YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE

PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP

PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP

GGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSWYVMHWVRQAPGK

LEWVSSIYPSSGGLTKYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVY

YCARQRYRGPKYYYYMDVWGQGTTTVSSGGGGSGGGSGGGSGGGSD

IVMTQSPLSLPVTPGEPASISCRSSQSLHSNGNYLDWYLQKPGQSPQ

LIYLGSNRASGVPDFRGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPW

TFGCGTKVEIKR

-continued

>620I-X0180-C11 (620I-X0177-G01 with IgG-C-term Lys mutation to Gly)

(SEQ ID NO: 146)

```
EVQLLESGGLVQPGGSRLSCAASGFTFSHYIMMWVRQAPGKGLEWVG  
IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR  
IGVPRRDEFDIWGQGTMVTSSASTKGPSVFPLAPSSKSTSGGTAALGCL  
VKDYFPEPVTVWNSGALTSGVHTFPABLQSSGLYSLSSVVTVPSSSLGT  
QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEELLGGPSVFLFPP  
KPKDTLMISRTPEVTCVVVDVSHEDPEVFKFNWYDGVEVHNAKTKPREEQ  
YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQPRE  
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP  
PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP  
GGSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSHYVMHWVRQAPGK  
CLEWVSSIYPSGGLTKYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV  
YYCARQRYPKYYYYMDVWGQGTTVTVSSGGGGSGGGSGGGSGGGSGGGGS  
DIVMTQSPLSLPVTPGEPEASISCRSSQSLHNSNGNYLDWYLQKPGQSPQ  
LIYLGSNRASGVPDFSGSGSTDFTLKISRVEAEDVGVYYCMQALQTP  
WTFGCGTKVEIKR
```

>620I-X0180-E07 (620I-X0177-E01 with IgG-C-term Lys deletion)

(SEQ ID NO: 147)

```
EVQLLESGGLVQPGGSRLSCAASGFTFSHYIMMWVRQAPGKGLEWVG  
IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR  
IGVPRRDEFDIWGQGTMVTSSASTKGPSVFPLAPSSKSTSGGTAALGCL  
VKDYFPEPVTVWNSGALTSGVHTFPABLQSSGLYSLSSVVTVPSSSLGT  
QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEELLGGPSVFLFPP  
KPKDTLMISRTPEVTCVVVDVSHEDPEVFKFNWYDGVEVHNAKTKPREEQ  
YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQPRE  
PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP  
PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP  
GGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFWSWYSMHWVRQAPGKC  
LEWVSVIYPSGGKTRYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVY  
YCARQRYPKYYYYMDVWGQGTTVTVSSGGGGSGGGSGGGSGGGSGGGSD  
IVMTQSPLSLPVTPGEPEASISCRSSQSLHNSNGNYLDWYLQKPGQSPQ  
LIYLGSNRASGVPDFSGSGSTDFTLKISRVEAEDVGVYYCMQALQTPW  
TFGCGTKVEIKR
```

>620I-X0180-G03 (620I-X0177-E01 with IgG-C-term Lys mutation to Glycine)

(SEQ ID NO: 148)

```
EVQLLESGGLVQPGGSRLSCAASGFTFSHYIMMWVRQAPGKGLEWVG  
IYSSGGITVYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAYRR  
IGVPRRDEFDIWGQGTMVTSSASTKGPSVFPLAPSSKSTSGGTAALGCL  
VKDYFPEPVTVWNSGALTSGVHTFPABLQSSGLYSLSSVVTVPSSSLGT
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QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEELLGGPSVFLFPP

KPKDTLMISRTPEVTCVVVDVSHEDPEVFKFNWYDGVEVHNAKTKPREEQ

YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQPRE

PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP

PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP

GGSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFWSWYSMHWVRQAPGK

CLEWVSVIYPSGGKTRYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV

YYCARQRYPKYYYYMDVWGQGTTVTVSSGGGGSGGGSGGGSGGGSGGGGS

DIVMTQSPLSLPVTPGEPEASISCRSSQSLHNSNGNYLDWYLQKPGQSPQ

LLIYLGSNRASGVPDFSGSGSTDFTLKISRVEAEDVGVYYCMQALQTP

WTFGCGTKVEIKR

[0179] Each of the exemplary bispecific antibodies including a deletion of the C-terminal lysine residue or a mutation of the C-terminal lysine to a glycine residue of the heavy chain of the first antibody was assessed by separating the bispecific antibodies on an SDS-PAGE 30 gel at t=0 (FIG. 17). Samples of each of the exemplary bispecific antibodies were also concentrated using an Amicon 10 kDa molecular weight cut-off spin filter to approximately 10 mg/mL in 50 mM Hepes, pH 7.5 and incubated at room temperature for 48 hours. The samples were then assessed by SDS-PAGE gel (FIG. 18). In each case, deletion or mutation of the C-terminal lysine reduced or eliminated cleavage of the scFv from the bispecific antibody.

[0180] Samples of the bispecific were also assessed by analytical size exclusion chromatography, demonstrating that the deletion or mutation of the C-terminal lysine reduced cleavage of the bispecific antibodies (FIGS. 19-20). Cleavage of the bispecific antibodies was also assessed by incubating the antibodies with EndoLysC at 37° C. for 1 hour followed by separation on an SDS-PAGE gel (FIG. 21). The protein bands at 50 kDa corresponded to the Fab portion of DX-2930, and the bands at 100 kDa corresponded to a homodimer of Fc-scFv, further indicating that the deletion or mutation of the heavy chain C-terminal lysine reduced cleavage of the bispecific antibodies.

[0181] The exemplary bispecific antibodies including a deletion or mutation of the C-terminal lysine were also characterized for the ability to inhibit pKal, FXIIa, and activated plasma compared to DX-2930 and DX-4012 control (Table 1, FIG. 22-24). Each of the exemplary bispecific antibodies was found to be functionally equivalent to the parent bispecific antibody (the bispecific antibody that does not comprise the deletion or mutation of the IgG1 heavy chain C-terminal lysine). The mutation may reduce charge heterogeneity of the bispecific antibody.

TABLE 6

Summary of bispecific antibodies used in the biochemical assays, as well as DX-2930 and DX-4012 control IgGs.
Assays were performed to measure inhibition of pKal, inhibition of FXIIa, and inhibition of activated plasma.

R-name	X-name (or DX-)	Parent Bispecific	IgG-C-term Lys alteration	FXII scFv	pKal inhibition Ki, app (pM)	FXIIa inhibition Ki, app (pM)	activated plasma inhibition IC50/ Ki, app (nM)
6201-R0052-A01	6201-X0179-A09	6201-X0177-A01	Lys-Delete	559C-M0192-H11 GL/GO/Disulfide H4L SCFv	225	90	7.6 (Ki)
6201-R0052-C01	6201-X0179-C01	6201-X0177-A01	Lys-Gly	559C-M0192-H11 GL/GO/Disulfide H4L SCFv	243	108	7.8 (KI)
6201-R0052-E01	6201-X0179-E05	6201-X0177-C01	Lys-Delete	559C-M0192-F06 GL/GO/Disulfide H4L SCFv	203	99	7.4 (Ki)
6201-R0052-G01	6201-X0179-G05	6201-X0177-C01	Lys-Gly	559C-M0192-F06 GL/GO/Disulfide H4L SCFv	226	52	8.1 (Ki)
5201-R0052-E03	6201-X0180-E07	6201-X0177-E01	Lys-Delete	559C-M0191-E09 GL/GO/Disulfide H4L ScFv	243	92	3.0 (Ki)
6201-R0052-G03	6201-X0180-G03	6201-X0177-E01	Lys-Gly	559C-M0191-E09 GL/GO/Disulfide H4L SCFv	208	71	2.8 (Ki)
6201-R0052-A03	6201-X0180-A05	6201-X0177-G01	Lys-Delete	559C-M0192-A01 GL/GO/Disulfide H4L scFv	254	116	7.3 (Ki)
6201-R0052-C03	6201-X0180-C11	6201-X0177-G01	Lys-Gly	559C-M0192-A01 GL/GO/Disulfide H4L scFv	232	140	9.2 (Ki)
DX-2930					127, 131, 151	n/a	90, 68, 74, 74, 66 (IC50)
DX-4012					n/a	8, 2, 9	279, 291 (IC50)

[0182] Alternatively or in addition, the Lys-Arg (KR) motif at the C-terminus of the anti-FXIIa scFvs noted above can be removed. Provided below are the amino acid sequences of the exemplary bispecific antibody polypeptides

including a deletion of the C-terminal lysine residue or a mutation of the C-terminal lysine to a glycine residue of the heavy chain of the first antibody and a deletion of the C-terminal lysine-arginine residues of the scFv.

```
>6201-X0186-C05 (6201-X0177-A01 with IgG-C-term Lys deletion and
C-terminal KR removal)
(SEQ ID NO: 151)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSGIYSSGGITVVADSVKGKF
TISRDNSKNTLYLOMNSLRAEDTAVYYCAYRRIGVPRRDEFIDIWGQGTMTVSSASTKGPSVFPLAPS
SKSTSGGTAALGCLVKDYFPEPVTVWSNSGALTSGVHTFPAVLOSSGLYSLSSVTVPSSSLGTQTYI
CNVNHKPSNTKVDKRVEPKSCDKTHCPPCPAPEELLGGPSVELFPPPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKITPPVLDSDGS
FFLYSKLTVDKSRWQQGNVFCSVHEALHNHYTOKSLSSLPGSGGGSEVOLLESGGLVOPGSSLRL
SCAASGFTFSQYVMHWVRQAPGKCLEWVSSIWPSGGHTRYADSVKGRFTISRDNSKNTLYLOMNSLRA
EDTAVYYCARQRYRGPKYYYYMDVVGQGTTVTSSGGGGSGGGSGGGSDIVMTQSPLSLPV
TPGEPASISCRSSQSLLHSNCNYLDWYLQKPGOSPQLIYLGSNRASCVPDRPSGSGSGTDFTLKIS
RVEAEDVGVYYCMQALQTPTWFGCGTKVEI
```

- continued

>620I-X0185-C01 (620I-X0177-A01 with IgG-C-term Lys mutation to Glycine and C-terminal KR removal)

(SEQ ID NO: 152)

```
EVQLLESGGLVQPGGSRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSGIYSSGGITVYADSVKGREF
TISRDNSKNTLYLQMNSLRAEDTAVYYCAYRRIGVPRRDEFDIWGQGTMTVSSASTKGPSVFPLAPS
SKSTSGGTAALGCLVKDYFPEPVTWNSGALISGVHTFPAVLOSSGLYSLSSVTVPSSSLGTQTYI
CNVNHKPSNTKVDKRVEPKSCDKTHCTPPCPAPELLGGPSVELFPPPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVGVEVHNNAKTPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS
FFLYSKLTVDKSRWQQGNFSCVMHEALHNHYTQKSLSLSPGGSGGGSEVOLLESGGGLVQPGGSLR
LSCAASGFTFSQYVMHWVRQAPGKCLEWVSSIWPSGGHTRYADSVKGRFTISRDNSKNTLYLQMNSLR
AEDTAVYYCARQRYRGPKYYYYMDVWGQGTTTVSSGGGSGGGSGGGSGGGSDIVMTQSPLSLP
VTPGEPAISCRSSQSLLHSNGNYLDWYLQKPGQSPOLLIYLGSNRASGVPDFRSGSGSGTDFTLK
SRVEAEDVGVYYCMQALQTPWTFGCGTKVEI
```

>620I-X0186-E05 (620I-X0177-C01 with IgG-C-term Lys deletion and C-terminal KR removal)

(SEQ ID NO: 153)

```
EVQLLESGGLVOPGGSLRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSGIYSSGGITVYADSVKGREF
TISRDNSKNTLYLQMNSLRAEDTAVYYCAYRRIGVPRRDEFDIWGQGTMTVSSASTKGPSVFPLAPS
SKSTSGGTAALGCLVKDYFPEPVTWNSGALISGVHTFPAVLOSSGLYSLSSVTVPSSSLGTQTYI
CNVNHKPSNTKVDKRVEPKSCDKTHCTPPCPAPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVGVEVHNNAKTPREEQYNSTYRVSVLIVLHQDWLNGKEYKCKVSNKALPAPIEKT
ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS
FFLYSKLTVDKSRWQQGNFSCVMHEALHNHYTQKSLSLSPGGSGGGSEVOLLESGGGLVQPGGSLR
SCAASGFTFSWYVMHWVRQAPGKCLEWVSSIYPSGGKTSYADSVKGRETISRDNSKNTLYLQMNSLRA
EDTAVYYCARQRYRGPKYYYYMDVWGQGTTTVSSGGGSGGGSGGGSGGGSDIVMTQSPLSLP
TPGEPAISCRSSQSLLHSNGNYLDWYLQKPGQSPOLLIYLGSNRASGVPDFRSGSGSGTDFTLK
RVEAEDVGVYYCMQALQTPWTFGCGTKVEI
```

>620I-X0185-E01 (620I-X0177-C01 with IgG-C-term Lys mutation to Glycine and C-terminal KR removal)

(SEQ ID NO: 154)

```
EVQLLESGGLVQPGGSRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSGIYSSGGITVYADSVKGREF
TISRDNSKNTLYLQMNSLRAEDTAVYYCAYRRIGVPRRDEFDIWGQGTMTVSSASTKGPSVFPLAPS
SKSTSGGTAALGCLVKDYFPEPVTWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYI
CNVNHKPSNTKVDKRVEPKSCDKTHCTPPCPAPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVGVEVHNNAKTPREEQYNSTYRVSVLIVLHQDWLNGKEYKCKVSNKALPAPIEKT
ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS
FFLYSKLTVDKSRWQQGNFSCVMHEALHNHYTQKSLSLSPGGSGGGSEVOLLESGGGLVQPGGSLR
LSCAASGFTFSWYVMHWVRQAPGKCLEWVSSIYPSGGKTSYADSVKGRFTISRDNSKNTLYLQMNSLR
EDTAVYYCARQRYRGPKYYYYMDVWGQGTTTVSSGGGSGGGSGGGSGGGSDIVMTQSPLSLP
VTPGEPAISCRSSQSLLHSNGNYLDWYLQKPGQSPOLLIYLGSNRASGVPDFRSGSGSGTDFTLK
SRVEAEDVGVYYCMQALQTPWTFGCGTKVEI
```

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>620I-X0186-A05 (620I-X0177-G01 with IgG-C-term Lys
deletion and C-terminal KRremoval) (SEQ ID NO: 155)

TISRDNSKNLTYLOMNSLRAEDTAVYYCAYRRIGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPS
SKSTSGGTAALGCLVKDYFPEPVTVWSNGALTSGVHTFPVALQSGLYLSLSSVTPSSSLGTQTYI
CNVNHKPSNTKVDKRVEPKSCDKTHCPCCPAPELLGGPSVLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYDGVEVHNAKTKPREEQYNSTYRVSVSLLVLHQDWLNGKEYKCKVSNKALPAPIEKT
ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESENQOPENNYKTTPPVLDSDGS
FFFLYSKLTVDKSRWQQGNFVSCVMHEALHNHYTQKSLSLSPGSGGGSEVOLLESGGGLVQPGGSLRL
SCAASGFTFSHYVMHWVRQAPGKCLEWVSSIYPSEGGLTKYADSVKGFRТИSRDNSKNLTYLOMNSLRA
EDTAVYYCARQRYRGPKYYYYMDVWQGQTTVTVSSGGGGGGGGGGGGGGSDIVMTQSPLSLPV
TPGEPAISCRSSQSLLHSNGYNYLDWYLQKPGOSPQLLIYLGNSNRASGVPDFRESGSGSGTDETLKIS

RVEAEDVGVYYCMQALQTPWIFGCGTKVEI
>620I-X0185-A03 (620I-X0177-G01 with IgG-C-term Lys mutation
to Glycine and C-terminal KR removal) (SEQ ID NO: 156)

TISRDN SKNTLYLOMNSLRAEDTAVYYCAYRRIGVPRRDEFDIWGOGTMVTSSASTKGPSVFPLAPS
SKSTSGGTAALGCLVKDYFPEPVTWSWNSGALTSGVHTFPAVLOSSGLYSLSSVTPSSSLGTQTYI
CNVNHKPSNTKVDKRVEPKSCDKTHTCPPCAPELLGGPSVFLFPPKPKDLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
ISAKAQGPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTPPVLDSDGS
FFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLPGGGGGSEVOLLESGGGLVQPGGSLR
LSCAASGFTFSHYMHWVRQAPGKCLEWSSIYPSGGLTKYADSVKGRFTISRDN SKNTLYLQMNSLR
AEDTAVYYCARQRYRGPKYYYMDVGQGTTVSSGGGGSGGGSGGGSGGGSDIVMTQSPLSLP
VTPGEPASISCRSSQSSLHNSGNYLDWYLOKPGQSPQLIYLGSNRASGVPDRESGSGGTDETLKI

TISRDN SKNTLYLOMNSLRAEDTAVYYCAYRRIGVPRRDEFDIWGQGTMVTVSSASTKGPSVFPLAPS
SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALISGVHTFPAPLOSSGLYSLSSVTPSSSLGTQTYI
CNVNHKPSNTKVDKRVEPKSCDKTHTCPPCAPELLGGPSVELFPPPKPDLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKIKPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
ISAKAQGPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAWEWESNGQPENNYKITPPVLDSDGS
FFFLYSKLTVDKSRWQQGNVFCSVMEALHNHYTQKSLSLPGSGGGSEVOLLESGGGLVQPGGSLRL
SCAASGFTFSWYSMHWVRQAGKCLEWVSVIYPSGGKTRYADSVKGRFTISRDN SKNTLYLQMNSLRA
EDTAVYYCARQRYRGPKYYYYMDVWQGQTTVTVSSGGGGGGGGGGGGSDIVMTQSPLSLPV
TPGEPASISCRSSOSLLHSNGNYLDWYLQKPGOSPQLIYLGSNRASGVPDFSGSGSGTDFTLKIS
RVEAEDVGVYYCMQALQTPWTFGCGTKVEI

- continued

>620I-X0185-G01 (620I-X0177-E01 with IgG-C-term Lys mutation to Glycine and C-terminal KR removal)
 (SEQ ID NO: 158)

