(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
22 December 2016 (22.12.2016)

WIPO | PCT

(10) International Publication Number
WO 2016/205427 A2

(51) International Patent Classification:
C07K 16/24 (2006.01)

(21) International Application Number:
PCT/US2016/037710

(22) International Filing Date:
15 June 2016 (15.06.2016)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
62/175,546 15 June 2015 (15.06.2015) US
62/291,964 5 February 2016 (05.02.2016) US

(71) Applicant: **ABBVIE INC.** [US/US]; 1 North Waukegan Road, North Chicago, IL 60064 (US).

(72) Inventors: **GU, Jijie**; 19 Crimson Drive, Shrewsbury, MA 01545 (US). **BOWLEY, Diana**; 12 Hylair Drive, Shrewsbury, MA 01545 (US). **EATON, Lucia**; 177 Magill Drive, Grafton, MA 01519 (US). **DONG, Feng**; 118 Veronica Lane, Lansdale, PA 19446 (US). **BENATUIL, Lorenzo**; 33 Mohawk Drive, Northborough, MA 01532 (US). **GHAYUR, Tariq**; 1014 Washington Street, Holliston, MA 01746 (US). **CHARI, Ravi**; 2 Clara Street, Apt. 2, Worcester, MA 01606 (US). **RIESER, Matthew**; 7 Cedar Gage Circle, Sugar Grove, IL 60554 (US). **CLABBERS, Anca**; 20 Haven Hill Road, Rutland, MA 01543 (US).

(74) Agents: **MCDONELL, Leslie A.** et al.; Finnegan, Henderson, Farabow, Garrett & Dunner LLP, 901 New York Avenue, NW, Washington, DC 20001 (US).

(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JP, KE, KG, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU,

[Continued on next page]

(54) Title: BINDING PROTEINS AGAINST VEGF, PDGF, AND/OR THEIR RECEPTORS

(57) Abstract: Binding proteins that bind one or more of VEGF, PDGF and/or their receptors, including antibodies, CDR-grafted antibodies, humanized antibodies, binding fragments, fusion proteins, and bispecific or multispecific proteins thereof are disclosed. Also disclosed are methods of making and using the binding proteins.

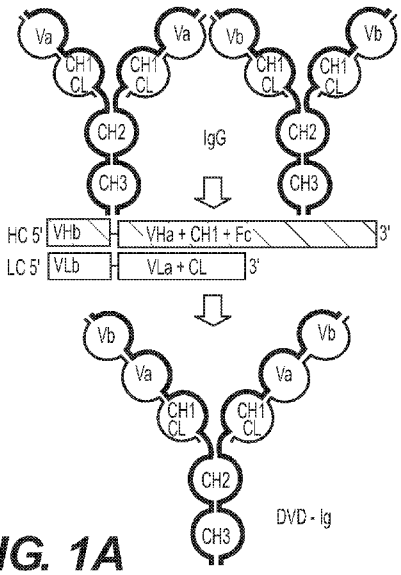


FIG. 1A

WO 2016/205427 A2

LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Published:

— *without international search report and to be republished upon receipt of that report (Rule 48.2(g))*

BINDING PROTEINS AGAINST VEGF, PDGF, AND/OR THEIR RECEPTORS

[001] This international application claims priority to U.S. Provisional Application Serial No. 62/175,546, filed June 15, 2015, and U.S. Provisional Application Serial No. 62/291,964, filed February 5, 2016, each of which is incorporated herein by reference in its entirety.

Field

[002] The invention relates to antibodies and antigen-binding fragments thereof, as well as multivalent and multispecific binding proteins, that bind vascular endothelial growth factor (VEGF) and/or platelet-derived growth factor (PDGF), as well as their receptors, and methods of making, and using the constructs in the diagnosis, prevention, and/or treatment of acute and chronic inflammatory diseases, cancer, and other disorders.

Background

[003] Angiogenesis, the formation of new blood vessels from pre-existing vasculature, plays a role in the pathogenesis of many diseases, including ocular diseases such as age-related macular degeneration (AMD) or diabetic macular edema (DME). Vascular endothelial growth factor (VEGF) plays a role in the regulation of normal and abnormal angiogenesis (Ferrara et al. (1997) Endocr. Rev. 18:4-25). Several anti-VEGF agents are provided in the art, e.g., in U.S. Patent No. 7,169,901, which discloses VEGF antibodies for inhibiting VEGF-induced cell proliferation, and U.S. Patent No. 7,070,959, which discloses isolated nucleic acid molecules encoding fusion proteins capable of binding VEGF.

[004] Targeting VEGF with currently available therapeutics is not effective in all patients or for all diseases associated with inflammation and/or angiogenesis. A significant population of non-responders present following anti-VEGF monotherapy, and the disease prevalence will only increase as the aging population increases globally.

[005] A currently preferred treatment for wet AMD consists of intravitreal injections of an anti-VEGF agent. However, athough anti-VEGF therapy reduces choroidal neovascularization, it does not have an effect on regression of the mature vasculature. Also, current agents do not provide an anti-fibrotic effect, so that once scarring of the retina occurs; visual acuity cannot be recovered. Other limitations of the existing treatments regimens include patient discomfort, the need for repeat injections with inherent complications including endophthalmitis, retinal tear and detachment, intraocular hemorrhage, and cataract formation. There is a substantial time burden on ophthalmologists to provide monthly intravitreal treatment and optical coherence tomography (OCT) measurements on a large volume patients. As a result,

there is a significant medical and economic need for an AMD therapeutic with greater efficacy, or that can be delivered less frequently and still achieve optimal efficacy.

[006] Platelet-derived growth factor (PDGF) is a growth factor involved in the regulation of blood vessels from pre-existing vessel tissue. PDGF binds to receptors on pericytes in newly-forming abnormal blood vessels. This may contribute to neovascularization of abnormal blood vessels by providing a protective perictye coating, for example, during ocular disorders such as wet AMD.

[007] Engineered proteins, such as antibodies, fragments, and multispecific binding proteins capable of binding two or more antigens, are known in the art. Such multispecific binding proteins can be generated using cell fusion, chemical conjugation, or recombinant DNA techniques. There are a variety of multispecific binding protein structures known in the art and many structures and methods have distinct disadvantages.

[008] Bispecific antibodies have been produced using quadroma technology. Bispecific antibodies can also be produced by chemical conjugation of two different mAbs. Other approaches include coupling of two parental antibodies with a hetero-bifunctional crosslinker, production of tandem single-chain Fv molecules, diabodies, bispecific diabodies, single-chain diabodies, and di-diabodies. In addition, a multivalent antibody construct comprising two Fab repeats in the heavy chain of an IgG and capable of binding four antigen molecules has been described (see PCT Publication No. WO 01/77342 and Miller et al. (2003) J. Immunol. 170(9):4854-61).

[009] US Patent No. 7,612,181 (incorporated herein by reference in its entirety) provides a novel family of binding proteins capable of binding two or more antigens with high affinity, which are called dual variable domain binding proteins (DVD-Ig binding protein) or dual variable domain immunoglobulins (DVD-Ig). DVD-Ig molecules are binding proteins that may be used to bind two distinct epitopes on the same molecule or two different molecules simultaneously. DVD-Ig molecules are unique binding proteins comprised of two variable domains fused to N-terminal constant regions. The variable domains may be directly fused to one another or connected via synthetic peptide linkers of assorted length and amino acid composition. DVD-Ig binding proteins may be engineered with intact and functional Fc domains, or otherwise modified constant domains, allowing them to mediate appropriate effector functions and exhibit other desired properties. The DVD-Ig format, due to its flexibility of choice of variable domain pair, orientation of two antigen-binding domains, and the length of the linker that joins them, may provide novel therapeutic modalities.

[010] Accordingly, while VEGF monotherapy has had some success in the art, there remains a need for constructs exhibiting better targeting, efficiency, and/or efficacy in binding to

VEGF, as well as improved targeting of other pathways involved in inflammation (such as ocular inflammation), e.g., the PDGF pathway. Improved targeting of either of these molecules, alone or in combination, may lead to improvements in, e.g., preventing, diagnosing, and/or treating disorders such as angiogenic, inflammatory, and/or ocular disorders. Also, while a variety of structures have been provided in the art, with various advantages and disadvantages, new variable domain sequences can further improve the properties of binding proteins targeting VEGF and/or PDGF, or their cognate receptors.

Summary

[011] Disclosed herein are binding proteins capable of binding VEGF and/or PDGF, and/or their cognate receptors. In some embodiments, the binding proteins are antibodies to VEGF and/or PDGF, or antigen-binding fragments thereof. In some embodiments, the binding proteins are bispecific and capable of binding VEGF and PDGF. In some embodiments, the binding proteins comprise one or more sequences from any one of Tables A, 27-30, 38-42, 46-50, or 56-58, or the CDR amino acid residues from those sequences.

[012] In various embodiments, the bnding proteins are bispecific or multispecific binding proteins capable of binding one or more of VEGF and/or PDGF, and/or their cognate receptors. In some embodiments, the binding proteins are dual variable domain immunoglobulins (DVD-Igs or DVD-Ig binding proteins) using the binding protein framework disclosed in U.S. Patent No. 7,612,181 (incorporated herein by reference in its entirety).

[013] In some embodiments, the DVD-Ig binding proteins contain particular first and second polypeptide chains, each comprising first and second variable domains comprising sequences (e.g., sequences selected from those listed in Tables A, 27-30, 38-42, 46-50, or 56-58, or the CDR amino acid residues from those sequences) that form functional binding sites for binding targets such as VEGF and/or PDGF, or their cognate receptors. In some embodiments, the first and second polypeptide chains of the binding protein each independently comprise VD1-(X1)n-VD2-C-X2, wherein VD1 is a first variable domain; VD2 is a second variable domain; C is a constant domain; X1 is a linker; X2 is an Fc region that is either present or absent; n is 0 or 1, and wherein the VD1 domains on the first and second polypeptide chains form a first functional target binding site for VEGF, PDGF, or a cognate receptor, and the VD2 domains on the first and second polypeptide chains form a second functional target binding site for VEGF, PDGF, or a cognate receptor. In some embodiments, (a) the first polypeptide chain of the binding protein comprises VD1-(X1)n-VD2-C-X2, wherein VD1 is a first heavy chain variable domain; VD2 is a second heavy chain variable domain; C is a heavy chain constant domain; X1 is a linker; X2 is an Fc region; and n is 0 or 1 (i.e., X1 and X2 are either present or absent, depending on whether n is independently chosen to be 0 or 1 for each position); and (b) the second polypeptide chain of the

binding protein comprises VD1-(X1)n-VD2-C-X2, wherein VD1 is a first light chain variable domain; VD2 is a second light chain variable domain; C is a light chain constant domain; X1 is a linker; X2 is an Fc region; and n is 0 or 1 for X1 and n is 0 for X2 (i.e., the Fc region is absent on the second polypeptide chain); and (c) wherein the VD1 domains on the first and second polypeptide chains form a first functional target binding site for VEGF, PDGF, or a cognate receptor, and the VD2 domains on the first and second polypeptide chains form a second functional target binding site for VEGF, PDGF, or a cognate receptor. In some embodiments, the VD1 position forms a binding site for VEGF and the VD2 position forms a binding site for PDGF. In some embodiments, the CDR and/or variable domains at the VD1 and VD2 positions are antibody variable domains and the constant domains are antibody constant domains. Any of the CDR and/or variable domain and/or first and second polypeptide chain sequences disclosed herein may be incorporated in these DVD-Ig binding protein structures to form binding domains for VEGF and/or PDGF, and/or their cognate receptors.

[014] In some embodiments, both the first and second binding sites of a DVD-Ig construct disclosed herein target VEGF. In some embodiments, both the first and second binding sites target PDGF. In some embodiments, the first binding site targets VEGF and the second binding site targets PDGF. In some embodiments, the first binding site targets PDGF and the second binding site targets VEGF. In some embodiments, an Fc domain is present on one polypeptide chain and absent on the other, or absent on both polypeptide chains. In some embodiments, the sequences of the first and second variable domains on each polypeptide chain (i.e., the VD1 and VD2 positions) are independently selected from the sequences in Table A, 27-30, 38-42, 46-50, or 56-58 to form functional binding sites. In some embodiments, the sequences of the first and second variable domains each contain the three complementarity determining regions (i.e., CDRs 1-3) from the selected sequences listed in Tables A, 27-30, 38-42, 46-50, or 56-58, and are arranged in the same order as shown in the Tables, thereby forming functional binding sites (i.e., the binding domains are capable of binding to their target antigen, VEGF or PDGF). In some embodiments, the paired variable domain sequences on the first and second polypeptide chains (i.e., the VD1 sequence on the first chain paired with the VD1 sequence on the second chain and the VD2 sequence on the first chain paired with the VD2 sequence on the second chain) form functional binding sites for binding targets VEGF and/or PDGF using the sequences in the Tables. In some embodiments, the binding proteins are capable of binding to VEGF and/or PDGF with improved binding affinity and/or neutralization potency, improved in vivo efficacy, improved expression, and/or improved drug-like properties (e.g., thermal stability, storage stability, solubility, etc.).

[015] Also disclosed herein are methods of making and using the claimed binding proteins, e.g., in the detection, inhibition, reduction, prevention, and/or treatment of cancers,

tumors, fibrosis, renal disease, inflammation, age-related macular degeneration (AMD), wet AMD, diabetic retinopathy, other angiogenesis-dependent diseases, or angiogenesis-independent diseases characterized by aberrant VEGF and/or PDGF expression or activity.

Brief Description of the Drawings

[016] Fig. 1A and Fig. 1B are schematic representations of a Dual Variable Domain (DVD) binding protein construct.

[017] Fig. 2A and Fig. 2B show the reactivity of anti-PDGF-BB antibodies and anti-VEGF-A/anti-PDGF-BB DVD-Ig molecules to ECM-associated PDGF-BB.

[018] Fig. 3 illustrates the inhibition of sprouting from a HUVEC/MSC co-culture sprouting assay by anti-VEGF-A/anti-PDGF-BB DVD-Ig molecules.

[019] Fig. 4 is a bar graph showing the area of subretinal neovascularization in Rho/huVEGF transgenic mice.

[020] Fig. 5 is a bar graph showing the area of choroidal neovascularization in Rho/huVEGF transgenic mice.

[021] Fig. 6 is a bar graph comparing choroidal neovascularization in the untreated eye among the different treatment groups.

[022] Fig. 7 is a bar graph showing number of partial, total, and undetached eyes in Tet/opsin/VEGF mice.

Detailed Description

[023] Vascular endothelial growth factor (VEGF) is a signal protein that regulates physiological angiogenesis during embryogenesis, skeletal growth, and reproductive functions. Aberrant expression of VEGF is implicated in pathological angiogenesis and is associated with tumors, intraocular neovascular disorders, and other diseases. The VEGF family members include VEGF-A, placenta growth factor (PGF), VEGF-B, VEGF-C, and VEGF-D. Multiple isoforms of VEGF-A exist that result from alternative splicing of a single, 8-exon *VEGFA* gene. The biological effects of VEGF are mediated by various receptors, including two receptor tyrosine kinases, VEGF receptor-1 (VEGFR1) and VEGF receptor-2 (VEGFR2), which differ in their signaling properties. When cells are deficient in oxygen, they produce hypoxia-inducible factor (HIF) which releases VEGF and other mediators triggering a tyrosine kinase pathway leading to angiogenesis (Ferrara et al. (2003) Nat. Med. 9:669-676). In various embodiments, the binding proteins disclosed herein can bind one or more of the VEGF family members, including alternate isoforms, and/or can bind one or more of the cognate VEGF receptors.

[024] Platelet-derived growth factor (PDGF) is a protein that stimulates growth, survival, and motility of mesenchymal cells and certain other cell types. It has significant functions during embryonal development and in the control of blood vessel formation as an adult. PDGF is composed of a dimeric glycoprotein made up of two A (-AA), two B (-BB) chains, or a combination of the two (-AB). There are five different isoforms of PDGF that moderate cellular responses through two receptors, alpha (PDGFRA) and beta (PDGFRB) (Heldin (2013) Cell Commun. Sig. 11:97). PDGF plays an important role in driving the proliferation of undifferentiated mesenchyme and some progenitor populations. Overactivity or inappropriate PDGF signaling is associated with the development of certain malignant diseases, as well as non-malignant diseases characterized by excessive cell proliferation and other inflammatory disorders. In various embodiments, the binding proteins disclosed herein can bind one or more of the PDGF isoforms, and/or can bind one or more of the cognate PDGF receptors.

Binding Proteins

[025] Disclosed herein are binding proteins capable of binding one or more of VEGF, PDGF, and their cognate receptors. In some embodiments, the binding protein is an antibody or an antigen-binding fragment thereof. In an embodiment, the binding protein is an antibody, a monoclonal antibody, a murine antibody, a human antibody, a humanized antibody, a bispecific antibody, a chimeric antibody, a Fab, a Fab′, a $F(ab')_2$, an ScFv, an SMIP, an affibody, an avimer, a versabody, a nanobody, a fynomab, a domain antibody, or an antigen binding fragment of any of the foregoing. In an embodiment, the binding protein comprises antibody heavy chain variable domain sequences and antibody light chain variable domain sequences that are capable of binding one or more of VEGF, PDGF, and their cognate receptors. In an embodiment, the binding protein comprises the paired heavy and light chain variable domain sequences of any of the binding sites disclosed in Tables 27-30, 38-42, 46-50, or the CDR sequences from those variable domains. The CDR sequences of the variable domains in the Tables are identified in bold.

[026] In some embodiments, the binding proteins disclosed herein is bispecific or multispecific. The bispecific or multispecific construct may be monovalent or bivalent. Various bispecific or multispecific constructs are known in the art (see e.g., Spiess et al. (2015) Mol. Immunol. 67; 95-106). Bispecific or multispecific constructs include, but are not limited to, an asymmetric bispecific antibody, an asymmetric bispecific IgG4, a CrossMab binding protein, a bispecific antibody, a bispecific binding protein, a multispecific binding protein, a DAF (dual action Fab antibody; two-in-one), a DAF (dual action Fab antibody; four-in-one), a DutaMab, a DT-IgG, a knobs-in-holes binding protein, a Charge pair binding protein, a Fab-arm exchange binding protein, a SEEDbody, a Triomab (Triomab quadroma bispecific or removab bispecific), a LUZ-Y, a Fcab, a κλ-body, an iMab (innovative multimer), and an Orthogonal Fab. In some

embodiments, the bispecific or multispecific construct is a DVD-Ig binding protein, an IgG(H)-scFv, an scFv-(H)IgG, an IgG(L)-scFv, an scFv-(L)IgG, an IgG(L, H)-Fv, an IgG(H)-V, a V(H)-IgG, an IgG(L)-V, a V(L)-IgG, a KIH IgG-scFab, a 2scFv-IgG, an IgG-2scFv, an scFv4-Ig, a Zybody, or a DVI-IgG (four-in-one). In some embodiments, the bispecific or multispecific construct also can be a nanobody (or VHH), a bispecific tandem nanobody, a bispecific trivalent tandem nanobody, a nanobody-HSA, a BiTE (bispecific T-cell engager) binding protein, a Diabody, a DART (dual affinity retargeting) binding protein, a TandAb (tetravalent bispecifc tandem antibody), an scDiabody, an scDiabody-CH3, a Diabody-CH3, a Triple Body, a Miniantibody, a Minibody, a TriBi minibody, an scFv-CH3 KIH, a Fab-scFv, an scFv-CH-CL-scFv, a F(ab')2, a F(ab')2 scFv2, an scFv-KIH, a Fab-scFv-Fc, a Tetravalent HCAb, an scDiabody-Fc, a Diabody-Fc, a Tandem scFv-Fc, a Fabsc, a bsFc-1/2, a CODV-Ig (cross-over dual variable immunoglobulin), a biclonics antibody or an Intrabody. Bispecific or multispecific constructs also include, for example, a Dock and Lock binding protein, an ImmTAC, an HSAbody, an scDiabody-HSA, a Tandem scFv-Toxin, an IgG-IgG binding protein, a Cov-X-Body, and an scFv1-PEG-scFv2. In some embodiments, the bispecific or multispecific construct is a DVD-Ig binding protein, a CrossMab binding protein, a diabody, a tandem single-chain Fv molecule, a bispecific diabody, a single-chain diabody molecule, or a di-diabody. In some embodiments, the binding protein is a DVD-Ig binding protein. See, e.g., US Patent No. 7,612,181 (incorporated herein by reference in its entirety). The bispecific or multispecific construct may comprise one or more binding sites for VEGF, PDGF, and/or their receptors. The bispecific or multispecific construct may comprise binding sites only for VEGF, PDGF, and/or their receptors, or may comprise additional binding sites for other antigen targets. The bispecific or multispecific construct may comprise binding sites for more than one epitope on VEGF, PDGF, and/or their receptors, e.g., using different CDR sets or variable domains from those disclosed herein to form binding sites targeting different epitopes.

[027] In various embodiments, the binding protein is capable of binding VEGF, and comprises CDRs 1-3 from SEQ ID NO: 17 and CDRs 1-3 from SEQ ID NO: 18, CDRs 1-3 from SEQ ID NO: 19 and CDRs 1-3 from SEQ ID NO: 20, CDRs 1-3 from SEQ ID NO: 21 and CDRs 1-3 from SEQ ID NO: 22, CDRs 1-3 from SEQ ID NO: 23 and CDRs 1-3 from SEQ ID NO: 24, CDRs 1-3 from SEQ ID NO: 25 and CDRs 1-3 from SEQ ID NO: 26, CDRs 1-3 from SEQ ID NO: 27 and CDRs 1-3 from SEQ ID NO: 28, CDRs 1-3 from SEQ ID NO: 29 and CDRs 1-3 from SEQ ID NO: 30, CDRs 1-3 from SEQ ID NO: 31 and CDRs 1-3 from SEQ ID NO: 32, CDRs 1-3 from SEQ ID NO: 33 and CDRs 1-3 from SEQ ID NO: 34, CDRs 1-3 from SEQ ID NO: 35 and CDRs 1-3 from SEQ ID NO: 36, CDRs 1-3 from SEQ ID NO: 37 and CDRs 1-3 from SEQ ID NO: 38, CDRs 1-3 from SEQ ID NO: 39 and CDRs 1-3 from SEQ ID NO: 40, CDRs 1-3 from SEQ ID NO: 41 and CDRs 1-3 from SEQ ID NO: 42, or CDRs 1-3 from SEQ ID NO: 43 and

CDRs 1-3 from SEQ ID NO: 44. In an embodiment, the binding protein is capable of binding VEGF, and comprises SEQ ID NO: 17 and SEQ ID NO: 18, SEQ ID NO: 19 and SEQ ID NO: 20, SEQ ID NO: 21 and SEQ ID NO: 22, SEQ ID NO: 23 and SEQ ID NO: 24, SEQ ID NO: 25 and SEQ ID NO: 26, SEQ ID NO: 27 and SEQ ID NO: 28, SEQ ID NO: 29 and SEQ ID NO: 30, SEQ ID NO: 31 and SEQ ID NO: 32, SEQ ID NO: 33 and SEQ ID NO: 34, SEQ ID NO: 35 and SEQ ID NO: 36, SEQ ID NO: 37 and SEQ ID NO: 38, SEQ ID NO: 39 and SEQ ID NO: 40, SEQ ID NO: 41 and SEQ ID NO: 42, or SEQ ID NO: 43 and SEQ ID NO: 44. Any of said binding proteins capable of binding VEGF may also be capable of binding PDGF, and may comprise any of the PDGF binding sequences as described herein.