```
EVQLLESGGGLVQPGGSRLSCAASGFTFSHYIMMWVRQAPGKGLEWVSGIYSSGGITVYADSVKGRE
TISRDNSKNTLYLQMNSLRAEDTAVYYCAYRRIGVPRRDEFIDIWGQGTMVTVSSASTKGPSVFPLAPS
SKSTSGGTAALGCLVKDVFPEPFTVSWNSGALTSGVHTFPAVLOSSGLYSLSSVVTVPSSSLGTQTYI
CNVNHKPSNTKVDRVEPKSCDKTHCPCCPAPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVGVEVHNAKTPKREEQYNSTYRVVSVLIVLHQDWLNGKEYKCKVSNKALPAPIEKT
ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS
FFLYSKLTVDKSRWQQGNVFCSVMHEALHNHYTQKSLSLSPGGSGGGSEVOLLESGGGLVQPGGSLR
LSCAASGFTFSWYSMHWRQAPGKCLEWVSVIYPSGGKTRYADSVKGRFTISRDNSKNTLYLQMNSLR
AEDTAVYYCARQRYRGPKYYYYMDVWGQGTTVTVSSGGGSGGGGSGGGGSGGGSDIVMTQSPLSLP
VTPGEPAISCRSSQSLLHSNGYNYLDWYLOKPGQSPQLLIYLGSNRASGVPDRESGSGSGTDETLKI
SRVEAEDVGYYYCMQALQTPWTFGCGTKVEI
```

[0183] The above-listed polypeptides can be paired with the light chain of DX-2930 to form bispecific antibodies, which are also within the scope of the present disclosure.

Other Embodiments

[0184] All of the features disclosed in this specification may be combined in any combination. Each feature disclosed in this specification may be replaced by an alternative feature serving the same, equivalent, or similar purpose.

Thus, unless expressly stated otherwise, each feature disclosed is only an example of a generic series of equivalent or similar features.

[0185] From the above description, one skilled in the art can easily ascertain the essential characteristics of the present invention, and without departing from the spirit and scope thereof, can make various changes and modifications of the invention to adapt it to various usages and conditions. Thus, other embodiments are also within the claims.

SEQUENCE LISTING

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Sequence total quantity: 164
SEQ ID NO: 1      moltype = AA  length = 122
FEATURE          Location/Qualifiers
REGION           1..122
note = Synthetic Polypeptide
source            1..122
mol_type = protein
organism = synthetic construct

SEQUENCE: 1
EVQLLESGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFIDIWGQGTMVTV 120
SS                           122

SEQ ID NO: 2      moltype = AA  length = 106
FEATURE          Location/Qualifiers
REGION           1..106
note = Synthetic Polypeptide
source            1..106
mol_type = protein
organism = synthetic construct

SEQUENCE: 2
DIQMTQSPST LSASVGDRVIT ITCRASQYSIS SWLAWYQQKP GKAPKLIIYK ASTLESGVPS 60
RFSGSGSGTE FTLTISLQP DDFATYYCQQ YNTYWTFGQG TKVEIK                  106

SEQ ID NO: 3      moltype = AA  length = 123
FEATURE          Location/Qualifiers
REGION           1..123
note = Synthetic Polypeptide
source            1..123
mol_type = protein
organism = synthetic construct

SEQUENCE: 3
EVQLLESGGG LVQPGGSLRL SCAASGFTFS GYIMMAWRQA PGKGLEWVSY IYPSGGITVY 60
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCTRQR YRGPKYYYYM DVWGKGTTVT 120
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VSS		123
SEQ ID NO: 4	moltype = AA length = 123	
FEATURE	Location/Qualifiers	
REGION	1..123	
	note = Synthetic Polypeptide	
source	1..123	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 4		
EVQLLESGGG LVQPGGSLRL SCAASGFTPS FYSMHWVRQA PGKGLEWVSR IYPSGGVTKY	60	
ADSVVKGRFTI SRDNSKNLTY LQMNSLRAED TAVYYCTRQR YRGPKYYYYM DVWGKGTTVT	120	
VSS		123
SEQ ID NO: 5	moltype = AA length = 113	
FEATURE	Location/Qualifiers	
REGION	1..113	
	note = Synthetic Polypeptide	
source	1..113	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 5		
DIQMTQSPSLS LPVTPGEPAS ISCRSSQSLL HSNGYNYLDW YLQKPGQSPQ LLIYLGSNRA	60	
SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCMQALQTP WFGQGKVEI IKR	113	
SEQ ID NO: 6	moltype = AA length = 112	
FEATURE	Location/Qualifiers	
REGION	1..112	
	note = Synthetic Polypeptide	
source	1..112	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 6		
DIQMTQSPSLS LSVAPGEPAS ISCRSSQSLL HRNGHNYLDW YLQKPGQSPQ LLIYLGSNRA	60	
SGVPERFSGS GSGTDFTLRI SRVEAEDVGV YYCMQALQAR TFGQGKVEI KR	112	
SEQ ID NO: 7	moltype = AA length = 112	
FEATURE	Location/Qualifiers	
REGION	1..112	
	note = Synthetic Polypeptide	
source	1..112	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 7		
DIQMTQSPSLS LPVTPGEPAS ISCRSSQSLL HSNGYNYLDW YLQKPGQSPQ LLIYLGSNRA	60	
SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCMQALQTR TFGQGKVEI KR	112	
SEQ ID NO: 8	moltype = AA length = 113	
FEATURE	Location/Qualifiers	
REGION	1..113	
	note = Synthetic Polypeptide	
source	1..113	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 8		
DIQMTQSPSLS LPVTPGEPAS ISCRSSQSLL HSNGYNYLDW YLQKPGQSPQ IMIYLGSNRA	60	
SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCMQALQTP RTFGQGKVE IKR	113	
SEQ ID NO: 9	moltype = AA length = 471	
FEATURE	Location/Qualifiers	
REGION	1..471	
	note = Synthetic Polypeptide	
source	1..471	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 9		
MGWSCLLFL VATATGAHSE VQLLESGGGL VQPGGSLRLS CAASGFTFSH YIMMWVRQAP	60	
GIGKLEWVSGI YSSGGITVVA DSVKGRFTIS RDNSKNLTYL QMNSLRAEDT AVYYCAYRRI	120	
GVPRRDEFDI WGQGTMVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV KDYFFPEPVTV	180	
SWNSGALTSG VHTFPAPLQS SGGLYSSLSSV TVPSSSLGTQ TYICNVNHKP SNTKVDKRV	240	
PKSCDKTHTC PPCPAPELLG GPSVFLFPKK PKDTLMISRT PEVTCVVVDV SHEDPEVKFN	300	
WYVDGVEVHN AKTKPREEQY NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI	360	
SKAKGQPREP QVYTLPPSRE EMTKNQVSLSI CLVKGFYPSD IAVEWESNGQ PENNYKTPP	420	
VLDSDGSFFL YSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG K	471	
SEQ ID NO: 10	moltype = AA length = 232	

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FEATURE	Location/Qualifiers
REGION	1..232
note	= Synthetic Polypeptide
source	1..232
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 10	
MGWSCIILFL VATATGVHSD	IQMTQSPSTL SASVGDRVTI TCRASQSISS WLAWYQQKPG 60
KAPKLLIYKA STLESGVPSR	FSGSGSGTEF TLTISSLQPD DFATYYCQOY NTYWTFGQGT 120
KVEIKRTVAA PSVFIFPPSD	EQLKSGTAVS VCLLNNFYPR EAKVQWKVDN ALQSGNSQES 180
VTEQDSKDST YSLSSTLTLS	KADYEKHKVY ACEVTHQGLS SPVTKSFNRG EC 232
SEQ ID NO: 11	moltype = AA length = 731
FEATURE	Location/Qualifiers
REGION	1..731
note	= Synthetic Polypeptide
source	1..731
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 11	
MGWSCIILFL VATATGAHSE	VQLLESGGGL VQPAGSLRLS CAASGFTFSH YIMMWVRQAP 60
GKGLEWWSGI YSSGGITVYA	DSVKGRFTIS RDNSKNTLYL QMNSLRAEDT AVYYCAYRRI 120
GVPRRDEFDI WGQGTMVTVS	SASTKGPSVF PLAPSSKSTS GGTAALGCLV KDYFPEPVTV 180
SWNSGALTSG VHTFPAVLQS	SGLYSLSSVV TVPSSSLGTQ TYICCNVNHKP SNTKVDKRVE 240
PKSCDTHTCP PCPAPELLGG	PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW 300
YVDGVEVHNA KTKPREEQYN	STYRVVSVLT VLHQDWLNKG EYKCKVSNKA LPAPIEKTTIS 360
KAKGQPREPQ VYTLPSSREE	MTKNQVSLTC LVKGFYPSDI AVEWESENQGP ENNYKTPPPV 420
LSDDGSSFFLY SKLTVDKSRW	QQGNVFSCSV MHEALHNHYT QKSLSLSPGK SGGSSEVQLL 480
ESGGGLVQPG GSLRLSCAAS	GFTFSFYSMH WVRQAPGKGL EWVSRIVYPSG GVTKYADSVK 540
GRFTISRDNS KNTLYLQMNS	LRAEDTAVYY CTRQRYRGPK YYYYYMDWYGK GTTVTVSSGG 600
GGSGGGGSGG GGSGGGGSDI	QMTQPLSLP VTPGEPASIS CRSSQSLLHS NGNYLDWYL 660
QKPGQSPOLL IYLGSRASG	VDPDRFSGSGS GTDFTLKR VEAEDGVVYY CMQALQTPWT 720
FGQGTKVEIK R	731
SEQ ID NO: 12	moltype = AA length = 732
FEATURE	Location/Qualifiers
REGION	1..732
note	= Synthetic Polypeptide
source	1..732
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 12	
MGWSCIILFL VATATGAHSE	VQLLESGGGL VQPAGSLRLS CAASGFTFSH YIMMWVRQAP 60
GKGLEWWSGI YSSGGITVYA	DSVKGRFTIS RDNSKNTLYL QMNSLRAEDT AVYYCAYRRI 120
GVPRRDEFDI WGQGTMVTVS	SASTKGPSVF PLAPSSKSTS GGTAALGCLV KDYFPEPVTV 180
SWNSGALTSG VHTFPAVLQS	SGLYSLSSVV TVPSSSLGTQ TYICCNVNHKP SNTKVDKRVE 240
PKSCDTHTCP PCPAPELLGG	PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW 300
YVDGVEVHNA KTKPREEQYN	STYRVVSVLT VLHQDWLNKG EYKCKVSNKA LPAPIEKTTIS 360
KAKGQPREPQ VYTLPSSREE	MTKNQVSLTC LVKGFYPSDI AVEWESENQGP ENNYKTPPPV 420
LSDDGSSFFLY SKLTVDKSRW	QQGNVFSCSV MHEALHNHYT QKSLSLSPGK SGGSIDIQMT 480
QSPLSPLVPT GEPAISICRS	SQSLLLHSNGY NYLDWYLQKGP QSPQQLIYL GSNRASGVPD 540
RFSGSGSGTD FTLKISRVEA	EDVGVYYCMQ ALQTPWTFQG GTKVEIKRTG GGGGGGGSG 600
GGGGGGGGSE VOLLESGGGL	VQPAGSLRLS CAASGFTFSF YSMHWVRQAP GKGLEWVSRI 660
YPSGGVTKYA DSVKGRFTIS	RDNSKNTLYL QMNSLRAEDT AVYYCTRQRY RGPKYYYYMD 720
VWGKGTTVTV SS	732
SEQ ID NO: 13	moltype = AA length = 730
FEATURE	Location/Qualifiers
REGION	1..730
note	= Synthetic Polypeptide
source	1..730
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 13	
MGWSCIILFL VATATGAHSE	VQLLESGGGL VQPAGSLRLS CAASGFTFSH YIMMWVRQAP 60
GKGLEWWSGI YSSGGITVYA	DSVKGRFTIS RDNSKNTLYL QMNSLRAEDT AVYYCAYRRI 120
GVPRRDEFDI WGQGTMVTVS	SASTKGPSVF PLAPSSKSTS GGTAALGCLV KDYFPEPVTV 180
SWNSGALTSG VHTFPAVLQS	SGLYSLSSVV TVPSSSLGTQ TYICCNVNHKP SNTKVDKRVE 240
PKSCDTHTCP PCPAPELLGG	PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW 300
YVDGVEVHNA KTKPREEQYN	STYRVVSVLT VLHQDWLNKG EYKCKVSNKA LPAPIEKTTIS 360
KAKGQPREPQ VYTLPSSREE	MTKNQVSLTC LVKGFYPSDI AVEWESENQGP ENNYKTPPPV 420
LSDDGSSFFLY SKLTVDKSRW	QQGNVFSCSV MHEALHNHYT QKSLSLSPGK SGGSSEVQLL 480
ESGGGLVQPG GSLRLSCAAS	GFTFSGYIMA WVRQAPGKGL EWVSYIYPSG GITVYADSVK 540
GRFTISRDNS KNTLYLQMNS	LRAEDTAVYY CTRQRYRGPK YYYYYMDWYGK GTTVTVSSGG 600
GGGGGGGGSE GGSGGGGSDI	QMTQPLSLS VAPGEPASIS CRSSQSLLHR NGHNYLDWYL 660
QKPGQSPOLL IYLGSRASG	VPERFSGSGS GTDFTLISR VEAEDGVVYY CMQALQARTF 720

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GQGTKVEIKR

730

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SEQ ID NO: 14      moltype = AA length = 731
FEATURE          Location/Qualifiers
REGION           1..731
note = Synthetic Polypeptide
source            1..731
mol_type = protein
organism = synthetic construct

SEQUENCE: 14
MGWSCIILFL VATATGAHSE VQLLESGGGL VQPGGSLRLS CAASGFTFSH YIMMWVRQAP 60
GKGLEWWSGI YSSGGITVYA DSVKGRTFIS RDNSKNTLYL QMNSLRAEDT AVYYCAYRRI 120
GVPRRDEFDI WGQGTMVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV KDYFPEPVT 180
SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSLGTQ TYICCNVNHKP SNTKVDKRVE 240
PKSCDTHTCP PCPAPELLGG PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW 300
YVDGVEVHNA KTKPREEQYN STYRVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTI 360
KAKGQPREPQ VYTLPSSREE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTPPV 420
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK SGGSIDIQMT 480
QSPLSLSVAP GEPASISCRS SQSLLHSNGY NYLDWYLQKP GQSPQLLIYL GSRRASGVPE 540
RFSGSGSGTQ FTLRISRVEA EDVGVYYCMQ ALQARTFGQG TKVEIKRTGG GGSGGGGSGG 600
GGSGGGGSEV QLLESGGGLV QPGGSLRLSC AASGFTFSGY IMAWVRQAPG KGLEWVSYIY 660
PSGGITVYAD SVKGRTFISR DNSKNTLYLQ MNNSLRAEDTA VYYCTRQRYR GPKYYYYMDV 720
WGKGTTTVTS S                                         731

SEQ ID NO: 15      moltype = AA length = 730
FEATURE          Location/Qualifiers
REGION           1..730
note = Synthetic Polypeptide
source            1..730
mol_type = protein
organism = synthetic construct

SEQUENCE: 15
MGWSCIILFL VATATGAHSE VQLLESGGGL VQPGGSLRLS CAASGFTFSH YIMMWVRQAP 60
GKGLEWWSGI YSSGGITVYA DSVKGRTFIS RDNSKNTLYL QMNSLRAEDT AVYYCAYRRI 120
GVPRRDEFDI WGQGTMVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV KDYFPEPVT 180
SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSLGTQ TYICCNVNHKP SNTKVDKRVE 240
PKSCDTHTCP PCPAPELLGG PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW 300
YVDGVEVHNA KTKPREEQYN STYRVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTI 360
KAKGQPREPQ VYTLPSSREE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTPPV 420
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK SGGSEVQLL 480
ESGGGLVQPG GSLRLSCAAS GFTFSGYIMA WVRQAPGKGL EWVSYIYPNG GITVYADSVK 540
GRFTISRDNS KNTLYLQMNS LRAEDTAVYY CTRQRYRGPK YYYYMDWLGK GTTVTVSSGG 600
GGSGGGGSGG GGSGGGGSDI QMTOQPLSLP VTPGEPASIS CRSSQSLLHS NGYNYLDWYL 660
QKPGQSPQLL IYLGNSNRASG VPDRFSGSGS GTDFTLKISR VEAEDVGVYY CMQALQTRTF 720
GQGTKVEIKR                                         730

SEQ ID NO: 16      moltype = AA length = 731
FEATURE          Location/Qualifiers
REGION           1..731
note = Synthetic Polypeptide
source            1..731
mol_type = protein
organism = synthetic construct

SEQUENCE: 16
MGWSCIILFL VATATGAHSE VQLLESGGGL VQPGGSLRLS CAASGFTFSH YIMMWVRQAP 60
GKGLEWWSGI YSSGGITVYA DSVKGRTFIS RDNSKNTLYL QMNSLRAEDT AVYYCAYRRI 120
GVPRRDEFDI WGQGTMVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV KDYFPEPVT 180
SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSLGTQ TYICCNVNHKP SNTKVDKRVE 240
PKSCDTHTCP PCPAPELLGG PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW 300
YVDGVEVHNA KTKPREEQYN STYRVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTI 360
KAKGQPREPQ VYTLPSSREE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTPPV 420
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK SGGSIDIQMT 480
QSPLSLVPTP GEPASISCRS SQSLLHSNGY NYLDWYLQKP GQSPQLLIYL GSRRASGVPD 540
RFSGSGSGTQ FTLRISRVEA EDVGVYYCMQ ALQARTFGQG TKVEIKRTGG GGSGGGGSGG 600
GGSGGGGSEV QLLESGGGLV QPGGSLRLSC AASGFTFSGY IMAWVRQAPG KGLEWVSYIY 660
PSGGITVYAD SVKGRTFISR DNSKNTLYLQ MNNSLRAEDTA VYYCTRQRYR GPKYYYYMDV 720
WGKGTTTVTS S                                         731

SEQ ID NO: 17      moltype = AA length = 731
FEATURE          Location/Qualifiers
REGION           1..731
note = Synthetic Polypeptide
source            1..731
mol_type = protein
organism = synthetic construct

SEQUENCE: 17

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MGWSCIILFL VATATGAHSE	VQLLESGGGL VQPGGSLRLS	CAASGFTFSH YIMMWVRQAP	60
GKGLEWVSGI YSSGGITVYA	DSVKGRFTIS RDNSKNTLYL	QMNSLRAEDT AVYYCAYRRI	120
GVPRRDEFDI WGQGTMVTVS	SASTKGPSVF PLAPSSKSTS	GGTAALGCLV KDYFPEPVT	180
SWNSGALTSG VHTFPAVLQS	SGLYSLSSVV TVPSSSLGTQ	TYICCNVNHKP SNTKVDKRVE	240
PKSCDTHTCP PCPAPELLGG	PSVFLFPPKP KDTLMISRTP	EVTCVVVDVS HEDPEVKFNW	300
YVDGVEVHNA KTKPREEQYN	STYRVSVLT VLHQDWLNGK	EYKCKVSNKA LPAPIEKTTIS	360
KAKGQPREPQ VTTLPPSREE	MTKNQVSLTC LVKGFYPSDI	AVEWESNGQP ENNYKTPPV	420
LSDGSFFLY SKLTVDKSRW	QOGNVFSCSV MHEALHNHYT	QKSLSLSPGK SGGSSEVQOLL	480
ESGGGLVQPG GSLRLSCAAS	GFTFSGYIMA WVRQAPGKGL	EWVSYIYPSG GITVYADSVK	540
GRFTISRDN S KNTLYLQMNS	LRAEDTAVYY CTRQRYRGPK	YYYYMDVWGK GTTVTVSSGG	600
GGGGGGGGCG CGGGGGGSDI	QMTQSPLSLP VTPGEPASIS	CRSSQSLLHS NGNYNLDWYL	660
QKPGQSPQIM IYLGSRASG	VPDRFSGSGS GTDFTLKISR	VEAEVGVYY CMQALQTPRT	720
FGQGTKVEIK R			731

SEQ ID NO: 18	moltype = AA length = 732		
FEATURE	Location/Qualifiers		
REGION	1..732		
	note = Synthetic Polypeptide		
source	1..732		
	mol_type = protein		
	organism = synthetic construct		
SEQUENCE: 18			
MGWSCIILFL VATATGAHSE	VQLLESGGGL VQPGGSLRLS	CAASGFTFSH YIMMWVRQAP	60
GKGLEWVSGI YSSGGITVYA	DSVKGRFTIS RDNSKNTLYL	QMNSLRAEDT AVYYCAYRRI	120
GVPRRDEFDI WGQGTMVTVS	SASTKGPSVF PLAPSSKSTS	GGTAALGCLV KDYFPEPVT	180
SWNSGALTSG VHTFPAVLQS	SGLYSLSSVV TVPSSSLGTQ	TYICCNVNHKP SNTKVDKRVE	240
PKSCDTHTCP PCPAPELLGG	PSVFLFPPKP KDTLMISRTP	EVTCVVVDVS HEDPEVKFNW	300
YVDGVEVHNA KTKPREEQYN	STYRVSVLT VLHQDWLNGK	EYKCKVSNKA LPAPIEKTTIS	360
KAKGQPREPQ VTTLPPSREE	MTKNQVSLTC LVKGFYPSDI	AVEWESNGQP ENNYKTPPV	420
LSDGSFFLY SKLTVDKSRW	QOGNVFSCSV MHEALHNHYT	QKSLSLSPGK SGGSIDIQMT	480
QSPSLPVT P GEPASISCRS	SQSLHHNSGY NYLDWYLQKP	GQSPQIMIYL GSRRASGVPD	540
RFGSGSGSTD FTLKISRVEA	EDVGVYYCMQ ALQTPRTFGQ	GTKVEIKRTG GGGSGGGGSG	600
GGGGGGGGSE VQLLESGGGL	VQPGGSLRLS CAASGFTFSG	YIMAWVRQAP GKGLEWVSYI	660
YPSGGITVYA DSVKGRFTIS	RDNSKNTLYL QMNSLRAEDT	AVYYCTRQRY RGPKYYYYMD	720
VWGKGITVTV SS			732

SEQ ID NO: 19	moltype = AA length = 731		
FEATURE	Location/Qualifiers		
REGION	1..731		
	note = Synthetic Polypeptide		
source	1..731		
	mol_type = protein		
	organism = synthetic construct		
SEQUENCE: 19			
MGWSCIILFL VATATGAHSE	VQLLESGGGL VQPGGSLRLS	CAASGFTFSH YIMMWVRQAP	60
GKGLEWVSGI YSSGGITVYA	DSVKGRFTIS RDNSKNTLYL	QMNSLRAEDT AVYYCAYRRI	120
GVPRRDEFDI WGQGTMVTVS	SASTKGPSVF PLAPSSKSTS	GGTAALGCLV KDYFPEPVT	180
SWNSGALTSG VHTFPAVLQS	SGLYSLSSVV TVPSSSLGTQ	TYICCNVNHKP SNTKVDKRVE	240
PKSCDTHTCP PCPAPELLGG	PSVFLFPPKP KDTLMISRTP	EVTCVVVDVS HEDPEVKFNW	300
YVDGVEVHNA KTKPREEQYN	STYRVSVLT VLHQDWLNGK	EYKCKVSNKA LPAPIEKTTIS	360
KAKGQPREPQ VTTLPPSREE	MTKNQVSLTC LVKGFYPSDI	AVEWESNGQP ENNYKTPPV	420
LSDGSFFLY SKLTVDKSRW	QOGNVFSCSV MHEALHNHYT	QKSLSLSPGK SGGSSEVQOLL	480
ESGGGLVQPG GSLRLSCAAS	GFTFSGYIMA WVRQAPGKGL	EWVSYIYPSG GITVYADSVK	540
GRFTISRDN S KNTLYLQMNS	LRAEDTAVYY CTRQRYRGPK	YYYYMDVWGK GTTVTVSSGG	600
GGGGGGGGCG CGGGGGGSDI	QMTQSPLSLP VTPGEPASIS	CRSSQSLLHS NGNYNLDWYL	660
QKPGQSPQIM IYLGSRASG	VPDRFSGSGS GTDFTLKISR	VEAEVGVYY CMQALQTPWT	720
FGQGTKVEIK R			731

SEQ ID NO: 20	moltype = AA length = 732
FEATURE	Location/Qualifiers
REGION	1..732
	note = Synthetic Polypeptide
source	1..732
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 20	

MGWSCIILFL VATATGAHSE	VQLLESGGGL VQPGGSLRLS	CAASGFTFSH YIMMWVRQAP	60
GKGLEWVSGI YSSGGITVYA	DSVKGRFTIS RDNSKNTLYL	QMNSLRAEDT AVYYCAYRRI	120
GVPRRDEFDI WGQGTMVTVS	SASTKGPSVF PLAPSSKSTS	GGTAALGCLV KDYFPEPVT	180
SWNSGALTSG VHTFPAVLQS	SGLYSLSSVV TVPSSSLGTQ	TYICCNVNHKP SNTKVDKRVE	240
PKSCDTHTCP PCPAPELLGG	PSVFLFPPKP KDTLMISRTP	EVTCVVVDVS HEDPEVKFNW	300
YVDGVEVHNA KTKPREEQYN	STYRVSVLT VLHQDWLNGK	EYKCKVSNKA LPAPIEKTTIS	360
KAKGQPREPQ VTTLPPSREE	MTKNQVSLTC LVKGFYPSDI	AVEWESNGQP ENNYKTPPV	420
LSDGSFFLY SKLTVDKSRW	QOGNVFSCSV MHEALHNHYT	QKSLSLSPGK SGGSIDIQMT	480
QSPSLPVT P GEPASISCRS	SQSLHHNSGY NYLDWYLQKP	GQSPQIMIYL GSRRASGVPD	540
RFGSGSGSTD FTLKISRVEA	EDVGVYYCMQ ALQTPRTFGQ	GTKVEIKRTG GGGSGGGGSG	600

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GGGSAGGGSE VQLLESGGGL VQPGGSLRLS CAASGFTFSG YIMAWVRQAP GKGLEWVSYI	660	
YPSGGITVYA DSVKGRFTIS RDNSKNTLYL QMNSLRAEDT AVYYCTRQRY RGPKYYYYYMD	720	
VWGKGTTVTV SS	732	
SEQ ID NO: 21	moltype = AA length = 248	
FEATURE	Location/Qualifiers	
REGION	1..248	
	note = Synthetic Polypeptide	
source	1..248	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 21		
IVGGTNSSWG EWPWQVSLQV	KLTAQRHLCG GSLIGHQWVL TAAHCFDGLP LQDVWRIYSG	60
IILNLSDITKD TPFSOIKEII	IHQNYKVSEG NHDIALIKLQ APLNYTEFQK PISLPSKGDT	120
STIYTNCWVT GWGFSKEKGE	IQNILQKVNI PLVTNEECQK RYQDYKITQR MVCAGYKEGG	180
KDACKGDSGG PLVCKHNGMW	RLVGITSWGE GCARREQPGV YTAKVAEYMDW ILEKTQSSDG	240
KAQMOSPA		248
SEQ ID NO: 22	moltype = AA length = 5	
FEATURE	Location/Qualifiers	
REGION	1..5	
	note = Synthetic Polypeptide	
source	1..5	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 22		5
SGGGS		
SEQ ID NO: 23	moltype = AA length = 20	
FEATURE	Location/Qualifiers	
REGION	1..20	
	note = Synthetic Polypeptide	
source	1..20	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 23		20
GGGGSGGGGS GGGGSGGGGS		
SEQ ID NO: 24	moltype = DNA length = 3535	
FEATURE	Location/Qualifiers	
misc_feature	1..3535	
	note = Synthetic Polynucleotide	
source	1..3535	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 24		
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atccagatga cccagtcacc	ctccacccctg tcggcctctg tggggcacag agtgaccatc	120
acctgtcggg cctcccaagtc	catctccago tggctggcct ggtatcagca gaagccccgc	180
aaggccccca agctgtgtat	ctacaaggcc agcaccctgg aatccggcgt gcccctccaga	240
tttcccggtt ctggctccgg	cacccggatc accctgacca tcagctccct gcagcccgac	300
gacttcggcca ctactactg	ccagcgtac aacacctact ggaccttccg ccagggcacc	360
aagggtggaaa tcaagcggac	cgtggcgcgt cccctccgtg tcatctccc accctccgac	420
gagcagctga agtccggcac	cgcctccgtg gtctgcctgc tgaacaacct ctaccccgcc	480
gaggccaaagg tgcagtggaa	gggtggacaaac gcccgtcagc cccggcaactc ccaggaatcc	540
gtgaccgagc aggactggaa	ggacacggacc tactccctgt cctctacccctt gaccctgtcc	600
aaggccgact accgaaagca	caagggtgtac gcttgcgaag tgacccacca gggctgtcc	660
agccccgtga ccaagtccct	caacccgggc gagtgtgtat gaggcgcggc ttgcgtcga	720
gcatgcattt atggggggccca	atccggccccc tccccccatac gttactggcc	780
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gggggtctttt ccctctcgcc	aaaggaaatgc aagggtctgtt gaatgtctgt aaggaaggcag	960
ttcctcttggaa agcttttga	agacaaacaa cgtctgtacg gacccttgc aggcagccga	1020
accccccacc tggccacagg	tgcctctgtgg gccaaaagcc acgttatcaa gatacacctg	1080
caaaggccgc acaaaaaccag	tgcacatgtt tgagtggat agtgtggaa agagtcaaat	1140
ggctcttc aacgttattc	aacaaggggc tgaaggatgc ccagaaggta ccccatgtta	1200
tgggatctga tctggggctt	cgggtcgatg gctttacatg tgtttagtcg aggttaaaaa	1260
aacgtcttagg ccccccgaac	cacggggacg tggttttctt ttgaaaaaca cgatgataat	1320
atggccacaa ccatggatg	gtcttcgcattt atctgtttc tggtggccac agccacaggc	1380
gctcaactcg aggtgtcaatt	gtctggatcc ggccggaggac tggtcagcc tggcggtcc	1440
cttgagactgt ctgcggccgc	ctccggcttc accttctccc actacatcat gatgtgggt	1500
cgacaggcctt ctggcaaggg	gcttggatgg gtgtccggca tctactcc tcggccgatc	1560
accctgtacg cggactccgt	gaaggggccgg ttcacccatct ctccggacaa ctccaagaac	1620
accctgtacc tgcagatgaa	ctccctgcgg gccgaggaca cccggctgtta ctactgcgcc	1680
taccggcggaa tcggcgtgcc	cagacgggac gagttcgaca tctggggca gggcaccatg	1740
gtgacagtgtt cctccgcctc	caccaaggcc cccctctgtt tcccgctagc accctccagc	1800

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gtgttcagg	ctccggcct	gtacacgc	ctgcgtcg	tgaccgtgcc	ctccagtc	1980
ctggccaccc	agacctacat	ctgaacgtg	aaccacaac	cttccaaacac	caaagtggac	2040
aaggcggtgg	aacccaagtc	ctgacgacacc	cacacgtc	ccccctgccc	tgccccgtaa	2100
ctgctggccg	gacccagcgt	gttccgtgtc	cccccaaaac	ccaaggacac	cctgtatgatc	2160
tcccgaccc	ccgaagtgc	ctgegtgg	ttggacgtgt	cccacggaga	ccctgaagt	2220
aagttaatt	ggtacgtgg	ccgggtggaa	gtgcataac	ccaagacaa	gccccagag	2280
gaacagtaca	actccaccta	ccgggtgg	ttcggtgt	ccgtgtgt	ccaggactgg	2340
ctgaacggca	aagaatcaca	gtgacgggt	tccaaacaac	ccctgtgtc	ccccatcgaa	2400
aagacatca	ccaaaggccaa	gggcacgt	cgcgagcccc	agggtatcac	cctgccccct	2460
agccggaaag	agatgacca	gaaccagg	ttccctgac	gtctggtcaa	gggttctac	2520
ccctccgata	tcgcccgtg	atgggatcc	aacggcc	ccgagaacaa	ctacaagacc	2580
accccccctg	tgctggacag	cgacggctca	ttttccgt	actccaaat	gaccgtggac	2640
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aaccactaca	cccaaaatc	cctgtccctg	tcccccgg	agtctggccg	aggatccgaa	2760
gtcagtc	tgaaaagcgg	cgaggcc	gtgcacgt	gaggcagc	gagactgtct	2820
tgcgctcoca	gggggttcac	ttttagt	ttacagcat	actgggtcc	acaggctcca	2880
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cagatgaaca	gcctggggc	cgaggac	ccgtgtact	actgcaccc	gcagcggtac	3060
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ggcagcgtaca	tccatgtac	ccagggcc	ctgagcgt	ccgtgtac	ttggcgaccc	3240
ggcagcatca	gtcgacaa	cagecag	ctgtgcac	gcaacggct	caactactg	3300
gactgttac	tgcacaa	cgccggat	ccccatgt	tgatctact	gggcagcaac	3360
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aagatcgcc	gggtggaa	cgaggac	ggcgtgt	attgtatc	ggccctgca	3480
acccctgg	cccccggca	ggggacca	gtggaaat	agagatgaat	ctaga	3535

SEQ ID NO: 25	moltype = DNA	length = 3538				
FEATURE	Location/Qualifiers					
misc_feature	1..3538					
source	note = Synthetic Polynucleotide					
	1..3538					
	mol_type = other DNA					
	organism = synthetic construct					
SEQUENCE: 25						
atgggatgt	cctgcacat	cctgtttctg	gtggctacag	ccacaggcg	gcactccgac	60
atccagatga	cccaatccc	ctccaccc	tccgcctcg	ttggcgcac	agtgaccatc	120
acctgtcg	cctccacgt	catccca	tggctggct	ggtatc	gaagccccc	180
aaggccccca	agctgtgt	ctacaaggc	agcacc	ccgtgt	gccctccaga	240
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gacttcgcca	cataactact	ccagcgt	aacacca	ttccgt	ccagggcacc	360
aagggttcaa	tcaacgg	cgtggcg	ccctccgt	ttatctcc	accctccgac	420
gagcagctg	agtccggc	cgccctccgt	gtctgc	tgaacaac	ctaccccg	480
gaggccaa	tgacgtgg	ggtgacaa	ccctgt	ccggcaact	ccaggaatcc	540
gtgacccgg	aggacttca	ggacac	tactccgt	ctcttac	gaccctgt	600
aaggccact	ccggaaagca	caagggt	gtctgc	tgacccac	gggcgtgtc	660
agcccccgt	ccaatgtt	caacccgg	gagtgt	gaggcgc	ttcgctcg	720
gcatgtat	aggccggc	atcccccc	tccccc	ccccctaa	gttactggc	780
gaagccgtt	gaaataaggc	cggtgt	ttgtctata	tttcc	accatatgc	840
cgtcttttt	caatgtt	ggccgg	aaac	cttgcctgt	tttctgtac	900
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acccccccctg	tgctggacag	cgacggctca	ttcttctgt	actcaacgt	gaccgtggac	2640
aagtcccggt	ggcggcgggg	caacgtgtt	tctgtctcg	tgtgtacgaa	ggccctgtc	2700
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ggcaaggggc	tggaaatgggt	gttacatc	tacccacgt	ccggcatcac	cggtacgc	2940
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caagatca	gtctggggc	cgaggacacc	ggcggtact	actgcaccc	gcagggtac	3060
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ggcagcgtac	tccatgtac	ccagggcccc	ctgacccgtc	ccgtgacacc	ttggcgacc	3240
gccagcatca	gttacgtac	cagccagago	ctgtgtcaca	gcaacggct	caactac	3300
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agagccacgc	gggtggccg	cagatcgt	ggcagccgg	ccggcacca	tttacccctg	3420
aagatcagcc	gggtggaa	cgaggacgt	ggcggtact	attgtatc	ggccctgtc	3480
accccttgc	gttacgtgg	gggcacca	gggttacatc	agagatgt	ctaga	3535

SEQ ID NO: 33 moltype = DNA length = 3538
 FEATURE Location/Qualifiers
 misc_feature 1..3538
 note = Synthetic Polynucleotide
 source 1..3538
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 33
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 acctgtcgcc ccccccgtc catctccatc tggctggctt ggtatcaca gaagcccgcc 180
 aaggccccca agctgtgtat ctacaaggcc agcaccctgg aatccggcg gcccctccaga 240
 ttctccggct ctggctccgg cacccggatc accctgttca tcagctccct gcagcccgac 300
 gacttcgcacca ctactactg ccagcgatc aacacatcttccgg ccagggcacc 360
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 gagcagctga agtccggac cgcctccgtg gtctgttgc tgaacaacctt ctaccccg 480
 gagggccaaagg tgcagtgaa ggtggacacaat cccctgttgc cccggcaatcc ccaggaaatcc 540
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 aaggccgactt accggaaatca acgggtgtac gtgtccggaa tgacccttccca gggctgtcc 660
 agccccgtga ccaagtctt caacccgggc gagtgttgc gaggcgccg ttcgtgtcga 720
 gcatgcattt atggggccca attccggcccc tctccccc ccccccataac gttactggcc 780
 gaaggccgtt ggaataaggcc cgggtgttgcgt ttgttctat gttatccatccatattgc 840
 cgtctttttgg ccatgttgcgg gcccggccctgtt ctccgttgc accatccatc 900
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 accccccacc tggcgacagg tgcctctgcg gccaaaacgc acgtgtataa gatacact 1080
 caaaggccgc acaaccccag tggccacgttg tgagttggat agtttgtggaa agagtcaat 1140
 ggctcttc aacgttattc aacaaggggc tgaaggatgc ccagaaggta ccccttgc 1200
 tggatctga tctggggctt cggtgcatg gctttacatg tggtttgcgtt aggttaaaaa 1260
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 ctgagactgtt ctggccgcgc ctccggctt accttctccc actacatcat gatgtgggt 1500
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taccggcga	tcggcgatgcc	cagacgggac	gagttcgaca	tctggggca	gggcacccatg	1740					
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aagtccac	ccggcgac	cgctgtctg	ggctgcctcg	tcaaggacta	cttccccgag	1860					
cccggtacg	tgtccggaa	ctctggcgcc	ctgaccacg	gagtgcatac	cttccctg	cc	1920				
gtgtccagt	ctccggcct	gtacacg	ctgtctgt	tgaccgt	g	ctccag	1980				
ctggccaccc	agacccat	ctgaac	tgta	ccat	cc	caaa	2040				
aaggcggtgg	aaccaagtc	ctg	cgacacc	cacac	cttgc	ccc	2100				
ctgtgtggcg	gacccagcgt	gtt	ctgtgt	ccccaa	ccaagg	acac	2160				
tccgggaccc	ccgaa	gtac	ctgtgtgt	gtggac	gagga	ccctga	2220				
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gaacagtaca	actccacta	ccgggtgg	tccgtgt	ccgtgt	gca	ccaggact	gg	2340			
ctgaacgcga	aagat	acgg	tccaa	ccat	cc	ccat	cgaa	2400			
aagaccatca	gcaaggccaa	gggc	ccgcgt	cg	gaccc	cc	agg	gtac	2460		
agccggaa	agat	gacca	gaa	ccat	cc	ctgtgt	cc	gggttctac	2520		
ccctccgata	tcg	ccgtg	gta	atggag	gtcc	aa	cgag	acaa	ctacaagacc	2580	
accccccctg	tg	ctgtgg	acag	cgac	gtc	t	tttct	ctgt	actccaa	gac	2640
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aaccactaca	ccca	aa	gtt	cc	cc	cc	ccat	cg	at	cc	2760
atccagatga	ccc	aa	gtt	cc	cc	cc	ccat	cg	at	cc	2820
agotgcagaa	g	aa	gtt	cc	cc	cc	ccat	cg	at	cc	2880
ctgcaga	ccgg	cc	gtt	cc	cc	cc	ccat	cg	at	cc	2940
ggcg	ccgc	cc	gtt	cc	cc	cc	ccat	cg	at	cc	3000
cggtcgaa	ccg	gg	gtt	cc	cc	cc	ccat	cg	at	cc	3060
ac	ttt	cc	gtt	cc	cc	cc	ccat	cg	at	cc	3120
gttggaa	gg	gg	gtt	cc	cc	cc	ccat	cg	at	cc	3180
ggggcgg	gg	gg	gtt	cc	cc	cc	ccat	cg	at	cc	3240
ac	ttt	cc	gtt	cc	cc	cc	ccat	cg	at	cc	3300
gttgcctaca	ttt	cc	gtt	cc	cc	cc	ccat	cg	at	cc	3360
tttacccat	cc	cc	gtt	cc	cc	cc	ccat	cg	at	cc	3420
ggcagg	cc	cc	gtt	cc	cc	cc	ccat	cg	at	cc	3480
tactatcg	ac	gtt	gggg	cc	cc	cc	ccat	cg	at	cc	3538

SEQ ID NO: 34 moltype = AA length = 16
 FEATURE Location/Qualifiers
 REGION 1..16
 source note = Synthetic Polypeptide
 1..16
 mol_type = protein
 organism = synthetic construct

SEQUENCE: 34 RSSQSLLHSN GNYLD 16

SEQ ID NO: 35 moltype = AA length = 16
 FEATURE Location/Qualifiers
 REGION 1..16
 source note = Synthetic Polypeptide
 1..16
 mol_type = protein
 organism = synthetic construct

SEQUENCE: 35 RSSQSLLHNR GHNYLD 16

SEQ ID NO: 36 moltype = AA length = 7
 FEATURE Location/Qualifiers
 REGION 1..7
 source note = Synthetic Polypeptide
 1..7
 mol_type = protein
 organism = synthetic construct

SEQUENCE: 36 LGSNRAS 7

SEQ ID NO: 37 moltype = AA length = 9
 FEATURE Location/Qualifiers
 REGION 1..9
 source note = Synthetic Polypeptide
 1..9
 mol_type = protein
 organism = synthetic construct

SEQUENCE: 37 MQALQTPWT 9

SEQ ID NO: 38 moltype = AA length = 8
 FEATURE Location/Qualifiers

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REGION	1..8	
source	note = Synthetic Polypeptide	
	1..8	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 38		
MQALQART		8
SEQ ID NO: 39	moltype = AA length = 8	
FEATURE	Location/Qualifiers	
REGION	1..8	
source	note = Synthetic Polypeptide	
	1..8	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 39		
MQALQTRT		8
SEQ ID NO: 40	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
REGION	1..9	
source	note = Synthetic Polypeptide	
	1..9	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 40		
MQALQTPRT		9
SEQ ID NO: 41	moltype = AA length = 5	
FEATURE	Location/Qualifiers	
REGION	1..5	
source	note = Synthetic Polypeptide	
	1..5	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 41		
GYIMA		5
SEQ ID NO: 42	moltype = AA length = 5	
FEATURE	Location/Qualifiers	
REGION	1..5	
source	note = Synthetic Polypeptide	
	1..5	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 42		
FYSMH		5
SEQ ID NO: 43	moltype = AA length = 17	
FEATURE	Location/Qualifiers	
REGION	1..17	
source	note = Synthetic Polypeptide	
	1..17	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 43		
YIYPSGGITV YADSVKG		17
SEQ ID NO: 44	moltype = AA length = 17	
FEATURE	Location/Qualifiers	
REGION	1..17	
source	note = Synthetic Polypeptide	
	1..17	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 44		
RIYPSGGVTK YADSVKG		17
SEQ ID NO: 45	moltype = AA length = 14	
FEATURE	Location/Qualifiers	
REGION	1..14	
source	note = Synthetic Polypeptide	
	1..14	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 45		

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QRYRGPKYYY YMDV	14
SEQ ID NO: 46	moltype = AA length = 213
FEATURE	Location/Qualifiers
REGION	1..213
	note = Synthetic Polypeptide
source	1..213
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 46	
DIQMTQSPST LSASVGDRVT ITCRASQISI SWLAWYQQKP GKAPKLLIYK ASTLESGVPS	60
RFSFGSGSGTE FTLTISLQP DDFATYYCQQ YNTYWTFQCGQ TKVEIKRTVA APSVIFPPS	120
DEQLKSGTAS VVCLLNNFYP REAKVQWKVD NALQSGNSQE SVTEQDSKDS TYSLSSTLTL	180
SKADYEKHVK YACEVTHQGL SSPVTKSFNR GEC	213
SEQ ID NO: 47	moltype = AA length = 713
FEATURE	Location/Qualifiers
REGION	1..713
	note = Synthetic Polypeptide
source	1..713
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 47	
EVOLLESGGG LVQPGGSSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY	60
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV	120
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTPAVLQ	180
SSGLYSLSSV VTVPSLSSGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL	240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDEPEVVF NWYVDGVEVH NAKTKPREEQ	300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR	360
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTPV VLSDSDGSFF LYSKLTVDKS	420
RWQQGNVFS SVMHEALHNH YTQKSLSLSP GKSGGGSEVQ LLESGGGLVQ PGGSLRLSCA	480
ASGFTFSWVY MHWRQAPGK CLEWVSSIYIP SGKKTRYADS VKGRFTISRD NSKNLTYLQM	540
NSLRAEDTAV YYCARQRYRG PKYYYYYMDW GQGTTVTVS GGGGSGGGGS GGGGSGGGGS	600
DIVMTQSPLS LPVTPGEPAS ISCRSSQSLL HSNGYNYLDW YLQKPGQSPQ LLIYLGSNRA	660
SGVPDRFSGS GSGTDFTLKI SRVSEADEVGV YYCMQALQTP WTFGCGTKVE IKR	713
SEQ ID NO: 48	moltype = AA length = 713
FEATURE	Location/Qualifiers
REGION	1..713
	note = Synthetic Polypeptide
source	1..713
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 48	
EVOLLESGGG LVQPGGSSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY	60
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV	120
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTPAVLQ	180
SSGLYSLSSV VTVPSLSSGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL	240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDEPEVVF NWYVDGVEVH NAKTKPREEQ	300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR	360
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTPV VLSDSDGSFF LYSKLTVDKS	420
RWQQGNVFS SVMHEALHNH YTQKSLSLSP GKSGGGSEVQ LLESGGGLVQ PGGSLRLSCA	480
ASGFTFSWVY MHWRQAPGK CLEWVSSIYIP SGKKTRYADS VKGRFTISRD NSKNLTYLQM	540
NSLRAEDTAV YYCARQRYRG PKYYYYYMDW GQGTTVTVS GGGGSGGGGS GGGGSGGGGS	600
DIVMTQSPLS LPVTPGEPAS ISCRSSQSLL HSNGYNYLDW YLQKPGQSPQ LLIYLGSNRA	660
SGVPDRFSGS GSGTDFTLKI SRVSEADEVGV YYCMQALQTP WTFGCGTKVE IKR	713
SEQ ID NO: 49	moltype = AA length = 713
FEATURE	Location/Qualifiers
REGION	1..713
	note = Synthetic Polypeptide
source	1..713
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 49	
EVOLLESGGG LVQPGGSSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY	60
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV	120
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTPAVLQ	180
SSGLYSLSSV VTVPSLSSGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL	240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDEPEVVF NWYVDGVEVH NAKTKPREEQ	300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR	360
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTPV VLSDSDGSFF LYSKLTVDKS	420
RWQQGNVFS SVMHEALHNH YTQKSLSLSP GKSGGGSEVQ LLESGGGLVQ PGGSLRLSCA	480
ASGFTFSWVY MHWRQAPGK CLEWVSSIYIP SGKKTRYADS VKGRFTISRD NSKNLTYLQM	540
NSLRAEDTAV YYCARQRYRG PKYYYYYMDW GQGTTVTVS GGGGSGGGGS GGGGSGGGGS	600
DIVMTQSPLS LPVTPGEPAS ISCRSSQSLL HSNGYNYLDW YLQKPGQSPQ LLIYLGSNRA	660

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SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCMQALQTP WTFGCGTKVE IKR	713
SEQ ID NO: 50	
FEATURE	moltype = AA length = 713
REGION	Location/Qualifiers
source	1..713 note = Synthetic Polypeptide 1..713 mol_type = protein organism = synthetic construct
SEQUENCE: 50	
EVQLLESGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60	
ADSVKGRFTI SRDNSKNTLY LQMNLSRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVT 120	
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPABLQ 180	
SSGLYSLSSV VTVPSSSLGT QTYICVNHHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240	
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDEPVKF NWYVDGVEVH NAKTKPREEQ 300	
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR 360	
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS 420	
RWQQGNVFSC SVMHEALHHN YTQKSLSLSP GKSGGGSEVQ LLESGGGLVQ PGGSRLSQA 480	
ASGFTFSHYV MHWRQRQAPGK CLEWVSSIYP SGGLTKYADS VKGRFTISRD NSKNTLYLQM 540	
NSLRAEDTAV YYCARQRYRG PKYYYYMDWV GQGTTVTVSS GGGGSGGGGS GGGGSGGGGS 600	
DIVMTQSPLS LPVTPGE PAS ISCRSSQSLL HSNGYNYLDW YLQKPGQSPQ LLIYLGSNRA 660	
SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCMQALQTP WTFGCGTKVE IKR	713
SEQ ID NO: 51	
FEATURE	moltype = AA length = 713
REGION	Location/Qualifiers
source	1..713 note = Synthetic Polypeptide 1..713 mol_type = protein organism = synthetic construct
SEQUENCE: 51	
EVQLLESGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60	
ADSVKGRFTI SRDNSKNTLY LQMNLSRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVT 120	
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPABLQ 180	
SSGLYSLSSV VTVPSSSLGT QTYICVNHHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240	
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDEPVKF NWYVDGVEVH NAKTKPREEQ 300	
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR 360	
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS 420	
RWQQGNVFSC SVMHEALHHN YTQKSLSLSP GKSGGGSEVQ LLESGGGLVQ PGGSRLSQA 480	
ASGFTFSHYV MWVWRQRQAPGK CLEWVSSIYP SGGLTKYADS VKGRFTISRD NSKNTLYLQM 540	
NSLRAEDTAV YYCARQRYRG PKYYYYMDWV GKGTGTTVSS GGGGSGGGGS GGGGSGGGGS 600	
DIVMTQSPLS LPVTPGE PAS ISCRSSQSLL HSNGYNYLDW YLQKPGQSPQ LLIYLGSNRA 660	
SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCMQALQTP WTFGCGTKVE IKR	713
SEQ ID NO: 52	
FEATURE	moltype = AA length = 714
REGION	Location/Qualifiers
source	1..714 note = Synthetic Polypeptide 1..714 mol_type = protein organism = synthetic construct
SEQUENCE: 52	
EVOLLESGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60	
ADSVKGRFTI SRDNSKNTLY LQMNLSRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVT 120	
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPABLQ 180	
SSGLYSLSSV VTVPSSSLGT QTYICVNHHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240	
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDEPVKF NWYVDGVEVH NAKTKPREEQ 300	
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR 360	
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS 420	
RWQQGNVFSC SVMHEALHHN YTQKSLSLSP GKSGGGSDIQ MTQSPSLPV TPGEIASISC 480	
RSSQSLLHSN GYNYLWDWLYQ KPGQSPQLLI YLGSNRASGV PDRFGSGGSG TDFTLKISR 540	
EAEDVGVYYC MQALQTPWTF GQGTTKVEIKR TGGGGSGGGG SGGGGSGGGG SEVQLLESGG 600	
GLVQPGGSLR LSCAASGFTF SRYIMMWVRQ APGKGLEWS RIYPSGGYTR YADSVKGRFT 660	
ISRDNSKNTL YLQMNLSRAE DTAVYYCTRQ RYRGPKYYY MDVWGKGTTV TVSS	714
SEQ ID NO: 53	
FEATURE	moltype = AA length = 713
REGION	Location/Qualifiers
source	1..713 note = Synthetic Polypeptide 1..713 mol_type = protein organism = synthetic construct
SEQUENCE: 53	
EVQLLESGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60	
ADSVKGRFTI SRDNSKNTLY LQMNLSRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVT 120	
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPABLQ 180	

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SSGLYSLSSV	VTVPSLSSGT	QTYICNVNHK	PSNTKVDKRV	EPKSCDKTHT	CPPCPAPELL	240
GGSVFLFPP	KPKDTLMISR	TPEVTCVVVD	VSHDPEVKF	NWYVDGVEVH	NAKTKPREEQ	300
YNSTYRVVSV	LTVLHQDWLN	GKEYCKVSN	KALPAPIEKT	ISKAKQPRE	PQVYTLPPSR	360
EEMTKNQVSL	TCLVKGFYPS	DIAVEWESNG	QPENNYKTPP	PVLSDSGSFF	LYSKLTVDKS	420
RWQGQNVFSC	SVMHEALHNH	YTQKSLSLSP	GKSGGGSEVQ	LLESGGGLVQ	PGGSLRLSCA	480
ASGFTFSFYH	MHWVRQAPGK	GLEWWSRIVP	SGGMTRADS	VKGRTFISRD	NSKNLTYLQM	540
NSLRAEDTAV	YYCTRQRYRG	PKYYYYMDW	GKGTTVTVSS	GGGGSGGGGS	GGGGSGGGGS	600
DIQMTQSPSLS	LPVTPGEPAS	ISCRSSQSLL	HSNGYNYLDW	YLQKPGQSPQ	LLIYLGSNRA	660
SGVPDRFSGS	GGGTDFTLKI	SRVEAEDGVG	YYCMQALQTP	WTFGQGTKVE	IKR	713

SEQ ID NO: 54	moltype = AA length = 714				
FEATURE	Location/Qualifiers				
REGION	1..714				
note = Synthetic Polypeptide					
source	1..714				
mol_type = protein					
organism = synthetic construct					
SEQUENCE: 54					
EVQLLESGGG LVQPGGSSLRL	SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY	60			
ADSVKGRFTI SRDNSKNTLY	LQMNLSRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV	120			
SSASTKGPSV FPLAPSSKST	SGGTAALGCL VKDYFPEPV	T VSWNSGALT	GVHTFP	PAVLQ	180
SSGLYSLSSV VTVPSLSSGT	QTYICNVNHK PSNTKVDKRV	EPKSCDKTHT	CPPCPAPELL	240	
GGSVFLFPP KPKDTLMISR	TPEVTCVVVD	VSHDPEVKF	NWYVDGVEVH	NAKTKPREEQ	300
YNSTYRVVSV LTVLHQDWLN	GKEYCKVSN	KALPAPIEKT	ISKAKQPRE	PQVYTLPPSR	360
EEMTKNQVSL TCLVKGFYPS	DIAVEWESNG	QPENNYKTPP	PVLSDSGSFF	LYSKLTVDKS	420
RWQGQNVFSC SVMHEALHNH	YTQKSLSLSP	GKSGGGSDIQ	MTQSPLSLPV	TPGEPASISC	480
RSSQSLHSN GYNYLDWYQ	KPGQSPQLLI	YLGSNRASGV	PDRFSGSGSG	TDFTLKISR	540
EAEDVGVYYC MQALQTPWTF	GQGKVEIKR	TGGGGSGGGG	GGGGSGGGG	SEVQLLES	600