[028] In varous embodiments, the binding protein is capable of binding PDGF, and comprises CDRs 1-3 from SEQ ID NO: 1 and CDRs 1-3 from SEQ ID NO: 2, CDRs 1-3 from SEQ ID NO: 3 and CDRs 1-3 from SEQ ID NO: 4, CDRs 1-3 from SEQ ID NO: 5 and CDRs 1-3 from SEQ ID NO: 6, CDRs 1-3 from SEQ ID NO: 7 and CDRs 1-3 from SEQ ID NO: 8, CDRs 1-3 from SEQ ID NO: 9 and CDRs 1-3 from SEQ ID NO: 10, CDRs 1-3 from SEQ ID NO: 11 and CDRs 1-3 from SEQ ID NO: 12, CDRs 1-3 from SEQ ID NO: 13 and CDRs 1-3 from SEQ ID NO: 14, CDRs 1-3 from SEQ ID NO: 15 and CDRs 1-3 from SEQ ID NO: 16, or CDRs 1-3 from SEQ ID NO: 211 and CDRs 1-3 from SEQ ID NO: 212. In an embodiment, the binding protein is capable of binding PDGF, and comprises SEQ ID NO: 1 and SEQ ID NO: 2, SEQ ID NO: 3 and SEQ ID NO: 4, SEQ ID NO: 5 and SEQ ID NO: 6, SEQ ID NO: 7 and SEQ ID NO: 8, SEQ ID NO: 9 and SEQ ID NO: 10, SEQ ID NO: 11 and SEQ ID NO: 12, SEQ ID NO: 13 and SEQ ID NO: 14, SEQ ID NO: 15 and SEQ ID NO: 16, or SEQ ID NO: 211 and SEQ ID NO: 212. Any of said binding proteins capable of binding PDGF may also be capable of binding VEGF, and may comprise any of the VEGF binding sequences as described herein.

[029] In an embodiment, the binding protein is a bispecific or multispecific antibody capable of binding one or more of VEGF, PDGF, and their cognate receptors, or another multispecific construct capable of binding the targets. In certain embodiments, the treatment is with bispecific antibodies that have been produced by quadroma technology (Milstein and Cuello (1983) Nature 305(5934): 537-40), by chemical conjugation of two different monoclonal antibodies (Staerz et al. (1985) Nature 314(6012): 628-31), or by knob-into-hole or similar approaches which introduces mutations in the Fc region (Holliger et al. (1993) Proc. Natl. Acad. Sci. USA 90(14): 6444-6448). In some embodiments, the multispecific binding protein is a dual variable domain immunoglobulin (DVD-Ig), e.g., as disclosed in U.S. Patent No. 7,612,181 (incorporated herein by reference in their entirety). In an embodiment, the DVD-Ig binding protein comprises one or more binding sites comprising the paired heavy and light chain variable domain sequences of any of the binding sites disclosed in Tables 27-30, 38-42, 46-50, or 56-58, or the CDR sequences from those variable domains. For instance, a binding site for VEGF can

comprise a paired set of heavy and light chain variable domain sequences from any one of Tables 27 or 38-42, or the CDR regions from those sequences, while the PDGF can comprise the paired heavy and light chain variable domain sequences in Tables 28 or 46-50, or the CDR regions from those sequences. The CDR regions of some of these sequences are shown in Table A and in Table 57.

[030] In some embodiments, a multispecific binding protein disclosed herein is capable of binding VEGF and PDGF, and allows for fewer injections or a lower concentration of active agent, as compared to combination antibody therapy.

[031] In some embodiments, the DVD-Ig binding protein comprises first and second polypeptide chains, each independently comprising VD1-(X1)n-VD2-C-X2, wherein: VD1 is a first variable domain; VD2 is a second variable domain; C is a constant domain; X1 is a linker; X2 is an Fc region that is either present or absent; n is independently 0 or 1 on the first and second chains, and wherein the VD1 domains on the first and second polypeptide chains form a first functional target binding site and the VD2 domains on the first and second polypeptide chains form a second functional target binding site. In some embodiments, the binding protein is capable of binding one or more of VEGF, PDGF, and their cognate receptors, e.g., using a paired set of sequences from any one of Tables 27-30, 38-42, 46-50, or 56-58. In some embodiments, the binding protein comprises VD1 sequences on the first and second polypeptide chains (i.e., a VD1 sequence on the first chain paired with a VD1 sequence on the second chain) that together form a binding domain capable of binding a target selected from VEGF, PDGF, and their cognate receptors. In some embodiments, the binding protein is capable of binding VEGF at both the VD1 and VD2 positions. In some embodiments, the binding protein is capable of binding PDGF at both the VD1 and VD2 positions. In some embodiments, the binding protein is capable of binding VEGF at the VD1 position and PDGF at the VD2 position. In some embodiments, the binding protein is capable of binding PDGF at the VD1 position and VEGF at the VD2 position.

[032] When a binding protein comprises the CDRs from a sequence selected from any one of Tables 27-30, 38-42, 46-50, or 56-58, the CDRs are arranged in the order specified by the sequence in the Table and separated by suitable framework sequences to form a functional binding site. The paired sequences selected from the Tables that form a functional binding site for a target (e.g., a binding site for VEGF and/or PDGF), or the CDRs from those sequences, may be placed in either the VD1 or VD2 positions on the first and second polypeptide chains to form a binding site at either the VD1 or VD2 domain.

[033] The binding proteins disclosed herein comprise VD1 and VD2 binding domains that are capable of binding to first and second target antigens. As used herein, a VD1 domain or a VD2 domain, or a VD1 position or VD2 position, may refer to either the variable domain

sequence on one polypeptide chain (e.g., a VD1 heavy chain sequence) or to the variable domain sequences on both the first and second polypeptide chain (e.g., a VD1 heavy chain sequence and a VD1 light chain sequence) that together form the functional binding site, as indicated by the context in which it is discussed.

[034] In some embodiments, a DVD-Ig binding protein can comprise two first and two second polypeptide chains forming four functional binding sites on two arms of the construct. An example of a four chain structure having two arms, each arm comprising a first and second polypeptide chain and two functional binding sites, is shown in Figure 1.

[035] In an embodiment, the DVD-Ig binding protein is capable of binding VEGF and PDGF, wherein the binding site for VEGF comprises CDRs 1-3 from SEQ ID NO: 17 and CDRs 1-3 from SEQ ID NO: 18, CDRs 1-3 from SEQ ID NO: 19 and CDRs 1-3 from SEQ ID NO: 20, CDRs 1-3 from SEQ ID NO: 21 and CDRs 1-3 from SEQ ID NO: 22, CDRs 1-3 from SEQ ID NO: 23 and CDRs 1-3 from SEQ ID NO: 24, CDRs 1-3 from SEQ ID NO: 25 and CDRs 1-3 from SEQ ID NO: 26, CDRs 1-3 from SEQ ID NO: 27 and CDRs 1-3 from SEQ ID NO: 28, CDRs 1-3 from SEQ ID NO: 29 and CDRs 1-3 from SEQ ID NO: 30, CDRs 1-3 from SEQ ID NO: 31 and CDRs 1-3 from SEQ ID NO: 32, CDRs 1-3 from SEQ ID NO: 33 and CDRs 1-3 from SEQ ID NO: 34, CDRs 1-3 from SEQ ID NO: 35 and CDRs 1-3 from SEQ ID NO: 36, CDRs 1-3 from SEQ ID NO: 37 and CDRs 1-3 from SEQ ID NO: 38, CDRs 1-3 from SEQ ID NO: 39 and CDRs 1-3 from SEQ ID NO: 40, CDRs 1-3 from SEQ ID NO: 41 and CDRs 1-3 from SEQ ID NO: 42, or CDRs 1-3 from SEQ ID NO: 43 and CDRs 1-3 from SEQ ID NO: 44. In an embodiment, the binding site for VEGF comprises SEQ ID NO: 17 and SEQ ID NO: 18, SEQ ID NO: 19 and SEQ ID NO: 20, SEQ ID NO: 21 and SEQ ID NO: 22, SEQ ID NO: 23 and SEQ ID NO: 24, SEQ ID NO: 25 and SEQ ID NO: 26, SEQ ID NO: 27 and SEQ ID NO: 28, SEQ ID NO: 29 and SEQ ID NO: 30, SEQ ID NO: 31 and SEQ ID NO: 32, SEQ ID NO: 33 and SEQ ID NO: 34, SEQ ID NO: 35 and SEQ ID NO: 36, SEQ ID NO: 37 and SEQ ID NO: 38, SEQ ID NO: 39 and SEQ ID NO: 40, SEQ ID NO: 41 and SEQ ID NO: 42, or SEQ ID NO: 43 and SEQ ID NO: 44.

[036] In an embodiment, a DVD-Ig binding protein is disclosed that is capable of binding VEGF and PDGF, wherein the binding site for PDGF comprises CDRs 1-3 from SEQ ID NO: 1 and CDRs 1-3 from SEQ ID NO: 2, CDRs 1-3 from SEQ ID NO: 3 and CDRs 1-3 from SEQ ID NO: 4, CDRs 1-3 from SEQ ID NO: 5 and CDRs 1-3 from SEQ ID NO: 6, CDRs 1-3 from SEQ ID NO: 7 and CDRs 1-3 from SEQ ID NO: 8, CDRs 1-3 from SEQ ID NO: 9 and CDRs 1-3 from SEQ ID NO: 10, CDRs 1-3 from SEQ ID NO: 11 and CDRs 1-3 from SEQ ID NO: 12, CDRs 1-3 from SEQ ID NO: 13 and CDRs 1-3 from SEQ ID NO: 14, CDRs 1-3 from SEQ ID NO: 15 and CDRs 1-3 from SEQ ID NO: 16, or CDRs 1-3 from SEQ ID NO: 211 and CDRs 1-3 from SEQ ID NO: 212. In an embodiment, the binding site for PDGF comprises SEQ ID NO: 1 and SEQ ID NO: 2, SEQ ID NO: 3 and SEQ ID NO: 4, SEQ ID NO: 5 and SEQ ID

NO: 6, SEQ ID NO: 7 and SEQ ID NO: 8, SEQ ID NO: 9 and SEQ ID NO: 10, SEQ ID NO: 11 and SEQ ID NO: 12, SEQ ID NO: 13 and SEQ ID NO: 14, SEQ ID NO: 15 and SEQ ID NO: 16, or SEQ ID NO: 211 and SEQ ID NO: 212.

[037] In an embodiment, the DVD-Ig binding protein is capable of binding VEGF and PDGF, wherein the binding site for VEGF comprises CDRs 1-3 from SEQ ID NO: 17 and CDRs 1-3 from SEQ ID NO: 18, CDRs 1-3 from SEQ ID NO: 19 and CDRs 1-3 from SEQ ID NO: 20, CDRs 1-3 from SEQ ID NO: 21 and CDRs 1-3 from SEQ ID NO: 22, CDRs 1-3 from SEQ ID NO: 23 and CDRs 1-3 from SEQ ID NO: 24, CDRs 1-3 from SEQ ID NO: 25 and CDRs 1-3 from SEQ ID NO: 26, CDRs 1-3 from SEQ ID NO: 27 and CDRs 1-3 from SEQ ID NO: 28, CDRs 1-3 from SEQ ID NO: 29 and CDRs 1-3 from SEQ ID NO: 30, CDRs 1-3 from SEQ ID NO: 31 and CDRs 1-3 from SEQ ID NO: 32, CDRs 1-3 from SEQ ID NO: 33 and CDRs 1-3 from SEQ ID NO: 34, CDRs 1-3 from SEQ ID NO: 35 and CDRs 1-3 from SEQ ID NO: 36, CDRs 1-3 from SEQ ID NO: 37 and CDRs 1-3 from SEQ ID NO: 38, CDRs 1-3 from SEQ ID NO: 39 and CDRs 1-3 from SEQ ID NO: 40, CDRs 1-3 from SEQ ID NO: 41 and CDRs 1-3 from SEQ ID NO: 42, or CDRs 1-3 from SEQ ID NO: 43 and CDRs 1-3 from SEQ ID NO: 44; and the binding site for PDGF comprises CDRs 1-3 from SEQ ID NO: 1 and CDRs 1-3 from SEQ ID NO: 2, CDRs 1-3 from SEQ ID NO: 3 and CDRs 1-3 from SEQ ID NO: 4, CDRs 1-3 from SEQ ID NO: 5 and CDRs 1-3 from SEQ ID NO: 6, CDRs 1-3 from SEQ ID NO: 7 and CDRs 1-3 from SEQ ID NO: 8, CDRs 1-3 from SEQ ID NO: 9 and CDRs 1-3 from SEQ ID NO: 10, CDRs 1-3 from SEQ ID NO: 11 and CDRs 1-3 from SEQ ID NO: 12, CDRs 1-3 from SEQ ID NO: 13 and CDRs 1-3 from SEQ ID NO: 14, CDRs 1-3 from SEQ ID NO: 15 and CDRs 1-3 from SEQ ID NO: 16, or CDRs 1-3 from SEQ ID NO: 211 and CDRs 1-3 from SEQ ID NO: 212. In an embodiment, the binding site for VEGF comprises SEQ ID NO: 17 and SEQ ID NO: 18, SEQ ID NO: 19 and SEQ ID NO: 20, SEQ ID NO: 21 and SEQ ID NO: 22, SEQ ID NO: 23 and SEQ ID NO: 24, SEQ ID NO: 25 and SEQ ID NO: 26, SEQ ID NO: 27 and SEQ ID NO: 28, SEQ ID NO: 29 and SEQ ID NO: 30, SEQ ID NO: 31 and SEQ ID NO: 32, SEQ ID NO: 33 and SEQ ID NO: 34, SEQ ID NO: 35 and SEQ ID NO: 36, SEQ ID NO: 37 and SEQ ID NO: 38, SEQ ID NO: 39 and SEQ ID NO: 40, SEQ ID NO: 41 and SEQ ID NO: 42, or SEQ ID NO: 43 and SEQ ID NO: 44; and the binding site for PDGF comprises SEQ ID NO: 1 and SEQ ID NO: 2, SEQ ID NO: 3 and SEQ ID NO: 4, SEQ ID NO: 5 and SEQ ID NO: 6, SEQ ID NO: 7 and SEQ ID NO: 8, SEQ ID NO: 9 and SEQ ID NO: 10, SEQ ID NO: 11 and SEQ ID NO: 12, SEQ ID NO: 13 and SEQ ID NO: 14, SEQ ID NO: 15 and SEQ ID NO: 16, or SEQ ID NO: 211 and SEQ ID NO: 212.

[038] In various embodiments, the DVD-Ig binding protein is capable of binding VEGF and PDGF, wherein the binding site for VEGF comprises CDRs 1-3 from SEQ ID NO: 35 and CDRs-1-3 from SEQ ID NO: 36, and the binding site for PDGF comprises CDRs 1-3 from SEQ ID NO: 15 and CDRs-1-3 from SEQ ID NO: 16. In an embodiment, the binding site for

VEGF comprises SEQ ID NO: 35 and SEQ ID NO: 36, and the binding site for PDGF comprises SEQ ID NO: 15 and SEQ ID NO: 16. In any of these embodiments, the binding site for VEGF may be the outer binding domain or VD1 position as described herein, and the binding site for PDGF may be the inner domain or VD2 position as described herein. In various embodiments, any of the DVD-Ig binding proteins disclosed herein can comprise one or more of the X1 linkers shown in Table 55. In an embodiment, the X1 linker on the heavy chain is a GS-H10 linker and the X1 linker on the light chain is a GS-L10(dR) linker. In an embodiment, the X1 linker on the heavy chain is a GS-H10 linker and the X1 linker on the light chain is a GS-L10 linker. In an embodiment, the X1 linker on the heavy chain is an HG-short linker and the X1 linker on the light chain is an LK-long linker.

[039] In various embodiments, any of the antibodies, binding proteins, or DVD-Ig binding proteins disclosed herein can comprise a human IgG (e.g., an IgG1) heavy chain constant region on the first polypeptide chain comprising substitutions of leucines at positions 234 and 235 with alanines, and optionally also (or alternatively) a substitution of histidine at position 435 with alanine, wherein the amino acid positions are numbered using EU index numbering. In various embodiments, the antibody, binding protein, or DVD-Ig binding protein can also comprise a human kappa or lambda light chain constant region on the second polypeptide chain. In an embodiment, the light chain comprises a wild-type human kappa light chain constant region sequence.

[040] In an embodiment, the DVD-Ig binding protein is capable of binding VEGF and PDGF, and comprises PR-1610561 (comprising SEQ ID NOs: 131 and 132). In an embodiment, the binding protein comprises a heavy chain constant region on the first polypeptide chain comprising a human IgG1 heavy chain sequence modified by one or more amino acid changes, wherein the changes comprise substitution of leucines at positions 234 and 235 with alanines, and optionally also comprising a substitution of histidine at position 435 with alanine, wherein the amino acid positions are numbered using EU index numbering; and a light chain constant region on the second polypeptide chain comprising a human kappa light chain constant region sequence. In an embodiment, the binding protein comprises an IgG1 constant region with substitution of leucines at positions 234 and 235 with alanines, and a substitution of histidine at position 435 with alanine, wherein the amino acid positions are numbered using EU index numbering; and a light chain constant region on the second polypeptide chain comprising a human kappa light chain constant region sequence. In some embodiments, the L234A, L235A, and H435 mutations are present in a DVD-Ig binding protein comprising PR-1610561 (comprising SEQ ID NOs: 131 and 132). In some embodiments, the binding protein carrying the constant region mutations has increased ocular duration over an antibody, but is rapidly cleared from systemic circulation (e.g., by altering FcRn recognition), as compared to an antibody or as compared to the same binding

protein lacking the constant region mutations. In some embodiments, the high ocular duration allows for less frequent administration and/or fewer overall injections while achieving a comparable or improved efficacy as compared to administration of a combination of anti-VEGF and anti-PDGF antibodies or as compared to administration of the binding protein lacking the constant region mutations. In some embodiments, the binding protein carrying the constant region mutations has decreased ADCC and CDC effector functions mediated by binding to extracellular matrix-associated VEGF-A and/or PDGF-BB, as compared to administration of the binding protein lacking the constant region mutations. In some embodiments, the binding protein carrying the constant region mutations does not bind to one or more Fc-gamma receptors. In some embodiments, systemic levels of the binding protein in a patient drops below detectable levels after less than 20, 25, 30, 35, or 40 hours following administration at 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 mg/kg, or more (or any concentration in between) in an intravenous bolus dose.

[041] In an embodiment, the DVD-Ig binding protein is capable of binding VEGF and PDGF, wherein the binding site for VEGF comprises CDRs 1-3 from SEQ ID NO: 17 and CDRs-1-3 from SEQ ID NO: 18, and the binding site for PDGF comprises CDRs 1-3 from SEQ ID NO: 1 and CDRs-1-3 from SEQ ID NO: 2. In an embodiment, the binding site for VEGF comprises SEQ ID NO: 17 and SEQ ID NO: 18, and the binding site for PDGF comprises SEQ ID NO: 1 and SEQ ID NO: 2. In an embodiment, the DVD-Ig binding protein is capable of binding VEGF and PDGF, wherein the binding site for VEGF comprises CDRs 1-3 from SEQ ID NO: 39 and CDRs-1-3 from SEQ ID NO: 40, and the binding site for PDGF comprises CDRs 1-3 from SEQ ID NO: 15 and CDRs-1-3 from SEQ ID NO: 16. In an embodiment, the binding site for VEGF comprises SEQ ID NO: 39 and SEQ ID NO: 40, and the binding site for PDGF comprises SEQ ID NO: 15 and SEQ ID NO: 16. In any of these embodiments, the binding site for VEGF may be the outer binding domain or VD1 sequence as described herein, and the binding site for PDGF may be the inner domain or VD2 sequence as dscribed herein. In various embodiments, the binding proteins can comprise one or more of the X1 linkers shown in Table 55. In an embodiment, the X1 linker on the heavy chain is a GS-H10 linker and the X1 linker on the light chain is a GS-L10(dR) linker. In an embodiment, the X1 linker on the heavy chain is a GS-H10 linker and the X1 linker on the light chain is a GS-L10 linker. In an embodiment, the X1 linker on the heavy chain is an HG-short linker and the X1 linker on the light chain is an LK-long linker. In an embodiment, the binding protein is capable of binding VEGF and PDGF, and comprises PR-1572102 (comprising SEQ ID NOs: 88 and 89) or PR-1572105 (comprising SEQ ID NOs: 94 and 95) or PR1611292 (comprising SEQ ID NOs: 141 and 142). In an embodiment, the binding protein comprises a heavy chain constant region on the first polypeptide chain comprising a human IgG1 heavy chain sequence modified by one or more amino acid changes, wherein the changes comprise substitution of leucines at positions 234 and 235 with alanines, and optionally

also comprising a substitution of histidine at position 435 with alanine, wherein the amino acid positions are numbered using EU index numbering; and a light chain constant region on the second polypeptide chain comprising a human kappa light chain constant region sequence.

[042] In an embodiment, the DVD-Ig binding protein comprises the first and second polypeptide chains of any of the DVD-Ig binding proteins disclosed in Tables 56-58. The CDR sequences of the variable domains in Tables 56-58 are in bold and the linker sequences are italicized.