GLVQPGGSSLR LSCAASGFTF	SFYIMHWVRQ	APGKGLEWVS	RIVPSGGMTR	YADSVKGRFT	660
ISRDNSKNTL YLQMNLSRAE	DTAVYYCTRQ	RYRGPKYYYY	MDVWGKGT	TV	713

SEQ ID NO: 55	moltype = AA length = 713					
FEATURE	Location/Qualifiers					
REGION	1..713					
note = Synthetic Polypeptide						
source	1..713					
mol_type = protein						
organism = synthetic construct						
SEQUENCE: 55						
EVQLLESGGG LVQPGGSSLRL	SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY	60				
ADSVKGRFTI SRDNSKNTLY	LQMNLSRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV	120				
SSASTKGPSV FPLAPSSKST	SGGTAALGCL VKDYFPEPV	T VSWNSGALT	GVHTFP	PAVLQ	180	
SSGLYSLSSV VTVPSLSSGT	QTYICNVNHK PSNTKVDKRV	EPKSCDKTHT	CPPCPAPELL	240		
GGSVFLFPP KPKDTLMISR	TPEVTCVVVD	VSHDPEVKF	NWYVDGVEVH	NAKTKPREEQ	300	
YNSTYRVVSV LTVLHQDWLN	GKEYCKVSN	KALPAPIEKT	ISKAKQPRE	PQVYTLPPSR	360	
EEMTKNQVSL TCLVKGFYPS	DIAVEWESNG	QPENNYKTPP	PVLSDSGSFF	LYSKLTVDKS	420	
RWQGQNVFSC SVMHEALHNH	YTQKSLSLSP	GKSGGGSEVQ	LLESGGGLVQ	PGGSLRLSCA	480	
ASGFTFSFYI MGWVRQAPGK	GLEWWSRIVP	SGGATQYADS	VKGRTFISRD	NSKNLTYLQM	540	
NSLRAEDTAV YYCTRQRYRG	PKYYYYMDW	GKGTTVTVSS	GGGGSGGGGS	GGGGSGGGGS	600	
DIQMTQSPSLS	LPVTPGEPAS	ISCRSSQSLL	HSNGYNYLDW	YLQKPGQSPQ	LLIYLGSNRA	660
SGVPDRFSGS GGGTDFTLKI	SRVEAEDGVG	YYCMQALQTP	WTFGQGTKVE	IKR	713	

SEQ ID NO: 56	moltype = AA length = 714				
FEATURE	Location/Qualifiers				
REGION	1..714				
note = Synthetic Polypeptide					
source	1..714				
mol_type = protein					
organism = synthetic construct					
SEQUENCE: 56					
EVQLLESGGG LVQPGGSSLRL	SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY	60			
ADSVKGRFTI SRDNSKNTLY	LQMNLSRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV	120			
SSASTKGPSV FPLAPSSKST	SGGTAALGCL VKDYFPEPV	T VSWNSGALT	GVHTFP	PAVLQ	180
SSGLYSLSSV VTVPSLSSGT	QTYICNVNHK PSNTKVDKRV	EPKSCDKTHT	CPPCPAPELL	240	
GGSVFLFPP KPKDTLMISR	TPEVTCVVVD	VSHDPEVKF	NWYVDGVEVH	NAKTKPREEQ	300
YNSTYRVVSV LTVLHQDWLN	GKEYCKVSN	KALPAPIEKT	ISKAKQPRE	PQVYTLPPSR	360
EEMTKNQVSL TCLVKGFYPS	DIAVEWESNG	QPENNYKTPP	PVLSDSGSFF	LYSKLTVDKS	420
RWQGQNVFSC SVMHEALHNH	YTQKSLSLSP	GKSGGGSDIQ	MTQSPLSLPV	TPGEPASISC	480
RSSQSLHSN GYNYLDWYQ	KPGQSPQLLI	YLGSNRASGV	PDRFSGSGSG	TDFTLKISR	540
EAEDVGVYYC MQALQTPWTF	GQGKVEIKR	TGGGGSGGGG	GGGGSGGGG	SEVQLLES	600
GLVQPGGSSLR LSCAASGFTF	SFYIMHWVRQ	APGKGLEWVS	RIVPSGGATQ	YADSVKGRFT	660
ISRDNSKNTL YLQMNLSRAE	DTAVYYCTRQ	RYRGPKYYYY	MDVWGKGT	TV	714

SEQ ID NO: 57	moltype = AA length = 713
FEATURE	Location/Qualifiers
REGION	1..713

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source          note = Synthetic Polypeptide
                1..713
                mol_type = protein
                organism = synthetic construct

SEQUENCE: 57
EVQVLLESGGG LVQPGGSSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60
ADSVKGRFTI SRDNSKNTLY LQMNLSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ 180
SSGLYSLSSV VTPVSSSLGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYCKVSN KALPAPIEKT ISKAKQPRE PQVYTLPPSR 360
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS 420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKSGGGSEVQ LLESGGGLVQ PGGSLRLSCA 480
ASGFTFSGYI MAWVRQAPGK GLEWVSYIYP SGHTKYADS VKGRFTISRD NSKNTLYLQM 540
NSLRAEDTAV YYCTRQRYRG PKYVYMDWV GKGTTVTVSS GGGGSGGGGS GGGGSGGGGS 600
DIQMTQSPLS LPVTPGE PAS ISCRSSQSLL HSNGNYLDW YLQKPGQSPQ LLIYLGSNRA 660
SGVPDRFSGS GSGTDFTLKI SRVEAEDIGV YYCMQGRHRP YTFGQGTRLE IKR 713

SEQ ID NO: 58      moltype = AA length = 714
FEATURE          Location/Qualifiers
REGION           1..714
source          note = Synthetic Polypeptide
                1..714
                mol_type = protein
                organism = synthetic construct

SEQUENCE: 58
EVQVLLESGGG LVQPGGSSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60
ADSVKGRFTI SRDNSKNTLY LQMNLSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ 180
SSGLYSLSSV VTPVSSSLGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYCKVSN KALPAPIEKT ISKAKQPRE PQVYTLPPSR 360
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS 420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKSGGGSDIQ MTQSPSLSPV TPGEPASISC 480
RSSQSLLHSN PDKDQLDWYLQ KPGQSPQLI YLGSNRASGV PDRFSGSGSG TDFTLKIISRV 540
EABDIGVY MCGRHRPYTF GQGTRLEIKR TGGGGSGGGG SGGGGSGGG SEVQLLESQG 600
GLVQPGGSLR LSCAASGFTF SGYIMAWVRQ APGKGLEWVS YIYPSSGGITV YADSVKGRFT 660
ISRDNSKNTL YLQMNLSLRAE DTAVYYCTRQ RYRGPKYYYY MDVWGKTTV TVSS 714

SEQ ID NO: 59      moltype = AA length = 713
FEATURE          Location/Qualifiers
REGION           1..713
source          note = Synthetic Polypeptide
                1..713
                mol_type = protein
                organism = synthetic construct

SEQUENCE: 59
EVQVLLESGGG LVQPGGSSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60
ADSVKGRFTI SRDNSKNTLY LQMNLSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ 180
SSGLYSLSSV VTPVSSSLGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYCKVSN KALPAPIEKT ISKAKQPRE PQVYTLPPSR 360
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS 420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKSGGGSEVQ LLESGGGLVQ PGGSLRLSCA 480
ASGFTFSGYI MQWVRQAPGK GLEWVSYIYP SGHTKYADS VKGRFTISRD NSKNTLYLQM 540
NSLRAEDTAV YYCTRQRYRG PKYVYMDWV GKGTTVTVSS GGGGSGGGGS GGGGSGGGGS 600
DIQMTQSPLS LPVTPGE PAS ISCRSSQSLL HSNGNYLDW YLQKPGQSPQ LLIYLGSNRA 660
SGVPDRFSGS GSGTDFTLKI SRVEAEDIGV YYCMQALQTP WTFGQGTRLE IKR 713

SEQ ID NO: 60      moltype = AA length = 714
FEATURE          Location/Qualifiers
REGION           1..714
source          note = Synthetic Polypeptide
                1..714
                mol_type = protein
                organism = synthetic construct

SEQUENCE: 60
EVQVLLESGGG LVQPGGSSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60
ADSVKGRFTI SRDNSKNTLY LQMNLSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ 180
SSGLYSLSSV VTPVSSSLGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYCKVSN KALPAPIEKT ISKAKQPRE PQVYTLPPSR 360
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS 420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKSGGGSDIQ MTQSPSLSPV TPGEPASISC 480

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SEQ ID NO: 61	moltype = AA length = 713
FEATURE	Location/Qualifiers
REGION	1..713
	note = Synthetic Polypeptide
source	1..713
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 61	
EVOLLESGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60	
ADSVKGRFTI SRDNSKNTLY LQMNLSRAED TAVYYCAYRIG VGPVRRDEFD IWGQGTMVT 120	
SSASTKGPSV FPLAPSSKST SGTTAALGCL VKDYFPEPVTV SWNSGALTGVHFTPAVLQ 180	
SSGLYSLSSV VTVPSSSLGT QTYICVNHHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240	
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVFKF NWYVDGVEVH NAKTKPREEQ 300	
YNSTYRVVSV LTVLHQDWLN GKEYCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR 360	
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTPPVLDSDGSFF LYSKLTVDKS 420	
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKSGGGSEVQ LLESGGGLVQ PGGSRLS 480	
ASGFTFSMYT MNWVRQAPGK GLEWVSRQAD SGGKTLYADS VKGRFTISRD NSKNTLYLQM 540	
NSLRAEDTAV YYCTRQRYRG PKYVYMDWV GKGTGTVTVSS GGGGSGGGGS GGGGSGGGGS 600	
DIQMTQSPSLP LPVTPGE PAS ISCRSSQSLL HSNQYNYLDW YLQKPGQSPQ LLIYLGSNRA 660	
SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCMQALQTP WTFGQGKVE IKR 713	
SEQ ID NO: 62	moltype = AA length = 714
FEATURE	Location/Qualifiers
REGION	1..714
	note = Synthetic Polypeptide
source	1..714
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 62	
EVOLLESGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60	
ADSVKGRFTI SRDNSKNTLY LQMNLSRAED TAVYYCAYRIG VGPVRRDEFD IWGQGTMVT 120	
SSASTKGPSV FPLAPSSKST SGTTAALGCL VKDYFPEPVTV SWNSGALTGVHFTPAVLQ 180	
SSGLYSLSSV VTVPSSSLGT QTYICVNHHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240	
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVFKF NWYVDGVEVH NAKTKPREEQ 300	
YNSTYRVVSV LTVLHQDWLN GKEYCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR 360	
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTPPVLDSDGSFF LYSKLTVDKS 420	
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKSGGGSDIQ MTQSPSLSPV TPGEPASISC 480	
RSSQSLHSN GYNYLWYLO KPGQSPQLI YLGSNRASGV PDRFSGSGSG TDFTLKISRV 540	
EAEDVGVYYC MQLQTPWTF GQGKTVKEIKR TGGGGSGGGG SEVQLLES 600	
GLVQPGGSLR LSCAASGFTS SMYTMMWVRQ APGKGLEWVS RIYPGKGTLY YADSVKGRFT 660	
ISRDNSKNTL YLQMNLSRAE DTAVYYCTRQ RYRGPKYYYY MDVWGKTTV TVSS 714	
SEQ ID NO: 63	moltype = AA length = 713
FEATURE	Location/Qualifiers
REGION	1..713
	note = Synthetic Polypeptide
source	1..713
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 63	
EVOLLESGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60	
ADSVKGRFTI SRDNSKNTLY LQMNLSRAED TAVYYCAYRIG VGPVRRDEFD IWGQGTMVT 120	
SSASTKGPSV FPLAPSSKST SGTTAALGCL VKDYFPEPVTV SWNSGALTGVHFTPAVLQ 180	
SSGLYSLSSV VTVPSSSLGT QTYICVNHHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240	
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVFKF NWYVDGVEVH NAKTKPREEQ 300	
YNSTYRVVSV LTVLHQDWLN GKEYCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR 360	
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTPPVLDSDGSFF LYSKLTVDKS 420	
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKSGGGSEVQ LLESGGGLVQ PGGSRLS 480	
ASGFTFSRYV MHWVRQAPGK GLEWVSSIWP SGGMTKYADS VKGRFTISRD NSKNTLYLQM 540	
NSLRAEDTAV YYCTRQRYRG PKYVYMDWV GKGTGTVTVSS GGGGSGGGGS GGGGSGGGGS 600	
DIQMTQSPSLP LPVTPGE PAS ISCRSSQSLL HSNQYNYLDW YLQKPGQSPQ LLIYLGSNRA 660	
SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCMQALQTP WTFGQGKVE IKR 713	
SEQ ID NO: 64	moltype = AA length = 714
FEATURE	Location/Qualifiers
REGION	1..714
	note = Synthetic Polypeptide
source	1..714
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 64	

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EVQLLESGGG	LVQPGGSLRL	SCAASGFTFS	HYIMMWVRQA	PGKGLEWVSG	IYSSGGITVY	60
ADSVKGRFTI	SRDNSKNTLY	LQMNSLRAED	TAVYYCAYRR	IGVPRRDEFD	IWGQGTMVTV	120
SSASTKGPSV	FPLAPSSKST	SGGTAAALGCL	VKDYFPEPVT	VSWNSGALTS	GVHTFPAVLQ	180
SSGLYSLSSV	VTPVSSSLGT	QTYICNVNHK	PSNTKVDRV	EPKSCDKTHT	CPPCPAPELL	240
GGPSVFLPPP	KPKDTLMISR	TPEVTCVVVD	VSHEDPEVKF	NWYVDGVEVH	NAKTKPREEQ	300
YNSTYRVVSV	LTVLHQDWLN	GKEYCKVSN	KALPAPIEK	ISKAKQPRE	PQVYTLPPSR	360
EEMTKNQVSL	TCLVKGFYPS	DAIWEWESNG	QPENNYKTTP	PVLDSDGSFF	LYSKLTVDKS	420
RWQQGNVFSC	SVMHEALHNH	YTQKSLSLSP	GKSGGGSDIQ	MTQSPSLSPV	TPGEPASISC	480
RSSQSLLSHSN	GYNYLDWYLQ	KPGQSPQLLI	YLGSNRASGV	PDRFSGSGSG	TDFTLKISR	540
EAEDVGVYYC	MQALQTPWTF	GQGTKEVIEKR	TGGGGSGGGG	SGGGGSGGGG	SEVQLLESGG	600
GLVQPGGSLR	LSCAASGFT	SRYVMHWVRQ	APGKGLEWVS	SIWPSCGMTK	YADSVKGRFT	660
ISRDNSKNTL	YLQMNSLRAE	DTAVYYCTRQ	RYRGPKYYYY	MDVWGKGT	TVSS	714

SEQ ID NO: 65	moltype = AA	length = 713				
FEATURE	Location/Qualifiers					
REGION	1..713					
source	note = Synthetic Polypeptide					
	1..713					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 65						
EVQLLESGGG	LVQPGGSLRL	SCAASGFTFS	HYIMMWVRQA	PGKGLEWVSG	IYSSGGITVY	60
ADSVKGRFTI	SRDNSKNTLY	LQMNSLRAED	TAVYYCAYRR	IGVPRRDEFD	IWGQGTMVTV	120
SSASTKGPSV	FPLAPSSKST	SGGTAAALGCL	VKDYFPEPVT	VSWNSGALTS	GVHTFPAVLQ	180
SSGLYSLSSV	VTPVSSSLGT	QTYICNVNHK	PSNTKVDRV	EPKSCDKTHT	CPPCPAPELL	240
GGPSVFLPPP	KPKDTLMISR	TPEVTCVVVD	VSHEDPEVKF	NWYVDGVEVH	NAKTKPREEQ	300
YNSTYRVVSV	LTVLHQDWLN	GKEYCKVSN	KALPAPIEK	ISKAKQPRE	PQVYTLPPSR	360
EEMTKNQVSL	TCLVKGFYPS	DAIWEWESNG	QPENNYKTTP	PVLDSDGSFF	LYSKLTVDKS	420
RWQQGNVFSC	SVMHEALHNH	YTQKSLSLSP	GKSGGGSEVQ	LLESGGGLVQ	PGGSLRLSCA	480
ASGFTFSWYI	MGWVRQAPGK	GLEWWSRIYP	SGGTTFYADS	VKGRFTISRD	NSKNLTYLQM	540
NSLRAEDTAV	YVCTRQYRG	PKYYYYMDW	GKGTGTVTSS	GGGGSGGGGS	GGGGSGGGGS	600
DIQMTQSPSL	LPVTGEPAS	ISCRSSQSLL	HSNGYNYLDW	YLQKPGQSPQ	LLIYLGSNRA	660
SGVPDRFSGS	GGSGTDFTLKI	SRVEAEDVGV	YYCMQALQTP	WTFQGQTKVE	IKR	713

SEQ ID NO: 66	moltype = AA	length = 714
FEATURE	Location/Qualifiers	
REGION	1..714	
source	note = Synthetic Polypeptide	
	1..714	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 66		

EVQLLESGGG	LVQPGGSLRL	SCAASGFTFS	HYIMMWVRQA	PGKGLEWVSG	IYSSGGITVY	60
ADSVKGRFTI	SRDNSKNTLY	LQMNSLRAED	TAVYYCAYRR	IGVPRRDEFD	IWGQGTMVTV	120
SSASTKGPSV	FPLAPSSKST	SGGTAAALGCL	VKDYFPEPVT	VSWNSGALTS	GVHTFPAVLQ	180
SSGLYSLSSV	VTPVSSSLGT	QTYICNVNHK	PSNTKVDRV	EPKSCDKTHT	CPPCPAPELL	240
GGPSVFLPPP	KPKDTLMISR	TPEVTCVVVD	VSHEDPEVKF	NWYVDGVEVH	NAKTKPREEQ	300
YNSTYRVVSV	LTVLHQDWLN	GKEYCKVSN	KALPAPIEK	ISKAKQPRE	PQVYTLPPSR	360
EEMTKNQVSL	TCLVKGFYPS	DAIWEWESNG	QPENNYKTTP	PVLDSDGSFF	LYSKLTVDKS	420
RWQQGNVFSC	SVMHEALHNH	YTQKSLSLSP	GKSGGGSDIQ	MTQSPSLSPV	TPGEPASISC	480
RSSQSLLSHSN	GYNYLDWYLQ	KPGQSPQLLI	YLGSNRASGV	PDRFSGSGSG	TDFTLKISR	540
EAEDVGVYYC	MQALQTPWTF	GQGTKEVIEKR	TGGGGSGGGG	SGGGGSGGGG	SEVQLLESGG	600
GLVQPGGSLR	LSCAASGFT	SRYVMHWVRQ	APGKGLEWVS	RIYPSGGT	YADSVKGRFT	660
ISRDNSKNTL	YLQMNSLRAE	DTAVYYCTRQ	RYRGPKYYYY	MDVWGKGT	TVSS	714

SEQ ID NO: 67	moltype = AA	length = 713
FEATURE	Location/Qualifiers	
REGION	1..713	
source	note = Synthetic Polypeptide	
	1..713	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 67		

EVQLLESGGG	LVQPGGSLRL	SCAASGFTFS	HYIMMWVRQA	PGKGLEWVSG	IYSSGGITVY	60
ADSVKGRFTI	SRDNSKNTLY	LQMNSLRAED	TAVYYCAYRR	IGVPRRDEFD	IWGQGTMVTV	120
SSASTKGPSV	FPLAPSSKST	SGGTAAALGCL	VKDYFPEPVT	VSWNSGALTS	GVHTFPAVLQ	180
SSGLYSLSSV	VTPVSSSLGT	QTYICNVNHK	PSNTKVDRV	EPKSCDKTHT	CPPCPAPELL	240
GGPSVFLPPP	KPKDTLMISR	TPEVTCVVVD	VSHEDPEVKF	NWYVDGVEVH	NAKTKPREEQ	300
YNSTYRVVSV	LTVLHQDWLN	GKEYCKVSN	KALPAPIEK	ISKAKQPRE	PQVYTLPPSR	360
EEMTKNQVSL	TCLVKGFYPS	DAIWEWESNG	QPENNYKTTP	PVLDSDGSFF	LYSKLTVDKS	420
RWQQGNVFSC	SVMHEALHNH	YTQKSLSLSP	GKSGGGSEVQ	LLESGGGLVQ	PGGSLRLSCA	480
ASGFTFSWYI	MWVVRQAPGK	GLEWWSRIYP	SGGITHYADS	VKGRFTISRD	NSKNLTYLQM	540
NSLRAEDTAV	YVCTRQYRG	PKYYYYMDW	GKGTGTVTSS	GGGGSGGGGS	GGGGSGGGGS	600
DIQMTQSPSL	LPVTGEPAS	ISCRSSQSLL	HSNGYNYLDW	YLQKPGQSPQ	LLIYLGSNRA	660
SGVPDRFSGS	GGSGTDFTLKI	SRVEAEDVGV	YYCMQALQTP	WTFQGQTKVE	IKR	713

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SEQ ID NO: 68	moltype = AA length = 714
FEATURE	Location/Qualifiers
REGION	1..714
note = Synthetic Polypeptide	
source	1..714
mol_type = protein	
organism = synthetic construct	
SEQUENCE: 68	
EVQPLESGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60	
ADSVKGRTI SRDNSKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120	
SSASTKGPSV FPLAPSSKST SGGAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAAVLQ 180	
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240	
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVGVEVH NAKTKPREEQ 300	
YNSTYRVVSV LTVLHQDWLN GKEYCKVSN KALPAPIEKT ISKAKQPRE PQVYTLPPSR 360	
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS 420	
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKSGGGSDIQ MTQSPSLSPV TPGEPASISC 480	
RSSQSLLSHN GNYLDWYLQ KPGQSPQLLI YLGSNRASGV PDRFSGSGSG TDFTLKISR 540	
EAEDVGVYVC MQALQTWPWT GQGKTVKEIKR TGGGGSGGGG SGGGGSGGGG SEVQLLESGG 600	
GLVQPGGSLR LSCAASGFTF SWYVMMWVRQ APGKGLEWVS RIYPSGGITH YADSVKGRTF 660	
ISRDNSKNTL YLQMNLSRAE DTAVYYCTRQ RYRGPKYYYY MDVWGKTTV TVSS 714	
SEQ ID NO: 69	moltype = AA length = 713
FEATURE	Location/Qualifiers
REGION	1..713
note = Synthetic Polypeptide	
source	1..713
mol_type = protein	
organism = synthetic construct	
SEQUENCE: 69	
EVOLLESGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60	
ADSVKGRTI SRDNSKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120	
SSASTKGPSV FPLAPSSKST SGGAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAAVLQ 180	
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240	
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVGVEVH NAKTKPREEQ 300	
YNSTYRVVSV LTVLHQDWLN GKEYCKVSN KALPAPIEKT ISKAKQPRE PQVYTLPPSR 360	
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS 420	
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKSGGGSEVQ LLESGGGLVQ PGGSLRLSCA 480	
ASGFTFSWYN MHWVRQAPGK GLEWWSYISP SGKTKYTDs VKGRFTISRD NSKNTLYLQM 540	
NSLRAEDTAV YYCTRQRYRQ PKYNNYMDW GKGTTVTVRS GGGGGSGGGG GGGGGSGGG 600	
DIQMTQSPLS LPVTPGEPAS ISCRNSQSLN HSNGNYLDWYLQ LQKPGQSPQ LLIYLGSNRA 660	
SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCMQALQTP WTFQGQTKVE IKR 713	
SEQ ID NO: 70	moltype = AA length = 714
FEATURE	Location/Qualifiers
REGION	1..714
note = Synthetic Polypeptide	
source	1..714
mol_type = protein	
organism = synthetic construct	
SEQUENCE: 70	
EVOLLESGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60	
ADSVKGRTI SRDNSKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120	
SSASTKGPSV FPLAPSSKST SGGAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAAVLQ 180	
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240	
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVGVEVH NAKTKPREEQ 300	
YNSTYRVVSV LTVLHQDWLN GKEYCKVSN KALPAPIEKT ISKAKQPRE PQVYTLPPSR 360	
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS 420	
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKSGGGSDIQ MTQSPSLSPV TPGEPASISC 480	
RSSQSLLSHN GNYLDWYLQ KPGQSPQLLI YLGSNRASGV PDRFSGSGSG TDFTLKISR 540	
EAEDVGVYVC MQALQTWPWT GQGKTVKEIKR TGGGGSGGGG SGGGGSGGGG SEVQLLESGG 600	
GLVQPGGSLR LSCAASGFTF SWYMMWVRQ APGKGLEWVS YISPSGGKTK YTDSVKGRFT 660	
ISRDNSKNTL YLQMNLSRAE DTAVYYCTRQ RYRGPKYYYY MDVWGKTTV TVSS 714	
SEQ ID NO: 71	moltype = AA length = 713
FEATURE	Location/Qualifiers
REGION	1..713
note = Synthetic Polypeptide	
source	1..713
mol_type = protein	
organism = synthetic construct	
SEQUENCE: 71	
EVOLLESGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60	
ADSVKGRTI SRDNSKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120	
SSASTKGPSV FPLAPSSKST SGGAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAAVLQ 180	
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240	
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVGVEVH NAKTKPREEQ 300	

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YNSTYRVVSV	LTVLHQDWLN	GKEYKCKVSN	KALPAPIEKI	ISKAKGQPRE	PQVYTLPPSR	360
EEMTKNQVSL	TCLVKGFYPS	DIAVEWESNG	QPENNYKTTP	PVLDSDGFFF	LYSKLTVDKS	420
RWQQGNVFSC	SVMHEALHNH	YTQKSLSLSP	GKSGGGSEVQ	LLESGGGLVQ	PGGSRLRSCA	480
ASGFTFSRYI	MGWVRQAPGK	GLEWSSIYP	SGGVTRYADS	VKGRTFTISRD	NSKNLTYLQM	540
NSLRAEDTAV	YYCTRQRYRG	PKYYYYYMDWV	GKGTTVTVSS	GGGGSGGGGS	GGGGSGGGGS	600
DJQMTQSPLS	LPVTGPGE PAS	ISCRSSQSLL	HSNGYNYL DW	YLQKPGQSPQ	LLIYLGSNRA	660
SGVPDRFSGS	GGSGTDFTLKI	SRVEAEDVG V	YYCMQALQTP	WTFGQGTKVE	IKR	713

SEQ ID NO: 72	moltype = AA	length = 714				
FEATURE	Location/Qualifiers					
REGION	1..714					
	note = Synthetic Polypeptide					
source	1..714					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 72						
EVQLLESGGG	LVQPGGSLRL	SCAASGFTFS	HYIMMWVRQA	PGKGLEWVSG	IYSSGGITVY	60
ADSVKGRFTI	SRD NSKNTLY	LQMN SLRAED	TAVYYCAYRR	IGVP RRD EFD	IWGQ GTMVT	120
SSASTKGPSV	FPLAPSSKST	SGGTA ALGCL	VKD YFPEPV T	VSWN SGA L TS	GVHTFP AVLQ	180
SSGLYSLSSV	VTV PSSLGT	QT YICNVN HK	PSNTKV D KRV	EPKSCD KTH T	CPPC PAPE LL	240
GGPSVFLFPP	KPKDTLMISR	TPEVTCVVVD	VSH EDPEVKF	NWY VDGV EVH	NAKTKPREEQ	300
YNSTYRVVSV	LTVLHQDWLN	GKEYKCKVSN	KALPAPIEKI	ISKAKGQPRE	PQVYTLPPSR	360
EEMTKNQVSL	TCLVKGFYPS	DIAVEWESNG	QPENNYKTTP	PVLDSDGFFF	LYSKLTVDKS	420
RWQQGNVFSC	SVMHEALHNH	YTQKSLSLSP	GKSGGGSDIQ	MTQSPSLSPV	TPGE PAS ISC	480
RSSQSLLSHN	GY NYLDWYL Q	KPGQSPQ LLI	Y LGSNRASGV	PDR FSGSGSG	TDF TLKIS RV	540
EAD DVGVYYC	MQALQT PWTF	GQGT KVEIKR	TGGGGSGGGG	S GGGGSGGGG	SEVQ LLES GG	600
GLVQPGGSLR	LSCAASGFTF	SR YIMGW VRQ	APGKG LEWV S	SIYPSGGVTR	YAD SVKGRFT	660
ISRD NSKNTL	YLQMN SLRAE	DTAV YYC TRQ	RYRG PKY YYY	MDV WKG GTTV	TVSS	714

SEQ ID NO: 73	moltype = AA	length = 713				
FEATURE	Location/Qualifiers					
REGION	1..713					
	note = Synthetic Polypeptide					
source	1..713					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 73						
EVQLLESGGG	LVQPGGSLRL	SCAASGFTFS	HYIMMWVRQA	PGKGLEWVSG	IYSSGGITVY	60
ADSVKGRFTI	SRD NSKNTLY	LQMN SLRAED	TAVYYCAYRR	IGVP RRD EFD	IWGQ GTMVT	120