[043] In an embodiment, the DVD-Ig binding protein comprises the first and second polypeptide chains of PR-1563988 (comprising SEQ ID NOs: 45 and 46), PR-1563990 (comprising SEQ ID NOs: 47 and 48), PR-1563998 (comprising SEQ ID NOs: 49 and 50), PR-1564009 (comprising SEQ ID NOs: 51 and 52), PR-1564010 (comprising SEQ ID NOs: 53 and 54), PR-1564011 (comprising SEQ ID NOs: 55 and 56), PR-1564012 (comprising SEQ ID NOs: 57 and 58), PR-1564013 (comprising SEQ ID NOs: 59 and 60), PR-1565031 (comprising SEQ ID NOs: 76 and 77), PR-1565032 (comprising SEQ ID NOs: 78 and 79), PR-1565035 (comprising SEQ ID NOs: 80 and 81), PR-1572102 (comprising SEQ ID NOs: 88 and 89), PR-1572103 (comprising SEQ ID NOs: 90 and 91), PR-1572104 (comprising SEQ ID NOs: 92 and 93), PR-1572105 (comprising SEQ ID NOs: 94 and 95), PR-1572106 (comprising SEQ ID NOs: 96 and 97), PR-1575832 (comprising SEQ ID NOs: 99 and 100), PR-1575834 (comprising SEQ ID NOs: 101 and 102), PR-1575835 (comprising SEQ ID NOs: 103 and 104), PR-1577165 (comprising SEQ ID NOs: 105 and 106), PR-1577166 (comprising SEQ ID NOs: 107 and 108), PR-1577547 (comprising SEQ ID NOs: 109 and 110), PR-1577548 (comprising SEQ ID NOs: 111 and 112), PR-1577550 (comprising SEQ ID NOs: 113 and 114), PR-1578137 (comprising SEQ ID NOs: 116 and 117), PR-1610560 (comprising SEQ ID NOs: 129 and 130), PR-1610561 (comprising SEQ ID NOs: 131 and 132), PR-1610562 (comprising SEQ ID NOs: 133 and 134), PR-1610563 (comprising SEQ ID NOs: 135 and 136), PR-1611291 (comprising SEQ ID NOs: 139 and 140), PR-1611292 (comprising SEQ ID NOs: 141 and 142), PR-1612489 (comprising SEQ ID NOs: 161 and 162), PR-1612491 (comprising SEQ ID NOs: 163 and 164), PR-1612492 (comprising SEQ ID NOs: 165 and 166), PR-1612495 (comprising SEQ ID NOs: 171 and 172), PR-1612496 (comprising SEQ ID NOs: 173 and 174), PR-1612499 (comprising SEQ ID NOs: 177 and 178), PR-1612500 (comprising SEQ ID NOs: 179 and 180), PR-1612501 (comprising SEQ ID NOs: 181 and 182), PR-1612502 (comprising SEQ ID NOs: 183 and 184), PR-1613183 (comprising SEQ ID NOs: 185 and 186), PR-1613184 (comprising SEQ ID NOs: 187 and 188), PR-1613185 (comprising SEQ ID NOs: 189 and 190), PR-1613190 (comprising SEQ ID NOs: 199 and 200), PR-1565040 (comprising SEQ ID NOs: 209 and 210), PR-1565042 (comprising SEQ ID NOs: XX and YY), PR-1565044 (comprising SEQ ID NOs: 213 and 214), PR-1565051 (comprising SEQ ID NOs: 215 and 216), PR-1565083 (comprising SEQ ID NOs: 217 and 218), PR-1565084

(comprising SEQ ID NOs: 219 and 220), PR-1565085 (comprising SEQ ID NOs: 221 and 222), PR-1565086 (comprising SEQ ID NOs: 223 and 224), PR-1571821 (comprising SEQ ID NOs: 225 and 226), PR-1571823 (comprising SEQ ID NOs: 227 and 228), PR-1575521 (comprising SEQ ID NOs: 229 and 230), PR-1571824 (comprising SEQ ID NOs: 231 and 232), PR-1571825 (comprising SEQ ID NOs: 233 and 234), PR-1571826 (comprising SEQ ID NOs: 235 and 236), PR-1571827 (comprising SEQ ID NOs: 237 and 238), PR-1571828 (comprising SEQ ID NOs: 239 and 240), PR-1571830 (comprising SEQ ID NOs: 241 and 242), PR-1571831 (comprising SEQ ID NOs: 243 and 244), PR-1571832 (comprising SEQ ID NOs: 245 and 246), PR-1571836 (comprising SEQ ID NOs: 247 and 248), PR-1577053 (comprising SEQ ID NOs: 249 and 250), or PR-1577056 (comprising SEQ ID NOs: 251 and 252.

[044] In some embodiments, a binding protein, including a DVD-Ig binding protein, antibody, or fragment thereof, is capable of binding VEGF and/or PDGF and has at least about 80%, 90%, 95%, or 99% homology to CDRs 1-3 or to the full variable domains of any of the sequences in Tables 27, 28, 38-42, or 46-50. As used herein, the term percent (%) homology defines the percentage of residues in the amino acid sequence variant that are identical after aligning the sequences and introducing gaps and other spacing, e.g., using the BLAST alignment software.

[045] In an embodiment, the binding protein has an on rate constant (K_{on}) to one or more targets of at least about $10^{2}M^{-1}s^{-1}$; at least about $10^{3}M^{-1}s^{-1}$; at least about $10^{4}M^{-1}s^{-1}$; at least about $10^{5}M^{-1}s^{-1}$; or at least about $10^{6}M^{-1}s^{-1}$, as measured by surface plasmon resonance. In an embodiment, the binding protein has an on rate constant (K_{on}) to one or more targets from about $10^{2}M^{-1}s^{-1}$ to about $10^{3}M^{-1}s^{-1}$; from about $10^{3}M^{-1}s^{-1}$ to about $10^{4}M^{-1}s^{-1}$; from about $10^{4}M^{-1}s^{-1}$ to about $10^{5}M^{-1}s^{-1}$; or from about $10^{5}M^{-1}s^{-1}$ to about $10^{6}M^{-1}s^{-1}$, as measured by surface plasmon resonance.

[046] In an embodiment, the binding protein has an off rate constant (K_{off}) for one or more targets of at most about $10^{-3}s^{-1}$; at most about $10^{-4}s^{-1}$; at most about $10^{-5}s^{-1}$; or at most about $10^{-6}s^{-1}$, as measured by surface plasmon resonance. In an embodiment, the binding protein has an off rate constant (K_{off}) to one or more targets of about $10^{-3}s^{-1}$ to about $10^{-4}s^{-1}$; of about $10^{-4}s^{-1}$ to about $10^{-5}s^{-1}$; or of about $10^{-5}s^{-1}$ to about $10^{-6}s^{-1}$, as measured by surface plasmon resonance.

[047] In an embodiment, the binding protein has a dissociation constant (K_d) to one or more targets of at most about $10^{-7}M$; at most about $10^{-8}M$; at most about $10^{-9}M$; at most about $10^{-10}M$; at most about $10^{-11}M$; at most about $10^{-12}M$; or at most $10^{-13}M$. In an embodiment, the binding protein has a dissociation constant (K_d) to its targets of about $10^{-7}M$ to about $10^{-8}M$; of about $10^{-8}M$ to about $10^{-9}M$; of about $10^{-9}M$ to about $10^{-10}M$; of about $10^{-10}M$ to about $10^{-11}M$; of about $10^{-11}M$ to about $10^{-12}M$; or of about 10^{-12} to M about $10^{-13}M$.

[048] In an embodiment, the binding protein is a conjugate further comprising an agent. In an embodiment, the agent is an immunoadhesion molecule, an imaging agent, a therapeutic agent, or a cytotoxic agent. In an embodiment, the imaging agent is a radiolabel, an enzyme, a fluorescent label, a luminescent label, a bioluminescent label, a magnetic label, or biotin. In another embodiment, the radiolabel is ^{3}H, ^{14}C, ^{35}S, ^{90}Y, ^{99}Tc, ^{111}In, ^{125}I, ^{131}I, ^{177}Lu, ^{166}Ho, or ^{153}Sm. In yet another embodiment, the therapeutic or cytotoxic agent is an anti-metabolite, an alkylating agent, an antibiotic, a growth factor, a cytokine, an anti-angiogenic agent, an anti-mitotic agent, an anthracycline, toxin, or an apoptotic agent, or an immunosuppressive agent.

[049] In an embodiment, the binding protein is a crystallized binding protein and exists as a crystal. In an embodiment, the crystal is a carrier-free pharmaceutical controlled release crystal. In another embodiment, the crystallized binding protein has a greater half-life in vivo than the soluble counterpart of the binding protein. In yet another embodiment, the crystallized binding protein retains biological activity.

[050] In certain embodiments, a binding protein disclosed herein can compete for binding to VEGF, PDGF, and/or a cognate receptor with any of the antibodies, binding proteins, or bispecific antibodies disclosed herein. In certain embodiments, a binding protein disclosed herein can compete for binding with an antibody, binding protein, or bispecific antibody comprising CDRs and/or variable domains selected from those identified in Tables 27, 28, 38-42, or 46-50. In certain embodiments, a binding protein disclosed herein can compete for binding with PR-1610561 (comprising SEQ ID NOs: 131 and 132) or a binding protein comprising the CDRs and/or variable domains of PR-1610561. In certain embodiments, a binding protein disclosed herein can compete for binding with PR-1572102 (comprising SEQ ID NOs: 88 and 89) or PR-1572105 (comprising SEQ ID NOs: 94 and 95) or PR1611292 (comprising SEQ ID NOs: 141 and 142).

[051] According to certain embodiments, a binding protein disclosed herein can bind to the same epitope of VEGF, PDGF, and/or a cognate receptor as any of the antibodies, binding proteins, or bispecific antibodies disclosed herein. In certain embodiments, a binding protein disclosed herein can bind to the same epitope of VEGF, PDGF, and/or a cognate receptor bound by an antibody, binding protein, or bispecific antibody comprising CDRs and/or variable domains selected from those identified in Tables 27, 28, 38-42, or 46-50. In certain embodiments, a binding protein disclosed herein can bind to the same epitope as PR-1610561 (comprising SEQ ID NOs: 131 and 132) or a binding protein comprising the CDRs and/or variable domains of PR-1610561. In certain embodiments, a binding protein disclosed herein binds to the same epitope as PR-1572102 (comprising SEQ ID NOs: 88 and 89) or PR-1572105 (comprising SEQ ID NOs: 94 and 95) or PR1611292 (comprising SEQ ID NOs: 141 and 142).

[052] In certain embodiments, competitive binding can be evaluated using a cross-blocking assay, such as the assay described in ANTIBODIES, A LABORATORY MANUAL, Cold Spring Harbor Laboratory, Ed Harlow and David Lane (1st edition 1988, 2nd edition 2014). In some embodiments, competitive binding is identified when a test antibody or binding protein reduces binding of a reference antibody or binding protein (e.g., a binding protein comprising CDRs and/or variable domains selected from those identified in Tables 27, 28, 38-42, or 46-50) to VEGF, PDGF, and/or a cognate receptor by at least about 50% in the cross-blocking assay (e.g., 50%, 60%, 70%, 80%, 90%, 95%, 99%, 99.5%, or more, or any percentage in between), and/or vice versa. In some embodiments, competitive binding can be due to shared or similar (e.g., partially overlapping) epitopes, or due to steric hindrance where antibodies or binding proteins bind at nearby epitopes. *See, e.g.*, Tzartos, Methods in Molecular Biology, vol. 66, Epitope Mapping Protocols, pages 55-66, Humana Press Inc. (1998). In some embodiments, competitive binding can be used to sort groups of binding proteins that share similar epitopes, e.g., those that compete for binding can be "binned" as a group of binding proteins that have overlapping or nearby epitopes, while those that do not compete are placed in a separate group of binding proteins that do not have overlapping or nearby epitopes

[053] In an embodiment, the binding protein described herein is glycosylated. For example, the glycosylation pattern may be a human glycosylation pattern.

[054] In various embodiments, a pharmaceutical composition comprising a binding protein disclosed herein and a pharmaceutically acceptable carrier is provided. In a further embodiment, the pharmaceutical composition comprises at least one additional agent such as a therapeutic agent for treating a disorder or a diagnostic agent. For example, the additional agent may be a therapeutic agent, an imaging agent, a cytotoxic agent, an angiogenesis inhibitor (including but not limited to an anti-VEGF antibody or a VEGF-trap), a kinase inhibitor (including but not limited to a KDR and a TIE-2 inhibitor), a co-stimulation molecule blocker (including but not limited to anti-B7.1, anti-B7.2, CTLA4-Ig, anti-CD20), an adhesion molecule blocker (including but not limited to an anti-LFA-1 antibody, an anti-E/L selectin antibody, a small molecule inhibitor), an anti-cytokine antibody or functional fragment thereof (including but not limited to an anti-IL-18, an anti-TNF, and an anti-IL-6/cytokine receptor antibody), methotrexate, cyclosporin, rapamycin, FK506, a detectable label or reporter, a TNF antagonist, an antirheumatic, a muscle relaxant, a narcotic, a non-steroid anti-inflammatory drug (NSAID), an analgesic, an anesthetic, a sedative, a local anesthetic, a neuromuscular blocker, an antimicrobial, an antipsoriatic, a corticosteriod, an anabolic steroid, an erythropoietin, an immunoglobulin, an immunosuppressive, a growth hormone, a hormone replacement drug, a radiopharmaceutical, an antidepressant, an antipsychotic, a stimulant, an asthma medication, a beta agonist, an inhaled steroid, an epinephrine or analog, a cytokine, or a cytokine antagonist.

[055] In various embodiments, a binding protein disclosed herein binds to VEGF and comprises CDRs and/or variable domains selected from those identified in Tables A, 2.4.1-2.4.9, 27, and 38-42. In some embodiments, the binding protein comprises a CDR set of heavy chain CDRs 1-3 and paired light chain CDRs 1-3 selected from any of the CDR sets listed in Tables A, 2.4.1-2.4.9, 27, and 38-42. In some embodiments, the binding protein comprises a heavy chain variable domain and paired light chain variable domain selected from any of the variable domains listed in Tables A, 2.4.1-2.4.9, 27, and 38-42. In some embodiments, the binding protein is a bispecific or multispecific binding protein, comprising CDRs and/or variable domains selected from Tables A, 2.4.1-2.4.9, 27, and 38-42. The binding protein may further comprise heavy and light chain constant domains selected from Table 3. In some embodiments, the binding protein is also capable of binding to PDGF.

[056] In some embodiments, a binding protein disclosed herein binds to PDGF and comprises CDRs and/or variable domains selected from those identified in Tables A, 1.4.1-1.4.7, 28, and 46-50. In some embodiments, the binding protein comprises a CDR set of heavy chain CDRs 1-3 and paired light chain CDRs 1-3 selected from any of the CDR sets listed in Tables A, 1.4.1-1.4.7, 28, and 46-50. In some embodiments, the binding protein comprises a heavy chain variable domain and paired light chain variable domain selected from any of the variable domains listed in Tables A, 1.4.1-1.4.7, 28, and 46-50. In some embodiments, the binding protein is a bispecific or multispecific binding protein, comprising CDRs and/or variable domains selected from Tables A, 1.4.1-1.4.7, 28, and 46-50. The binding protein may further comprise heavy and light chain constant domains selected from Table 3. In some embodiments, the binding protein is also capable of binding to VEGF.

[057] In some embodiments, a binding protein disclosed herein binds to VEGF and PDGF, wherein the binding site for VEGF comprises CDRs and/or variable domains selected from those identified in Tables A, 2.4.1-2.4.9, 27, and 38-42 and the binding site for PDGF comprises CDRs and/or variable domains selected from those identified in Tables A, 1.4.1-1.4.7, 28, and 46-50. In some embodiments, the binding sites for VEGF and PDGF comprises CDRs and/or variable domains selected from any of the variable domains listed in Tables 56-59, 95, and 96. In some embodiments, binding proteins disclosed herein comprise binding sites for VEGF and PDGF comprising the paired CDRs and/or variable domains from any one of the bispecific binding proteins selected from Tables 56-59, 95, and 96. In some embodiments, the binding proteins are DVD-Ig binding proteins, or any of the other bispecific or multispecific formats disclosed herein. The binding protein described herein may further comprise one or more linkers between the VEGF and PDGF binding sites, wherein the linkers comprise sequences that are selected from Table 55. The binding protein described herein may also comprise heavy and light chain constant domains selected from Table 3.

[058] In some embodiments, a binding protein is capable of binding VEGF and PDGF, wherein the binding site for VEGF comprises CDRs 1-3 from SEQ ID NO: 17 and CDRs-1-3 from SEQ ID NO: 18, and the binding site for PDGF comprises a CDR set of heavy chain CDRs 1-3 and paired light chain CDRs 1-3 selected from any of Tables A, 1.4.1-1.4.7, 28, and 46-50. In some embodiments, the binding site for VEGF comprises CDRs 1-3 from SEQ ID NO: 35 and CDRs-1-3 from SEQ ID NO: 36, and the binding site for PDGF comprises a CDR set of heavy chain CDRs 1-3 and paired light chain CDRs 1-3 selected from any of Tables A, 1.4.1-1.4.7, 28, and 46-50. In some embodiments, the binding site for VEGF comprises CDRs 1-3 from SEQ ID NO: 39 and CDRs-1-3 from SEQ ID NO: 40, and the binding site for PDGF comprises a CDR set of heavy chain CDRs 1-3 and paired light chain CDRs 1-3 selected from any of Tables A, 1.4.1-1.4.7, 28, and 46-50. In some embodiments, the binding site for VEGF comprises SEQ ID NO: 17 and SEQ ID NO: 18, and the binding site for PDGF comprises a heavy chain variable domain and paired light chain variable domain selected from any of the variable domains listed in Tables A, 1.4.1-1.4.7, 28, and 46-50. In some embodiments, the binding site for VEGF comprises SEQ ID NO: 35 and SEQ ID NO: 36, and the binding site for PDGF comprises a heavy chain variable domain and paired light chain variable domain selected from any of the variable domains listed in Tables A, 1.4.1-1.4.7, 28, and 46-50. In some embodiments, the binding site for VEGF comprises SEQ ID NO: 39 and SEQ ID NO: 40, and the binding site for PDGF comprises a heavy chain variable domain and paired light chain variable domain selected from any of the variable domains listed in Tables A, 1.4.1-1.4.7, 28, and 46-50. The binding protein described herein may further comprise one or more linkers between the VEGF and PDGF binding sites, wherein the linkers comprise sequences that are selected from Table 55. The binding protein described herein may also comprise heavy and light chain constant domains selected from Table 3.

[059] In some embodiments, a binding protein is capable of binding VEGF and PDGF, wherein the binding site for PDGF comprises CDRs 1-3 from SEQ ID NO: 1 and CDRs-1-3 from SEQ ID NO: 2, and the binding site for VEGF comprises a CDR set of heavy chain CDRs 1-3 and paired light chain CDRs 1-3 selected from any of Tables A, 2.4.1-2.4.9, 27, and 38-42. In some embodiments, the binding site for PDGF comprises CDRs 1-3 from SEQ ID NO: 15 and CDRs-1-3 from SEQ ID NO: 16, and the binding site for VEGF comprises a CDR set of heavy chain CDRs 1-3 and paired light chain CDRs 1-3 selected from any of Tables A, 2.4.1-2.4.9, 27, and 38-42. In some embodiments, the binding site for PDGF comprises SEQ ID NO: 1 and SEQ ID NO: 2, and the binding site for VEGF comprises a heavy chain variable domain and paired light chain variable domain selected from any of the variable domains listed in Tables A, 2.4.1-2.4.9, 27, and 38-42. In some embodiments, the binding site for PDGF comprises SEQ ID NO: 15 and SEQ ID NO: 16, and the binding site for VEGF comprises a heavy chain variable domain and paired light chain variable domain selected from any of the variable domains listed in

Tables A, 2.4.1-2.4.9, 27, and 38-42. The binding protein described herein may further comprise one or more linkers between the VEGF and PDGF binding sites, wherein the linkers comprise sequences that are selected from Table 55. The binding protein described herein may also comprise heavy and light chain constant domains selected from Table 3.

[060] In some embodiments, a binding protein is capable of binding VEGF and PDGF, wherein the binding site for VEGF comprises CDRs 1-3 from SEQ ID NO: 17 and CDRs-1-3 from SEQ ID NO: 18, and the binding site PDGF comprises CDRs 1-3 from SEQ ID NO: 1 and CDRs-1-3 from SEQ ID NO: 2. In some embodiments, the binding site for VEGF comprises CDRs 1-3 from SEQ ID NO: 35 and CDRs-1-3 from SEQ ID NO: 36, and the binding site for PDGF comprises CDRs 1-3 from SEQ ID NO: 15 and CDRs-1-3 from SEQ ID NO: 16. In some embodiments, the binding site for VEGF comprises CDRs 1-3 from SEQ ID NO: 39 and CDRs-1-3 from SEQ ID NO: 40, and the binding site for PDGF comprises CDRs 1-3 from SEQ ID NO: 15 and CDRs-1-3 from SEQ ID NO: 16. The binding protein described herein may further comprise one or more linkers between the VEGF and PDGF binding sites, wherein the linkers comprise sequences that are selected from Table 55. The binding protein described herein may also comprise heavy and light chain constant domains selected from Table 3.

[061] In some embodiments, a binding protein is capable of binding VEGF and PDGF, wherein the binding site for VEGF comprises SEQ ID NO: 17 and SEQ ID NO: 18, and the binding site PDGF comprises SEQ ID NO: 1 and SEQ ID NO: 2. In some embodiments, the binding site for VEGF comprises SEQ ID NO: 35 and SEQ ID NO: 36, and the binding site for PDGF comprises SEQ ID NO: 15 and SEQ ID NO: 16. In some embodiments, the binding site for VEGF comprises SEQ ID NO: 39 and SEQ ID NO: 40, and the binding site for PDGF comprises SEQ ID NO: 15 and SEQ ID NO: 16. The binding protein described herein may further comprise one or more linkers between the VEGF and PDGF binding sites, wherein the linkers comprise sequences that are selected from Table 55. The binding protein described herein may also comprise heavy and light chain constant domains selected from Table 3.

[062] In some embodiments, the binding protein is a DVD-Ig binding protein, capable of binding VEGF and PDGF. In some embodiment, the heavy chain of the binding protein comprises a DVD-Ig heavy chain variable domain and paired DVD-Ig light chain variable domain selected from Tables 56-59, 95, and 96. In some embodiments, the binding protein comprises DVD-Ig heavy and light chain variable domains of SEQ ID NO: 131 and SEQ ID NO: 132. In some embodiments, the binding protein comprises DVD-Ig heavy and light chain variable domains of SEQ ID NO: 88 and SEQ ID NO: 89. In some embodiments, the binding protein comprises DVD-Ig heavy and light chain variable domains of SEQ ID NO: 94 and SEQ ID NO: 95. In some embodiments, the binding protein comprises DVD-Ig heavy and light chain variable

domains of SEQ ID NO: 141 and SEQ ID NO: 142. The DVD-Ig binding protein described herein may further comprise heavy and light chain constant domains selected from Table 3.

[063] In certain embodiments, a binding protein disclosed herein is a DVD-Ig binding protein, comprising first and second polypeptide chains of SEQ ID NO: 131 and SEQ ID NO: 132. In some embodiments, the DVD-Ig binding protein comprises first and second polypeptide chains of SEQ ID NO: 88 and SEQ ID NO: 89. In some embodiments, the DVD-Ig binding protein comprises first and second polypeptide chains of SEQ ID NO: 94 and SEQ ID NO: 95. In some embodiments, the DVD-Ig binding protein comprises first and second polypeptide chains of SEQ ID NO: 141 and SEQ ID NO: 142.

Binding Protein Properties

[064] The development and production of a binding protein for use as a human therapeutic agent, e.g., as an anti-inflammatory agent or oncologic agent, may require more than the identification of a binding protein capable of binding to a desired target or targets. The binding proteins disclosed herein exhibit favorable properties in one or more of the following categories (a) the binding kinetics (on-rate, off-rate and affinity) for both the inner and outer antigen-binding domains, (b) potencies in various biochemical and cellular bioassays, (c) in vivo efficacies in relevant tumor models, (d) pharmacokinetic and pharmacodynamics properties, (e) manufacturability, including protein expression level in selected cell lines, scalability, post-translational modification, physicochemical properties such as monomer percentage, solubility, and stability (intrinsic, freeze/thaw, storage stability, etc.), (f) formulation properties, (g) potential immunogenicity risk, (h) toxicological properties, and (i) binding mode and valency. Binding mode and valency may affect binding properties and cellular potencies of a molecule.

[065] The binding proteins disclosed herein exhibit favorable properties in some or each of the categories listed above, including surprisingly high binding affinity at both the VD1 and VD2 positions.

[066] In some embodiments a binding protein or binding proteins disclosed herein targeting VEGF and PDGF serve to both reduce choroidal neovascularization and increase regression of mature vasculature, e.g., in ocular conditions such as AMD. In some embodiments a binding protein or binding proteins disclosed herein targeting VEGF and PDGF neutralize VEGF and PDGF simultaneously. In some embodiments, the binding protein exhibits one or more of high potency to VEGF and/or PDGF, extended ocular duration, and rapid clearance from systemic circulation. In some embodiments, the binding protein is a bispecific and allows for a single injection of an agent to both targets (VEGF and PDGDF), reducing injection volume/frequency while still retaining the drug-like products of a traditional antibody.

[067] In some embodiments, the disclosed binding protein exhibits superior in vivo efficacy (e.g., in a preclinical model of choroidal neovascularization or AMD) as compared to existing treatments for AMD (e.g., Elyea™ and/or Lucentis™). In some embodiments, the disclosed binding protein is a DVD-Ig binding protein and exhibits a high ocular duration. In some embodiments, the DVD-Ig binding protein may be, e.g., 150-200 kDa in weight or greater, and may provide for a longer ocular duration as compared to lower weight agents such as monoclonal antibodies. In some embodiments, the binding protein disclosed herein is a DVD-Ig binding protein and has an ocular half life of at least about 4 days, or at least about 4. 6 days, or at least about 5 days, or at least about 6 days, or at least about 6.5 days, or more. In some embodiments, the DVD-Ig ocular half life is greater than the half-life of an antibody or other construct having a smaller size, while retaining a more rapid systemic clearance similar to that of the antibody. In some embodiments, the DVD-Ig binding protein has an ocular half life of at least about 4 (or at least about 4.6) days after intravitreoius administration at 0.25 mg.

[068] In some embodiments, the disclosed binding proteins are DVD-Ig binding proteins and exhibit improved drug-like properties, including one or more of high theromstability (e.g., a T_{onset} of greater than 50°, 55°, 60°, 61°, 62°, 63°, 64°, or 65° C), a solubility of at least about 70, 72, 74, 76, 78, or 80 mg/ml, a viscosity at room temperature and at a concentration of 100 mg/ml of about 7.2 centipoise, an effective storage stability in a universal buffer, and/or high freeze-thaw stability. In some embodiments, the DVD-Ig binding protein does not exhibit a significant change in monomer percentage at low concentration after storage at 5°C or 40°C for 10, 15, 20, 21, 22, 23, 24, 25, or more days, and/or does not exhibit a significant increase in aggregation at 50-150 mg/ml (or 100 +/-10 mg/ml) after 1, 2, 3, 4, 5, or more freeze/thaw cycles.

[069] In certain embodiments, a binding protein exhibiting particularly favorable properties in some or each of the categories listed above is a DVD-Ig binding protein capable of binding VEGF and PDGF, wherein the binding site for VEGF comprises CDRs 1-3 from SEQ ID NO: 35 and CDRs-1-3 from SEQ ID NO: 36, and the binding site for PDGF comprises CDRs 1-3 from SEQ ID NO: 15 and CDRs-1-3 from SEQ ID NO: 16. In an embodiment, the binding site for VEGF comprises SEQ ID NO: 35 and SEQ ID NO: 36, and the binding site for PDGF comprises SEQ ID NO: 15 and SEQ ID NO: 16. In an embodiment, the binding protein is capable of binding VEGF and PDGF, and comprises PR-1610561 (comprising SEQ ID NOs: 131 and 132). In an embodiment, the binding protein comprises a heavy chain constant region on the first polypeptide chain comprising a human IgG1 heavy chain sequence modified by one or more amino acid changes, wherein the changes comprise substitution of leucines at positions 234 and 235 with alanines, and optionally also comprising a substitution of histidine at position 435 with alanine, wherein the amino acid positions are numbered using EU index numbering; and a light

chain constant region on the second polypeptide chain comprising a human kappa light chain constant region sequence

[070] In certain embodiments, a binding protein exhibiting particularly favorable properties in some or each of the categories listed above is a DVD-Ig binding protein capable of binding VEGF and PDGF, wherein the binding site for VEGF comprises CDRs 1-3 from SEQ ID NO: 17 and CDRs-1-3 from SEQ ID NO: 18, and the binding site for PDGF comprises CDRs 1-3 from SEQ ID NO: 1 and CDRs-1-3 from SEQ ID NO: 2. In an embodiment, the binding site for VEGF comprises SEQ ID NO: 17 and SEQ ID NO: 18, and the binding site for PDGF comprises SEQ ID NO: 1 and SEQ ID NO: 2. In an embodiment, the binding protein is capable of binding VEGF and PDGF, and comprises PR-1572102 (comprising SEQ ID NOs: 88 and 89) or PR-1572105 (comprising SEQ ID NOs: 94 and 95) or PR1611292 (comprising SEQ ID NOs: 141 and 142). In an embodiment, the binding protein comprises a heavy chain constant region on the first polypeptide chain comprising a human IgG1 heavy chain sequence modified by one or more amino acid changes, wherein the changes comprise substitution of leucines at positions 234 and 235 with alanines, and optionally also comprising a substitution of histidine at position 435 with alanine, wherein the amino acid positions are numbered using EU index numbering; and a light chain constant region on the second polypeptide chain comprising a human kappa light chain constant region sequence.

[071] For instance, in some embodiments, the binding protein disclosed herein (e.g., PR-1610561, PR-1572102, PR-1572105, or PR1611292) may exhibit one or more of the following features: enhanced in vivo efficacy in human VEGF transgenic mice, enhanced potency (as measured, e.g., via BIACORE, ELISA, or co-culture sprouting assay), improved expression (e.g., in HEK293 or CHO cells), and improved drug-like properties (e.g., thermal stability, storage stability, solubility, physicochemical properties, and/or pharmacokinetics) as compared to another binding protein or combination of binding proteins targeting VEGF and PDGF.

Preparation of Binding Proteins

[072] In another aspect, the disclosure provides a method of making a binding protein that binds PDGF, VEGF, and/or either or both cognate receptors. In an embodiment, the method of making a binding protein comprises the steps of a) obtaining a first parent antibody, or antigen binding portion thereof, that binds PDGF, VEGF, or a cognate receptor; b) obtaining a second parent antibody, or antigen binding portion thereof, that binds PDGF, VEGF, or a cognate receptor; c) determining the sequences of the variable domains of the parent antibodies or antigen binding portions thereof; d) preparing construct(s) encoding any of the binding proteins described herein using those variable domain sequences; and e) expressing the polypeptide chains, such that a binding protein that binds PDGF, VEGF, and/or either or both cognate receptors is generated.

[073] In any of the embodiments herein, the VD1 heavy chain variable domain, if present, and light chain variable domain, if present, can be from a first parent antibody or antigen binding portion thereof; the VD2 heavy chain variable domain, if present, and light chain variable domain, if present, can be from a second parent antibody or antigen binding portion thereof. The first and second parent antibodies can be the same or different.

[074] In one embodiment, the first parent antibody or antigen binding portion thereof, binds a first antigen, and the second parent antibody or antigen binding portion thereof, binds a second antigen. In an embodiment, the first and second antigens are the same antigen. In another embodiment, the parent antibodies bind different epitopes on the same antigen. In another embodiment, the first and second antigens are different antigens. In another embodiment, the first parent antibody or antigen binding portion thereof, binds the first antigen with a potency different from the potency with which the second parent antibody or antigen binding portion thereof, binds the second antigen. In yet another embodiment, the first parent antibody or antigen binding portion thereof, binds the first antigen with an affinity different from the affinity with which the second parent antibody or antigen binding portion thereof, binds the second antigen.

[075] In another embodiment, the first parent antibody or antigen binding portion thereof, and the second parent antibody or antigen binding portion thereof, are a human antibody, CDR grafted antibody, humanized antibody, and/or affinity matured antibody. The "parent antibody", which provides at least one antigen binding specificity of the multivalent and or multispecific binding protein, may be one that is internalized (and/or catabolized) by a cell expressing an antigen to which the antibody binds; and/or may be an agonist, cell death-inducing, and/or apoptosis-inducing antibody, and the multivalent and or multispecific binding protein as described herein may display improvement(s) in one or more of these properties. Moreover, the parent antibody may lack any one or more of these properties, but may acquire one or more of them when constructed as a multivalent binding protein as described herein. For example, different Fc mutants may prevent FcR, FcR-gamma, complement, or C' binding, or extend half-life.

[076] In various embodiments, an isolated nucleic acid encoding any one of the binding proteins disclosed herein is also provided. Also provided is a composition comprising one or more nucleic acids wherein said one or more nucleic acids encode a nucleic acid encoding any one of the binding proteins disclosed herein. For example, the composition may comprise a nucleic acid that encodes a first polypeptide and a nucleic acid that encodes a second polypeptide, wherein said first and second polypeptide together form a binding protein as described herein. A further embodiment provides a vector (e.g., an expression vector) comprising the isolated nucleic acid disclosed herein. Also provided is a vector (e.g. an expression vector) that comprises one or more nucleic acids that encode a binding protein as described herein. Also provided is a

composition comprising one or more vectors that encode a binding protein as escribd herein. For example, the composition may comprise a vector that encodes a first polypeptide and a vector that encodes a second polypeptide, wherein said first and second polypeptide together form a binding protein as described herein. In some embodiments, the vector is pcDNA; pTT (Durocher et al. (2002) Nucleic Acids Res. 30(2):e9; pTT3 (pTT with additional multiple cloning site; pEFBOS (Mizushima and Nagata (1990) Nucleic Acids Res. 18:17); pBV; pJV; pcDNA3.1 TOPO; pEF6 TOPO; pBOS; pHybE; or pBJ. In an embodiment, the vector is a vector disclosed in U.S. Patent No. 8,187,836.

[077] In another aspect, a host cell is transformed with the vector disclosed herein. In an embodiment, the host cell is a prokaryotic cell, for example, E.coli. In another embodiment, the host cell is a eukaryotic cell, for example, a protist cell, an animal cell, a plant cell, or a fungal cell. In an embodiment, the host cell is a mammalian cell including, but not limited to, CHO, COS, NS0, SP2, PER.C6, or a fungal cell, such as *Saccharomyces cerevisiae*, or an insect cell, such as Sf9. In an embodiment, two or more binding proteins, e.g., with different specificities, are produced in a single recombinant host cell. For example, the expression of a mixture of antibodies has been called Oligoclonics™ (Merus B.V., The Netherlands) disclosed in U.S. Patent Nos. 7,262,028 and 7,429,486.

[078] In various embodiments, a binding proteins disclosed herein can be prepared by culturing any one of the host cells disclosed herein in a culture medium under conditions sufficient to produce the binding protein.

[079] One embodiment provides a composition for the release of a binding protein wherein the composition comprises a crystallized binding protein, an ingredient, and at least one polymeric carrier. In an embodiment, the polymeric carrier is poly (acrylic acid), a poly (cyanoacrylate), a poly (amino acid), a poly (anhydride), a poly (depsipeptide), a poly (ester), poly (lactic acid), poly (lactic-co-glycolic acid) or PLGA, poly (b-hydroxybutryate), poly (caprolactone), poly (dioxanone), poly (ethylene glycol), poly ((hydroxypropyl) methacrylamide, poly [(organo)phosphazene], a poly (ortho ester), poly (vinyl alcohol), poly (vinylpyrrolidone), a maleic anhydride- alkyl vinyl ether copolymer, a pluronic polyol, albumin, alginate, cellulose, a cellulose derivative, collagen, fibrin, gelatin, hyaluronic acid, an oligosaccharide, a glycaminoglycan, a sulfated polysaccharide, or blends and copolymers thereof. In an embodiment, the ingredient is albumin, sucrose, trehalose, lactitol, gelatin, hydroxypropyl-β- cyclodextrin, methoxypolyethylene glycol, or polyethylene glycol.

[080] The binding proteins provided herein, such as DVD-Ig binding proteins, may be produced by any of a number of techniques known in the art. For example, expression from host cells, wherein expression vector(s) encoding the DVD-Ig heavy and DVD-Ig light chains is (are)

transfected into a host cell by standard techniques. Although it is possible to express the DVD-Ig binding proteins provided herein in either prokaryotic or eukaryotic host cells, DVD-Ig binding proteins are preferably expressed in eukaryotic cells, for example, mammalian host cells.

[081] In an exemplary system for recombinant expression of DVD-Ig proteins, a recombinant expression vector encoding both the DVD-Ig heavy chain and the DVD-Ig light chain is introduced into dhfr- CHO cells by calcium phosphate-mediated transfection. Within the recombinant expression vector, the DVD-Ig heavy and light chain sequences are each operatively linked to CMV enhancer/AdMLP promoter regulatory elements 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 DVD-Ig heavy and light chains and intact DVD-Ig protein is recovered from the culture medium. Standard molecular biology techniques may be used to prepare the recombinant expression vector, transfect the host cells, select for transformants, culture the host cells and recover the DVD-Ig protein from the culture medium. In some embodiments, a method of synthesizing a DVD-Ig binding protein by culturing a host cell provided herein in a suitable culture medium until a DVD-Ig binding protein is synthesized is also provided. The method may further comprise isolating the DVD-Ig protein from the culture medium.

[082] A feature of a DVD-Ig binding protein is that it can be produced and purified in a similar way to a conventional antibody. The design of the full length DVD-Ig binding protein heavy and light chains provided herein leads to assemble primarily to the desired dual-specific multivalent full length binding proteins. In an embodiment, 50%-75% of the binding protein produced by this method is a dual specific tetravalent binding protein (e.g., a DVD-Ig binding protein). In another embodiment, 75%-90% of the binding protein produced by this method is a dual specific tetravalent binding protein. In another embodiment, 90%-95% of the binding protein produced is a dual specific tetravalent binding protein. In some embodiments, at least 50%, at least 75% and at least 90% of the assembled, and expressed dual variable domain immunoglobulin molecules are the desired dual-specific tetravalent protein.

[083] In various embodiments, the disclosure provides methods of expressing a dual variable domain light chain and a dual variable domain heavy chain in a single cell leading to a primary product of a dual-specific tetravalent full length binding protein, where the primary product is more than 50%, such as more than 75% and more than 90%, of all assembled protein, comprising a dual variable domain light chain and a dual variable domain heavy chain.

Therapeutic and Diagnostic Uses

[084] Also disclosed herein, in various embodiments, are methods for diagnosing and treating a mammal (e.g., a human) comprising the step of administering to the mammal, or a sample taken from the mammal, an effective amount of a composition disclosed herein. A binding protein as described herein may be used in a method for therapy or diagnosis.

[085] Given their ability to bind VEGF, PLGF, and/or their cognate receptors, in some embodiments, the binding proteins provided herein can be used to detect one or more of those antigens (e.g., in a biological sample, such as serum or plasma), using a conventional immunoassay, such as an enzyme linked immunosorbent assays (ELISA), a radioimmunoassay (RIA), or tissue immunohistochemistry. The binding protein is directly or indirectly labeled with a detectable substance to facilitate detection of the bound or unbound antibody. Suitable detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β-galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin. An example of a luminescent material is luminol and examples of suitable radioactive materials include ^{3}H, ^{14}C, ^{35}S, ^{90}Y, ^{99}Tc, ^{111}In, ^{125}I, ^{131}I, ^{177}Lu, ^{166}Ho, and ^{153}Sm.

[086] In some embodiments, a method is disclosed for treating a human subject suffering from a disorder in which the target, or targets, capable of being bound by the binding proteins disclosed herein is/are detrimental, comprising administering to the human subject a binding protein disclosed herein such that the activity of the target, or targets, in the human subject is inhibited and one or more symptoms is alleviated or treatment is achieved is provided. In various embodiments, treatment comprises reducing, improving, or ameliorating one or more symptom of a disorder. Treatment includes but does not necessarily require curing (i.e., completely eliminating) a disorder or a symptom of a disorder.

[087] The binding proteins provided herein can be used to treat humans suffering from diseases such as, for example, those associated with increased angiogenesis and/or inflammation (e.g., ocular inflammation). In an embodiment, the binding proteins provided herein or antigen-binding portions thereof, are used to treat an autoimmune disorder, asthma, ocular inflammation, Crohn's disease, ulcerative colitis, inflammatory bowel disease (IBD), insulin dependent diabetes mellitus, rheumatoid arthritis, osteoarthritis, systemic lupus erythematosus (SLE), multiple sclerosis, sepsis, a neurodegenerative disease, or an oncological disorder. In an embodiment, a binding protein disclosed herein is used to treat an eye disorder

(e.g., an angiogenic eye disorder). In an embodiment, the eye disorder is a macular degeneration, such as wet macular degeneration, dry macular degeneration, age related macular degeneration (AMD), exudative AMD, dry eye, glaucoma, diabetic retinopathy, diabetic macular edema, central retinal vein occlusion, corneal neovascularization, , iris neovascularization, neovascular glaucoma, post-surgical fibrosis in glaucoma, proliferative vitreoretinopathy (PVR), choroidal neovascularization, optic disc neovascularization, retinal neovascularization, vitreal neovascularization, pannus, pterygium, macular edema, diabetic macular edema (DME), vascular retinopathy, retinal degeneration, uveitis, keratoconjunctivitis sicca, blepharitis, keratitis or another inflammatory disease of the eye.

[088] In an embodiment, the binding proteins provided herein are capable of neutralizing the activity of their antigen targets both *in vitro* and *in vivo*. Accordingly, such binding proteins can be used to inhibit antigen activity, e.g., in a cell culture containing the antigens, in human subjects or in other mammalian subjects having the antigens with which a binding protein provided herein cross-reacts. In another embodiment, a method for reducing antigen activity in a subject suffering from a disease or disorder in which the antigen activity is detrimental is provided. A binding protein provided herein may be administered to a human subject for therapeutic purposes. In some embodiments, the binding protein (e.g., the DVD-Ig binding protein) is administered to a patient, e.g., a patient suffering from wet AMD, and can have one or more effects selected from regressing mature vasculature (e.g., via VEGF binding), reducing choroidal neovascularization (e.g., via VEGF binding), allowing access to blood vessels by stripping off pericytes (e.g., via PDGF binding), and/or providing anti-fibrotic effects to reduce visual loss from scarring (e.g., via PDGF binding). In some embodiments, the binding protein is multispecific for VEGF and PDGF, and is administered at a reduced number of injections and/or a reduced injection frequency, as compared to a combination antibody therapy.

[089] The term "a disorder in which antigen activity is detrimental" encompasses diseases and other disorders in which the presence of the antigen in a subject suffering from the disorder has been shown to be or is suspected of being either responsible for the pathophysiology of the disorder or a factor that contributes to a worsening of the disorder. Accordingly, a disorder in which antigen activity is detrimental is a disorder in which reduction of antigen activity is expected to alleviate the symptoms and/or progression of the disorder. Such disorders may be evidenced, for example, by an increase in the concentration of the antigen in a biological fluid of a subject suffering from the disorder (e.g., an increase in the concentration of antigen in serum, plasma, synovial fluid, etc., of the subject). Non-limiting examples of disorders that can be treated with the binding proteins provided herein include those disorders discussed below and in the section pertaining to pharmaceutical compositions comprising the binding proteins.

[090] Binding proteins disclosed herein, such as the DVD-Ig binding proteins, can be employed in some embodiments for tissue-specific delivery (target a tissue marker and a disease mediator for enhanced local PK thus higher efficacy and/or lower toxicity), including intracellular delivery (targeting an internalizing receptor and an intracellular molecule), delivering through a biological barrier, such as to the inside of the eye or brain (e.g., targeting transferrin receptor and a CNS disease mediator for crossing the blood-brain barrier). The binding proteins may also serve as carrier proteins to deliver an antigen to a specific location via binding to a non-neutralizing epitope of that antigen and also to increase the half-life of the antigen. Furthermore, the binding protein may be designed to either be physically linked to medical devices implanted into patients or target these medical devices (see Burke et al. (2006) Advanced Drug Deliv. Rev. 58(3): 437-446; Hildebrand et al. (2006) Surface and Coatings Technol. 200(22-23): 6318-6324; Drug/ device combinations for local drug therapies and infection prophylaxis, Wu (2006) Biomaterials 27(11):2450-2467; Mediation of the cytokine network in the implantation of orthopedic devices, Marques (2005) Biodegradable Systems in Tissue Engineer. Regen. Med. 377-397).

[091] In an embodiment, diseases that can be treated or diagnosed with the compositions and methods disclosed herein include, but are not limited to, primary and metastatic cancers, including carcinomas of breast, colon, rectum, lung, oropharynx, hypopharynx, esophagus, stomach, pancreas, liver, gallbladder and bile ducts, small intestine, urinary tract (including kidney, bladder and urothelium), female genital tract (including cervix, uterus, and ovaries as well as choriocarcinoma and gestational trophoblastic disease), male genital tract (including prostate, seminal vesicles, testes and germ cell tumors), endocrine glands (including the thyroid, adrenal, and pituitary glands), and skin, as well as hemangiomas, melanomas, sarcomas (including those arising from bone and soft tissues as well as Kaposi's sarcoma), tumors of the brain, nerves, eyes, and meninges (including astrocytomas, gliomas, glioblastomas, retinoblastomas, neuromas, neuroblastomas, Schwannomas, and meningiomas), solid tumors arising from hematopoietic malignancies such as leukemias, and lymphomas (both Hodgkin's and non-Hodgkin's lymphomas).