SSASTKGPSV	FPLAPSSKST	SGGTA ALGCL	VKD YFPEPV T	VSWN SGA L TS	GVHTFP AVLQ	180
SSGLYSLSSV	VTV PSSLGT	QT YICNVN HK	PSNTKV D KRV	EPKSCD KTH T	CPPC PAPE LL	240
GGPSVFLFPP	KPKDTLMISR	TPEVTCVVVD	VSH EDPEVKF	NWY VDGV EVH	NAKTKPREEQ	300
YNSTYRVVSV	LTVLHQDWLN	GKEYKCKVSN	KALPAPIEKI	ISKAKGQPRE	PQVYTLPPSR	360
EEMTKNQVSL	TCLVKGFYPS	DIAVEWESNG	QPENNYKTTP	PVLDSDGFFF	LYSKLTVDKS	420
RWQQGNVFSC	SVMHEALHNH	YTQKSLSLSP	GKSGGGSEVQ	LLESGGGLVQ	PGGSRLRSCA	480
ASGFTFSRYI	MHW VRQAPGK	GLEWSSIYP	SGGVTRYADS	VKGRTFTISRD	NSKNLTYLQM	540
NSLRAEDTAV	YYCTRQRYRG	PKY YYYYMDWV	GKGT TVTVSS	GGGGSGGGGS	GGGGSGGGGS	600
DJQMTQSPLS	LPVTGPGE PAS	ISCRSSQSLL	HSNGYNYL DW	YLQKPGQSPQ	LLIYLGSNRA	660
SGVPDRFSGS	GGSGTDFTLKI	SRVEAEDVG V	YYCMQALQTP	WTFGQGTKVE	IKR	713

SEQ ID NO: 74	moltype = AA	length = 714				
FEATURE	Location/Qualifiers					
REGION	1..714					
	note = Synthetic Polypeptide					
source	1..714					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 74						
EVOLLESGGG	LVQPGGSLRL	SCAASGFTFS	HYIMMWVRQA	PGKGLEWVSG	IYSSGGITVY	60
ADSVKGRFTI	SRD NSKNTLY	LQMN SLRAED	TAVYYCAYRR	IGVP RRD EFD	IWGQ GTMVT	120
SSASTKGPSV	FPLAPSSKST	SGGTA ALGCL	VKD YFPEPV T	VSWN SGA L TS	GVHTFP AVLQ	180
SSGLYSLSSV	VTV PSSLGT	QT YICNVN HK	PSNTKV D KRV	EPKSCD KTH T	CPPC PAPE LL	240
GGPSVFLFPP	KPKDTLMISR	TPEVTCVVVD	VSH EDPEVKF	NWY VDGV EVH	NAKTKPREEQ	300
YNSTYRVVSV	LTVLHQDWLN	GKEYKCKVSN	KALPAPIEKI	ISKAKGQPRE	PQVYTLPPSR	360
EEMTKNQVSL	TCLVKGFYPS	DIAVEWESNG	QPENNYKTTP	PVLDSDGFFF	LYSKLTVDKS	420
RWQQGNVFSC	SVMHEALHNH	YTQKSLSLSP	GKSGGGSDIQ	MTQSPSLSPV	TPGE PAS ISC	480
RSSQSLLSHN	GY NYLDWYL Q	KPGQSPQ LLI	Y LGSNRASGV	PDR FSGSGSG	TDF TLKIS RV	540
EAD DVGVYYC	MQALQT PWTF	GQGT KVEIKR	TGGGGSGGGG	S GGGGSGGGG	SEVQ LLES GG	600
GLVQPGGSLR	LSCAASGFTF	SR YIMH W VRQ	APGKG LEWV S	SIYPSGGVTK	YAD SVKGRFT	660
ISRD NSKNTL	YLQMN SLRAE	DTAV YYC TRQ	RYRG PKY YYY	MDV WKG GTTV	TVSS	714

SEQ ID NO: 75	moltype = AA	length = 713
FEATURE	Location/Qualifiers	
REGION	1..713	
	note = Synthetic Polypeptide	
source	1..713	

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mol_type = protein
organism = synthetic construct

SEQUENCE: 75
EVQLESGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120
SSASTKGPSV FPLAPSSKST SGGAALGCL VKYFPEPVT VSWNSGALTS GVHTPPAVLQ 180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR 360
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTTP PVLDSDGSFF LYSKLTVDKS 420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKSGGGSEVQ LLESGGGLVQ PGGSLRLSCA 480
ASGFTFSFY S MHWRQAPGK GLEWWSRIYP SGGLTQYADS VKGRFTISRD NSKNTLYLQM 540
NSLRAEDTAV YYCTRQRYRG PKYYYYMDW GKTTTVTSS GGGGSGGGGS GGGGSGGGGS 600
DIQMTQSPSLS LPVTPGEPEAS ISCRSSQSLL HSNGYNYLDW YLQKPGQSPQ LLIYLGSNRA 660
SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCMQALQTP WFGQGKVE IKR 713

SEQ ID NO: 76      moltype = AA length = 714
FEATURE           Location/Qualifiers
REGION            1..714
note = Synthetic Polypeptide
source             1..714
mol_type = protein
organism = synthetic construct

SEQUENCE: 76
EVQLESGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120
SSASTKGPSV FPLAPSSKST SGGAALGCL VKYFPEPVT VSWNSGALTS GVHTPPAVLQ 180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR 360
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTTP PVLDSDGSFF LYSKLTVDKS 420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP MTQSPSLPV TPGEPASTISC 480
RSSQSLLHSN GNYLDWYLQ KPGQSPQLLI YLGSNRASGV PDRFSGSGSG TDFTLKISR 540
EADBDVGVYYC MQLQTPWTF GQGKVEIKR TGGGGSGGGG SGGGGSGGGG SEVQLESGG 600
GLVQPGGSLR LSCAASGFTF SFYSMHWVRQ APGKGLEWVS RIYPSGGVTK YADSVKGRFT 660
ISRDNSKNTL YLQMNLSRAE DTAVYYCTRQ RYRGPKYYYY MDVWKGKTTV TVSS 714

SEQ ID NO: 77      moltype = AA length = 713
FEATURE           Location/Qualifiers
REGION            1..713
note = Synthetic Polypeptide
source             1..713
mol_type = protein
organism = synthetic construct

SEQUENCE: 77
EVQLESGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120
SSASTKGPSV FPLAPSSKST SGGAALGCL VKYFPEPVT VSWNSGALTS GVHTPPAVLQ 180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR 360
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTTP PVLDSDGSFF LYSKLTVDKS 420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKSGGGSEVQ LLESGGGLVQ PGGSLRLSCA 480
ASGFTFSFY S MHWRQAPGK GLEWWSRIYP SGGLTQYADS VKGRFTISRD NSKNTLYLQM 540
NSLRAEDTAV YYCTRQRYRG PKYYYYMDW GKTTTVTSS GGGGSGGGGS GGGGSGGGGS 600
DIQMTQSPSLS LPVTPGEPEAS ISCRSSQSLL HSNGYNYLDW YLQKPGQSPQ LLIYLGSNRA 660
SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCMQALQTP WFGQGKVE IKR 713

SEQ ID NO: 78      moltype = AA length = 714
FEATURE           Location/Qualifiers
REGION            1..714
note = Synthetic Polypeptide
source             1..714
mol_type = protein
organism = synthetic construct

SEQUENCE: 78
EVQLESGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120
SSASTKGPSV FPLAPSSKST SGGAALGCL VKYFPEPVT VSWNSGALTS GVHTPPAVLQ 180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR 360
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTTP PVLDSDGSFF LYSKLTVDKS 420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP MTQSPSLPV TPGEPASTISC 480
RSSQSLLHSN GNYLDWYLQ KPGQSPQLLI YLGSNRASGV PDRFSGSGSG TDFTLKISR 540
EADBDVGVYYC MQLQTPWTF GQGKVEIKR TGGGGSGGGG SGGGGSGGGG SEVQLESGG 600

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GLVQPGGSLR LSCAASGFTF SFYVMGWVRQ APGKGLEWVS RIYPSGLLTO YADSVKGRFT 660	
ISRDNSKNTL YLQMNSLRAE DTAVYYCTRQ RYRGPKYYYY MDVWKGKTTV TVSS 714	
SEQ ID NO: 79	moltype = AA length = 713
FEATURE	Location/Qualifiers
REGION	1..713
	note = Synthetic Polypeptide
source	1..713
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 79	
EVQLLESGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60	
ADSVKGRFTI SRDNEKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120	
SSASTKGPV FPLAPSSKST SGGAALGCL VKYDFPEPVT VSWNNGALTS GVHTFPAVLQ 180	
SSGLYSLSSV VTVPSLSSGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240	
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ 300	
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR 360	
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTPV PVLDSDGSFF LYSKLTVDKS 420	
RWQQGNVFSC SVMHEALHNH YTQKSLSP GKSGGGSEVQ LLESGGGLVQ PGGSLRLSCA 480	
ASGFTFSWYV MHWVRQAPGK GLEWVSSILP SGGRKTVYADS VKGRFTISRD NSKNTLYLQM 540	
NSLRAEDTAV YYCTRQRYRG PKYYYYMDVW GKTTTVTSS GGGGSGGGGS GGGGSGGGGS 600	
DIQMTQSPSLS LPVTGEPAS ISCRSSQSLL HSNGYNYLDW YLQKPGQSPQ LLIYLGSNRA 660	
SGVPDRFSGS GSGTDFTLKI SRVEADEVGV YYCMQALQTP WFGQGKVE IKR 713	
SEQ ID NO: 80	moltype = AA length = 714
FEATURE	Location/Qualifiers
REGION	1..714
	note = Synthetic Polypeptide
source	1..714
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 80	
EVQLLESGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60	
ADSVKGRFTI SRDNEKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120	
SSASTKGPV FPLAPSSKST SGGAALGCL VKYDFPEPVT VSWNNGALTS GVHTFPAVLQ 180	
SSGLYSLSSV VTVPSLSSGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240	
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ 300	
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR 360	
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTPV PVLDSDGSFF LYSKLTVDKS 420	
RWQQGNVFSC SVMHEALHNH YTQKSLSP GKSGGGSDIQ MTQSPSLSPV TPGEPASISC 480	
RSSQSLLHSN GYNLYDWYLQ KPGQSPQLLI YLGSNRASGV PDRFSGSGSG TDFTLKISR 540	
EADBDVGVYYC MQLALQTPWTF GQGTTKVEIKR TGGGGSGGGG SGGGSGGGG SEVOLLESGG 600	
GLVQPGGSLR LSCAASGFTF SWYMMQWVRQ APGKGLEWVS SIWPSGGKTV YADSVKGRFT 660	
ISRDNEKNTL YLQMNSLRAE DTAVYYCTRQ RYRGPKYYYY MDVWKGKTTV TVSS 714	
SEQ ID NO: 81	moltype = AA length = 713
FEATURE	Location/Qualifiers
REGION	1..713
	note = Synthetic Polypeptide
source	1..713
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 81	
EVQLLESGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60	
ADSVKGRFTI SRDNEKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120	
SSASTKGPV FPLAPSSKST SGGAALGCL VKYDFPEPVT VSWNNGALTS GVHTFPAVLQ 180	
SSGLYSLSSV VTVPSLSSGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240	
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ 300	
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR 360	
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTPV PVLDSDGSFF LYSKLTVDKS 420	
RWQQGNVFSC SVMHEALHNH YTQKSLSP GKSGGGSEVQ LLESGGGLVQ PGGSLRLSCA 480	
ASGFTFSWYV MHWVRQAPGK GLEWVSGIWP SGGRKTVYADS VKGRFTISRD NSKNTLYLQM 540	
NSLRAEDTAV YYCTRQRYRG PKYYYYMDVW GKTTTVTSS GGGGSGGGGS GGGGSGGGGS 600	
DIQMTQSPSLS LPVTGEPAS ISCRSSQSLL HSNGYNYLDW YLQKPGQSPQ LLIYLGSNRA 660	
SGVPDRFSGS GSGTDFTLKI SRVEADEVGV YYCMQALQTP WFGQGKVE IKR 713	
SEQ ID NO: 82	moltype = AA length = 714
FEATURE	Location/Qualifiers
REGION	1..714
	note = Synthetic Polypeptide
source	1..714
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 82	
EVQLLESGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60	
ADSVKGRFTI SRDNEKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120	

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SSASTKGPSV	FPLAPSSKST	SGGTAALGCL	VKDYFPEPVT	VSWNSGALTS	GVHTFPAAVLQ	180
SSGLYSLFPP	VTVPSSSLGT	QTYICNVNHK	PSNTKVDKRV	EPKSCDKTHT	CPPCPAPELL	240
GGPSVFLPPP	KPKDTLMISR	TPEVTCVVVD	VSHEDPEVKF	NWYVDGVEVH	NAKTKPREEQ	300
YNSTYRVVSV	LTVLHQDWLN	GKEYKCKVSN	KALPAPIEKT	ISAKAKGQPRE	PQVYTLPPSR	360
EEMTKNQVSL	TCLVKGFYPS	DIAVEWESNG	QPENNYKTTP	PVLDSDGSFF	LYSKLTVDKS	420
RWQGNVFSC	SVMHEALHNH	YTQKSLSLSP	GKSGGGSDIQ	MTOQSPLSLPV	TPGEPASISC	480
RSSQSLLHSN	GYNLYDWYLQ	KPGQSPQLLI	YLGSNRASGV	PDRFSGSGSG	TDFTLKISRV	540
EAEDVGVYYC	MQALQTPWTF	GQGTKVEIKR	TGGGGSGGGG	SGGGGSGGGG	SEVQLLESGG	600
GLVQPGGSLR	LSCAASGFTF	SWYVMHWVRQ	APGKGLEWVS	GIWPSGGRTK	YADSVKGRFT	660
ISRDNSKNTL	YLQMNSLRAE	DTAVYYCTRQ	RYRGPKYYYY	MDVWGKTTV	TVSS	714

SEQ ID NO: 83	moltype = AA length = 713					
FEATURE	Location/Qualifiers					
REGION	1..713					
	note = Synthetic Polypeptide					
source	1..713					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 83						
EVOLLESGGG	LVQPGGSLRL	SCAASGFTFS	HYIMMWVRQA	PGKGLEWVSG	IYSSGGITVY	60
ADSVKGRFTI	SRDNSKNTLY	LQMNSLRAED	TAVYYCAYRR	IGVPRRDEFD	IWGQGTMVTV	120
SSASTKGPSV	FPLAPSSKST	SGGTAALGCL	VKDYFPEPVT	VSWNSGALTS	GVHTFPAAVLQ	180
SSGLYSLFPP	VTVPSSSLGT	QTYICNVNHK	PSNTKVDKRV	EPKSCDKTHT	CPPCPAPELL	240
GGPSVFLPPP	KPKDTLMISR	TPEVTCVVVD	VSHEDPEVKF	NWYVDGVEVH	NAKTKPREEQ	300
YNSTYRVVSV	LTVLHQDWLN	GKEYKCKVSN	KALPAPIEKT	ISAKAKGQPRE	PQVYTLPPSR	360
EEMTKNQVSL	TCLVKGFYPS	DIAVEWESNG	QPENNYKTTP	PVLDSDGSFF	LYSKLTVDKS	420
RWQGNVFSC	SVMHEALHNH	YTQKSLSLSP	GKSGGGSEVQ	LLESGGGLVQ	PGGSLRLSCA	480
ASGFTFSQYI	MHWVRQAPGK	GLEWVSIY	SGGNTKYADS	VKGRTFTISRD	NSKNLTYLQM	540
NSLRAEDTAV	YYCTRQRYRG	PKYYYYMDWV	GKGTGTVVSS	GGGGSGGGGS	GGGGSGGGGS	600
DIQMTQSPS	LPVTGPGE PAS	ISCRSSQSLL	HSNGYNLYDW	YLQKPGQSPQ	LLIYLGSNRA	660
SGVPDRFSGS	GGSGTDFTLKI	SRVEAEDVGV	YYCMQALQTP	WTFGQGKVE	IKR	713

SEQ ID NO: 84	moltype = AA length = 714					
FEATURE	Location/Qualifiers					
REGION	1..714					
	note = Synthetic Polypeptide					
source	1..714					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 84						
EVOLLESGGG	LVQPGGSLRL	SCAASGFTFS	HYIMMWVRQA	PGKGLEWVSG	IYSSGGITVY	60
ADSVKGRFTI	SRDNSKNTLY	LQMNSLRAED	TAVYYCAYRR	IGVPRRDEFD	IWGQGTMVTV	120
SSASTKGPSV	FPLAPSSKST	SGGTAALGCL	VKDYFPEPVT	VSWNSGALTS	GVHTFPAAVLQ	180
SSGLYSLFPP	VTVPSSSLGT	QTYICNVNHK	PSNTKVDKRV	EPKSCDKTHT	CPPCPAPELL	240
GGPSVFLPPP	KPKDTLMISR	TPEVTCVVVD	VSHEDPEVKF	NWYVDGVEVH	NAKTKPREEQ	300
YNSTYRVVSV	LTVLHQDWLN	GKEYKCKVSN	KALPAPIEKT	ISAKAKGQPRE	PQVYTLPPSR	360
EEMTKNQVSL	TCLVKGFYPS	DIAVEWESNG	QPENNYKTTP	PVLDSDGSFF	LYSKLTVDKS	420
RWQGNVFSC	SVMHEALHNH	YTQKSLSLSP	GKSGGGSDIQ	MTOQSPLSLPV	TPGEPASISC	480
RSSQSLLHSN	GYNLYDWYLQ	KPGQSPQLLI	YLGSNRASGV	PDRFSGSGSG	TDFTLKISRV	540
EAEDVGVYYC	MQALQTPWTF	GQGTKVEIKR	TGGGGSGGGG	SGGGGSGGGG	SEVQLLESGG	600
GLVQPGGSLR	LSCAASGFTF	SQYIMMWVRQ	APGKGLEWVS	SIYPSGGNTK	YADSVKGRFT	660
ISRDNSKNTL	YLQMNSLRAE	DTAVYYCTRQ	RYRGPKYYYY	MDVWGKTTV	TVSS	714

SEQ ID NO: 85	moltype = AA length = 487
FEATURE	Location/Qualifiers
REGION	1..487
	note = Synthetic Polypeptide
source	1..487
	mol_type = protein
	organism = synthetic construct

SEQUENCE: 85						
EVOLLESGGG	LVQPGGSLRL	SCAASGFTFS	HYIMMWVRQA	PGKGLEWVSG	IYSSGGITVY	60
ADSVKGRFTI	SRDNSKNTLY	LQMNSLRAED	TAVYYCAYRR	IGVPRRDEFD	IWGQGTMVTV	120
SSASTKGPSV	FPLAPSSKST	SGGTAALGCL	VKDYFPEPVT	VSWNSGALTS	GVHTFPAAVLQ	180
SSGLYSLFPP	VTVPSSSLGT	QTYICNVNHK	PSNTKVDKRV	EPKSCDKTHT	CPPCPAPELL	240
GGPSVFLPPP	KPKDTLMISR	TPEVTCVVVD	VSHEDPEVKF	NWYVDGVEVH	NAKTKPREEQ	300
YNSTYRVVSV	LTVLHQDWLN	GKEYKCKVSN	KALPAPIEKT	ISAKAKGQPRE	PQVYTLPPSR	360
EEMTKNQVSL	TCLVKGFYPS	DIAVEWESNG	QPENNYKTTP	PVLDSDGSFF	LYSKLTVDKS	420
RWQGNVFSC	SVMHEALHNH	YTQKSLSLSP	GKSGGGSEVQ	LLESGGGLVQ	PGGSLRLSCA	480
ASGFTFS						487

SEQ ID NO: 86	moltype = AA length = 621
FEATURE	Location/Qualifiers
REGION	1..621
	note = Synthetic Polypeptide
source	1..621

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mol_type = protein
organism = synthetic construct

SEQUENCE: 86
EVOLLESGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKYFPEPVT VSWNSGALTS GVHTPPAVLQ 180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEK I SKAKGQPRE PQVYTLPPSR 360
EEMTKKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS 420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKSGGGSDIQ MTQSPSLPV TPGEPASISC 480
RSSQSLLHSN GNYLDWYLO KPGQSPQLLI YLGSNRASGV PDRFSGSGSG TDFTLKISR 540
EAEDVGVYYC MQALQTPWTF GQGKTKVEIKR TGGGGSGGGG SGGGGSGGGG SEVQLLESGG 600
GLVQPGGSLR LSCAASGFTF S 621

SEQ ID NO: 87      moltype = AA length = 713
FEATURE          Location/Qualifiers
REGION           1..713
source            note = Synthetic Polypeptide
                  1..713
mol_type = protein
organism = synthetic construct

SEQUENCE: 87
EVOLLESGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKYFPEPVT VSWNSGALTS GVHTPPAVLQ 180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEK I SKAKGQPRE PQVYTLPPSR 360
EEMTKKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS 420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKSGGGSDIQ MTQSPSLPV TPGEPASISC 480
ASGFTFSPII MHWRQAPGK GLEWWSRIYP SGATVYADS VKGRFTISRD NSKNTLYLQM 540
NSLRAEDTAV YYCTRQRYRG PKYYYYYMDW GKTTVTVSS GGGGGGGG GGGGGGGG 600
DIQMTQSPLS LPVTPGEPAS ISCRSSQSLL HSNGYNYLDW YLQKPGQSPQ LLIYLSNRA 660
SGVPDRFSGS GSGTDFTLKI SRVVAEDGVV YYCMQALQTP WFGQGKVE IKR 713

SEQ ID NO: 88      moltype = AA length = 714
FEATURE          Location/Qualifiers
REGION           1..714
source            note = Synthetic Polypeptide
                  1..714
mol_type = protein
organism = synthetic construct

SEQUENCE: 88
EVOLLESGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKYFPEPVT VSWNSGALTS GVHTPPAVLQ 180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEK I SKAKGQPRE PQVYTLPPSR 360
EEMTKKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS 420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKSGGGSDIQ MTQSPSLPV TPGEPASISC 480
RSSQSLLHSN GNYLDWYLO KPGQSPQLLI YLGSNRASGV PDRFSGSGSG TDFTLKISR 540
EAEDVGVYYC MQALQTPWTF GQGKTKVEIKR TGGGGSGGGG SGGGGSGGGG SEVQLLESGG 600
GLVQPGGSLR LSCAASGFTF SPYIMMWVRQ APGKGLEWVS RIYPSGGATV YADSVKGRFT 660
ISRDNSKNTL YLQMNLSRAE DTAVYYCTRQ RYRGPKYYYY MDVWKGKTTV TVSS 714

SEQ ID NO: 89      moltype = AA length = 713
FEATURE          Location/Qualifiers
REGION           1..713
source            note = Synthetic Polypeptide
                  1..713
mol_type = protein
organism = synthetic construct

SEQUENCE: 89
EVOLLESGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKYFPEPVT VSWNSGALTS GVHTPPAVLQ 180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEK I SKAKGQPRE PQVYTLPPSR 360
EEMTKKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS 420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKSGGGSEVQ LLESGGGLVQ PGGSLRLSCA 480
ASGFTFSMYI MHWRQAPGK GLEWWSRIYP SGGMKYADS VKGRFTISRD NSKNTLYLQM 540
NSLRAEDTAV YYCTRQRYRG PKYYYYYMDW GKTTVTVSS GGGGGGGG GGGGGGGG 600
DIQMTQSPLS LPVTPGEPAS ISCRSSQSLL HSNGYNYLDW YLQKPGQSPQ LLIYLSNRA 660

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SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCMQALQTP WTFQGQTKVE IKR	713
SEQ ID NO: 90	
FEATURE moltype = AA length = 714	
REGION Location/Qualifiers	
1..714	
note = Synthetic Polypeptide	
source 1..714	
mol_type = protein	
organism = synthetic construct	
SEQUENCE: 90	
EVQLLESGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60	
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVT 120	
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ 180	
SSGLYSLSSV VTVPSSSLGT QTYICVNHHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240	
GGPSVFLPFP KPKDTLMISR TPEVTCVVVD VSHEDPVEKF NWYVDGVEVH NAKTKPREEQ 300	
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEK I SKAKGQPRE PQVYTLPPSR 360	
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS 420	
RWQQGNVFSC SVMHEALHHN YTQKSLSLSP GKSGGGSDIQ MTQSPPLSLPV TPGEPASISC 480	
RSSQSLHSN GYNYLDSLWYQ KPGQSPQLLI YLGSNRASGV PDRFSGSGSG TDFTLKISR 540	
EAEDVGVYYC MQALQTPTWTF GQGTKEVIEK TGGGGSGGGG SGGGGSGGGG SEVQLLESGG 600	
GLVQPGGSLR LSACAASGFTF SMYIMHWVRQ APGKGLEWVS SIYPSGGMTK YADSVKGRFT 660	
ISRDNSKNTL YLQMNLSLRAE DTAVYYCTRQ RYRGPKYYYY MDVWGKTTV TVSS 714	
SEQ ID NO: 91	
FEATURE moltype = AA length = 713	
REGION Location/Qualifiers	
1..713	
note = Synthetic Polypeptide	
source 1..713	
mol_type = protein	
organism = synthetic construct	
SEQUENCE: 91	
EVQLLESGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60	
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVT 120	
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ 180	
SSGLYSLSSV VTVPSSSLGT QTYICVNHHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240	
GGPSVFLPFP KPKDTLMISR TPEVTCVVVD VSHEDPVEKF NWYVDGVEVH NAKTKPREEQ 300	
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEK I SKAKGQPRE PQVYTLPPSR 360	
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS 420	
RWQQGNVFSC SVMHEALHHN YTQKSLSLSP GKSGGGSEVQ LLESGGGLVQ PGGSRLRS 480	
ASGFTFSWYS MHWRQAPGK GLEWWSVIYP SGGKTRYADS VKGRFTISRD NSKNLYLQM 540	
NSLRAEDTAV YYCTQRQYRG PKYYYYMDW GKTTVTVSS GGGGGGGG GGGGGGGG 600	
DIQMTQSPS LPPVTPGEPAS ISCRSSQSLL HSNGYNLYDW YLQKPGQSPQ LLIYLGSNRA 660	
SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCMQALQTP WTFQGQTKVE IKR 713	
SEQ ID NO: 92	
FEATURE moltype = AA length = 714	
REGION Location/Qualifiers	
1..714	
note = Synthetic Polypeptide	
source 1..714	
mol_type = protein	
organism = synthetic construct	
SEQUENCE: 92	
EVQLLESGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60	
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVT 120	
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ 180	
SSGLYSLSSV VTVPSSSLGT QTYICVNHHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240	
GGPSVFLPFP KPKDTLMISR TPEVTCVVVD VSHEDPVEKF NWYVDGVEVH NAKTKPREEQ 300	
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEK I SKAKGQPRE PQVYTLPPSR 360	
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS 420	
RWQQGNVFSC SVMHEALHHN YTQKSLSLSP GKSGGGSDIQ MTQSPPLSLPV TPGEPASISC 480	
RSSQSLHSN GYNYLDSLWYQ KPGQSPQLLI YLGSNRASGV PDRFSGSGSG TDFTLKISR 540	
EAEDVGVYYC MQALQTPTWTF GQGTKEVIEK TGGGGSGGGG SGGGGSGGGG SEVQLLESGG 600	
GLVQPGGSLR LSACAASGFTF SWYIMHWVRQ APGKGLEWVS VIYPSGGKTR YADSVKGRFT 660	
ISRDNSKNTL YLQMNLSLRAE DTAVYYCTRQ RYRGPKYYYY MDVWGKTTV TVSS 714	
SEQ ID NO: 93	
FEATURE moltype = AA length = 713	
REGION Location/Qualifiers	
1..713	
note = Synthetic Polypeptide	
source 1..713	
mol_type = protein	
organism = synthetic construct	
SEQUENCE: 93	
EVQLLESGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60	
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVT 120	
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ 180	