[092] Another embodiment provides for the use of the binding protein in the treatment of a disease or disorder, wherein the disorder is arthritis, osteoarthritis, juvenile chronic arthritis, septic arthritis, Lyme arthritis, psoriatic arthritis, reactive arthritis, spondyloarthropathy, systemic lupus erythematosus, Crohn's disease, ulcerative colitis, inflammatory bowel disease, insulin dependent diabetes mellitus, thyroiditis, asthma, allergic diseases, psoriasis, dermatitis scleroderma, graft versus host disease, organ transplant rejection, acute or chronic immune disease associated with organ transplantation, sarcoidosis, atherosclerosis, disseminated intravascular coagulation, Kawasaki's disease, Grave's disease, nephrotic syndrome, chronic

fatigue syndrome, Wegener's granulomatosis, Henoch-Schoenlein purpurea, microscopic vasculitis of the kidneys, chronic active hepatitis, uveitis, septic shock, toxic shock syndrome, sepsis syndrome, cachexia, infectious diseases, parasitic diseases, acute transverse myelitis, Huntington's chorea, Parkinson's disease, Alzheimer's disease, stroke, primary biliary cirrhosis, hemolytic anemia, malignancies, heart failure, myocardial infarction, Addison's disease, sporadic polyglandular deficiency type I and polyglandular deficiency type II, Schmidt's syndrome, adult (acute) respiratory distress syndrome, alopecia, alopecia areata, seronegative arthopathy, arthropathy, Reiter's disease, psoriatic arthropathy, ulcerative colitic arthropathy, enteropathic synovitis, chlamydia, yersinia and salmonella associated arthropathy, spondyloarthopathy, atheromatous disease/arteriosclerosis, atopic allergy, autoimmune bullous disease, pemphigus vulgaris, pemphigus foliaceus, pemphigoid, linear IgA disease, autoimmune haemolytic anaemia, Coombs positive haemolytic anaemia, acquired pernicious anaemia, juvenile pernicious anaemia, myalgic encephalitis/Royal Free Disease, chronic mucocutaneous candidiasis, giant cell arteritis, primary sclerosing hepatitis, cryptogenic autoimmune hepatitis, Acquired Immunodeficiency Syndrome, Acquired Immunodeficiency Related Diseases, Hepatitis B, Hepatitis C, common varied immunodeficiency (common variable hypogammaglobulinaemia), dilated cardiomyopathy, female infertility, ovarian failure, premature ovarian failure, fibrotic lung disease, cryptogenic fibrosing alveolitis, post-inflammatory interstitial lung disease, interstitial pneumonitis, connective tissue disease associated interstitial lung disease, mixed connective tissue disease associated lung disease, systemic sclerosis associated interstitial lung disease, rheumatoid arthritis associated interstitial lung disease, systemic lupus erythematosus associated lung disease, dermatomyositis/polymyositis associated lung disease, Sjögren's disease associated lung disease, ankylosing spondylitis associated lung disease, vasculitic diffuse lung disease, haemosiderosis associated lung disease, drug-induced interstitial lung disease, fibrosis, radiation fibrosis, bronchiolitis obliterans, chronic eosinophilic pneumonia, lymphocytic infiltrative lung disease, postinfectious interstitial lung disease, gouty arthritis, autoimmune hepatitis, type-1 autoimmune hepatitis (classical autoimmune or lupoid hepatitis), type-2 autoimmune hepatitis (anti-LKM antibody hepatitis), autoimmune mediated hypoglycaemia, type B insulin resistance with acanthosis nigricans, hypoparathyroidism, acute immune disease associated with organ transplantation, chronic immune disease associated with organ transplantation, osteoarthrosis, primary sclerosing cholangitis, psoriasis type 1, psoriasis type 2, idiopathic leucopaenia, autoimmune neutropaenia, renal disease NOS, glomerulonephritides, microscopic vasulitis of the kidneys, lyme disease, discoid lupus erythematosus, male infertility idiopathic or NOS, sperm autoimmunity, multiple sclerosis (all subtypes), sympathetic ophthalmia, pulmonary hypertension secondary to connective tissue disease, Goodpasture's syndrome, pulmonary manifestation of polyarteritis nodosa, acute rheumatic fever, rheumatoid spondylitis, Still's disease, systemic sclerosis, Sjörgren's syndrome, Takayasu's disease/arteritis, autoimmune thrombocytopaenia,

idiopathic thrombocytopaenia, autoimmune thyroid disease, hyperthyroidism, goitrous autoimmune hypothyroidism (Hashimoto's disease), atrophic autoimmune hypothyroidism, primary myxoedema, phacogenic uveitis, primary vasculitis, vitiligo acute liver disease, chronic liver diseases, alcoholic cirrhosis, alcohol-induced liver injury, cholestasis, idiosyncratic liver disease, Drug-Induced hepatitis, Non-alcoholic Steatohepatitis, allergy and asthma, group B streptococci (GBS) infection, mental disorders (*e.g.*, depression and schizophrenia), Th2 Type and Th1 Type mediated diseases, acute and chronic pain (different forms of pain), and cancers such as lung, breast, stomach, bladder, colon, pancreas, ovarian, prostate and rectal cancer and hematopoietic malignancies (leukemia and lymphoma) abetalipoproteinemia, Acrocyanosis, acute and chronic parasitic or infectious processes, acute leukemia, acute lymphoblastic leukemia (ALL), acute myeloid leukemia (AML), acute or chronic bacterial infection, acute pancreatitis, acute renal failure, adenocarcinomas, aerial ectopic beats, AIDS dementia complex, alcohol-induced hepatitis, allergic conjunctivitis, allergic contact dermatitis, allergic rhinitis, allograft rejection, alpha-l- antitrypsin deficiency, amyotrophic lateral sclerosis, anemia, angina pectoris, anterior horn cell degeneration, anti cd3 therapy, antiphospholipid syndrome, anti-receptor hypersensitivity reactions, aordic and peripheral aneuryisms, aortic dissection, arterial hypertension, arteriosclerosis, arteriovenous fistula, ataxia, atrial fibrillation (sustained or paroxysmal), atrial flutter, atrioventricular block, B cell lymphoma, bone graft rejection, bone marrow transplant (BMT) rejection, bundle branch block, Burkitt's lymphoma, burns, cardiac arrhythmias, cardiac stun syndrome, cardiac tumors, cardiomyopathy, cardiopulmonary bypass inflammation response, cartilage transplant rejection, cerebellar cortical degenerations, cerebellar disorders, chaotic or multifocal atrial tachycardia, chemotherapy associated disorders, chronic myelocytic leukemia (CML), chronic alcoholism, chronic inflammatory pathologies, chronic lymphocytic leukemia (CLL), chronic obstructive pulmonary disease (COPD), chronic salicylate intoxication, colorectal carcinoma, congestive heart failure, conjunctivitis, contact dermatitis, cor pulmonale, coronary artery disease, Creutzfeldt-Jakob disease, culture negative sepsis, cystic fibrosis, cytokine therapy associated disorders, Dementia pugilistica, demyelinating diseases, dengue hemorrhagic fever, dermatitis, dermatologic conditions, diabetes, diabetes mellitus, diabetic ateriosclerotic disease, Diffuse Lewy body disease, dilated congestive cardiomyopathy, disorders of the basal ganglia, Down's Syndrome in middle age, drug- induced movement disorders induced by drugs which block CNS dopamine receptors, drug sensitivity, eczema, encephalomyelitis, endocarditis, endocrinopathy, epiglottitis, epstein-barr virus infection, erythromelalgia, extrapyramidal and cerebellar disorders, familial hematophagocytic lymphohistiocytosis, fetal thymus implant rejection, Friedreich's ataxia, functional peripheral arterial disorders, fungal sepsis, gas gangrene, gastric ulcer, graft rejection of any organ or tissue, gram negative sepsis, gram positive sepsis, granulomas due to intracellular organisms, hairy cell leukemia, Hallerrorden-Spatz disease, hashimoto's thyroiditis, hay fever, heart transplant

rejection, hemachromatosis, hemodialysis, hemolytic uremic syndrome/thrombolytic thrombocytopenic purpura, hemorrhage, hepatitis A, His bundle arryhthmias, HIV infection/HIV neuropathy, Hodgkin's disease, hyperkinetic movement disorders, hypersensitity reactions, hypersensitivity pneumonitis, hypertension, hypokinetic movement disorders, hypothalamic-pituitary-adrenal axis evaluation, idiopathic Addison's disease, idiopathic pulmonary fibrosis, antibody mediated cytotoxicity, Asthenia, infantile spinal muscular atrophy, inflammation of the aorta, influenza a, ionizing radiation exposure, iridocyclitis/uveitis/optic neuritis, ischemia-reperfusion injury, ischemic stroke, juvenile rheumatoid arthritis, juvenile spinal muscular atrophy, Kaposi's sarcoma, kidney transplant rejection, legionella, leishmaniasis, leprosy, lesions of the corticospinal system, lipedema, liver transplant rejection, lymphederma, malaria, malignamt Lymphoma, malignant histiocytosis, malignant melanoma, meningitis, meningococcemia, metabolic/idiopathic, migraine headache, mitochondrial multi.system disorder, mixed connective tissue disease, monoclonal gammopathy, multiple myeloma, multiple systems degenerations (Mencel Dejerine-Thomas Shy-Drager and Machado-Joseph), myasthenia gravis, mycobacterium avium intracellulare, mycobacterium tuberculosis, myelodyplastic syndrome, myocardial ischemic disorders, nasopharyngeal carcinoma, neonatal chronic lung disease, nephritis, nephrosis, neurodegenerative diseases, neurogenic I muscular atrophies , neutropenic fever, non- hodgkins lymphoma, occlusion of the abdominal aorta and its branches, occulsive arterial disorders, okt3 therapy, orchitis/epidydimitis, orchitis/vasectomy reversal procedures, organomegaly, osteoporosis, pancreas transplant rejection, pancreatic carcinoma, paraneoplastic syndrome/hypercalcemia of malignancy, parathyroid transplant rejection, pelvic inflammatory disease, perennial rhinitis, pericardial disease, peripheral atherlosclerotic disease, peripheral vascular disorders, peritonitis, pernicious anemia, pneumocystis carinii pneumonia, pneumonia, POEMS syndrome (polyneuropathy, organomegaly, endocrinopathy, monoclonal gammopathy, and skin changes syndrome), post perfusion syndrome, post pump syndrome, post-MI cardiotomy syndrome, preeclampsia, Progressive supranucleo Palsy, primary pulmonary hypertension, radiation therapy, Raynaud's phenomenon and disease, Raynoud's disease, Refsum's disease, regular narrow QRS tachycardia, renovascular hypertension, reperfusion injury, restrictive cardiomyopathy, sarcomas, scleroderma, senile chorea, Senile Dementia of Lewy body type, seronegative arthropathies, shock, sickle cell anemia, skin allograft rejection, skin changes syndrome, small bowel transplant rejection, solid tumors, specific arrythmias, spinal ataxia, spinocerebellar degenerations, streptococcal myositis, structural lesions of the cerebellum, Subacute sclerosing panencephalitis, Syncope, syphilis of the cardiovascular system, systemic anaphalaxis, systemic inflammatory response syndrome, systemic onset juvenile rheumatoid arthritis, T-cell or FAB ALL, Telangiectasia, thromboangitis obliterans, thrombocytopenia, toxicity, transplants, trauma/hemorrhage, type III hypersensitivity reactions, type IV hypersensitivity, unstable angina, uremia, urosepsis, urticaria, valvular heart diseases, varicose

veins, ,vasculitis, venous diseases, venous thrombosis, ventricular fibrillation, viral and fungal infections, vital encephalitis/aseptic meningitis, vital-associated hemaphagocytic syndrome, Wernicke- Korsakoff syndrome, Wilson's disease, xenograft rejection of any organ or tissue, acute coronary syndromes, acute idiopathic polyneuritis, acute inflammatory demyelinating polyradiculoneuropathy, acute ischemia, adult Still's disease, anaphylaxis, anti-phospholipid antibody syndrome, aplastic anemia, atopic eczema, atopic dermatitis, autoimmune dermatitis, autoimmune disorder associated with streptococcus infection, autoimmune enteropathy, autoimmune hearing loss, autoimmune lymphoproliferative syndrome (ALPS), autoimmune myocarditis, autoimmune premature ovarian failure, blepharitis, bronchiectasis, bullous pemphigoid, cardiovascular disease, catastrophic antiphospholipid syndrome, celiac disease, cervical spondylosis, chronic ischemia, cicatricial pemphigoid, clinically isolated syndrome (cis) with risk for multiple sclerosis, childhood onset psychiatric disorder, dacryocystitis, dermatomyositis, diabetic retinopathy, disk herniation, disk prolaps, drug induced immune hemolytic anemia, endometriosis, endophthalmitis, episcleritis, erythema multiforme, erythema multiforme major, gestational pemphigoid, Guillain-Barré syndrome (GBS), hay fever, Hughes syndrome, idiopathic Parkinson's disease, idiopathic interstitial pneumonia, IgE-mediated allergy, immune hemolytic anemia, inclusion body myositis, infectious ocular inflammatory disease, inflammatory demyelinating disease, inflammatory heart disease, inflammatory kidney disease, IPF/UIP, iritis, keratitis, keratoconjunctivitis sicca, Kussmaul disease or Kussmaul-Meier disease, Landry's paralysis, Langerhan's cell histiocytosis, livedo reticularis, macular degeneration, microscopic polyangiitis, morbus bechterev, motor neuron disorders, mucous membrane pemphigoid, multiple organ failure, myelodysplastic syndrome, myocarditis, nerve root disorders, neuropathy, non-A non-B hepatitis, optic neuritis, osteolysis, ovarian cancer, pauciarticular JRA, peripheral artery occlusive disease (PAOD), peripheral vascular disease (PVD), peripheral artery, disease (PAD), phlebitis, polyarteritis nodosa (or periarteritis nodosa), polychondritis, polymyalgia rheumatica, poliosis, polyarticular JRA, polyendocrine deficiency syndrome, polymyositis, post-pump syndrome, primary Parkinsonism, prostate and rectal cancer and hematopoietic malignancies (leukemia and lymphoma), prostatitis, pure red cell aplasia, primary adrenal insufficiency, recurrent neuromyelitis optica, restenosis, rheumatic heart disease, sapho (synovitis, acne, pustulosis, hyperostosis, and osteitis), scleroderma, secondary amyloidosis, shock lung, scleritis, sciatica, secondary adrenal insufficiency, silicone associated connective tissue disease, sneddon-wilkinson dermatosis, spondilitis ankylosans, Stevens-Johnson syndrome (SJS), systemic inflammatory response syndrome, temporal arteritis, toxoplasmic retinitis, toxic epidermal necrolysis, transverse myelitis, TRAPS (tumor necrosis factor receptor, type 1 allergic reaction, type II diabetes, usual interstitial pneumonia (UIP), vernal conjunctivitis, viral retinitis, Vogt-Koyanagi-Harada syndrome (VKH syndrome), wet macular degeneration, wound healing, fibrosis, renal disease, wet macular degeneration, wound healing, age related macular

degeneration (AMD), diabetic retinopathy, diabetic macular edema, central retinal vein occlusion, corneal neovascularization, exudative AMD, iris neovascularization, neovascular glaucoma, post-surgical fibrosis in glaucoma, proliferative vitreoretinopathy (PVR), choroidal neovascularization, optic disc neovascularization, retinal neovascularization, vitreal neovascularization, pannus, pterygium, macular edema, diabetic macular edema (DME), vascular retinopathy, retinal degeneration, uveitis, or an inflammatory disease of the eye.

[093] In some embodiments, any one of the binding proteins disclosed herein can be used to treat a disorder listed above. In certain embodiments, the binding protein used to treat any of the disorders discussed herein is one or more of the binding proteins listed in Tables 27-30, 38-42, 46-50, or 55-58. In certain embodiments, the binding protein used to treat any of the disorders discussed herein is one or more of the binding proteins listed in Tables 56-58. In certain embodiments, the binding protein is PR-1572102, PR-1572105, PR-1610561, or PR1611292.

[094] In some embodiments, a binding protein (e.g., PR-1572102, PR-1572105, PR1611292, or PR-1610561) may be used to treat wet AMD that is non-responsive to anti-VEGF monotherapy. For instance, a binding protein targeting VEGF and PDGF (e.g., PR-1572102, PR-1572105, or PR-1610561) may lead to better regression of angiogenesis, thereby providing for a more effective treatment (this does not necessarily mean, however, that such a binding protein would have a reduced administration frequency; whether that is the case is presently unknown). The dual inhibition of both VEGF and PDGF may provide for certain improved treatment outcomes, as compared to anti-VEGF monotherapy.

[095] In another aspect, methods of treating a patient suffering from a disorder are disclosed, comprising the step of administering any one of the binding proteins disclosed herein before, concurrently, or after the administration of a second agent, are provided. In an embodiment, the second agent is an imaging agent, cytotoxic agent, angiogenesis inhibitor, kinase inhibitor, co-stimulation molecule blocker, adhesion molecule blocker, anti-cytokine antibody or functional fragment thereof, methotrexate, cyclosporin, rapamycin, FK506, detectable label or reporter, TNF antagonist, antirheumatic, muscle relaxant, narcotic, non-steroid anti-inflammatory drug (NSAID), analgesic, anesthetic, sedative, local anesthetic, neuromuscular blocker, antimicrobial, antipsoriatic, corticosteriod, anabolic steroid, erythropoietin, immunization, immunoglobulin, immunosuppressive, growth hormone, hormone replacement drug, radiopharmaceutical, antidepressant, antipsychotic, stimulant, asthma medication, beta agonist, inhaled steroid, epinephrine or analog, cytokine, or cytokine antagonist.

[096] Also disclosed, in various embodiments, are anti-idiotype antibodies to the binding proteins disclosed herein. An anti-idiotype antibody includes any protein or peptide-containing molecule that comprises at least a portion of an immunoglobulin molecule such as, but

not limited to, at least one complementarily determining region (CDR) of a heavy or light chain or a ligand binding portion thereof, a heavy chain or light chain variable region, a heavy chain or light chain constant region, a framework region, or any portion thereof, that can be incorporated into a binding protein provided herein.

[097] Also disclosed herein, in various embodiments, are methods of determining the presence, amount or concentration of VEGF and/or PDGF, or fragment thereof, in a test sample. In some embodiments, the methods comprise assaying the test sample for the antigen, or fragment thereof, by an immunoassay. The immunoassay (i) employs at least one binding protein and at least one detectable label and (ii) comprises comparing a signal generated by the detectable label as a direct or indirect indication of the presence, amount or concentration of the antigen, or fragment thereof, in the test sample to a signal generated as a direct or indirect indication of the presence, amount or concentration of the antigen, or fragment thereof, in a control or a calibrator. The calibrator is optionally part of a series of calibrators in which each of the calibrators differs from the other calibrators in the series by the concentration of the antigen, or fragment thereof. The method can comprise (i) contacting the test sample with at least one capture agent, which binds to an epitope on the antigen, or fragment thereof, so as to form a capture agent/antigen, or fragment thereof, complex, (ii) contacting the capture agent/antigen, or fragment thereof, complex with at least one detection agent, which comprises a detectable label and binds to an epitope on the antigen, or fragment thereof, that is not bound by the capture agent, to form a capture agent/antigen, or fragment thereof/detection agent complex, and (iii) determining the presence, amount or concentration of the antigen, or fragment thereof, in the test sample based on the signal generated by the detectable label in the capture agent/antigen, or fragment thereof/detection agent complex formed in (ii), wherein at least one capture agent and/or at least one detection agent is the at least one binding protein.

[098] Alternatively, the method may comprise (i) contacting the test sample with at least one capture agent, which binds to an epitope on the antigen, or fragment thereof, so as to form a capture agent/antigen, or fragment thereof, complex, and simultaneously or sequentially, in either order, contacting the test sample with detectably labeled antigen, or fragment thereof, which can compete with any antigen, or fragment thereof, in the test sample for binding to the at least one capture agent, wherein any antigen, or fragment thereof, present in the test sample and the detectably labeled antigen compete with each other to form a capture agent/antigen, or fragment thereof, complex and a capture agent/detectably labeled antigen, or fragment thereof, complex, respectively, and (ii) determining the presence, amount or concentration of the antigen, or fragment thereof, in the test sample based on the signal generated by the detectable label in the capture agent/detectably labeled antigen, or fragment thereof, complex formed in (ii), wherein at least one capture agent is the at least one binding protein and wherein the signal generated by the

detectable label in the capture agent/detectably labeled antigen, or fragment thereof, complex is inversely proportional to the amount or concentration of antigen, or fragment thereof, in the test sample.

[099] In some embodiments, the test sample is from a patient, in which case the method can further comprise diagnosing, prognosticating, or assessing the efficacy of therapeutic/prophylactic treatment of the patient. If the method further comprises assessing the efficacy of therapeutic/prophylactic treatment of the patient, the method optionally further comprises modifying the therapeutic/prophylactic treatment of the patient as needed to improve efficacy. The method can be adapted for use in an automated system or a semi-automated system. Accordingly, the methods described herein also can be used to determine whether or not a subject has or is at risk of developing a given disease, disorder or condition. Specifically, such a method can comprise the steps of: (a) determining the concentration or amount in a test sample from a subject of analyte, or fragment thereof, (e.g., using the methods described herein, or methods known in the art); and (b) comparing the concentration or amount of analyte, or fragment thereof, determined in step (a) with a predetermined level, wherein, if the concentration or amount of analyte determined in step (a) is favorable with respect to a predetermined level, then the subject is determined not to have or be at risk for a given disease, disorder or condition. However, if the concentration or amount of analyte determined in step (a) is unfavorable with respect to the predetermined level, then the subject is determined to have or be at risk for a given disease, disorder or condition.

[0100] Additionally, in various embodiments, provided herein are methods of monitoring the progression of disease in a subject. In some embodiments, the method can comprise the steps of: (a) determining the concentration or amount in a test sample from a subject of analyte; (b) determining the concentration or amount in a later test sample from the subject of analyte; and (c) comparing the concentration or amount of analyte as determined in step (b) with the concentration or amount of analyte determined in step (a), wherein if the concentration or amount determined in step (b) is unchanged or is unfavorable when compared to the concentration or amount of analyte determined in step (a), then the disease in the subject is determined to have continued, progressed or worsened. By comparison, if the concentration or amount of analyte as determined in step (b) is favorable when compared to the concentration or amount of analyte as determined in step (a), then the disease in the subject is determined to have discontinued, regressed or improved.

[0101] Optionally, the method further comprises comparing the concentration or amount of analyte as determined in step (b), for example, with a predetermined level. Further, optionally the method comprises treating the subject with one or more pharmaceutical compositions for a period of time if the comparison shows that the concentration or amount of

analyte as determined in step (b), for example, is unfavorably altered with respect to the predetermined level.

[0102] Also provided, in various embodiments, are kits for assaying a test sample for VEGF and/or PDGF, or fragment thereof. The kit may comprise at least one component for assaying the test sample for an antigen, or fragment thereof, and instructions for assaying the test sample for an antigen, or fragment thereof, wherein the at least one component includes at least one composition comprising the binding protein disclosed herein, wherein the binding protein is optionally detectably labeled.

[0103] Unless otherwise defined herein, scientific and technical terms used herein have the meanings that are commonly understood by those of ordinary skill in the art. In the event of any latent ambiguity, definitions provided herein take precedent over any dictionary or extrinsic definition. Unless otherwise required by context, singular terms shall include pluralities and plural terms shall include the singular. The use of "or" means "and/or" unless stated otherwise. The use of the term "including", as well as other forms, such as "includes" and "included", is not limiting. Any range disclosed herein is intended to encompass the endpoints of that range unless stated otherwise.

[0104] Generally, nomenclatures used in connection with cell and tissue culture, molecular biology, immunology, microbiology, genetics and protein and nucleic acid chemistry and hybridization described herein are those known and commonly used in the art. The methods and techniques provided herein are generally performed according to conventional methods well known in the art and as described in various general and more specific references that are cited and discussed throughout the present specification unless otherwise indicated. Enzymatic reactions and purification techniques are performed according to manufacturer's specifications, as commonly accomplished in the art or as described herein. The nomenclatures used in connection with, and the laboratory procedures and techniques of, analytical chemistry, synthetic organic chemistry, and medicinal and pharmaceutical chemistry described herein are those well-known and commonly used in the art. Standard techniques are used for chemical syntheses, chemical analyses, pharmaceutical preparation, formulation, and delivery, and treatment of patients.

[0105] That the disclosure may be more readily understood, select terms are defined below.

[0106] The term "antibody" refers to an immunoglobulin (Ig) molecule, which is may comprise four polypeptide chains, two heavy (H) chains and two light (L) chains, or it may comprise a functional fragment, mutant, variant, or derivative thereof, that retains the epitope binding features of an Ig molecule. Such fragment, mutant, variant, or derivative antibody formats are known in the art. In an embodiment of a full-length antibody, each heavy chain is

comprised of a heavy chain variable region (VH) and a heavy chain constant region (CH). In the case of an IgG molecule, the CH comprises three domains, CH1, CH2 and CH3. Each light chain is comprised of a light chain variable region (VL) and a light chain constant region (CL). The CL is comprised of a single CL domain. The VH and VL can be further subdivided into regions of hypervariability, termed complementarity determining regions (CDRs), interspersed with regions that are more conserved, termed framework regions (FRs). Generally, each VH and VL is composed of three CDRs and four FRs, arranged from amino-terminus to carboxy-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, and FR4. CDR regions may be determined by standard methods, e.g., those of Kabat et al. Immunoglobulin molecules can be of any type (e.g., IgG, IgE, IgM, IgD, IgA and IgY), class (e.g., IgG1, IgG2, IgG3, IgG4, IgA1 and IgA2), or subclass.

[0107] The term "bispecific antibody" refers to an antibody that binds one antigen (or epitope) on one of its two binding arms (one pair of HC/LC), and binds a different antigen (or epitope) on its second binding arm (a different pair of HC/LC). A bispecific antibody is a type of bispecific binding protein. A bispecific antibody may have two distinct antigen binding arms (in both specificity and CDR sequences), and may be monovalent for each antigen to which it binds. Bispecific antibodies include those generated by quadroma technology (Milstein and Cuello (1983) Nature 305(5934): 537-40), by chemical conjugation of two different monoclonal antibodies (Staerz et al. (1985) Nature 314(6012): 628-31), or by knob-into-hole or similar approaches which introduces mutations in the Fc region (Holliger et al. (1993) Proc. Natl. Acad. Sci. USA 90(14): 6444-6448).

[0108] The term "affinity matured" refers to an antibody or binding protein with one or more alterations in one or more CDR or framework (FR) regions thereof, which may result in an improvement in the affinity for an antigen, compared to a parent antibody or binding protein which does not possess those alteration(s). Exemplary affinity matured antibodies or binding protein will have nanomolar or even picomolar affinities for the target antigen. Affinity matured antibodies or binding protein may be produced by procedures known in the art, e.g., Marks et al. (1992) BioTechnology 10:779-783 describes affinity maturation by VH and VL domain shuffling. Random mutagenesis of CDR and/or framework residues is described by Barbas et al. (1994) Proc. Nat. 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; Hawkins et al. (1992) J. Mol. Biol. 226:889-896 and mutation at selective mutagenesis positions, contact or hypermutation positions with an activity enhancing amino acid residue as described in U.S. Patent No. 6,914,128.

[0109] The term "CDR-grafted" refers to an antibody or binding protein that comprises heavy and light chain variable region sequences in which the sequences of one or more of the

CDR regions of VH and/or VL are replaced with CDR sequences of another antibody or binding protein. For example, the two antibodies or binding protein can be from different species, such as antibodies or binding protein having murine heavy and light chain variable regions in which one or more of the murine CDRs has been replaced with human CDR sequences.

[0110] The term "humanized" refers to an antibody or binding protein from a non-human species that has been altered to be more "human-like", i.e., more similar to human germline sequences. One type of humanized antibody or binding protein is a CDR-grafted antibody or binding protein, in which non-human CDR sequences are introduced into human VH and VL sequences to replace the corresponding human CDR sequences. A humanized antibody or binding protein also encompasses a variant, derivative, analog or fragment of an antibody or binding protein that comprises framework region (FR) sequences having substantially (e.g., at least 80%, at least 85%, at least 90%, at least 95%, at least 98% or at least 99% identity to) the amino acid sequence of a human antibody and at least one CDR having substantially the amino acid sequence of a non-human antibody. A humanized antibody or binding protein may comprise substantially all of at least one variable domain (Fab, Fab', F(ab') 2, FabC, Fv) in which the sequence of all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin (i.e., donor antibody) and the sequence of all or substantially all of the FR regions are those of a human immunoglobulin. The humanized antibody or binding protein also may include the CH1, hinge, CH2, CH3, and/or CH4 regions of the heavy chain. In an embodiment, a humanized antibody or binding protein may also comprise at least a portion of a human immunoglobulin Fc region. In some embodiments, a humanized antibody or binding protein only contains a humanized light chain. In some embodiments, a humanized antibody or binding protein only contains a humanized heavy chain. In some embodiments, a humanized antibody or binding protein only contains a humanized variable domain of a light chain and/or humanized variable domain of a heavy chain. In some embodiments, a humanized antibody or binding protein contains a humanized light chain as well as at least a variable domain of a heavy chain. In some embodiments, a humanized antibody or binding protein contains a humanized heavy chain as well as at least a variable domain of a light chain.

[0111] The term "anti-idiotypic antibody" refers to an antibody raised against the amino acid sequence of the antigen combining site of another antibody. Anti-idiotypic antibodies may be administered to enhance an immune response against an antigen.

[0112] The term "biological activity" refers to any one or more biological properties of a molecule (whether present naturally as found in vivo, or provided or enabled by recombinant means). Biological properties include, but are not limited to, binding a receptor, inducing cell proliferation, inhibiting cell growth, inducing other cytokines, inducing apoptosis, and enzymatic activity.

[0113] The term "neutralizing" refers to counteracting the biological activity of an antigen when a binding protein specifically binds to the antigen. In an embodiment, a neutralizing binding protein binds to an antigen (e.g., VEGF and/or PDGF or their receptors) and reduces the antigen's biological activity by at least about 20%, about 40%, about 60%, about 80%, about 85%, about 90%, about 95%, or about 100% (or any percentage in between).

[0114] The term "specificity" refers to the ability of a binding protein to selectively bind an antigen.

[0115] The term "affinity" refers to the strength of the interaction between a binding protein and an antigen, and is determined by the sequence of the CDRs of the binding protein as well as by the nature of the antigen, such as its size, shape, and/or charge. Binding proteins may be selected for affinities that provide desired therapeutic end-points while minimizing negative side-effects. Affinity may be measured using methods known to one skilled in the art (see, e.g., U.S. Patent Appl. No. 20090311253 and U.S. Patent No. 7,612,181).

[0116] The term "potency" refers to the ability of a binding protein to achieve a desired effect, and is a measurement of its therapeutic efficacy. Potency may be assessed using methods known to one skilled in the art (see, e.g., U.S. Patent Appl. No. 20090311253 and U.S. Patent No. 7,612,181).

[0117] The term "cross-reactivity" refers to the ability of a binding protein to bind a target other than that against which it was raised. Generally, a binding protein will bind its target tissue(s)/antigen(s) with an appropriately high affinity, but will display an appropriately low affinity for non-target normal tissues. Methods of assessing cross-reactivity are known to one skilled in the art (see, e.g., U.S. Patent Appl. No. 20090311253 and U.S. Patent No. 7,612,181).

[0118] The term "biological function" refers the specific *in vitro* or *in vivo* actions of a binding protein. Binding proteins may target several classes of antigens and achieve desired therapeutic outcomes through multiple mechanisms of action. Binding proteins may target soluble proteins, cell surface antigens, as well as extracellular protein deposits. Binding proteins may agonize, antagonize, or neutralize the activity of their targets. Binding proteins may assist in the clearance of the targets to which they bind, or may result in cytotoxicity when bound to cells. Portions of two or more antibodies may be incorporated into a multivalent format to achieve distinct functions in a single binding protein molecule. The *in vitro* assays and *in vivo* models used to assess biological function are known to one skilled in the art (see, e.g., U.S. Patent Appl. No. 20090311253 and U.S. Patent No. 7,612,181).

[0119] A "stable" binding protein refers to one in which the binding protein retains some level of its physical stability, chemical stability and/or biological activity upon storage. Methods of stabilizing binding proteins and assessing their stability at various temperatures are

known to one skilled in the art (see, e.g., U.S. Patent Appl. No. 20090311253 and U.S. Patent No. 7,612,181).

[0120] The term "solubility" refers to the ability of a protein to remain dispersed within an aqueous solution. The solubility of a protein in an aqueous formulation depends upon the proper distribution of hydrophobic and hydrophilic amino acid residues, and therefore, solubility can correlate with the production of correctly folded proteins. A person skilled in the art will be able to detect an increase or decrease in solubility of a binding protein using routine HPLC techniques and methods known to one skilled in the art (see, e.g., U.S. Patent Appl. No. 20090311253 and U.S. Patent No. 7,612,181).

[0121] Binding proteins may be produced using a variety of host cells or may be produced in vitro, and the relative yield per effort determines the "production efficiency." Factors influencing production efficiency include, but are not limited to, host cell type (prokaryotic or eukaryotic), choice of expression vector, choice of nucleotide sequence, and methods employed. The materials and methods used in binding protein production, as well as the measurement of production efficiency, are known to one skilled in the art (see, e.g., U.S. Patent Appl. No. 20090311253 and U.S. Patent No. 7,612,181).

[0122] The term "immunogenicity" means the ability of a substance to induce an immune response. Administration of a therapeutic binding protein may result in a certain incidence of an immune response. Potential elements that might induce immunogenicity in a multivalent format may be analyzed during selection of the parental antibodies, and steps to reduce such risk can be taken to optimize the parental antibodies prior to incorporating their sequences into a multivalent binding protein format. Methods of reducing the immunogenicity of antibodies and binding proteins are known to one skilled in the art (U.S. Patent Appl. No. 20090311253 and U.S. Patent No. 7,612,181).

[0123] The terms "label" and "detectable label" refer to a moiety attached to a member of a specific binding pair, such as an antibody/binding protein or its analyte to render a reaction (e.g., binding) between the members of the specific binding pair, detectable. The labeled member of the specific binding pair is referred to as "detectably labeled." Thus, the term "labeled binding protein" refers to a protein with a label incorporated that provides for the identification of the binding protein. In an embodiment, the label is a detectable marker that can produce a signal that is detectable by visual or instrumental means, e.g., incorporation of a radiolabeled amino acid or attachment to a polypeptide of biotinyl moieties that can be detected by marked avidin (e.g., streptavidin containing a fluorescent marker or enzymatic activity that can be detected by optical or colorimetric methods). Examples of labels for polypeptides include, but are not limited to, the following: radioisotopes or radionuclides (e.g., ^{3}H, ^{14}C, ^{35}S, ^{90}Y, ^{99}Tc, ^{111}In, ^{125}I, ^{131}I, ^{177}Lu, ^{166}Ho,

or ^{153}Sm); chromogens, fluorescent labels (e.g., FITC, rhodamine, lanthanide phosphors), enzymatic labels (e.g., horseradish peroxidase, luciferase, alkaline phosphatase); chemiluminescent markers; biotinyl groups; predetermined polypeptide epitopes recognized by a secondary reporter (e.g., leucine zipper pair sequences, binding sites for secondary antibodies, metal binding domains, epitope tags); and magnetic agents, such as gadolinium chelates. Representative examples of labels commonly employed for immunoassays include moieties that produce light, e.g., acridinium compounds, and moieties that produce fluorescence, e.g., fluorescein. In this regard, the moiety itself may not be detectably labeled but may become detectable upon reaction with yet another moiety.

[0124] The term "conjugate" refers to a binding protein that is chemically linked to a second chemical moiety, such as a therapeutic or cytotoxic agent. The term "agent" includes a chemical compound, a mixture of chemical compounds, a biological macromolecule, or an extract made from biological materials. In an embodiment, the therapeutic or cytotoxic agents include, but are not limited to, pertussis toxin, taxol, cytochalasin B, gramicidin D, ethidium bromide, emetine, mitomycin, etoposide, tenoposide, vincristine, vinblastine, colchicin, doxorubicin, daunorubicin, dihydroxy anthracin dione, mitoxantrone, mithramycin, actinomycin D, 1-dehydrotestosterone, glucocorticoids, procaine, tetracaine, lidocaine, propranolol, and puromycin and analogs or homologs thereof. When employed in the context of an immunoassay, the conjugate antibody may be a detectably labeled antibody used as the detection antibody.

[0125] The terms "crystal" and "crystallized" refer to a binding protein (e.g., an antibody), or antigen binding portion thereof, that exists in the form of a crystal. Crystals are one form of the solid state of matter, which is distinct from other forms such as the amorphous solid state or the liquid crystalline state. Crystals are composed of regular, repeating, three-dimensional arrays of atoms, ions, molecules (e.g., proteins such as antibodies), or molecular assemblies (e.g., antigen/antibody complexes). These three-dimensional arrays are arranged according to specific mathematical relationships that are well-understood in the field. The fundamental unit, or building block, that is repeated in a crystal is called the asymmetric unit. Repetition of the asymmetric unit in an arrangement that conforms to a given, well-defined crystallographic symmetry provides the "unit cell" of the crystal. Repetition of the unit cell by regular translations in all three dimensions provides the crystal. (See Giege and Ducruix (1999) CRYSTALLIZATION OF NUCLEIC ACIDS AND PROTEINS, A PRACTICAL APPROACH, 2nd ed., pp. 20 1-16, Oxford University Press, NY, NY).

[0126] The term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid," which refers to a circular double stranded DNA loop into which additional DNA segments may be ligated. Another type of vector is a viral vector, wherein additional DNA segments may be ligated into the

viral genome. Other vectors include RNA vectors. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (e.g., bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (e.g., non-episomal mammalian vectors) can be integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "recombinant expression vectors" (or simply, "expression vectors"). In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" may be used interchangeably as the plasmid is the most commonly used form of vector. However, other forms of expression vectors are also included, such as viral vectors (e.g., replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions. A group of pHybE vectors (e.g., U.S. Patent No. 8,187,836) may be used for parental antibody and DVD-binding protein cloning. V1, derived from pJP183; pHybE-hCg1,z,non-a V2; and pJP184, may be used for cloning of antibody and DVD heavy chains with a wild type constant region or modified constant region (e.g., a L234, L235, H435A modified IgG1 constant region). V2, derived from pJP191 (with or without modifications to the Kozak site); pHybE-hCk V3, may be used for cloning of antibody and DVD light chains with a kappa constant region. V3, derived from pJP192; pHybE-hCl V2, may be used for cloning of antibody and DVD light chains with a lambda constant region. V4, built with a lambda signal peptide and a kappa constant region, may be used for cloning of DVD light chains with a lambda-kappa hybrid V domain. V5, built with a kappa signal peptide and a lambda constant region, may be used for cloning of DVD light chains with a kappa-lambda hybrid V domain. V7, derived from pJP183; pHybE-hCg1,z,non-a V2, may be used for cloning of antibody and DVD heavy chains with a (234,235 AA) mutant constant region.

[0127] The terms "recombinant host cell" or "host cell" refer to a cell into which exogenous, e.g., recombinant, DNA has been introduced. Such terms refer not only to the particular subject cell, but to the progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term "host cell" as used herein. In an embodiment, host cells include prokaryotic and eukaryotic cells. In an embodiment, eukaryotic cells include protist, fungal, plant and animal cells. In another embodiment, host cells include but are not limited to the prokaryotic cell line *E. coli*; mammalian cell lines CHO, HEK 293, COS, NS0, SP2 and PER.C6; the insect cell line Sf9; and the fungal cell *Saccharomyces cerevisiae*.

[0128] The term "transfection" encompasses a variety of techniques commonly used for the introduction of exogenous nucleic acid (e.g., DNA) into a host cell, e.g., electroporation, calcium-phosphate precipitation, DEAE-dextran transfection and the like.

[0129] The term "cytokine" refers to a protein released by one cell population that acts on another cell population as an intercellular mediator. The term "cytokine" includes proteins from natural sources or from recombinant cell culture and biologically active equivalents of the native sequence cytokines.

[0130] The term "biological sample" refers to a quantity of a substance from a living thing or formerly living thing. Such substances include, but are not limited to, blood, plasma, serum, urine, amniotic fluid, synovial fluid, endothelial cells, leukocytes, monocytes, other cells, organs, tissues, bone marrow, lymph nodes and spleen.

[0131] The term "component" refers to an element of a composition. In relation to a diagnostic kit, for example, a component may be a capture antibody, a detection or conjugate antibody, a control, a calibrator, a series of calibrators, a sensitivity panel, a container, a buffer, a diluent, a salt, an enzyme, a co-factor for an enzyme, a detection reagent, a pretreatment reagent/solution, a substrate (e.g., as a solution), a stop solution, and the like that can be included in a kit for assay of a test sample. Thus, a "component" can include a polypeptide or other analyte as above, that is immobilized on a solid support, such as by binding to an anti-analyte (e.g., anti-polypeptide) antibody. Some components can be in solution or lyophilized for reconstitution for use in an assay.

[0132] "Control" refers to a composition known to not analyte ("negative control") or to contain analyte ("positive control"). A positive control can comprise a known concentration of analyte. A "positive control" can be used to establish assay performance characteristics and is a useful indicator of the integrity of reagents (e.g., analytes).

[0133] "Predetermined cutoff" and "predetermined level" refer generally to an assay cutoff value that is used to assess diagnostic/prognostic/therapeutic efficacy results by comparing the assay results against the predetermined cutoff/level, where the predetermined cutoff/level already has been linked or associated with various clinical parameters (e.g., severity of disease, progression/nonprogression/improvement, etc.). While the present disclosure may provide exemplary predetermined levels, it is well-known that cutoff values may vary depending on the nature of the immunoassay (e.g., antibodies employed, etc.). It further is well within the ordinary skill of one in the art to adapt the disclosure herein for other immunoassays to obtain immunoassay-specific cutoff values for those other immunoassays based on this disclosure. Whereas the precise value of the predetermined cutoff/level may vary between assays, correlations as described herein (if any) may be generally applicable.

[0134] "Pretreatment reagent," e.g., lysis, precipitation and/or solubilization reagent, as used in a diagnostic assay as described herein refers to one that lyses any cells and/or solubilizes any analyte that is/are present in a test sample. Pretreatment is not necessary for all samples, as described further herein. Among other things, solubilizing the analyte (e.g., polypeptide of interest) may entail release of the analyte from any endogenous binding proteins present in the sample. A pretreatment reagent may be homogeneous (not requiring a separation step) or heterogeneous (requiring a separation step). With use of a heterogeneous pretreatment reagent there is removal of any precipitated analyte binding proteins from the test sample prior to proceeding to the next step of the assay.

[0135] "Quality control reagents" in the context of immunoassays and kits described herein, include, but are not limited to, calibrators, controls, and sensitivity panels. A "calibrator" or "standard" typically is used (e.g., one or more, such as a plurality) in order to establish calibration (standard) curves for interpolation of the concentration of an analyte, such as an antibody or an analyte. Alternatively, a single calibrator, which is near a predetermined positive/negative cutoff, can be used. Multiple calibrators (i.e., more than one calibrator or a varying amount of calibrator(s)) can be used in conjunction so as to comprise a "sensitivity panel."

[0136] The term "specific binding partner" refers to a member of a specific binding pair. A specific binding pair comprises two different molecules that specifically bind to each other through chemical or physical means. Therefore, in addition to antigen and antibody specific binding, other specific binding pairs can include biotin and avidin (or streptavidin), carbohydrates and lectins, complementary nucleotide sequences, effector and receptor molecules, cofactors and enzymes, enzyme inhibitors and enzymes, and the like. Furthermore, specific binding pairs can include members that are analogs of the original specific binding members, for example, an analyte-analog. Immunoreactive specific binding members include antigens, antigen fragments, and antibodies, including monoclonal and polyclonal antibodies as well as complexes, fragments, and variants (including fragments of variants) thereof, whether isolated or recombinantly produced.

[0137] The term "Fc region" refers to the C-terminal region of an immunoglobulin heavy chain, which may be generated by papain digestion of an intact antibody or binding protein. The Fc region may be a native sequence Fc region or a variant Fc region. The Fc region of an immunoglobulin generally comprises two constant domains, a CH2 domain and a CH3 domain, and optionally comprises a CH4 domain. Replacements of amino acid residues in the Fc portion to alter effector function are known in the art (e.g., U.S. Patent Nos. 5,648,260 and 5,624,821). The Fc region mediates several important effector functions, e.g., cytokine induction, antibody dependent cell mediated cytotoxicity (ADCC), phagocytosis, complement dependent cytotoxicity

(CDC), and half-life/ clearance rate of antibody or binding protein and antigen-antibody or antigen-binding protein complexes. In some cases these effector functions are desirable for a therapeutic immunoglobulin but in other cases might be unnecessary or even deleterious, depending on the therapeutic objectives.

[0138] The term "antigen-binding portion" of a binding protein refers to one or more fragments of a binding protein that retain the ability to specifically bind to an antigen. The antigen-binding function of a binding protein may be performed by fragments of a full-length binding protein, including bispecific, dual specific, or multi-specific formats; for instance, binding to two or more different antigens. Examples of binding fragments encompassed within the term "antigen-binding portion" of an binding protein include (i) an Fab fragment, a monovalent fragment consisting of the VL, VH, CL and CH1 domains; (ii) an $F(ab')_2$ fragment, a bivalent fragment comprising two Fab fragments linked by a disulfide bridge at the hinge region; (iii) an Fd fragment consisting of the VH and CH1 domains; (iv) an Fv fragment consisting of the VL and VH domains of a single arm of an antibody or binding protein, (v) a dAb fragment, which comprises a single variable domain; and (vi) an isolated complementarity determining region (CDR). Furthermore, although the two domains of the Fv fragment, VL and VH, are encoded by separate genes, they may be joined, e.g., using recombinant methods, by a synthetic linker that enables them to be made as a single protein chain in which the VL and VH regions pair to form monovalent molecules (known as single chain Fv (scFv). Such single chain antibodies or binding proteins are also intended to be encompassed within the term "antigen-binding portion" of an antibody or binding protein. Other forms of single chain antibodies, such as diabodies are also encompassed. In addition, single chain antibodies or binding protein also include "linear" antibodies or binding protein comprising a pair of tandem Fv segments (VH-CH1-VH-CH1) which, together with complementary light chain polypeptides, form a pair of antigen binding regions.

[0139] The term "multivalent binding protein" refers to a binding protein comprising two or more antigen binding sites. In an embodiment, the multivalent binding protein is engineered to have three or more antigen binding sites, and may not be a naturally occurring antibody. The term "multispecific binding protein" refers to a binding protein capable of binding two or more related or unrelated targets. In an embodiment, the dual variable domain (DVD) binding proteins provided herein comprise two or more antigen binding sites and are tetravalent or multivalent binding proteins.

[0140] The term "linker" refers to an amino acid residue or a polypeptide comprising two or more amino acid residues joined by peptide bonds that are used to link two polypeptides (e.g., two VH or two VL domains). Such linker polypeptides are well known in the art (see, e.g.,

Holliger et al. (1993) Proc. Natl. Acad. Sci. USA 90:6444-6448; Poljak et al. (1994) Structure 2:1121-1123). A number of suitable linkers for use in the binding proteins described herein are set out in Table 55. In some embodiments, the X1 linker on the heavy chain is a GS-H10 linker and the X1 linker on the light chain is a GS-L10(dR) linker. In some embodiments, the X1 linker on the heavy chain is a GS-H10 linker and the X1 linker on the light chain is a GS-L10 linker. In some embodiments, the X1 linker on the heavy chain is an HG-short linker and the X1 linker on the light chain is an LK-long linker.