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SSGLYSLSSV	VTVPSLSSGT	QTYICNVNHK	PSNTKVDKRV	EPKSCDKTHT	CPPCPAPELL	240
GGPSVFLPPP	KPKDTLMISR	TPEVTCVVVD	VSHEDPEVKF	NWYVDGVEVH	NAKTKPREEQ	300
YNSTYRVVSV	LTVLHQDWLN	GKEYCKVSN	KALPAPIEKT	ISKAKQPRE	PQVYTLPPSR	360
EEMTKNQVSL	TCLVKGFYPS	DIAVEWESNG	QPENNYKTPP	PVLSDSGSFF	LYSKLTVDKS	420
RWQGQNVFSC	SVMHEALHNH	YTQKSLSLSP	GKSGGGSEVQ	LLESGGGLVQ	PGGSLRLSCA	480
ASGFTFSMVY	MHWVRQAPGK	GLEWVSSIYP	SGGLTKYADS	VKGRTFISRD	NSKNLTYLQM	540
NSLRAEDTAV	YYCTRQRYRG	PKYYYYMDW	GKGTTVTVSS	GGGGSGGGGS	GGGGSGGGGS	600
DIQMTQSPLS	LPVTPGEPAS	ISCRSSQSLL	HSNGYNYLDW	YLQKPGQSPQ	LLIYLGSNRA	660
SGVPDRFSGS	GGGTDFTLKI	SRVEAEDGVG	YYCMQALQTP	WTFGQGTKVE	IKR	713

SEQ ID NO: 94	moltype = AA length = 714	
FEATURE	Location/Qualifiers	
REGION	1..714	
note = Synthetic Polypeptide		
source	1..714	
mol_type = protein		
organism = synthetic construct		
SEQUENCE: 94		
EVQLLESGGG LVQPGGSSLRL	SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY	60
ADSVKGRFTI SRDNSKNTLY	LQMNLSRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV	120
SSASTKGPSV FPLAPSSKST	SGGTAALGCL VKDYFPEPVF VSWNSGALT GVHTFPAVLQ	180
SSGLYSLSSV VTVPSLSSGT	QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL	240
GGPSVFLPPP KPKDTLMISR	TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ	300
YNSTYRVVSV LTVLHQDWLN	GKEYCKVSN KALPAPIEKT ISKAKQPRE PQVYTLPPSR	360
EEMTKNQVSL TCLVKGFYPS	DIAVEWESNG QPENNYKTPP PVLSDSGSFF LYSKLTVDKS	420
RWQGQNVFSC SVMHEALHNH	YTQKSLSLSP GKSGGGSDIQ MTQSPLSLPV TPGEPASISC	480
RSSQSLLHSN GYNYLDWYLQ	KPGQSPQLLI YLGSNRASGV PDRFSGGSG TDFTLKISR	540
EAEDVGVYYC MQALQTPWTF	GQGKVEIKR TGGGGSGGGG SGGGGSGGGG SEVQLLESGG	600
GLVQPGGSSLR LSCAASGFTF	SMYVMHHWRQ APGKGLEWVS SIYPSGGLTK YADSVKGRFT	660
ISRDNSKNTL YLQMNLSRAE	DTAVYYCTRQ RYRGPKYYYY MDVWGKTTV TVSS	714

SEQ ID NO: 95	moltype = AA length = 713	
FEATURE	Location/Qualifiers	
REGION	1..713	
note = Synthetic Polypeptide		
source	1..713	
mol_type = protein		
organism = synthetic construct		
SEQUENCE: 95		
EVQLLESGGG LVQPGGSSLRL	SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY	60
ADSVKGRFTI SRDNSKNTLY	LQMNLSRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV	120
SSASTKGPSV FPLAPSSKST	SGGTAALGCL VKDYFPEPVF VSWNSGALT GVHTFPAVLQ	180
SSGLYSLSSV VTVPSLSSGT	QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL	240
GGPSVFLPPP KPKDTLMISR	TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ	300
YNSTYRVVSV LTVLHQDWLN	GKEYCKVSN KALPAPIEKT ISKAKQPRE PQVYTLPPSR	360
EEMTKNQVSL TCLVKGFYPS	DIAVEWESNG QPENNYKTPP PVLSDSGSFF LYSKLTVDKS	420
RWQGQNVFSC SVMHEALHNH	YTQKSLSLSP GKSGGGSEVQ LLESGGGLVQ PGGSLRLSCA	480
ASGFTFSWYT MHWVRQAPGK	GLEWVSSIYP SGGLTRYADS VKGRTFISRD NSKNLTYLQM	540
NSLRAEDTAV YYCTRQRYRG	PKYYYYMDW GKGTTVTVSS GGGGGSGGGG GGGGGSGGGGS	600
DIQMTQSPLS LPVTPGEPAS	ISCRSSQSLL HSNGYNYLDW YLQKPGQSPQ LLIYLGSNRA	660
SGVPDRFSGS GGGTDFTLKI	SRVEAEDGVG YYCMQALQTP WTFGQGTKVE IKR	713

SEQ ID NO: 96	moltype = AA length = 714	
FEATURE	Location/Qualifiers	
REGION	1..714	
note = Synthetic Polypeptide		
source	1..714	
mol_type = protein		
organism = synthetic construct		
SEQUENCE: 96		
EVOLLESGGG LVQPGGSSLRL	SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY	60
ADSVKGRFTI SRDNSKNTLY	LQMNLSRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV	120
SSASTKGPSV FPLAPSSKST	SGGTAALGCL VKDYFPEPVF VSWNSGALT GVHTFPAVLQ	180
SSGLYSLSSV VTVPSLSSGT	QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL	240
GGPSVFLPPP KPKDTLMISR	TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ	300
YNSTYRVVSV LTVLHQDWLN	GKEYCKVSN KALPAPIEKT ISKAKQPRE PQVYTLPPSR	360
EEMTKNQVSL TCLVKGFYPS	DIAVEWESNG QPENNYKTPP PVLSDSGSFF LYSKLTVDKS	420
RWQGQNVFSC SVMHEALHNH	YTQKSLSLSP GKSGGGSDIQ MTQSPLSLPV TPGEPASISC	480
RSSQSLLHSN GYNYLDWYLQ	KPGQSPQLLI YLGSNRASGV PDRFSGGSG TDFTLKISR	540
EAEDVGVYYC MQALQTPWTF	GQGKVEIKR TGGGGSGGGG SGGGGSGGGG SEVQLLESGG	600
GLVQPGGSSLR LSCAASGFTF	SMYVMHHWRQ APGKGLEWVS SIYPSGGLTK YADSVKGRFT	660
ISRDNSKNTL YLQMNLSRAE	DTAVYYCTRQ RYRGPKYYYY MDVWGKTTV TVSS	714

SEQ ID NO: 97	moltype = AA length = 713
FEATURE	Location/Qualifiers
REGION	1..713

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source          note = Synthetic Polypeptide
                1..713
                mol_type = protein
                organism = synthetic construct

SEQUENCE: 97
EVQVLLESGGG LVQPGGSSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60
ADSVKGRFTI SRDNSKNTLY LQMNLSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ 180
SSGLYSLSSV VTPVSSSLGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYCKVSN KALPAPIEKT ISKAKQPRE PQVYTLPPSR 360
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS 420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKSGGGSEVQ LLESGGGLVQ PGGSLRLSCA 480
ASGFTFSHYV MHWRQAPGK GLEWVSSIYP SGGLTKYADS VKGRFTISRD NSKNTLYLQM 540
NSLRAEDTAV YYCTRQRYRG PKYVYMDWV GKGTTVTVSS GGGGSGGGGS GGGGSGGGGS 600
DIQMTQSPLS LPVTPGE PAS ISCRSSQSLL HSNGYNYLDW YLQKPGQSPQ LLIYLGSNRA 660
SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCMQALQTP WTFGQGTKVE IKR 713

SEQ ID NO: 98      moltype = AA length = 714
FEATURE          Location/Qualifiers
REGION           1..714
source          note = Synthetic Polypeptide
                1..714
                mol_type = protein
                organism = synthetic construct

SEQUENCE: 98
EVQVLLESGGG LVQPGGSSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60
ADSVKGRFTI SRDNSKNTLY LQMNLSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ 180
SSGLYSLSSV VTPVSSSLGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYCKVSN KALPAPIEKT ISKAKQPRE PQVYTLPPSR 360
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS 420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKSGGGSDIQ MTQSPSLSPV TPGEPASISC 480
RSSQSLLHSN GQYNDWYLQ KPGQSPQLI YLGSNRASGV PDRFSGSGSG TDFTLKIISRV 540
EAEDVGVQYV MQALQTPTWTF GQGTCKVEIKR TGGGGSGGGG SGGGSGGGG SEVQLESQGG 600
GLVQPGGSLR LSCAASGFTF SHYVMHWVRQ APGKGLEWVS SIYPSGGLTK YADSVKGRFT 660
ISRDNSKNTL YLQMNLSLRAE DTAVYYCTRQ RYRGPKYYYY MDVWGKTTV TVSS 714

SEQ ID NO: 99      moltype = AA length = 713
FEATURE          Location/Qualifiers
REGION           1..713
source          note = Synthetic Polypeptide
                1..713
                mol_type = protein
                organism = synthetic construct

SEQUENCE: 99
EVQVLLESGGG LVQPGGSSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60
ADSVKGRFTI SRDNSKNTLY LQMNLSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ 180
SSGLYSLSSV VTPVSSSLGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYCKVSN KALPAPIEKT ISKAKQPRE PQVYTLPPSR 360
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS 420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKSGGGSEVQ LLESGGGLVQ PGGSLRLSCA 480
ASGFTFSHYV MQWVRQAPGK GLEWVSSIYP SGGLTKYADS VKGRFTISRD NSKNTLYLQM 540
NSLRAEDTAV YYCTRQRYRG PKYVYMDWV GKGTTVTVSS GGGGSGGGGS GGGGSGGGGS 600
DIQMTQSPLS LPVTPGE PAS ISCRSSQSLL HSNGYNYLDW YLQKPGQSPQ LLIYLGSNRA 660
SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCMQALQTP WTFGQGTKVE IKR 713

SEQ ID NO: 100     moltype = AA length = 714
FEATURE          Location/Qualifiers
REGION           1..714
source          note = Synthetic Polypeptide
                1..714
                mol_type = protein
                organism = synthetic construct

SEQUENCE: 100
EVQVLLESGGG LVQPGGSSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60
ADSVKGRFTI SRDNSKNTLY LQMNLSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ 180
SSGLYSLSSV VTPVSSSLGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYCKVSN KALPAPIEKT ISKAKQPRE PQVYTLPPSR 360
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS 420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKSGGGSDIQ MTQSPSLSPV TPGEPASISC 480

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RSSQSLLHSN	GYNYLDWYLQ	KPGQSPQLLI	YLGSNRASGV	PDRFSGSGSG	TDFTLKISR	540
EAEDVGVYYC	MQALQTPWTF	GQGTTKVEIKR	TGGGGSGGGG	SGGGGSGGGG	SEVOLLESGG	600
GLVQPGGSLR	LSCAASGFTF	SWYVMQWVRQ	APGKGLEWVS	SIYPSGGMTK	YADSVKGRFT	660
ISRDNSKNTL	YLQMNSLRAE	DTAVYYCTRQ	RYRGPKYYYY	MDVWGKTTV	TVSS	714

SEQ ID NO: 101	moltype = AA length = 713
FEATURE	Location/Qualifiers
REGION	1..713
	note = Synthetic Polypeptide
source	1..713
	mol_type = protein
	organism = synthetic construct

SEQUENCE: 101						
EVOLLESGGG	LVQPGGSLRL	SCAASGFTFS	HYIMMWVRQA	PGKGLEWVSG	IYSSGGITVY	60
ADSVKGRFTI	SRDNSKNTLY	LQMNLSRAED	TAVYYCAYRR	IGVPRRDEFD	IWGQCTMVT	120
SSASTKGPSV	FPLAPSSKST	SGGTAALGCL	VKDYPPEPVT	VSWNSGALTS	GVHTFPAVLQ	180
SSGLYSLSSV	VTPVSSSLGT	QTYICVNHHK	PSNTKVDKRV	EPKSCDKTHT	CPPCPAPELL	240
GGPSVFLFPP	KPKDTLMISR	TPEVTCVVVD	VSHEDPEVKF	NWYVDGVEVH	NAKTKPREEQ	300
YNSTYRVVSV	LTVLHQDWLN	GKEYCKVSN	KALPAPIEKT	ISKAKGQPRE	PQVYTLPPSR	360
EEMTKNQVSL	TCLVKGFYPS	DIAVEWESNG	QPENNYKTPP	PVLDSDGFFF	LYSKLTVDKS	420
RWQQGNVESC	SVMHEALHNH	YTQKSLSLSP	GKSGGGSEVQ	LLESGGGLVQ	PGGSLRLSCA	480
ASGFTFSQYV	MHWVRQAPGK	GLEWVSSIWP	SGGFTKYADS	VKGRFTISRD	NSKNLTYLQM	540
NSLRAEDTAV	YYCTRQYRG	PKYYYMDWV	GKGTTVTVSS	GGGGSGGGGS	GGGGSGGGGS	600
DIQMTQSPS	LPVTPGEPAS	ISCRSSQSSL	HSGNYNYLDW	YLQKPGQSPQ	LLIYLGSNRA	660
SGVPDRFSGS	SGSGTDFTLKI	SRVEAEDVGV	YYCMQALQTP	WTFGQGKVE	IKR	713

SEQ ID NO: 102	moltype = AA length = 714
FEATURE	Location/Qualifiers
REGION	1..714
	note = Synthetic Polypeptide
source	1..714
	mol_type = protein
	organism = synthetic construct

SEQUENCE: 102						
EVOLLESGGG	LVQPGGSLRL	SCAASGFTFS	HYIMMWVRQA	PGKGLEWVSG	IYSSGGITVY	60
ADSVKGRFTI	SRDNSKNTLY	LQMNLSRAED	TAVYYCAYRR	IGVPRRDEFD	IWGQCTMVT	120
SSASTKGPSV	FPLAPSSKST	SGGTAALGCL	VKDYPPEPVT	VSWNSGALTS	GVHTFPAVLQ	180
SSGLYSLSSV	VTPVSSSLGT	QTYICVNHHK	PSNTKVDKRV	EPKSCDKTHT	CPPCPAPELL	240
GGPSVFLFPP	KPKDTLMISR	TPEVTCVVVD	VSHEDPEVKF	NWYVDGVEVH	NAKTKPREEQ	300
YNSTYRVVSV	LTVLHQDWLN	GKEYCKVSN	KALPAPIEKT	ISKAKGQPRE	PQVYTLPPSR	360
EEMTKNQVSL	TCLVKGFYPS	DIAVEWESNG	QPENNYKTPP	PVLDSDGFFF	LYSKLTVDKS	420
RWQQGNVESC	SVMHEALHNH	YTQKSLSLSP	GKSGGGSDIQ	MTQSPLSLPV	TPGEPASISC	480
RSSQSLLHSN	GYNYLDWYLQ	KPGQSPQLLI	YLGSNRASGV	PDRFSGSGSG	TDFTLKISR	540
EAEDVGVYYC	MQALQTPWTF	GQGTTKVEIKR	TGGGGSGGGG	SGGGSGGGGS	SEVOLLESGG	600
GLVQPGGSLR	LSCAASGFTF	SWYVMQWVRQ	APGKGLEWVS	SIYPSGGMTK	YADSVKGRFT	660
ISRDNSKNTL	YLQMNSLRAE	DTAVYYCTRQ	RYRGPKYYYY	MDVWGKTTV	TVSS	714

SEQ ID NO: 103	moltype = AA length = 713
FEATURE	Location/Qualifiers
REGION	1..713
	note = Synthetic Polypeptide
source	1..713
	mol_type = protein
	organism = synthetic construct

SEQUENCE: 103						
EVOLLESGGG	LVQPGGSLRL	SCAASGFTFS	HYIMMWVRQA	PGKGLEWVSG	IYSSGGITVY	60
ADSVKGRFTI	SRDNSKNTLY	LQMNLSRAED	TAVYYCAYRR	IGVPRRDEFD	IWGQCTMVT	120
SSASTKGPSV	FPLAPSSKST	SGGTAALGCL	VKDYPPEPVT	VSWNSGALTS	GVHTFPAVLQ	180
SSGLYSLSSV	VTPVSSSLGT	QTYICVNHHK	PSNTKVDKRV	EPKSCDKTHT	CPPCPAPELL	240
GGPSVFLFPP	KPKDTLMISR	TPEVTCVVVD	VSHEDPEVKF	NWYVDGVEVH	NAKTKPREEQ	300
YNSTYRVVSV	LTVLHQDWLN	GKEYCKVSN	KALPAPIEKT	ISKAKGQPRE	PQVYTLPPSR	360
EEMTKNQVSL	TCLVKGFYPS	DIAVEWESNG	QPENNYKTPP	PVLDSDGFFF	LYSKLTVDKS	420
RWQQGNVESC	SVMHEALHNH	YTQKSLSLSP	GKSGGGSEVQ	LLESGGGLVQ	PGGSLRLSCA	480
ASGFTFSQYV	MHWVRQAPGK	GLEWVSSIWP	SGGFTKYADS	VKGRFTISRD	NSKNLTYLQM	540
NSLRAEDTAV	YYCTRQYRG	PKYYYMDWV	GKGTTVTVSS	GGGGSGGGGS	GGGGSGGGGS	600
DIQMTQSPS	LPVTPGEPAS	ISCRSSQSSL	HSGNYNYLDW	YLQKPGQSPQ	LLIYLGSNRA	660
SGVPDRFSGS	SGSGTDFTLKI	SRVEAEDVGV	YYCMQALQTP	WTFGQGKVE	IKR	713

SEQ ID NO: 104	moltype = AA length = 714
FEATURE	Location/Qualifiers
REGION	1..714
	note = Synthetic Polypeptide
source	1..714
	mol_type = protein
	organism = synthetic construct

SEQUENCE: 104

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EVQLLESGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY	60
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV	120
SSASTKGPSV FPLAPSSKST SGGAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ	180
SSGLYSLSSV VTPVSSSLGT QTYICNVNHK PSNTKVDRV EPKSCDKTHT CPPCPAPELL	240
GGPSVFLPP KPKDTLMISR TPEVTCVVVD VSHEDEPEVKF NWYVDGVEVH NAKTKPREEQ	300
YNSTYRVVSV LTVLHQDWLN GKEYCKVSN KALPAPIEKI ISKAKQPRE PQVYTLPPSR	360
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS	420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKSGGGSDIQ MTQSPSLSPV TPGEPASISC	480
RSSQSLLSHSN GYNYLDWYLQ KPGQSPQLLI YLGSNRASGV PDRFSGSGSG TDFTLKISR	540
EAEDVGVYYC MQALQTPTWTF GQGTKEVIEKR TGGGGSGGGG SGGGGSGGGG SEVQLLES	600
GLVQPGGSLR LSCHAASGFTF SWYIMQWVRQ APGKGLEWVS SIYPSGGRKT YADSVKGRFT	660
ISRDNSKNTL YLQMNLSRAE DTAVYYCTRQ RYRGPKYYYY MDVWGKGTTV TVSS	714

SEQ ID NO: 105	moltype = AA length = 713
FEATURE	Location/Qualifiers
REGION	1..713
note = Synthetic Polypeptide	
source	1..713
mol_type = protein	
organism = synthetic construct	
SEQUENCE: 105	
EVQLLESGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY	60
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV	120
SSASTKGPSV FPLAPSSKST SGGAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ	180
SSGLYSLSSV VTPVSSSLGT QTYICNVNHK PSNTKVDRV EPKSCDKTHT CPPCPAPELL	240
GGPSVFLPP KPKDTLMISR TPEVTCVVVD VSHEDEPEVKF NWYVDGVEVH NAKTKPREEQ	300
YNSTYRVVSV LTVLHQDWLN GKEYCKVSN KALPAPIEKI ISKAKQPRE PQVYTLPPSR	360
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS	420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKSGGGSEVQ LLESGGGLVQ PGGSLRLSCA	480
ASGFTFSWYV MAWVRQAPGK GLEWVSRQIY SGGMTQYADS VKGRFTISRD NSKNTLYLQM	540
NSLRAEDTAV YCCTRQYRG PKYYYYYMDW GKGTGTTVTVSS GGGGSGGGGS GGGGSGGGG	600
DIQMTQSPSLI LPVTPGEPAS ISCRSSQSLL HSNGYNYLDW YLQKPGQSPQ LLIYLSNRA	660
SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCMQALQTP WTFGQGKVE IKR	713

SEQ ID NO: 106	moltype = AA length = 714
FEATURE	Location/Qualifiers
REGION	1..714
note = Synthetic Polypeptide	
source	1..714
mol_type = protein	
organism = synthetic construct	
SEQUENCE: 106	
EVQLLESGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY	60
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV	120
SSASTKGPSV FPLAPSSKST SGGAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ	180
SSGLYSLSSV VTPVSSSLGT QTYICNVNHK PSNTKVDRV EPKSCDKTHT CPPCPAPELL	240
GGPSVFLPP KPKDTLMISR TPEVTCVVVD VSHEDEPEVKF NWYVDGVEVH NAKTKPREEQ	300
YNSTYRVVSV LTVLHQDWLN GKEYCKVSN KALPAPIEKI ISKAKQPRE PQVYTLPPSR	360
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS	420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKSGGGSDIQ MTQSPSLSPV TPGEPASISC	480
RSSQSLLSHSN GYNYLDWYLQ KPGQSPQLLI YLGSNRASGV PDRFSGSGSGG TDFTLKISR	540
EAEDVGVYYC MQALQTPTWTF GQGTKEVIEKR TGGGGSGGGG SGGGGSGGGG SEVQLLES	600
GLVQPGGSLR LSCHAASGFTF SWYIMQWVRQ APGKGLEWVS RIYPSGGMTO YADSVKGRFT	660
ISRDNSKNTL YLQMNLSRAE DTAVYYCTRQ RYRGPKYYYY MDVWGKGTTV TVSS	714

SEQ ID NO: 107	moltype = AA length = 713
FEATURE	Location/Qualifiers
REGION	1..713
note = Synthetic Polypeptide	
source	1..713
mol_type = protein	
organism = synthetic construct	
SEQUENCE: 107	
EVQLLESGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY	60
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV	120
SSASTKGPSV FPLAPSSKST SGGAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ	180
SSGLYSLSSV VTPVSSSLGT QTYICNVNHK PSNTKVDRV EPKSCDKTHT CPPCPAPELL	240
GGPSVFLPP KPKDTLMISR TPEVTCVVVD VSHEDEPEVKF NWYVDGVEVH NAKTKPREEQ	300
YNSTYRVVSV LTVLHQDWLN GKEYCKVSN KALPAPIEKI ISKAKQPRE PQVYTLPPSR	360
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS	420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKSGGGSEVQ LLESGGGLVQ PGGSLRLSCA	480
ASGFTFSWYV MHWVRQAPGK GLEWVSSIY SGGKTSYADS VKGRFTISRD NSKNTLYLQM	540
NSLRAEDTAV YCCTRQYRG PKYYYYYMDW GKGTGTTVTVSS GGGGSGGGGS GGGGSGGGG	600
DIQMTQSPSLI LPVTPGEPAS ISCRSSQSLL HSNGYNYLDW YLQKPGQSPQ LLIYLSNRA	660
SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCMQALQTP WTFGQGKVE IKR	713

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SEQ ID NO: 108      moltype = AA length = 714
FEATURE          Location/Qualifiers
REGION           1..714
note = Synthetic Polypeptide
source            1..714
mol_type = protein
organism = synthetic construct
SEQUENCE: 108
EVQLESAGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60
ADSVKGRTI SRDNSKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120
SSASTKGPSV FPLAPSSKST SGGAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAAVLQ 180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYCKVSN KALPAPIEKT ISKAKQPRE PQVYTLPPSR 360
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS 420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKSGGGSDIQ MTQSPSLSPV TPGEPASISC 480
RSSQSLLSHN GNYLDWYLQ KPGQSPQLLI YLGSNRASGV PDRFSGSGSG TDFTLKISR 540
EAEDVGVYVC MQALQTWPWT GQGTVKVEIKR TGGGGSGGGG SGGGGSGGGG SEVQLLESGG 600
GLVQPGGSLR LSCAASGFTF SWYVMHWVRQ APGKGLEWVS SIYPSGGKTS YADSVKGRTF 660
ISRDNSKNTL YLQMNLSLRAE DTAVYYCTRQ RYRGPKYYYY MDVWGKGTIV TVSS 714

SEQ ID NO: 109      moltype = AA length = 713
FEATURE          Location/Qualifiers
REGION           1..713
note = Synthetic Polypeptide
source            1..713
mol_type = protein
organism = synthetic construct
SEQUENCE: 109
EVOLLESAGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60
ADSVKGRTI SRDNSKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120
SSASTKGPSV FPLAPSSKST SGGAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAAVLQ 180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYCKVSN KALPAPIEKT ISKAKQPRE PQVYTLPPSR 360
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS 420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKSGGGSEVQ LLESGGGLVQ PGGSLRLSCA 480
ASGFTFSQYV MSWVRQAPGK GLEWSRRIYP SGGVTKYADS VKGRFTISRD NSKNTLYLQM 540
NSLRAEDTAV YYCTRQRYRG PKYNNYMDW GKGTGTVTWS GGGGGSGGGG GGGGGSGGG 600
DIQMTQSPLS LPVTPGEPAS ISCRVQSLN HSNGNYLDW YLQKPGQSPQ LLIYLGSNRA 660
SGVPDFRSGS GSGTDFTLKI SRVEAEDVGV YYCMQALQTP WTFGGQGKTE IKR 713

SEQ ID NO: 110      moltype = AA length = 714
FEATURE          Location/Qualifiers
REGION           1..714
note = Synthetic Polypeptide
source            1..714
mol_type = protein
organism = synthetic construct
SEQUENCE: 110
EVOLLESAGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60
ADSVKGRTI SRDNSKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120
SSASTKGPSV FPLAPSSKST SGGAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAAVLQ 180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYCKVSN KALPAPIEKT ISKAKQPRE PQVYTLPPSR 360
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS 420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKSGGGSDIQ MTQSPSLSPV TPGEPASISC 480
RSSQSLLSHN GNYLDWYLQ KPGQSPQLLI YLGSNRASGV PDRFSGSGSG TDFTLKISR 540
EAEDVGVYVC MQALQTWPWT GQGTVKVEIKR TGGGGSGGGG SGGGGSGGGG SEVQLLESGG 600
GLVQPGGSLR LSCAASGFTF SQYVMSWVRQ APGKGLEWVS RIYPSGGVTK YADSVKGRTF 660
ISRDNSKNTL YLQMNLSLRAE DTAVYYCTRQ RYRGPKYYYY MDVWGKGTIV TVSS 714

SEQ ID NO: 111      moltype = AA length = 713
FEATURE          Location/Qualifiers
REGION           1..713
note = Synthetic Polypeptide
source            1..713
mol_type = protein
organism = synthetic construct
SEQUENCE: 111
EVOLLESAGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60
ADSVKGRTI SRDNSKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120
SSASTKGPSV FPLAPSSKST SGGAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAAVLQ 180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVGVEVH NAKTKPREEQ 300

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YNSTYRVVSV	LTVLHQDWLN	GKEYKCKVSN	KALPAPIEKI	ISKAKGQPRE	PQVYTLPPSR	360
EEMTKNQVSL	TCLVKGFYPS	DIAVEWESNG	QPENNYKTTP	PVLDSDGFFF	LYSKLTVDKS	420
RWQQGNVFSC	SVMHEALHNH	YTQKSLSLSP	GKSGGGSEVQ	LLESGGGLVQ	PGGSRLSCA	480
ASGFTFSQYQ	MVWRQAPGK	GLEWWSRIWP	SGGKTTYADS	VKGRTFTISRD	NSKNLTYLQM	540
NSLRAEDTAV	YYCTRQRYRG	PKYYYYYMDWV	GKGTTVTVSS	GGGGSGGGGS	GGGGSGGGGS	600
DIQMTQSPSLS	LPVTGPGE PAS	ISCRSSQSLL	HSNGYNYLDW	YLQKPGQSPQ	LLIYLGSNRA	660
SGVPDRFSGS	GGSGTDFTLKI	SRVEAEDVG	YYCMQALQTP	WTFQGQTKVE	IKR	713

SEQ ID NO: 112	moltype = AA	length = 714				