[0141] The terms "Kabat numbering", "Kabat definitions" and "Kabat labeling" are used interchangeably herein. These terms, which are recognized in the art, refer to a system of numbering amino acid residues which are more variable (i.e., hypervariable) than other amino acid residues in the heavy and light chain variable regions of an antibody or binding protein, or an antigen binding portion thereof (Kabat et al. (1971) Ann. NY Acad. Sci. 190:382-391 and, Kabat et al. (1991) Sequences of Proteins of Immunological Interest, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242). For the heavy chain variable region, the hypervariable region ranges from amino acid positions 31 to 35 for CDR1, amino acid positions 50 to 65 for CDR2, and amino acid positions 95 to 102 for CDR3. For the light chain variable region, the hypervariable region ranges from amino acid positions 24 to 34 for CDR1, amino acid positions 50 to 56 for CDR2, and amino acid positions 89 to 97 for CDR3. In some embodiments, the CDR sequences, framework sequences, and or constant region sequences are identified using Kabat numbering.

[0142] The term "CDR" refers to a complementarity determining region within an immunoglobulin variable region sequence. There are three CDRs in each of the variable regions of the heavy chain and the light chain, which are designated CDR1, CDR2 and CDR3, for each of the heavy and light chain variable regions. The term "CDR set" refers to a group of three CDRs that occur in a single variable region capable of binding the antigen. The exact boundaries of these CDRs have been defined differently according to different systems. The system described by Kabat (Kabat et al. (1987) and (1991)) not only provides an unambiguous residue numbering system applicable to any variable region of an antibody or binding protein, but also provides precise residue boundaries defining the three CDRs in each heavy or light chain sequence. These CDRs may be referred to as Kabat CDRs. Chothia and coworkers (Chothia and Lesk (1987) J. Mol. Biol. 196:901-917; Chothia et al. (1989) Nature 342:877-883) found that certain sub-portions within Kabat CDRs adopt nearly identical peptide backbone conformations, despite having great diversity at the level of amino acid sequence. These sub-portions were designated as L1, L2 and L3 or H1, H2 and H3 where the "L" and the "H" designates the light chain and the heavy chain regions, respectively. These regions may be referred to as Chothia CDRs, which have boundaries that overlap with Kabat CDRs. Other boundaries defining CDRs overlapping

with the Kabat CDRs have been described by Padlan (1995) FASEB J. 9:133-139 and MacCallum (1996) J. Mol. Biol. 262(5):732-45). Still other CDR boundary definitions may not strictly follow one of the herein systems, but will nonetheless overlap with the Kabat CDRs, although they may be shortened or lengthened in light of prediction or experimental findings that particular residues or groups of residues or even entire CDRs do not significantly impact antigen binding. The methods used herein may utilize CDRs defined according to any of these systems, although certain embodiments use Kabat or Chothia defined CDRs.

[0143] The term "epitope" refers to a region of an antigen that is specifically bound by a binding protein disclosed herein. In certain embodiments, epitope determinants include chemically active surface groupings of molecules such as amino acids, sugar side chains, phosphoryl, or sulfonyl, and, in certain embodiments, may have specific three dimensional structural characteristics, and/or specific charge characteristics. An antigen or fragment can contain more than one epitope. An epitope may be determined by obtaining an X-ray crystal structure of an antibody:antigen complex and determining which residues on the antigen (e.g., VEGF or PDGF or a receptor) are within a specified distance of residues on the antibody of interest, wherein the specified distance is, 5 Å or less, e.g., 5Å, 4Å , 3Å, 2Å, 1Å or less, or any distance in between. In some embodiments, the epitope is defined as a stretch of 8 or more contiguous amino acid residues along the antigen sequence in which at least 50%, 70% or 85% of the residues are within the specified distance of the antibody or binding protein in the X-ray crystal structure.

[0144] In certain embodiments, a binding protein specifically binds an antigen when it preferentially recognizes its target antigen in a complex mixture of proteins and/or macromolecules. Binding proteins that bind to the same or similar epitopes will likely cross-compete (one prevents the binding or modulating effect of the other). Cross-competition, however, can occur even without partial or complete epitope overlap, e.g., if epitopes are adjacent in three-dimensional space and/or due to steric hindrance.

[0145] The term "pharmacokinetic(s)" refers to the process by which a drug is absorbed, distributed, metabolized, and excreted by an organism. To generate a multivalent binding protein molecule with a desired pharmacokinetic profile, parent monoclonal antibodies with similarly desired pharmacokinetic profiles are selected. The PK profiles of the selected parental monoclonal antibodies can be easily determined in rodents using methods known to one skilled in the art (see, e.g., U.S. Patent No. 7,612,181).

[0146] The term "bioavailability" refers to the degree and rate at which a drug is absorbed into a living system or is made available at the site of physiological activity. Bioavailability can be a function of several of the previously described properties, including

stability, solubility, immunogenicity and pharmacokinetics, and can be assessed using methods known to one skilled in the art (see, e.g., U.S. Patent No. 7,612,181).

[0147] The term "surface plasmon resonance" refers to an optical phenomenon that allows for the analysis of real-time biospecific interactions by detection of alterations in protein concentrations within a biosensor matrix, for example using the BIAcore® system (BIAcore International AB, a GE Healthcare company, Uppsala, Sweden and Piscataway, NJ). For further descriptions, see Jönsson et al. (1993) Ann. Biol. Clin. 51:19-26. The term "K_{on}" refers to the on rate constant for association of a binding protein (e.g., an antibody or DVD-Ig) to the antigen to form the, e.g., DVD-Ig/antigen complex. The term "K_{on}" also refers to "association rate constant", or "ka", as is used interchangeably herein. This value indicating the binding rate of a binding protein to its target antigen or the rate of complex formation between a binding protein, e.g., an antibody, and antigen also is shown by the equation below:

$$\text{Antibody ("Ab") + Antigen ("Ag")} \rightarrow \text{Ab-Ag}$$

[0148] The term "K_{off}" refers to the off rate constant for dissociation, or "dissociation rate constant", of a binding protein (e.g., an antibody or DVD-Ig) from the, e.g., DVD-Ig/antigen complex as is known in the art. This value indicates the dissociation rate of a binding protein, e.g., an antibody, from its target antigen or separation of Ab-Ag complex over time into free antibody and antigen as shown by the equation below:

$$\text{Ab + Ag} \leftarrow \text{Ab-Ag}$$

[0149] The terms "K_d" and "equilibrium dissociation constant" may refer to the value obtained in a titration measurement at equilibrium, or by dividing the dissociation rate constant (K_{off}) by the association rate constant (K_{on}). The association rate constant, the dissociation rate constant and the equilibrium dissociation constant, are used to represent the binding affinity of a binding protein (e.g., an antibody or DVD-Ig) to an antigen. Methods for determining association and dissociation rate constants are well known in the art. Using fluorescence–based techniques offers high sensitivity and the ability to examine samples in physiological buffers at equilibrium. Other experimental approaches and instruments such as a BIAcore® (biomolecular interaction analysis) assay, can be used (e.g., instrument available from BIAcore International AB, a GE Healthcare company, Uppsala, Sweden). Additionally, a KinExA® (Kinetic Exclusion Assay) assay, available from Sapidyne Instruments (Boise, Idaho), can also be used.

[0150] The term "variant" refers to a polypeptide that differs from a given polypeptide in amino acid sequence by the addition (e.g., insertion), deletion, or conservative substitution of amino acids, but that retains the biological activity of the given polypeptide (e.g., a variant VEGF antibody can compete with anti-VEGF antibody for binding to VEGF). A conservative

substitution of an amino acid, i.e., replacing an amino acid with a different amino acid of similar properties (e.g., hydrophilicity and degree and distribution of charged regions) is recognized in the art as typically involving a minor change. These minor changes can be identified, in part, by considering the hydropathic index of amino acids, as understood in the art (see, e.g., Kyte et al. (1982) J. Mol. Biol. 157: 105-132). The hydropathic index of an amino acid is based on a consideration of its hydrophobicity and charge. It is known in the art that amino acids of similar hydropathic indexes in a protein can be substituted and the protein still retains protein function. In one aspect, amino acids having hydropathic indexes of ± 2 are substituted. The hydrophilicity of amino acids also can be used to reveal substitutions that would result in proteins retaining biological function. A consideration of the hydrophilicity of amino acids in the context of a peptide permits calculation of the greatest local average hydrophilicity of that peptide, a useful measure that has been reported to correlate well with antigenicity and immunogenicity (see, e.g., U.S. Patent No. 4,554,101). Substitution of amino acids having similar hydrophilicity values can result in peptides retaining biological activity, for example immunogenicity, as is understood in the art. In one aspect, substitutions are performed with amino acids having hydrophilicity values within ± 2 of each other. Both the hydrophobicity index and the hydrophilicity value of amino acids are influenced by the particular side chain of that amino acid. Consistent with that observation, amino acid substitutions that are compatible with biological function are understood to depend on the relative similarity of the amino acids, and particularly the side chains of those amino acids, as revealed by the hydrophobicity, hydrophilicity, charge, size, and other properties. The term "variant" also includes polypeptide or fragment thereof that has been differentially processed, such as by proteolysis, phosphorylation, or other post-translational modification, yet retains its biological activity or antigen reactivity, e.g., the ability to bind to VEGF. The term "variant" encompasses fragments of a variant unless otherwise defined. A variant may be about 99%, 98%, 97%, 96%, 95%, 94%, 93%, 92%, 91%, 90%, 89%, 88%, 87%, 86%,85%, 84%, 83%, 82%, 81%, 80%, 79%, 78%, 77%, 76%, or 75% identical to the wild type sequence.

Use Of Disclosed Binding Proteins In Treating Various Diseases

[0151] The binding protein molecules provided herein are useful as therapeutic molecules to treat various diseases, e.g., wherein the targets that are recognized by the binding proteins are detrimental. Such binding proteins may bind one or more targets involved in a specific disease.

[0152] Without limiting the disclosure, further information on certain disease conditions is provided.

1. Age-Related Macular Degeneration (AMD)

[0153] In various embodiments, one or more of the binding proteins disclosed herein that are capable of binding to VEGF and PDGF and/or their cognate receptors (e.g., a combination of an anti-VEGF and an anti-PDGF binding protein, or a multispecific binding protein capable of targeting both VEGF and PDGF) can be used to treat AMD. In some embodiments, any of the binding proteins disclosed herein can be used to treat AMD, or a binding protein comprising the CDR and/or variable domain sequences from any of the binding disclosed herein. In certain embodiments, the binding protein used to treat AMD is one or more of the binding proteins listed in Tables 27-30, 38-42, 46-50, or 55-58. In certain embodiments, the binding protein used to treat AMD is one or more of the binding proteins listed in Tables 56-58. In certain embodiments, the binding protein is PR-1572102, PR-1572105, or PR-1610561.

[0154] Age-Related Macular Degeneration (AMD) is the leading cause of irreversible vision loss in individuals over the age of 50 in the United States and a major cause of blindness worldwide. Globally more than 160 million people suffer from AMD. AMD is an age-related ocular disease that results in blindness due to damage to the macula; the region of the retina responsible for sharp central vision. It is associated with the degeneration of the macula and in particular the retinal pigmented epithelium (RPE).

[0155] The disease occurs in two forms, the dry or non-exudative AMD form and the wet or exudative form. The most common form of macular degeneration, dry AMD (non-neovascular), is an early stage of the disease and may result from aging and thinning of macular tissues, deposition of pigment in the macula, or a combination of both processes. Dry AMD is diagnosed when yellowish spots known as drusen accumulate in and around the macula. Drusen are thought to be deposits or debris from nearby deteriorating tissue. The onset of dry AMD is usually associated with age-related changes in Bruch's membrane, a highly specialized matrix for adhesion of retinal pigment epithelial (RPE) cells. These alterations in Bruch's membrane can result in death of RPE cells in the macula, accumulation of drusen, and damage to photoreceptor cells. Gradual central loss of vision may occur with dry AMD, but the symptoms are typically not nearly as severe as with the wet form of the disease. Dry AMD can slowly progress to late-stage geographic atrophy (GA) resulting in a gradual deterioration of retinal cells that can cause severe vision loss. Dry AMD (both early and late stage) is the most common form of AMD representing more than 85% of all diagnosed cases.

[0156] The wet or exudative form of the disease usually results in more severe vision loss. Wet macular degeneration mainly affects central vision, causing "blind spots" in the central line of vision. Approximately 10-15% of dry AMD cases progress to wet AMD. Wet AMD is characterized by new blood vessel growth beneath the retina. Clinically, this is referred to as

choroidal neovascularization (CNV). Wet AMD accounts for about 10-15% of all cases of AMD. Progression of dry AMD to wet AMD is marked by the development of neovascularization within Bruch's membrane, as well as in the subretinal space. Wet AMD occurs when abnormal blood vessels behind the retina grow under the macula. These new blood vessels tend to be fragile and often leak blood and fluid. The blood and fluid result in macula inflammation and thickening and disrupts the connection between the photoreceptors and the RPE, leading to vision loss. In wet AMD, neovascularization is stimulated by many angiogenic factors; including vascular endothelial growth factor (VEGF), which appears to be the primary angiogenic factor in patients with wet AMD (Miller et al. (1994) Am. J. Pathol. 145(3):574-584). Additionally, VEGF can act as a powerful endothelial cell mitogen, increasing vascular permeability. The primary goals of current AMD treatment are to block or inhibit choroidal neovascularization (CNV) and macular edema following retinal vein occlusion (RVO), stabilize or improve vision, and to reduce the occurrence of adverse effects.

[0157] Anti-VEGF agents may reduce choroidal neovascularization (CNV) and leakage, but do not lead to regression of CNV itself. Emerging evidence indicates the important role of pericytes on the maturation of new blood vessels. Anti-PDGF agents can directly block pericyte recruitment and prevent the maturation and stabilization of choroidal neovascularization. If pericytes can be stripped away from new blood vessels, vascular endothelial cells may become more susceptible to VEGF blockade, ultimately leading to a regression of angiogenesis.

[0158] Among other functions, VEGF stimulates endothelial cell proliferation/growth, increases vascular permeability, and promotes leukocyte activity capable of damaging retinal endothelial cells (Leung et al. (1989) Science 246(4935):1306-9). In wet AMD, retinal tissues produce and release angiogenic growth factors such as VEGF that bind to specific receptors located on the endothelial cells of nearby preexisting blood vessels. Activation of endothelial cells can result in the release of enzymes targeting tight junctions. These enzymes act on the basement membrane surrounding all existing blood vessels and lead to the formation of holes in the membrane. The endothelial cells proliferate and migrate out through these holes toward the diseased tissue. Specialized adhesion molecules such as integrins promote formation of new blood vessel sprouts, and matrix metalloproteinases (MMPs) dissolve the tissue in front of the sprouting vessel tip in order to accommodate it. Finally, smooth muscle cells (pericytes) provide structural support to these newly formed blood vessel loops and blood flow begins in these new immature vessels. Thus, VEGF may serve as a rate-limiting step in angiogenesis. VEGF also increases vascular permeability by leukocyte-mediated endothelial cell injury, formation of fenestrations, and the dissolution of tight junctions. This leads to intra-retinal fluid accumulation and a detrimental effect on visual acuity. Moreover, VEGF can also cause the release of inflammatory cytokines that further reinforce the cycle of inflammation and angiogenesis.

[0159] In some embodiments, treatments inhibiting VEGF, PDGF, and/or the receptors (in a combination therapy or in one molecule) using the binding proteins disclosed herein may offer improved options for patients with wet AMD, while reducing the number of injections, reducing the safety concerns associated with multiple injections, and reducing cost.

2. Diabetic Retinopathy

[0160] Diabetic retinopathy is the most common diabetic eye disease and a leading cause of blindness in American adults. It is caused by changes in the blood vessels of the retina. In some people with diabetic retinopathy, blood vessels may swell and leak fluid. In other people, abnormal new blood vessels grow on the surface of the retina. The retina is the light-sensitive tissue at the back of the eye. A healthy retina is necessary for good vision.

[0161] Diabetic retinopathy has four stages: (1) Mild Nonproliferative Retinopathy. At this earliest stage, microaneurysms occur. They are small areas of balloon-like swelling in the retina's tiny blood vessels. (2) Moderate Nonproliferative Retinopathy. As the disease progresses, some blood vessels that nourish the retina are blocked. (3) Severe Nonproliferative Retinopathy. Many more blood vessels are blocked, depriving several areas of the retina with their blood supply. These areas of the retina send signals to the body to grow new blood vessels for nourishment. (4) Proliferative Retinopathy. At this advanced stage, the signals sent by the retina for nourishment trigger the growth of new blood vessels. This condition is called proliferative retinopathy. These new blood vessels are abnormal and fragile. They grow along the retina and along the surface of the clear, vitreous gel that fills the inside of the eye. By themselves, these blood vessels do not cause symptoms or vision loss. However, they have thin, fragile walls. If they leak blood, severe vision loss and even blindness can result.

[0162] Blood vessels damaged from diabetic retinopathy can cause vision loss in two ways: (1) Fragile, abnormal blood vessels can develop and leak blood into the center of the eye, blurring vision. This is proliferative retinopathy and is the fourth and most advanced stage of the disease. (2) Fluid can leak into the center of the macula, the part of the eye where sharp, straight-ahead vision occurs. The fluid makes the macula swell, blurring vision. This condition is called macular edema. It can occur at any stage of diabetic retinopathy, although it is more likely to occur as the disease progresses. About half of the people with proliferative retinopathy also have macular edema.

[0163] In some embodiments, the binding proteins disclosed herein may be used to inhibit VEGF, PDGF, and/or the receptors (in a combination therapy or in one molecule) to treat diabetic retinopathy.

[0164] In various embodiments, other diseases may be treated using the binding proteins disclosed herein, including but not limited to other eye disorders, cancers, fibrosis, renal

disease, pathologic angiogenesis, wound healing, bone formation, or other diseases associated with aberrant (e.g., elevated) PDGF and/or VEGF expression.

Pharmaceutical Compositions

[0165] In various embodiments, pharmaceutical compositions comprising one or more of the binding proteins disclosed herein, either alone or in combination with other prophylactic agents, therapeutic agents, and/or pharmaceutically acceptable carriers, are provided. The pharmaceutical compositions comprising binding proteins provided herein are for use in, but not limited to, diagnosing, detecting, or monitoring a disorder, in preventing, treating, managing, or ameliorating a disorder or one or more symptoms thereof, and/or in research. The formulation of pharmaceutical compositions, either alone or in combination with prophylactic agents, therapeutic agents, and/or pharmaceutically acceptable carriers, are known to one skilled in the art (see, e.g., U.S. Patent Appl. No. 20090311253 and U.S. Patent No. 7,612,181).

[0166] Methods of administering a pharmaceutical composition or a prophylactic or therapeutic agent provided herein include, but are not limited to, parenteral administration (e.g., intradermal, intramuscular, intraperitoneal, intravitreous, intravenous and subcutaneous), epidural administration, intratumoral administration, mucosal administration (e.g., intranasal and oral routes) and pulmonary administration (e.g., aerosolized compounds administered with an inhaler or nebulizer). In an embodiment, the methods of administering a pharmaceutical composition or a prophylactic or therapeutic agent provided herein include topical eye drops, gels, or creams. The formulation of pharmaceutical compositions for specific routes of administration, and the materials and techniques necessary for the various methods of administration are available and known to one skilled in the art (U.S. Patent Appl. No. 20090311253 and U.S. Patent No. 7,612,181).

[0167] Dosage regimens may be adjusted to provide the optimum desired response (e.g., a therapeutic or prophylactic response). For example, a single bolus may be administered, several divided doses may be administered over time or the dose may be proportionally reduced or increased as indicated by the exigencies of the therapeutic situation. It is especially advantageous to formulate parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. The term "dosage unit form" refers to physically discrete units suited as unitary dosages for the mammalian subjects to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms provided herein are dictated by and directly dependent on (a) the unique characteristics of the active compound and the particular therapeutic or prophylactic effect to be achieved, and (b) the limitations inherent in the art of compounding such an active compound for the treatment of

sensitivity in individuals. An exemplary, non-limiting range for a therapeutically or prophylactically effective amount of a binding protein provided herein is 0.1-20 mg/kg, for example, 1-10 mg/kg. It is to be noted that dosage values may vary with the type and severity of the condition to be alleviated. It is to be further understood that for any particular subject, specific dosage regimens may be adjusted over time according to the individual need and the professional judgment of the person administering or supervising the administration of the compositions, and that dosage ranges set forth herein are exemplary only and are not intended to limit the scope or practice of the claimed composition.

Combination Therapy

[0168] In various embodiments, a binding protein provided herein may also be administered with one or more additional therapeutic agents useful in the treatment of various diseases, the additional agent being selected by the skilled artisan for its intended purpose. For example, the additional agent can be a therapeutic agent art-recognized as being useful to treat the disease or condition being treated by the antibody provided herein, such as AMD. The combination can also include more than one additional agent, e.g., two or three additional agents.

[0169] Combination therapy agents include, but are not limited to imaging agents, cytotoxic agents, angiogenesis inhibitors, kinase inhibitors, tyrosine kinase inhibitors, tyrosine kinase receptor inhibitors, co-stimulation molecule blockers, adhesion molecule blockers, anti-cytokine antibodies or functional fragments thereof, methotrexate, cyclosporin, rapamycin, FK506, detectable labels or reporters, TNF antagonists, antirheumatics, muscle relaxants, narcotics, non-steroid anti-inflammatory drugs (NSAIDs), analgesics, anesthetics, local anesthetics, sedatives, a hyaluronidase enzyme, neuromuscular blockers, antimicrobials, antipsoriatics, corticosteriods, anabolic steroids, erythropoietin, immunizations, immunoglobulins, immunosuppressives, growth hormones, hormone replacement drugs, radiopharmaceuticals, antidepressants, antipsychotics, stimulants, asthma medications, beta agonists, inhaled steroids, epinephrine or analogs, cytokines, or cytokine antagonists.

Diagnostics

[0170] The disclosure herein also provides, in various embodiments, diagnostic applications including, but not limited to, diagnostic assay methods, diagnostic kits containing one or more binding proteins, and adaptation of the methods and kits for use in automated and/or semi-automated systems. The methods, kits, and adaptations provided may be employed in the detection, monitoring, and/or treatment of a disease or disorder in an individual. This is further elucidated below.

[0171] The present disclosure also provides a method for determining the presence, amount or concentration of an analyte, or fragment thereof, in a test sample using at least one

binding protein as described herein. Any suitable assay as is known in the art can be used in the method. Examples include, but are not limited to, immunoassays and/or methods employing mass spectrometry.

[0172] Immunoassays provided by the present disclosure may include sandwich immunoassays, radioimmunoassay (RIA), enzyme immunoassay (EIA), enzyme-linked immunosorbent assay (ELISA), competitive-inhibition immunoassays, fluorescence polarization immunoassay (FPIA), enzyme multiplied immunoassay technique (EMIT), bioluminescence resonance energy transfer (BRET), and homogenous chemiluminescent assays, among others.

[0173] A chemiluminescent microparticle immunoassay, in particular one employing the ARCHITECT® automated analyzer (Abbott Laboratories, Abbott Park, IL), is an example of an immunoassay.