FEATURE	Location/Qualifiers					
REGION	1..714					
	note = Synthetic Polypeptide					
source	1..714					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 112						
EVQLLESGGG	LVQPGGSLRL	SCAASGFTFS	HYIMMWVRQA	PGKGLEWVSG	IYSSGGITVY	60
ADSVKGRFTI	SRDNEKNTLY	LQMNLSRAED	TAVYYCAYRR	IGVPRRDEFD	IWGQGTMVTV	120
SSASTKGPSV	FPLAPSSKST	SGGTAALGCL	VKDYFPEPV	PTVWNSGALTS	GVHTFPAVLQ	180
SSGLYSLSSV	VTVPSSSLGT	QTYICNVNHK	PSNTKVDKRV	EPKSCDKTHT	CPPCPAPELL	240
GGPSVFLFPP	KPKDTLMISR	TPEVTCVVVD	VSHEDPEVFK	NWYVDGVEVH	NAKTKPREEQ	300
YNSTYRVVSV	LTVLHQDWLN	GKEYKCKVSN	KALPAPIEKI	ISKAKGQPRE	PQVYTLPPSR	360
EEMTKNQVSL	TCLVKGFYPS	DIAVEWESNG	QPENNYKTTP	PVLDSDGFFF	LYSKLTVDKS	420
RWQQGNVFSC	SVMHEALHNH	YTQKSLSLSP	GKSGGGSDIQ	MTQSPSLSPV	TPGEPASISC	480
RSSQSLLSHN	GYNYLDWYLQ	KPGQSPQLLI	YLGSNRASGV	PDRFSGSGSG	TDFTLKISR	540
EADVGVYYC	MQALQTPTWTF	GQGTKEVIEKR	TGGGGSGGGG	SGGGGSGGGG	SEVQLESGG	600
GLVQPGGSLR	LSCAASGFTF	SQYTMWVRQ	APGKGLEWVS	RIWPSGGKTT	YADSVKGRFT	660
ISRDNSKNTL	YLQMNLSRAE	DTAVYYCTRQ	RYRGPKYyyy	MDVWKGKTTV	TVSS	714

SEQ ID NO: 113	moltype = AA	length = 713				
FEATURE	Location/Qualifiers					
REGION	1..713					
	note = Synthetic Polypeptide					
source	1..713					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 113						
EVQLLESGGG	LVQPGGSLRL	SCAASGFTFS	HYIMMWVRQA	PGKGLEWVSG	IYSSGGITVY	60
ADSVKGRFTI	SRDNEKNTLY	LQMNLSRAED	TAVYYCAYRR	IGVPRRDEFD	IWGQGTMVTV	120
SSASTKGPSV	FPLAPSSKST	SGGTAALGCL	VKDYFPEPV	PTVWNSGALTS	GVHTFPAVLQ	180
SSGLYSLSSV	VTVPSSSLGT	QTYICNVNHK	PSNTKVDKRV	EPKSCDKTHT	CPPCPAPELL	240
GGPSVFLFPP	KPKDTLMISR	TPEVTCVVVD	VSHEDPEVFK	NWYVDGVEVH	NAKTKPREEQ	300
YNSTYRVVSV	LTVLHQDWLN	GKEYKCKVSN	KALPAPIEKI	ISKAKGQPRE	PQVYTLPPSR	360
EEMTKNQVSL	TCLVKGFYPS	DIAVEWESNG	QPENNYKTTP	PVLDSDGFFF	LYSKLTVDKS	420
RWQQGNVFSC	SVMHEALHNH	YTQKSLSLSP	GKSGGGSEVQ	LLESGGGLVQ	PGGSRLSCA	480
ASGFTFSQYQ	MVWRQAPGK	GLEWWSRIYP	SGGVTQYADS	VKGRTFTISRD	NSKNLTYLQM	540
NSLRAEDTAV	YYCTRQRYRG	PKYYYYYMDWV	GKGTTVTVSS	GGGGSGGGGS	GGGGSGGGGS	600
DIQMTQSPSLS	LPVTGPGE PAS	ISCRSSQSLL	HSNGYNYLDW	YLQKPGQSPQ	LLIYLGSNRA	660
SGVPDRFSGS	GGSGTDFTLKI	SRVEAEDVG	YYCMQALQTP	WTFQGQTKVE	IKR	713

SEQ ID NO: 114	moltype = AA	length = 714				
FEATURE	Location/Qualifiers					
REGION	1..714					
	note = Synthetic Polypeptide					
source	1..714					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 114						
EVOLLESGGG	LVQPGGSLRL	SCAASGFTFS	HYIMMWVRQA	PGKGLEWVSG	IYSSGGITVY	60
ADSVKGRFTI	SRDNEKNTLY	LQMNLSRAED	TAVYYCAYRR	IGVPRRDEFD	IWGQGTMVTV	120
SSASTKGPSV	FPLAPSSKST	SGGTAALGCL	VKDYFPEPV	PTVWNSGALTS	GVHTFPAVLQ	180
SSGLYSLSSV	VTVPSSSLGT	QTYICNVNHK	PSNTKVDKRV	EPKSCDKTHT	CPPCPAPELL	240
GGPSVFLFPP	KPKDTLMISR	TPEVTCVVVD	VSHEDPEVFK	NWYVDGVEVH	NAKTKPREEQ	300
YNSTYRVVSV	LTVLHQDWLN	GKEYKCKVSN	KALPAPIEKI	ISKAKGQPRE	PQVYTLPPSR	360
EEMTKNQVSL	TCLVKGFYPS	DIAVEWESNG	QPENNYKTTP	PVLDSDGFFF	LYSKLTVDKS	420
RWQQGNVFSC	SVMHEALHNH	YTQKSLSLSP	GKSGGGSDIQ	MTQSPSLSPV	TPGEPASISC	480
RSSQSLLSHN	GYNYLDWYLQ	KPGQSPQLLI	YLGSNRASGV	PDRFSGSGSG	TDFTLKISR	540
EADVGVYYC	MQALQTPTWTF	GQGTKEVIEKR	TGGGGSGGGG	SGGGGSGGGG	SEVQLESGG	600
GLVQPGGSLR	LSCAASGFTF	SQYTMWVRQ	APGKGLEWVS	RIYPSGGVTQ	YADSVKGRFT	660
ISRDNSKNTL	YLQMNLSRAE	DTAVYYCTRQ	RYRGPKYyyy	MDVWKGKTTV	TVSS	714

SEQ ID NO: 115	moltype = AA	length = 713
FEATURE	Location/Qualifiers	
REGION	1..713	
	note = Synthetic Polypeptide	
source	1..713	

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mol_type = protein
organism = synthetic construct

SEQUENCE: 115
EVQLESGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120
SSASTKGPSV FPLAPSSKST SGGAALGCL VKYFPEPVT VSWNSGALTS GVHTPPAVLQ 180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR 360
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTTP PVLDSDGSFF LYSKLTVDKS 420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKSGGGSEVQ LLESGGGLVQ PGGSLRLSCA 480
ASGFTFSQYV MHWVRQAPGK GLEWVSSRIYP SGGLTNYADS VKGRFTISRD NSKNTLYLQM 540
NSLRAEDTAV YYCTQRQRYRG PKYYYYMDVW GKGTGTVTSS GGGGSGGGGS GGGGSGGGGS 600
DIQMTQSPSLS LPVTPGEPEAS ISCRSSQSLL HSNGYNYLDW YLQKPGQSPQ LLIYLGSNRA 660
SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCMQALQTP WFGQGKVE IKR 713

SEQ ID NO: 116      moltype = AA length = 714
FEATURE           Location/Qualifiers
REGION            1..714
note = Synthetic Polypeptide
source             1..714
mol_type = protein
organism = synthetic construct

SEQUENCE: 116
EVQLESGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120
SSASTKGPSV FPLAPSSKST SGGAALGCL VKYFPEPVT VSWNSGALTS GVHTPPAVLQ 180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR 360
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTTP PVLDSDGSFF LYSKLTVDKS 420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP MTQSPSLPV TPGEPASTISC 480
RSSQSLLHSN GNYLDWYLQ KPGQSPQLLI YLGSNRASGV PDRFSGSGSG TDFTLKISR 540
EAEDVGVYYC MQALQTPWTF GQGKVEIKR TGGGGSGGGG SGGGGSGGGG SEVQLESGG 600
GLVQPGGSLR LSCAASGFTF SQYVMHWVRQ APGKGLEWVS RIYPSGGLTN YADSVKGRFT 660
ISRDNSKNTL YLQMNLSRAE DTAVYYCTRQ RYRGPKYyyy MDVWKGKTTV TVSS 714

SEQ ID NO: 117      moltype = AA length = 713
FEATURE           Location/Qualifiers
REGION            1..713
note = Synthetic Polypeptide
source             1..713
mol_type = protein
organism = synthetic construct

SEQUENCE: 117
EVQLESGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120
SSASTKGPSV FPLAPSSKST SGGAALGCL VKYFPEPVT VSWNSGALTS GVHTPPAVLQ 180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR 360
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTTP PVLDSDGSFF LYSKLTVDKS 420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKSGGGSEVQ LLESGGGLVQ PGGSLRLSCA 480
ASGFTFSQYV MHWVRQAPGK GLEWVSSRIYP SGGLTNYADS VKGRFTISRD NSKNTLYLQM 540
NSLRAEDTAV YYCTQRQRYRG PKYYYYMDVW GKGTGTVTSS GGGGSGGGGS GGGGSGGGGS 600
DIQMTQSPSLS LPVTPGEPEAS ISCRSSQSLL HSNGYNYLDW YLQKPGQSPQ LLIYLGSNRA 660
SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCMQALQTP WFGQGKVE IKR 713

SEQ ID NO: 118      moltype = AA length = 714
FEATURE           Location/Qualifiers
REGION            1..714
note = Synthetic Polypeptide
source             1..714
mol_type = protein
organism = synthetic construct

SEQUENCE: 118
EVQLESGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120
SSASTKGPSV FPLAPSSKST SGGAALGCL VKYFPEPVT VSWNSGALTS GVHTPPAVLQ 180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR 360
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTTP PVLDSDGSFF LYSKLTVDKS 420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKSGGGSDIQ MTQSPSLPV TPGEPASTISC 480
RSSQSLLHSN GNYLDWYLQ KPGQSPQLLI YLGSNRASGV PDRFSGSGSG TDFTLKISR 540
EAEDVGVYYC MQALQTPWTF GQGKVEIKR TGGGGSGGGG SGGGGSGGGG SEVQLESGG 600

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GLVQPGGSLR LSCAASGFTF SQYVMHWVRQ APKGLEWVS SIWPSGGHTR YADSVKGRFT	660
ISRDNSKNTL YLQMNSLRAE DTAVYYCTRQ RYRGPKYYYY MDVWKGTTV TVSS	714
SEQ ID NO: 119	moltype = AA length = 713
FEATURE	Location/Qualifiers
REGION	1..713
	note = Synthetic Polypeptide
source	1..713
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 119	
EVQLLESGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY	60
ADSVKGRFTI SRDNEKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV	120
SSASTKGPSV FPLAPSSKST SGGAALGCL VKYDFPEPVT VSWNSGALTS GVHTFPAVLQ	180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL	240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ	300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR	360
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTPV PVLDSDGSFF LYSKLTVDKS	420
RWQQGNVFSC SVMHEALHNH YTQKSLSP GKSGGGSEVQ LLESGGGLVQ PGGSLRLSCA	480
ASGFTFSNYY MHWRQRQAPGK GLEWVSSILP SGKTKYADS VKGRFTISRD NSKNTLYLQM	540
NSLRAEDTAV YYCTRQRYRG PKYYYYMDAW GQGTTVTVSS GGGGSGGGGS GGGGSGGGGS	600
DIQMTQSPSLS LPVTGEPAS ISCRSSQSLL HSNGYNYLDW YLQKPGQSPQ LLIYLGSNRA	660
SGVPDRFSGS GSGTDFTLKI SRVEADEVGV YYCMQALQTP WFGQGTTKVE IKR	713
SEQ ID NO: 120	moltype = AA length = 714
FEATURE	Location/Qualifiers
REGION	1..714
	note = Synthetic Polypeptide
source	1..714
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 120	
EVQLLESGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY	60
ADSVKGRFTI SRDNEKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV	120
SSASTKGPSV FPLAPSSKST SGGAALGCL VKYDFPEPVT VSWNSGALTS GVHTFPAVLQ	180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL	240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ	300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR	360
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTPV PVLDSDGSFF LYSKLTVDKS	420
RWQQGNVFSC SVMHEALHNH YTQKSLSP GKSGGGSDIQ MTQSPSLSPV TPGEPASISC	480
RSSQSLLHSN GYNLYDWYLQ KPGQSPQLLI YLGSNRASGV PDRFSGSGSG TDFTLKISR	540
EADBDVGVYYC MQALQTPTWTF GQGTTKVEIKR TGGGGSGGGG SGGGSGGGG SEVOLLESGG	600
GLVQPGGSLR LSCAASGFTF SNYVMHWVRQ APKGLEWVS SIWPSGGKTK YADSVKGRFT	660
ISRDNEKNTL YLQMNSLRAE DTAVYYCTRQ RYRGPKYYYY MDWQGQGTTV TVSS	714
SEQ ID NO: 121	moltype = AA length = 713
FEATURE	Location/Qualifiers
REGION	1..713
	note = Synthetic Polypeptide
source	1..713
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 121	
EVQLLESGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY	60
ADSVKGRFTI SRDNEKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV	120
SSASTKGPSV FPLAPSSKST SGGAALGCL VKYDFPEPVT VSWNSGALTS GVHTFPAVLQ	180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL	240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ	300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR	360
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTPV PVLDSDGSFF LYSKLTVDKS	420
RWQQGNVFSC SVMHEALHNH YTQKSLSP GKSGGGSEVQ LLESGGGLVQ PGGSLRLSCA	480
ASGFTFSFYS MHWRQRQAPGK GLEWVSRVYI PGGITSYADS VKGRFTISRD NSKNTLYLQM	540
NSLRAEDTAV YYCTRQRYRG PKYYYYMDW GQGTTVTVSS GGGGSGGGGS GGGGSGGGGS	600
DIQMTQSPSLS LPVTGEPAS ISCRSSQSLL HSNGYNYLDW YLQKPGQSPQ LLIYLGSNRA	660
SGVPDRFSGS GSGTDFTLKI SRVEADEVGV YYCMQALQTP WFGQGTTKVE IKR	713
SEQ ID NO: 122	moltype = AA length = 714
FEATURE	Location/Qualifiers
REGION	1..714
	note = Synthetic Polypeptide
source	1..714
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 122	
EVQLLESGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY	60
ADSVKGRFTI SRDNEKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV	120

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SSASTKGPSV	FPLAPSSKST	SGGTAALGCL	VKDYFPEPV	VSWNSGALTS	GVHTFPAVLQ	180
SSGLYSLSPV	VTVPSSLPP	QTYCIVNVHK	PSNTKVVDKRV	EPKSCDKTHT	CPPCPAPELL	240
GGPSVFLFPP	KPKDTLMISR	TPEVTCVVVD	VSHEDPEVKF	NWYVVDGVEVH	NAKTKPREEQ	300
YNSTYRVVSV	LTVLHQDWLN	GKEYCKVSN	KALPAPIEKT	ISKAKQPRE	PQVYTLPPSR	360
EEMTKNQVSL	TCLVKGFYPS	DIAVEWESNG	QPENNYKTTP	PVLSDGSFF	LYSKLTVDKS	420
RWQGQNVESC	SVMHEALHNH	YTQKSLSLSP	GKSGGGSDIQ	MTQSPPLSLPV	TPGEPAISC	480
RSSQSLLHSN	GYNQYLDWYLQ	KPGQSPQLLI	YLGSNRASGV	PDRFSGSGSG	TDFTLKISRV	540
EAEDVGYYIC	MQALQTPWTF	GQQGTKEIIR	TGGGGSGGGG	SGGGGSGGGG	SEVQLESQGG	600
GLVQPGGSLR	LSCAASGFTF	SFYSMHWVRQ	APGKGLEWVS	RIYPSGGITS	YADSVKGRFT	660
ISRDNSKNTL	YLQMNSLRAE	DTAVYYCTRQ	RYRGPKYYYY	MDVWGKTTV	TVSS	714
 SEQ ID NO: 123		moltype = AA	length = 123			
FEATURE		Location/Qualifiers				
REGION		1..123				
		note = Synthetic Polypeptide				
source		1..123				
		mol_type = protein				
		organism = synthetic construct				
 SEQUENCE: 123						
EVQELLESGGG	LVQPGGSLRL	SCAASGFTFS	QYVMHWVRQA	PGKCLEWVSS	IWPSGGHTRY	60
ADSVKGRFTI	SRDNSKNTLY	LQMNSLRAED	TAVYYCARQR	YRGPKYYYYYM	DVWGQGTTVT	120
VSS						123
 SEQ ID NO: 124		moltype = AA	length = 123			
FEATURE		Location/Qualifiers				
REGION		1..123				
		note = Synthetic Polypeptide				
source		1..123				
		mol_type = protein				
		organism = synthetic construct				
 SEQUENCE: 124						
EVQELLESGGG	LVQPGGSLRL	SCAASGFTFS	WYVMHWVRQA	PGKCLEWVSS	IYPSGGKTSY	60
ADSVKGRFTI	SRDNSKNTLY	LQMNSLRAED	TAVYYCARQR	YRGPKYYYYYM	DVWGQGTTVT	120
VSS						123
 SEQ ID NO: 125		moltype = AA	length = 123			
FEATURE		Location/Qualifiers				
REGION		1..123				
		note = Synthetic Polypeptide				
source		1..123				
		mol_type = protein				
		organism = synthetic construct				
 SEQUENCE: 125						
EVQELLESGGG	LVQPGGSLRL	SCAASGFTFS	WYSMHWVRQA	PGKCLEWVSV	IYPSGGKTRY	60
ADSVKGRFTI	SRDNSKNTLY	LQMNSLRAED	TAVYYCARQR	YRGPKYYYYYM	DVWGQGTTVT	120
VSS						123
 SEQ ID NO: 126		moltype = AA	length = 123			
FEATURE		Location/Qualifiers				
REGION		1..123				
		note = Synthetic Polypeptide				
source		1..123				
		mol_type = protein				
		organism = synthetic construct				
 SEQUENCE: 126						
EVQELLESGGG	LVQPGGSLRL	SCAASGFTFS	HYVMHWVRQA	PGKCLEWVSS	IYPSGLLTKY	60
ADSVKGRFTI	SRDNSKNTLY	LQMNSLRAED	TAVYYCARQR	YRGPKYYYYYM	DVWGQGTTVT	120
VSS						123
 SEQ ID NO: 127		moltype = AA	length = 113			
FEATURE		Location/Qualifiers				
REGION		1..113				
		note = Synthetic Polypeptide				
source		1..113				
		mol_type = protein				
		organism = synthetic construct				
 SEQUENCE: 127						
DIVMTQSPPLS	LPVTPGEPAS	ISCRSSQSLL	HSNGYNYLDW	YLQKPGQSPQ	LLIYLGSNRA	60
SGVPDRFGS	GSGTDFTLKI	SRVEAEDVGV	YYCMQALQTP	WTFGCGTKVE	IKR	113
 SEQ ID NO: 128		moltype = AA	length = 113			
FEATURE		Location/Qualifiers				
REGION		1..113				
		note = Synthetic Polypeptide				
source		1..113				
		mol_type = protein				

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SEQUENCE: 128          organism = synthetic construct
DIVMTQSPLS LPVTPGEPAS ISCRSSQSLL HSNGYNYLDW YLQKPGQSPQ LLIYLGSNRA 60
SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCMQALQTP WTFGCGTKVE IKR      113

SEQ ID NO: 129          moltype = AA length = 113
FEATURE
REGION
1..113
note = Synthetic Polypeptide
source
1..113
mol_type = protein
organism = synthetic construct

SEQUENCE: 129          moltype = AA length = 113
DIVMTQSPLS LPVTPGEPAS ISCRSSQSLL HSNGYNYLDW YLQKPGQSPQ LLIYLGSNRA 60
SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCMQALQTP WTFGCGTKVE IKR      113

SEQ ID NO: 130          moltype = AA length = 113
FEATURE
REGION
1..113
note = Synthetic Polypeptide
source
1..113
mol_type = protein
organism = synthetic construct

SEQUENCE: 130          moltype = AA length = 113
DIVMTQSPLS LPVTPGEPAS ISCRSSQSLL HSNGYNYLDW YLQKPGQSPQ LLIYLGSNRA 60
SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCMQALQTP WTFGCGTKVE IKR      113

SEQ ID NO: 131          moltype = AA length = 16
FEATURE
REGION
1..16
note = Synthetic Polypeptide
source
1..16
mol_type = protein
organism = synthetic construct

SEQUENCE: 131          moltype = AA length = 16
RSSQSLLHSN GNYLD
16

SEQ ID NO: 132          moltype = AA length = 5
FEATURE
REGION
1..5
note = Synthetic Polypeptide
source
1..5
mol_type = protein
organism = synthetic construct

SEQUENCE: 132          moltype = AA length = 5
QYVMH
5

SEQ ID NO: 133          moltype = AA length = 17
FEATURE
REGION
1..17
note = Synthetic Polypeptide
source
1..17
mol_type = protein
organism = synthetic construct

SEQUENCE: 133          moltype = AA length = 17
SIWPSGGHTR YADSVKG
17

SEQ ID NO: 134          moltype = AA length = 14
FEATURE
REGION
1..14
note = Synthetic Polypeptide
source
1..14
mol_type = protein
organism = synthetic construct

SEQUENCE: 134          moltype = AA length = 14
QRYRGPKYYY YMDV
14

SEQ ID NO: 135          moltype = AA length = 5
FEATURE
REGION
1..5
note = Synthetic Polypeptide
source
1..5
mol_type = protein
organism = synthetic construct

SEQUENCE: 135          moltype = AA length = 5
WYVMH
5

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-continued

SEQ ID NO: 136	moltype = AA length = 17	
FEATURE	Location/Qualifiers	
REGION	1..17	
source	note = Synthetic Polypeptide	
	1..17	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 136		
SIYPSGGKTS YADSVKG		17
SEQ ID NO: 137	moltype = AA length = 5	
FEATURE	Location/Qualifiers	
REGION	1..5	
source	note = Synthetic Polypeptide	
	1..5	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 137		
WYSMH		5
SEQ ID NO: 138	moltype = AA length = 17	
FEATURE	Location/Qualifiers	
REGION	1..17	
source	note = Synthetic Polypeptide	
	1..17	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 138		
VIYPSGGKTR YADSVKG		17
SEQ ID NO: 139	moltype = AA length = 5	
FEATURE	Location/Qualifiers	
REGION	1..5	
source	note = Synthetic Polypeptide	
	1..5	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 139		
HYVMH		5
SEQ ID NO: 140	moltype = AA length = 17	
FEATURE	Location/Qualifiers	
REGION	1..17	
source	note = Synthetic Polypeptide	
	1..17	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 140		
SIYPSGGLTK YADSVKG		17
SEQ ID NO: 141	moltype = AA length = 712	
FEATURE	Location/Qualifiers	
REGION	1..712	
source	note = Synthetic	
	1..712	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 141		
EVQLLESGG LVQPGGSLRL SCAASGFTFS HYIMMMWVRQA PGKGLEWVSG IYSSGGITVY	60	
ADSVVKGRFTI SRDNSKNTLY LQMNLSRAED TAVYYCAVRR IGVPRRDEFD IWGQGTMVT	120	
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVTT VSWNSGALT GVHTFPAVLQ	180	
SSGLYSLSSLV VIVPSSSLGT QTYICNVNHK PSNTKVVDKRV EPKSCDKTHT CPPCPAPELL	240	
GGPSPVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ	300	
YNSTTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKI ISKAKQPRE PQVYTLPPSR	360	
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTPP PVLDSDGSFF LYSKLTVDKS	420	
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GSGGGSEVQL LESGGGLVQP GGSLRLSCAA	480	
SGPTFSQYVM HWVRQAPGKC LEWVSSIWPS GGHTTRYADSV KGRFTISRDN SKNTLYLQMN	540	
SIRAEADTAVY YCARQRYRGP KYYYYMDVWG QGTTVTVSSG GGGSGGGGSG GGGSGGGGSD	600	
IVMTQSPLSL PVTGEPASI SCRSSQSLHH SNGYNYLDWY LQKPGQSPQL LIYLGSNRAS	660	
GVPDFRSGSG SGTDFTLKIS RVEAEDVGVY YCMQALQTPW TFGCGTKVEI KR	712	
SEQ ID NO: 142	moltype = AA length = 713	
FEATURE	Location/Qualifiers	
REGION	1..713	
source	note = Synthetic Polypeptide	

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source          1..713
               mol_type = protein
               organism = synthetic construct

SEQUENCE: 142
EVOLLESGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60
ADSVKGRTI SRDNSKNTLY LQMNLSRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120
SSASTKGPSV FPLAPSSKST SGGAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ 180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKQPRE PQVYTLPPSR 360
EEMTKNQVSL TCVKGFYPS DIAVEWESNG QPENNYKTPP PVLDSDGSFF LYSKLTVDKS 420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GGSGGGSEVQ LLESGGGLVQ PGGSLRLSCA 480
ASGFTFSQYV MHWVRQAPGK CLEWVSSIWP SGHGTRYADS VKGRFTISRD NSKNTLYLQM 540
NSLRAEDTAV YYCARQRYRG PKYYYYMDWV GQGTTVTVSS GGGGSGGGGS GGGGSGGGGS 600
DIVMTQSPLS LPVTPGEPAS ISCRSSQSLL HSNGYNYLDWV LQKPGQSQPQ LLIYLGSNRA 660
GVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCMQALQTP WTFCGCTKVE IKR 713

SEQ ID NO: 143      moltype = AA length = 712
FEATURE           Location/Qualifiers
REGION            1..712
                  note = Synthetic Polypeptide
source             1..712
               mol_type = protein
               organism = synthetic construct

SEQUENCE: 143
EVOLLESGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60
ADSVKGRTI SRDNSKNTLY LQMNLSRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120
SSASTKGPSV FPLAPSSKST SGGAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ 180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKQPRE PQVYTLPPSR 360
EEMTKNQVSL TCVKGFYPS DIAVEWESNG QPENNYKTPP PVLDSDGSFF LYSKLTVDKS 420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GGSGGGSEVQ LLESGGGLVQ PGGSLRLSCA 480
SGFTFSWVYV HWVRQAPGK CLEWVSSIYP SGKTSYADS VKGRFTISRD NSKNTLYLQM 540
SIRRAEDTAV YYCARQRYRG PKYYYYMDWV GQGTTVTVSS GGGGSGGGGS GGGGSGGGSD 600
IVMTQSPLS LPVTPGEPAS ISCRSSQSLL HSNGYNYLDWV LQKPGQSQPQ LLIYLGSNRA 660
GVPDRFSGS GSGTDFTLKIS RVEAEDVGV YYCMQALQTP WTFCGCTKVEI KR 712

SEQ ID NO: 144      moltype = AA length = 713
FEATURE           Location/Qualifiers
REGION            1..713
                  note = Synthetic Polypeptide
source             1..713
               mol_type = protein
               organism = synthetic construct

SEQUENCE: 144
EVOLLESGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60
ADSVKGRTI SRDNSKNTLY LQMNLSRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120
SSASTKGPSV FPLAPSSKST SGGAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ 180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKQPRE PQVYTLPPSR 360
EEMTKNQVSL TCVKGFYPS DIAVEWESNG QPENNYKTPP PVLDSDGSFF LYSKLTVDKS 420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GGSGGGSEVQ LLESGGGLVQ PGGSLRLSCA 480
ASGFTFSWVYV MHWVRQAPGK CLEWVSSIYP SGKTSYADS VKGRFTISRD NSKNTLYLQM 540
NSLRAEDTAV YYCARQRYRG PKYYYYMDWV GQGTTVTVSS GGGGSGGGGS GGGGSGGGSD 600
IVMTQSPLS LPVTPGEPAS ISCRSSQSLL HSNGYNYLDWV LQKPGQSQPQ LLIYLGSNRA 660
GVPDRFSGS GSGTDFTLKIS RVEAEDVGV YYCMQALQTP WTFCGCTKVEI KR 713

SEQ ID NO: 145      moltype = AA length = 712
FEATURE           Location/Qualifiers
REGION            1..712
                  note = Synthetic Polypeptide
source             1..712
               mol_type = protein
               organism = synthetic construct

SEQUENCE: 145
EVOLLESGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60
ADSVKGRTI SRDNSKNTLY LQMNLSRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120
SSASTKGPSV FPLAPSSKST SGGAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ 180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKQPRE PQVYTLPPSR 360
EEMTKNQVSL TCVKGFYPS DIAVEWESNG QPENNYKTPP PVLDSDGSFF LYSKLTVDKS 420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GGSGGGSEVQ LLESGGGLVQ PGGSLRLSCA 480
SGFTFSHYVM HWVRQAPGK CLEWVSSIYP GGGLTKYADSV KGRFTISRD NSKNTLYLQM 540

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SLRAEDTAVY YCARQRYRGP KYYYYMDVWG QGTTVTVSSG GGGSGGGGSG GGGSGGGSD 600
IVMTQSPLS PVTGPGEASI SCRQQSLLH SNGYNYLDWY LQKPGQSPQL LIYLGSNRAS 660
GVPDRFSGSG SGTDFTLKIS RVEAEDVGYY YCMQALQTPW TFGCGTKVEI KR 712
SEQ ID NO: 146 moltype = AA length = 713
FEATURE Location/Qualifiers
REGION 1..713
note = Synthetic Polypeptide
source 1..713
mol_type = protein
organism = synthetic construct
 SEQUENCE: 146
EVQLLESGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120
SSASTKGPSV FPLAPSSKST SGGAALGCL VKYDFPEPV T VSWNSGALT GVHTFPAVLQ 180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVFK NWYVDGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKQPRE PQVYTLPPSR 360
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTPV PVLDSDGSFF LYSKLTVDKS 420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GGSGGGSEVQ LLESGGGLVQ PGSSLRLSCA 480
ASGFTFSHYV MHWRQAPGK CLEWVSSIYP SGGLTKYADS VKGRFTISRD NSKNTLYLQM 540
NSLRAEDTAV YCARQRYRGP PKYYYYMDVW GQGTTVTVSS GGGSGGGGSG GGGSGGGSD 600
DIVMTQSPLS LPVTGPGEIASI SCRQQSLLH SNGYNYLDWY LQKPGQSPQL LIYLGSNRAS 660
GVPDRFSGSG SGTDFTLKIS RVEAEDVGYY YCMQALQTPW TFGCGTKVEI KR 713
SEQ ID NO: 147 moltype = AA length = 712
FEATURE Location/Qualifiers
REGION 1..712
note = Synthetic Polypeptide
source 1..712
mol_type = protein
organism = synthetic construct
 SEQUENCE: 147
EVQLLESGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120
SSASTKGPSV FPLAPSSKST SGGAALGCL VKYDFPEPV T VSWNSGALT GVHTFPAVLQ 180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVFK NWYVDGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKQPRE PQVYTLPPSR 360
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTPV PVLDSDGSFF LYSKLTVDKS 420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GGSGGGSEVQ LLESGGGLVQ PGSSLRLSCA 480
SGFTFSWYSM HWVRQAPGK CLEWVSSIYP GGKTRYADS KGRFTISRDN SKNTLYLQM 540
SLRAEDTAVY YCARQRYRGP KYYYYMDVW GQGTTVTVSS GGGSGGGGSG GGGSGGGSD 600
IVMTQSPLS PVTGPGEASI SCRQQSLLH SNGYNYLDWY LQKPGQSPQL LIYLGSNRAS 660
GVPDRFSGSG SGTDFTLKIS RVEAEDVGYY YCMQALQTPW TFGCGTKVEI KR 712
SEQ ID NO: 148 moltype = AA length = 713
FEATURE Location/Qualifiers
REGION 1..713
note = Synthetic Polypeptide
source 1..713
mol_type = protein
organism = synthetic construct
 SEQUENCE: 148
EVQLLESGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120
SSASTKGPSV FPLAPSSKST SGGAALGCL VKYDFPEPV T VSWNSGALT GVHTFPAVLQ 180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVFK NWYVDGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKQPRE PQVYTLPPSR 360
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTPV PVLDSDGSFF LYSKLTVDKS 420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GGSGGGSEVQ LLESGGGLVQ PGSSLRLSCA 480
ASGFTFSWYS MHWRQAPGK CLEWVSSIYP SGKTRYADS VKGRFTISRD NSKNTLYLQM 540
NSLRAEDTAV YCARQRYRGP PKYYYYMDVW GQGTTVTVSS GGGSGGGGSG GGGSGGGSD 600
DIVMTQSPLS LPVTGPGEIASI SCRQQSLLH SNGYNYL DWY LQKPGQSPQL LIYLGSNRAS 660
GVPDRFSGSG SGTDFTLKIS RVEAEDVGYY YCMQALQTPW TFGCGTKVEI KR 713
SEQ ID NO: 149 moltype = AA length = 470
FEATURE Location/Qualifiers
REGION 1..470
note = Synthetic Polypeptide
source 1..470
mol_type = protein
organism = synthetic construct
 SEQUENCE: 149
MGWSCIILFL VATATGAHSE VQLLESGGGL VQPGGSLRLS CAASGFTFSH YIMMWVRQAP 60

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GKGLEWVSGI	YSSGGITVYA	DSVKGRFTIS	RDNSKNTLYL	QMNSLRAEDT	AVYYCAYRRI	120
GVPRRDEFDI	WGQGTMVTVS	SASTKGPSVF	PLAPSSKSTS	GGTAALGCLV	KDYFPEPVTV	180
SWNSGALTSG	VHTFPAVLQS	SGLYSLSSVV	TVPSSSLGTQ	TYICCNVNHKP	SNTKVDKRVE	240
PKSCDKTHTC	PPCPAPELLG	GPSVFLFPKK	PKDLMISR	PEVTCVVVDV	SHEDPEVKFN	300
WYVDGVEVHN	AKTKPREEQY	NSTYRVVSVL	TVLHQDWLNG	KEYKCKVSNK	ALPAPIEKTI	360
SKAKGQPREP	QVYTLPPSRE	EMTKNQVSLT	CLVKGFYPSD	IAVEWESNGQ	PENNYKTPP	420
VLDSDGSFFL	YSKLTVDKSR	WQQGNVFSCS	VMHEALHNHY	TQKSLSSLSPG		470

SEQ ID NO: 150	moltype = AA	length = 471				
FEATURE	Location/Qualifiers					
REGION	1..471					
	note = Synthetic Polypeptide					
source	1..471					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 150						
MGWSCIILFL	VATATGAHSE	VQLLESGGGL	VQPGGSLRLS	CAASGFTSH	YIMMWVRQAP	60
GKGLEWVSGI	YSSGGITVYA	DSVKGRFTIS	RDNSKNTLYL	QMNSLRAEDT	AVYYCAYRRI	120
GVPRRDEFDI	WGQGTMVTVS	SASTKGPSVF	PLAPSSKSTS	GGTAALGCLV	KDYFPEPVTV	180
SWNSGALTSG	VHTFPAVLQS	SGLYSLSSVV	TVPSSSLGTQ	TYICCNVNHKP	SNTKVDKRVE	240
PKSCDKTHTC	PPCPAPELLG	GPSVFLFPKK	PKDLMISR	PEVTCVVVDV	SHEDPEVKFN	300
WYVDGVEVHN	AKTKPREEQY	NSTYRVVSVL	TVLHQDWLNG	KEYKCKVSNK	ALPAPIEKTI	360
SKAKGQPREP	QVYTLPPSRE	EMTKNQVSLT	CLVKGFYPSD	IAVEWESNGQ	PENNYKTPP	420
VLDSDGSFFL	YSKLTVDKSR	WQQGNVFSCS	VMHEALHNHY	TQKSLSSLSPG	G	471

SEQ ID NO: 151	moltype = AA	length = 710				
FEATURE	Location/Qualifiers					
REGION	1..710					
	note = Synthetic Polypeptide					
source	1..710					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 151						
EVQLLESQGG	LVQPGGSLRL	SCAASGFTFS	HYIMMWVRQA	PGKGLEWVSG	IYSSGGITVY	60
ADSVKGRFTI	SRDNSKNTLY	LQMNSLRAED	TAVYYCAYRR	IGVPRRDEFD	IWGQGTMVTV	120
SSASTKGPSV	FPLAPSSKST	SGGTAALGCL	VKDYFPEPV	VSWNSGALT	GVHTFPAVLQ	180
SSGLYSLSSV	VTVPSSSLGT	QTYICCNVNHK	PSNTKVDKR	EPKSCDKTH	CPPCPAPELL	240
GGPSVFLFPP	KPKDTLMISR	TPEVTCVVVD	VSHEDPEVKF	NWYVDGVEVH	NAKTKPREEQ	300
YNSTYRVVSV	LTVLHQDWLN	GKEYKCKVSN	KALPAPIEKT	ISKAKGQPRE	PQVYTLPPSR	360
EEMTKNQVSL	TCLVKGFYPS	DAIEWESNG	QPENNYKTPP	PVLDSDGFFF	LYSKLTVDKS	420
RWQQGNVFSC	SVMHEALHNH	YTQKSLSSL	GSGGGSEVOL	LESGGGLVQP	GGSLRLSCAA	480
SGFTFSQYVM	HWWVRQAPGK	LEWVSSIWPS	GGHTRYADS	KGRFTISRDN	SKNTLYLQMN	540
SLRAEDTAVY	YCARQRYRG	KYYYYMDWV	QGTIVTVSSG	GGGSGGGGSG	GGGSGGGGSD	600
IVMTQSPLS	PVTPGEPASI	SCRSSQSLL	SNGYNYLDWY	LQKPGQSPQ	LIYLGSNRAS	660
GVPDFRSGSG	SGSTDFTLKIS	RVEAEDVGVY	YCMQALQTPW	WTFGCGTKVEI		710

SEQ ID NO: 152	moltype = AA	length = 711				
FEATURE	Location/Qualifiers					
REGION	1..711					
	note = Synthetic Polypeptide					
source	1..711					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 152						
EVQLLESQGG	LVQPGGSLRL	SCAASGFTFS	HYIMMWVRQA	PGKGLEWVSG	IYSSGGITVY	60
ADSVKGRFTI	SRDNSKNTLY	LQMNSLRAED	TAVYYCAYRR	IGVPRRDEFD	IWGQGTMVTV	120
SSASTKGPSV	FPLAPSSKST	SGGTAALGCL	VKDYFPEPV	VSWNSGALT	GVHTFPAVLQ	180
SSGLYSLSSV	VTVPSSSLGT	QTYICCNVNHK	PSNTKVDKR	EPKSCDKTH	CPPCPAPELL	240
GGPSVFLFPP	KPKDTLMISR	TPEVTCVVVD	VSHEDPEVKF	NWYVDGVEVH	NAKTKPREEQ	300
YNSTYRVVSV	LTVLHQDWLN	GKEYKCKVSN	KALPAPIEKT	ISKAKGQPRE	PQVYTLPPSR	360
EEMTKNQVSL	TCLVKGFYPS	DAIEWESNG	QPENNYKTPP	PVLDSDGFFF	LYSKLTVDKS	420
RWQQGNVFSC	SVMHEALHNH	YTQKSLSSL	GSGGGSEVOL	LESGGGLVQP	GGGSLRLSCAA	480
ASGFTFSQYVM	MHWVRQAPGK	CLEWVSSIWPS	GGGHTTRYADS	VKGRFTISRD	NSKNTLYLQMN	540
NSLRAEDTAVY	YCARQRYRG	KYYYYMDWV	QGTIVTVSSG	GGGSGGGGSG	GGGSGGGGSD	600
DIVMTQSPLS	PVTPGEPASI	SCRSSQSLL	SNGYNYLDWY	LQKPGQSPQ	LIYLGSNRAS	660
SGVPDFRSGSG	SGSTDFTLKIS	RVEAEDVGVY	YCMQALQTPW	WTFGCGTKVEI		711

SEQ ID NO: 153	moltype = AA	length = 710				
FEATURE	Location/Qualifiers					
REGION	1..710					
	note = Synthetic Polypeptide					
source	1..710					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 153						
EVQLLESQGG	LVQPGGSLRL	SCAASGFTFS	HYIMMWVRQA	PGKGLEWVSG	IYSSGGITVY	60

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ADSVKGRFTI	SRDNSKNTLY	LQMNLSLRAED	TAVYYCAYRR	IGVPRRDEFD	IWGQGTMVTV	120
SSASTKGPSV	FPLAPSSKST	SGGTAAALGCL	VKDYFPEPVT	VSWNSGALT	GVHTFPAVLQ	180
SSGLYSLSSV	VTVPSSSLGT	QTYICNVNHK	PSNTKVDKRV	EPKSCDKTHT	CPPCPAPELL	240
GGPSVFLFPP	KPKDTLMISR	TPEVTCVVVD	VSHDPEVF	NWYVGVEVH	NAKTKPREEQ	300
YNSTYRVVSV	LTVLHQDWLN	GKEYKCKVSN	KALPAPIEKT	ISKAKGQPRE	PQVYTLPPSR	360
EEMTKNQVSL	TCLVKGFYPS	DIAVEWESNG	QPENNYKTTP	PVLDSDGSFF	LYSKLTVDKS	420
RWQQGNVFSC	SVMHEALHNH	YTQKSLSLSP	GSGGGSEVQL	LESGGGLVQP	GGSLRLSCAA	480
SGFTFSWVY	MHWVRQAPGK	LEWVSSIYPS	GGKTSYADS	KGRFTISRDN	SKNTLYLQMN	540
SLRAEDTAVY	YCARQRYRGP	KYYYYMDVW	QGTTTVTSSG	GGGSGGGGSG	GGGSGGGGSD	600
DIVMTQSPLS	PVTPGEPEAS	SCRSSQSLLH	SNGYNYLDWY	LQKPGQSPQL	LIYLGSNRAS	660
GVDPDRFSGSG	SGTDFTLKIS	RVEAEDVGVY	YCMQALQTPW	WTFCGCKVEI		710

SEQ ID NO: 154	moltype = AA length = 711					
FEATURE	Location/Qualifiers					
REGION	1..711					
	note = Synthetic Polypeptide					
source	1..711					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 154						
EVQLLESGGG LVQPGGSLRL	SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY	60				
ADSVKGRFTI	SRDNSKNTLY	LQMNLSLRAED	TAVYYCAYRR	IGVPRRDEFD	IWGQGTMVTV	120
SSASTKGPSV	FPLAPSSKST	SGGTAAALGCL	VKDYFPEPVT	VSWNSGALT	GVHTFPAVLQ	180
SSGLYSLSSV	VTVPSSSLGT	QTYICNVNHK	PSNTKVDKRV	EPKSCDKTHT	CPPCPAPELL	240
GGPSVFLFPP	KPKDTLMISR	TPEVTCVVVD	VSHDPEVF	NWYVGVEVH	NAKTKPREEQ	300
YNSTYRVVSV	LTVLHQDWLN	GKEYKCKVSN	KALPAPIEKT	ISKAKGQPRE	PQVYTLPPSR	360
EEMTKNQVSL	TCLVKGFYPS	DIAVEWESNG	QPENNYKTTP	PVLDSDGSFF	LYSKLTVDKS	420
RWQQGNVFSC	SVMHEALHNH	YTQKSLSLSP	GSGGGSEVQL	LESGGGLVQP	GGSLRLSCAA	480
ASGFTFSWVY	MHWVRQAPGK	LEWVSSIYPS	GGKTSYADS	KGRFTISRDN	SKNTLYLQMN	540
NSLRAEDTAV	YCARQRYRGP	PKYYYYMDVW	QGTTTVTSSG	GGGSGGGGSG	GGGSGGGGSD	600
DIVMTQSPLS	PVTPGEPEAS	SCRSSQSLLH	SNGYNYLDWY	LQKPGQSPQL	LIYLGSNRAS	660
GVDPDRFSGSG	SGTDFTLKIS	RVEAEDVGVY	YCMQALQTPW	WTFCGCKVEI		711

SEQ ID NO: 155	moltype = AA length = 710					
FEATURE	Location/Qualifiers					
REGION	1..710					
	note = Synthetic Polypeptide					
source	1..710					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 155						
EVQLLESGGG LVQPGGSLRL	SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY	60				
ADSVKGRFTI	SRDNSKNTLY	LQMNLSLRAED	TAVYYCAYRR	IGVPRRDEFD	IWGQGTMVTV	120
SSASTKGPSV	FPLAPSSKST	SGGTAAALGCL	VKDYFPEPVT	VSWNSGALT	GVHTFPAVLQ	180
SSGLYSLSSV	VTVPSSSLGT	QTYICNVNHK	PSNTKVDKRV	EPKSCDKTHT	CPPCPAPELL	240
GGPSVFLFPP	KPKDTLMISR	TPEVTCVVVD	VSHDPEVF	NWYVGVEVH	NAKTKPREEQ	300
YNSTYRVVSV	LTVLHQDWLN	GKEYKCKVSN	KALPAPIEKT	ISKAKGQPRE	PQVYTLPPSR	360
EEMTKNQVSL	TCLVKGFYPS	DIAVEWESNG	QPENNYKTTP	PVLDSDGSFF	LYSKLTVDKS	420
RWQQGNVFSC	SVMHEALHNH	YTQKSLSLSP	GSGGGSEVQL	LESGGGLVQP	GGSLRLSCAA	480
SGFTFSHYV	MHWVRQAPGK	LEWVSSIYPS	GGLTKYADS	KGRFTISRDN	SKNTLYLQMN	540
SLRAEDTAV	YCARQRYRGP	KYYYYMDVW	QGTTTVTSSG	GGGSGGGGSG	GGGSGGGGSD	600
DIVMTQSPLS	PVTPGEPEAS	SCRSSQSLLH	SNGYNYLDWY	LQKPGQSPQL	LIYLGSNRAS	660
GVDPDRFSGSG	SGTDFTLKIS	RVEAEDVGVY	YCMQALQTPW	WTFCGCKVEI		710

SEQ ID NO: 156	moltype = AA length = 711					
FEATURE	Location/Qualifiers					
REGION	1..711					
	note = Synthetic Polypeptide					
source	1..711					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 156						
EVOLLESGGG LVQPGGSLRL	SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY	60				
ADSVKGRFTI	SRDNSKNTLY	LQMNLSLRAED	TAVYYCAYRR	IGVPRRDEFD	IWGQGTMVTV	120
SSASTKGPSV	FPLAPSSKST	SGGTAAALGCL	VKDYFPEPVT	VSWNSGALT	GVHTFPAVLQ	180
SSGLYSLSSV	VTVPSSSLGT	QTYICNVNHK	PSNTKVDKRV	EPKSCDKTHT	CPPCPAPELL	240
GGPSVFLFPP	KPKDTLMISR	TPEVTCVVVD	VSHDPEVF	NWYVGVEVH	NAKTKPREEQ	300
YNSTYRVVSV	LTVLHQDWLN	GKEYKCKVSN	KALPAPIEKT	ISKAKGQPRE	PQVYTLPPSR	360
EEMTKNQVSL	TCLVKGFYPS	DIAVEWESNG	QPENNYKTTP	PVLDSDGSFF	LYSKLTVDKS	420
RWQQGNVFSC	SVMHEALHNH	YTQKSLSLSP	GSGGGSEVQL	LESGGGLVQP	GGSLRLSCAA	480
ASGFTFSHYV	MHWVRQAPGK	LEWVSSIYPS	GGLTKYADS	KGRFTISRDN	SKNTLYLQMN	540
NSLRAEDTAV	YCARQRYRGP	PKYYYYMDVW	QGTTTVTSSG	GGGSGGGGSG	GGGSGGGGSD	600
DIVMTQSPLS	PVTPGEPEAS	SCRSSQSLLH	SNGYNYLDWY	LQKPGQSPQL	LIYLGSNRAS	660
GVDPDRFSGSG	SGTDFTLKIS	RVEAEDVGVY	YCMQALQTPW	WTFCGCKVEI		711

SEQ ID NO: 157	moltype = AA length = 710
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-continued

FEATURE	Location/Qualifiers
REGION	1..710
source	note = Synthetic Polypeptide 1..710 mol_type = protein organism = synthetic construct
SEQUENCE: 157	
EVOLLESGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60	
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120	
SSASTKGPSV FPLAPSSKST SGGAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ 180	
SSGLYSLSSV VTVPPSSLGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240	
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDEPEVKF NWYVDGVEVH NAKTKPREEQ 300	
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR 360	
EEMTKNQVSL TCLVKGFYPS DIAWEVESNG QPENNYKTTPV PVLDSDGSSFF LYSKLTVDKS 420	
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GGSGGSEVQL LESGGGLVQP GGSSLRLSCAA 480	
SGFTFSWYSM HWVRQAPGK LEWWSVIYPS GGKTRYADSV KGRFTISRDN SKNTLYLQM 540	
SLRAEDTAVY YCARQRYRGP KYYYYYMDVWQ QGTTTVTSSG GGGSGGGGSG GGGSGGGGSD 600	
DIVMTQSPLS LPVTPGEPASI SCRSSLQSLH SNGYNYLDWY LQKPGQSPQL LIYLGSNRAS 660	
GVPDRFSGSG SGTDFTLKIS RVEAEDVGVY YCMQALQTPW TFGCGTKVEI 710	
SEQ ID NO: 158	moltype = AA length = 711
FEATURE	Location/Qualifiers
REGION	1..711
source	note = Synthetic Polypeptide 1..711 mol_type = protein organism = synthetic construct
SEQUENCE: 158	
EVQLLESGGG LVQPGGSLRL SCAASGFTFS HYIMMWVRQA PGKGLEWVSG IYSSGGITVY 60	
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAYRR IGVPRRDEFD IWGQGTMVTV 120	
SSASTKGPSV FPLAPSSKST SGGAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ 180	
SSGLYSLSSV VTVPPSSLGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 240	
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDEPEVKF NWYVDGVEVH NAKTKPREEQ 300	
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR 360	
EEMTKNQVSL TCLVKGFYPS DIAWEVESNG QPENNYKTTPV PVLDSDGSSFF LYSKLTVDKS 420	
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GGSGGSEVQL LESGGGLVQP GGSSLRLSCAA 480	
ASGFTFSWYSM MHWRQAPGK CLEWWSVIYPS GGKTRYADSV VKGRFTISRD NSKNTLYLQM 540	
NSLRAEDTAV YCARQRYRGP PKYYYYMDVW QGTTTVTSSG GGGGSGGGGS GGGGSGGGGS 600	
DIVMTQSPLS LPVTPGEPASI SCRSSLQSLH SNGYNYLDWY LQKPGQSPQL LIYLGSNRAS 660	
GVPDRFSGSG SGTDFTLKIS RVEAEDVGVY YYCMQALQTPW TFGCGTKVEI 711	
SEQ ID NO: 159	moltype = AA length = 5
FEATURE	Location/Qualifiers
REGION	1..5
source	note = Synthetic 1..5 mol_type = protein organism = synthetic construct
SEQUENCE: 159	
HYIMM	5
SEQ ID NO: 160	moltype = AA length = 17
FEATURE	Location/Qualifiers
REGION	1..17
source	note = Synthetic 1..17 mol_type = protein organism = synthetic construct
SEQUENCE: 160	
GIYSSGGITV YADSVKG	17
SEQ ID NO: 161	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = Synthetic 1..13 mol_type = protein organism = synthetic construct
SEQUENCE: 161	
RRIGVPRRDE FDI	13
SEQ ID NO: 162	moltype = AA length = 11
FEATURE	Location/Qualifiers
REGION	1..11
source	note = Synthetic 1..11

-continued

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mol_type = protein
organism = synthetic construct

SEQUENCE: 162
RASQSISSWL A                                11

SEQ ID NO: 163      moltype = AA length = 7
FEATURE          Location/Qualifiers
REGION           1..7
source            note = Synthetic
                 1..7
mol_type = protein
organism = synthetic construct

SEQUENCE: 163
KASTLES                               7

SEQ ID NO: 164      moltype = AA length = 8
FEATURE          Location/Qualifiers
REGION           1..8
source            note = Synthetic
                 1..8
mol_type = protein
organism = synthetic construct

SEQUENCE: 164
QQYNTYWT                                8

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1-54. (canceled)

55. A bispecific antibody, comprising a first antibody that binds to plasma kallikrein (pKal) and a second antibody that binds to Factor XII (FXIIa);

wherein the bispecific antibody comprises a first polypeptide comprising a sequence set forth as SEQ ID NO: 46 and a second polypeptide comprising a sequence set forth as any one of SEQ ID NOS: 51-122.

56. An isolated nucleic acid or nucleic acid set, comprising a first nucleotide sequence encoding the first polypeptide set forth in claim **55** and a second nucleotide sequence encoding the second polypeptide set forth in claim **55**.

57. The nucleic acid or nucleic acid set of claim **56**, wherein the first and second nucleotide sequences are located on two separate nucleic acid molecules.

58. The nucleic acid or nucleic acid set of claim **56**, wherein the first and second nucleotide sequences are located on one nucleic acid molecule.

59. The nucleic acid or nucleic acid set of claim **56**, which is a vector set comprising a first vector that comprises the first nucleotide sequence and a second vector that comprises the second nucleotide sequence.

60. The nucleic acid or nucleic acid set of claim **59**, wherein the first and second vectors are expression vectors, in which the first and second nucleotide sequences are each operably linked to a common promoter or a different promoter.

61. The nucleic acid or nucleic acid set of claim **56**, which is a vector comprising both the first and second nucleotide sequences.

62. The nucleic acid or nucleic acid set of claim **61**, wherein the vector is an expression vector, in which the first and second nucleotide sequences are each operably linked to a common promoter or a different promoter.

63. A host cell or host cell set, comprising the nucleic acid or nucleic acid set of claim **56**.

64. A method for preparing a bispecific antibody, comprising:

culturing the host cell or host cell set of claim **63** under conditions allowing for expression of the first polypeptide and the second polypeptide; and isolating the bispecific antibody that comprises the first polypeptide and the second polypeptide.

65. A pharmaceutical composition comprising (i) the bispecific antibody of claim **55**, and (ii) a pharmaceutically acceptable carrier.

66. A method of treating a disease associated with contact activation system, comprising administering to the subject in need thereof the pharmaceutical composition of claim **65**.

67. The method of claim **66**, wherein the disease associated with the contact activation system is hereditary angioedema (HAE) or thrombosis.

68. The method of claim **67**, wherein the HAE is type I HAE, type II HAE, or type III HAE.

69. The method of claim **67**, wherein the thrombosis is associated with atrial fibrillation, deep vein thrombosis (DVT), pulmonary embolism, stroke, or an arterial or venous thrombotic event.

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