[0174] Methods employing mass spectrometry are provided by the present disclosure and include, but are not limited to MALDI (matrix-assisted laser desorption/ionization) or by SELDI (surface-enhanced laser desorption/ionization).

[0175] Methods for collecting, handling, processing, and analyzing biological test samples using immunoassays and mass spectrometry would be well-known to one skilled in the art, are provided for in the practice of the present disclosure (see, e.g., U.S. Patent No. 7,612,181).

Kits

[0176] In various embodiments, a kit for assaying a test sample for the presence, amount or concentration of an analyte, or fragment thereof, in a test sample is also provided. The kit comprises at least one component for assaying the test sample for the analyte, or fragment thereof, and instructions for assaying the test sample for the analyte, or fragment thereof. The at least one component for assaying the test sample for the analyte, or fragment thereof, can include a composition comprising a binding protein, as disclosed herein, and/or an anti-analyte binding protein (or a fragment, a variant, or a fragment of a variant thereof), which is optionally immobilized on a solid phase.

[0177] Optionally, the kit may comprise a calibrator or control, which may comprise isolated or purified analyte. The kit can comprise at least one component for assaying the test sample for an analyte by immunoassay and/or mass spectrometry. The kit components, including the analyte, binding protein, and/or anti-analyte binding protein, or fragments thereof, may be optionally labeled using any art-known detectable label. The materials and methods for the creation provided for in the practice of the present disclosure would be known to one skilled in the art (see, e.g., U.S. Patent No. 7,612,181).

[0178] The kit (or components thereof), as well as the method of determining the presence, amount or concentration of an analyte in a test sample by an assay, such as an immunoassay as described herein, can be adapted for use in a variety of automated and semi-automated systems (including those wherein the solid phase comprises a microparticle), as described, for example, in U.S. Patent Nos. 5,089,424 and 5,006,309, and as commercially marketed, for example, by Abbott Laboratories (Abbott Park, IL) as ARCHITECT®.

[0179] Other platforms available from Abbott Laboratories include, but are not limited to, AxSYM®, IMx® (see, for example, U.S. Patent No. 5,294,404, PRISM®, EIA (bead), and Quantum™ II, as well as other platforms. Additionally, the assays, kits and kit components can be employed in other formats, for example, on electrochemical or other hand-held or point-of-care assay systems. The present disclosure is, for example, applicable to the commercial Abbott Point of Care (i-STAT®, Abbott Laboratories) electrochemical immunoassay system that performs sandwich immunoassays. Immunosensors and their methods of manufacture and operation in single-use test devices are described, for example in, U.S. Patent No. 5,063,081, 7,419,821, 7,682,833, 7,723,099, and 9,035,027; and U.S. Publication No. 20040018577.

Sequences

[0180] Table 1 discloses amino acid and nucleotide sequences encoding VEGF-A from different human isoforms and different species. Table 2 discloses amino acid and nucleotide sequences encoding PDGF-BB from different human isoforms and different species. Table 3 discloses human IgG heavy chain and light chain constant domains, including sequences with the indicated amino acid modifications relative to the wild-type sequence. In various embodiments, the constant domains listed in Table 3 can be used with any of the binding proteins disclosed herein. The variable domains of the binding proteins disclosed herein may be attached to constant regions of any immunoglobulin species, isotypes, or mutants. Exemplary modifications in constant domain mutants include those with amino acid mutations intended to increase or reduce constant domain interactions with Fc-gamma receptors, C1q and FcRn, and/or mutations intended to modulate protein stability or valency (full-length and half molecule, heterodimer molecule, etc.). Tables 4 and 5 disclose exemplary heavy and light chain acceptor framework sequences that can be used with any of the CDR sets disclosed herein (i.e., heavy chain acceptor sequences paired with any of the heavy chain CDRs 1-3 disclosed herein, and/or light chain acceptor sequences paired with any of the light chain CDRs 1-3 disclosed herein) to form functional binding sites for PDGF, VEGF, and/or their cognate receptors.

Table 1. Amino Acid and Nucleotide Sequences for VEGF-A

Kind of Sequence	Sequence Identifier	Sequence
		12345678901234567890123456789 0
Human VEGF-A 165 Amino Acid Sequence	SEQ ID NO:x	APMAEGGGQNHHEVVKFMDVYQRSYCHPIE TLVDIFQEYPDEIEYIFKPSCVPLMRCGGC CNDEGLECVPTEESNITMQIMRIKPHQGQH IGEMSFLQHNKCECRPKKDRARQENPCGPC SERRKHLFVQDPQTCKCSCKNTDSRCKARQ LELNERTCRCDKPRR
Human VEGF-A 121 Amino Acid Sequence	SEQ ID NO:x	APMAEGGGQNHHEVVKFMDVYQRSYCHPIE TLVDIFQEYPDEIEYIFKPSCVPLMRCGGC CNDEGLECVPTEESNITMQIMRIKPHQGQH IGEMSFLQHNKCECRPKKDRARQEKCDKPR R
Human VEGF-A 110 Amino Acid Sequence	SEQ ID NO:x	APMAEGGGQNHHEVVKFMDVYQRSYCHPIE TLVDIFQEYPDEIEYIFKPSCVPLMRCGGC CNDEGLECVPTEESNITMQIMRIKPHQGQH IGEMSFLQHNKCECRCDKPRR
Cynomolgus monkey VEGF-A 165 Amino Acid Sequence	SEQ ID NO:x	APMAEGGGQNHHEVVKFMDVYQRSYCHPIE TLVDIFQEYPDEIEYIFKPSCVPLMRCGGC CNDEGLECVPTEESNITMQIMRIKPHQGQH IGEMSFLQHNKCECRPKKDRARQENPCGPC SERRKHLFVQDPQTCKCSCKNTDSRCKARQ LELNERTCRCDKPRR
Mouse VEGF-A 164 Amino Acid Sequence	SEQ ID NO:x	APTTEGEQKSHEVIKFMDVYQRSYCRPIET LVDIFQEYPDEIEYIFKPSCVPLMRCAGCC NDEALECVPTSESNITMQIMRIKPHQSQHI ERMSFLQHSRCECRPKKDRTKPENHCEPCS ERRKHLFVQDPQTCKCSCKNTDSRCKARQL ELNERTCRCDKPRR
Rat VEGF-A 164 Amino Acid Sequence	SEQ ID NO:x	APTTEGEQKAHEVVKFMDVYQRSYCRPIET LVDIFQEYPDEIEYIFKPSCVPLMRCAGCC NDEALECVPTSESNVTMQIMRIKPHQSQHI GEMSFLQHSRCECRPKKDRTKPENHCEPCS ERRKHLFVQDPQTCKCSCKNTDSRCKARQL ELNERTCRCDKPRR
Rabbit VEGF-A Amino Acid Sequence	SEQ ID NO:x	MNFLLSWVHWSLALLLYLHHAKWSQAAPMA EEGDNKPHEVVKFMEVYRRSYCQPIETLVD IFQEYPDEIEYIFKPSCVPLVRCGGCCNDE SLECVPTEEFNVTMQIMRIKPHQGQHIGEM SFLQHNKCECRPKKDRARQENPCGPCSERR KHLFVQDPQTCKCSCKNTDSRCKARQLELN ERTCRCDKPRR

Table 2. Amino Acid and Nucleotide Sequences for PDGF-BB

Kind of Sequence	Sequence Identifier	Sequence
		12345678901234567890123456789 0
Human PDGF-BB Amino Acid Sequence	SEQ ID NO:x	SLGSLTIAEPAMIAECKTRTEVFEISRRLI DRTNANFLVWPPCVEVQRCSGCCNNRNVQC RPTQVQLRPVQVRKIEIVRKKPIFKKATVT LEDHLACKCETVAAARPVT
Human PDGF-BB-RM (Retention Motif) Amino Acid Sequence	SEQ ID NO:x	MNRCWALFLSLCCYLRLVSAEGDPIPEELY EMLSDHSIRSFDDLQRLLHGDPGEEDGAEL DLNMTRSHSGGELESLARGRR**SLGSLTIAE PAMIAECKTRTEVFEISRRLIDRTNANFLV WPPCVEVQRCSGCCNNRNVQCRPTQVQLRP VQVRKIEIVRKKPIFKKATVTLEDHLACKC ETVAAARPVT**RSPGGSQEQRAKTPQTRVTI RTVRVRRPPKGKHRKFKHTHDKTALKETLG A
Cynomolgus monkey PDGF-BB Amino Acid Sequence	SEQ ID NO:x	SLGSLTVAEPAMIAECKTRTEVFEISRRLI DRTNANFLVWPPCVEVQRCSGCCNNRNVQC RPTQVQLRPVQVRKIEIVRKKPIFKKATVT LEDHLACKCETVAAARPVT
Mouse PDGF-BB Amino Acid Sequence	SEQ ID NO:x	SLGSLAAAEPAVIAECKTRTEVFQISRNLI DRTNANFLVWPPCVEVQRCSGCCNNRNVQC RASQVQMRPVQVRKIEIVRKKPIFKKATVT LEDHLACKCETIVTPRPVT
Rat PDGF-BB Amino Acid Sequence	SEQ ID NO:x	SLGSLAAAEPAVIAECKTRTEVFQISRNLI DRTNANFLVWPPCVEVQRCSGCCNNRNVQC RASQVQMRPVQVRKIEIVRKKPVFKKATVT LEDHLACKCETVVTPRPVT
Rabbit PDGF-BBA Amino Acid Sequence	SEQ ID NO:x	SLGSLAAAEPAVIAECKTRTEVFQISRNLI DRTNANFLVWPPCVEVQRCSGCCNNRNVQC RASQVQMRPVQVRKIEIVRKKPVFKKATVT LEDHLACKCETVVTPRPVT

Table 3. Amino Acid Sequences of Human IgG Heavy Chain and Light Chain Constant Domains

Protein	Sequence Identifier	Sequence
		12345678901234567890123456789 0
Ig gamma-1 constant region	SEQ ID NO:x	ASTKGPSVFFLAPSSKSTSGGTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSREE MTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
Ig gamma-1 constant	SEQ ID	ASTKGPSVFPLAPSSKSTSGGTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSS

Protein	Sequence Identifier	Sequence
		12345678901234567890123456789O
region L234A, L235A	NO:x	GLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSREE MTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
Ig gamma-1 constant region L234A, L235A, H435A	SEQ ID NO:x	ASTKGPSVFPLAPSSKSTSGGTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSREE MTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNAYTQKSLSLSPGK
Ig gamma-1 constant region L234A, L235A, H435R	SEQ ID NO:x	ASTKGPSVFPLAPSSKSTSGGTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSREE MTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNRYTQKSLSLSPGK
Ig gamma-1 constant region C226A, C229A, N297A, F405R (Half body)	SEQ ID NO:x	ASTKGPSVFPLAPSSKSTSGGTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTAPPAPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQYA STYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSREE MTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFRLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
Ig Kappa constant region	SEQ ID NO:x	RTVAAPSVFIFPPSDEQLKSGTASVVCLLN NFYPREAKVQWKVDNALQSGNSQESVTEQD SKDSTYSLSSTLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC
Ig Lambda constant region	SEQ ID NO:x	GQPKAAPSVTLFPPSSEELQANKATLVCLI SDFYPGAVTVAWKADSSPVKAGVETTTPSK QSNNKYAASSYLSLTPEQWKSHRSYSCQVT HEGSTVEKTVAPTECS

Table 4. Amino Acid Sequences of Heavy Chain Acceptor Frameworks

SEQ ID NO:	Protein region/ Closest Germline Family	Amino Acid Sequence
		12345678901234567890123456789012
	VH3-7 FR1	EVQLVESGGGLVQPGGSLRLSCAASGFTFS
	VH3-7 FR2	WVRQAPGKGLEWVA
	VH3-7 FR3	RFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR
	JH4 FR4	WGQGTLVTVSS
	VH3 CONSENUSUS FR1	EVQLVESGGGLVQPGGSLRLSCAASGFTFS
	VH3 CONSENUSUS FR2	WVRQAPGKGLEWVS
	VH3 CONSENUSUS FR3	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR
	JH4 FR4	WGQGTLVTVSS
	VH1-46 FR1	QVQLVQSGAEVKKPGASVKVSCKASGYTFT
	VH1-46 FR2	WVRQAPGQGLEWMG
	VH1-46 FR3	RVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR
	JH4 FR4	WGQGTLVTVSS
	VH3-30 FR1	QVQLVESGGGVVQPGRSLRLSCAASGFTFS
	VH3-30 FR2	WVRQAPGKGLEWVA
	VH3-30 FR3	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR
	JH3 FR4	WGQGTMVTVSS
	VH3 CONSENUSUS FR1	EVQLVESGGGLVQPGGSLRLSCAASGFTFS
	VH3 CONSENUSUS FR2	WVRQAPGKGLEWVS
	VH3 CONSENUSUS FR3	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR
	JH3 FR4	WGQGTMVTVSS
	VH2-70/JH6 FR1	EVTLRESGPALVKPTQTLTLTCTFSGFSLS
	VH2-70/JH6 FR2	WIRQPPGKALEWLA
	VH2-70/JH6 FR3	RLTISKDTSKNQVVLTMTNMDPVDTATYYCAR
	VH2-70/JH6 FR4	WGQGTTVTVSS
	VH2-26/JH6 FR1	EVTLKESGPVLVKPTETLTLTCTVSGFSLS
	VH2-26/JH6 FR2	WIRQPPGKALEWLA
	VH2-26/JH6 FR3	RLTISKDTSKSQVVLTMTNMDPVDTATYYCAR
	VH2-26/JH6 FR4	WGQGTTVTVSS
	VH3-72/JH6 FR1	EVQLVESGGGLVQPGGSLRLSCAASGFTFS
	VH3-72/JH6 FR2	WVRQAPGKGLEWVG
	VH3-72/JH6 FR3	RFTISRDDSKNSLYLQMNSLKTEDTAVYYCAR
	VH3-72/JH6 FR4	WGQGTTVTVSS
	VH3-21/JH6 FR1	EVQLVESGGGLVKPGGSLRLSCAASGFTFS
	VH3-21/JH6 FR2	WVRQAPGKGLEWVS
	VH3-21/JH6 FR3	RFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR
	VH3-21/JH6 FR4	WGQGTTVTVSS
	VH1-69/JH6 FR1	EVQLVQSGAEVKKPGSSVKVSCKASGGTFS
	VH1-69/JH6 FR2	WVRQAPGQGLEWMG
	VH1-69/JH6 FR3	RVTITADKSTSTAYMELSSLRSEDTAVYYCAR
	VH1-69/JH6 FR4	WGQGTTVTVSS
	VH1-18/JH6 FR1	EVQLVQSGAEVKKPGASVKVSCKASGYTFT
	VH1-18/JH6 FR2	WVRQAPGQGLEWMG
	VH1-18/JH6 FR3	RVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR
	VH1-18/JH6 FR4	WGQGTTVTVSS
	IGHV4-59 FR1	EVQLQESGPGLVKPSETLSLTCTVSGGSIS
	IGHV4-59 FR2	WIRQPPGKGLEWIG
	IGHV4-59 FR3	RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR

SEQ ID NO:	Protein region/ Closest Germline Family	Amino Acid Sequence
	IGHV4-59/JH FR4	WGQGTLVTVSS
	IGHV3-66 FW1	EVQLVESGGGLVQPGGSLRLSCAVSGGSIS
	IGHV3-66 FW2	WIRQAPGKGLEWIG
	IGHV3-66 FW3	RVTISVDTSKNSFYLQMNSLRAEDTAVYYCAR
	IGHV3-66/JH FW4	WGQGTLVTVSS
	IGHV4-59 FR1	EVQLQESGPGLVKPGETLSLTCTVSGGSIS
	IGHV4-59 FR2	WIRQAPGKGLEWIG
	IGHV4-59 FR3	RVTISVDTSKNQFYLKLSSVRAEDTAVYYCAR
	IGHV4-59/JH FR4	WGQGTLVTVSS
	IGHV5-51 FR1	EVQLVQSGTEVKKPGESLKISCKVSGGSIS
	IGHV5-51 FR2	WIRQMPGKGLEWIG
	IGHV5-51 FR3	QVTISVDTSFNTFFLQWSSLKASDTAMYYCAR
	IGHV5-51/JH FR4	WGQGTMVTVSS
	IGHV2-70 FR1	EVTLRESGPALVKPTQTLTLTCTVSGGSIS
	IGHV2-70 FR2	WIRQPPGKGLEWIG
	IGHV2-70 FR3	RVTISVDTSKNQFVLTMTNMDPVDTATYYCAR
	IGHV2-70/JH FR4	WGQGTTVTVSS
	IGHV3-15 FR1	EVQLLESGGGLVKSGGSLRLSCAASGFTFR
	IGHV3-15 FR2	WVRQAPGKGLEWVA
	IGHV3-15 FR3	RFTISRDNSKNTLYLQLNSLRAEDTAVYYCAK
	IGHV3-15/JH FR4	WGQGTMVTVSS
	IGHV3-43 FR1	EVQLVESGGGVVQPGGSLRLSCAASGFTFG
	IGHV3-43 FR2	WVRQAPGKGLEWVA
	IGHV3-43 FR3	RFTISRDNSKNTLYLQLNSLRAEDTAVYYCAK
	IGHV3-43/JH FR4	WGQGTMVTVSS

Table 5. Amino Acid Sequences of Light Chain Acceptor Frameworks

SEQ ID NO:	Protein region/ Closest Germline Family	Sequence
		12345678901234567890123456789012
	O2 FR1	DIQMTQSPSSLSASVGDRVTITC
	O2 FR2	WYQQKPGKAPKLLIY
	O2 FR3	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
	JK2 FR4	FGQGTKLEIK
	L2 FR1	EIVMTQSPATLSVSPGERATLSC
	L2 FR2	WYQQKPGQAPRLLIY
	L2 FR3	GIPARFSGSGSGTEFTLTISSLQSEDFAVYYC
	JK2 FR4	FGQGTKLEIK
	B3/JK4 FR1	DIVMTQSPDSLAVSLGERATINC
	B3/JK4 FR2	WYQQKPGQPPKLLIY
	B3/JK4 FR3	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC
	B3/JK4 FR4	FGGGTKVEIKR
	L2/JK4 FR1	EIVMTQSPATLSVSPGERATLSC
	L2/JK4 FR2	WYQQKPGQAPRLLIY
	L2/JK4 FR3	GIPARFSGSGSGTEFTLTISSLQSEDFAVYYC
	L2/JK4 FR4	FGGGTKVEIKR
	L15/JK4 FR1	DIQMTQSPSSLSASVGDRVTITC
	L15/JK4 FR2	WYQQKPEKAPKSLIY

SEQ ID NO:	Protein region/ Closest Germline Family	Sequence
	L15/JK4 FR3	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
	L15/JK4 FR4	FGGGTKVEIKR
	L5/JK4 FR1	DIQMTQSPSSVSASVGDRVTITC
	L5/JK4 FR2	WYQQKPGKAPKLLIY
	L5/JK4 FR3	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
	L5/JK4 FR4	FGGGTKVEIKR
	IGLV3-1 FR1	SYELTQPPSVSVSPGQTASITC
	IGLV3-1 FR2	WYQQKPGQSPVLVIY
	IGLV3-1 FR3	GIPERFSGSNSGDTATLTISGTQPMDEADYYC
	IGLV3-1/JL FR4	FGYGTKVTVL
	IGLV3-1 FR1	SYELTQPPSVSVSPGQTASITC
	IGLV3-1 FR2	WYQQKPGQSPVLVIY
	IGLV3-1 FR3	GIPERFSGSNSGDTATLTISGTQPMDEADYYC
	IGLV3-1/JL FR4	GGGTKLTVLG
	IGLV3-1 FR1	YELTQPPSVSVSPGQTASITC
	IGLV3-1 FR2	WYQQKPGQSPVLVIY
	IGLV3-1 FR3	GIPERFSGSNSGDTATLTISGTQPMDEADYYC
	IGLV3-1/JL FR4	GGGTKLTVLG
	IGLV3-1 FR1	LYVLTQPPSVSVSPGQTASITC
	IGLV3-1 FR2	WYQQKPGQSPVLVIY
	IGLV3-1 FR3	GIPERFSGSNSGDTATLTISGTQTMDEADYLC
	IGLV3-1/JL FR4	FGGGTKVTVLG
	IGKV6D-21 FR1	EYVLTQSPDFQSVTPKEKVTITC
	IGKV6D-21 FR2	WYQQKPDQSPKLVIY
	IGKV6D-21 FR3	GVPSRFSGSNSGDDATLTINSLEAEDAATYYC
	IGKV6D-21/JK FR4	FGQGTKVEIKR
	IGKV3D-15 FR1	EYVLTQSPATLSVSPGERATLSC
	IGKV3D-15 FR2	WYQQKPGQSPRLVIY
	IGKV3D-15 FR3	DIPARFSGSNSGDEATLTISSLQSEDFAVYYC
	IGKV3D-15/JK FR4	FGQGTRLEIKR
	IGKV4-1 FR1	DYVLTQSPDSLAVSLGERATINC
	IGKV4-1 FR2	WYQQKPGQSPKLVIY
	IGKV4-1 FR3	GIPDRFSGSNSGDDATLTISSLQAEDVAVYYC
	IGKV4-1/JK FR4	FGGGTKVEIKR
	IGLV3-1 FR1	LPVLTQPPSVSVSPGQTASITC
	IGLV3-1 FR2	WYQQKPGQSPVLVIY
	IGLV3-1 FR3	GIPERFSGSNSGNTATLTISGTQTMDEADYLC
	IGLV3-1/JL FR4	FGGGTKVTVL
	IGLV3-1 FR1	SYELTQPPSVSVSPGQTASITC
	IGLV3-1 FR2	WYQQKPGQSPVLVIY
	IGLV3-1 FR3	GIPERFSGSNSGNTATLTISGTQTMDEADYLC
	IGLV3-1/JL FR4	FGGGTKLTVL

Table A. Select Heavy Chain and Light Chain Variable Domain Sequences (CDRs in bold)

SEQ ID NO	VD name	Sequence 12345678901234567890123456789012
1	hBDI-9E8.4 VH (PDGF)	EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPPGKAL EWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTNMDPVDTAT YYCAR**IESIGTTYSFDY**WGQGTMVTVSS
2	hBDI-9E8.4 VL (PDGF)	EFVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKPGQAPR LVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QSYD INIDIV**FGGGTKVEIK
3	hBDI-5H1.9 VH (PDGF)	EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTFGMGVG**WIRQPPGKAL EWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQAVLTITNMDPVDTAT YYCAR**ISTGISSYYVMDA**WGQGTTVTVSS
4	hBDI-5H1.9 VL (PDGF)	DFVLTQSPDSLAVSLGERATINC**ERSSGDIGDTYVS**WYQQKPGQPPK NVIY**GNDQRPS**GVPDRFSGSGSGNSATLTISSLQAEDVAVYFC**QSYD SDIDIV**FGGGTKVEIK
5	hBDI-9E8.12 VH (PDGF)	EVQLVESGGGLVQPGGSLRLSCAFS**GFSLSTYGMGVG**WIRQAPGKGL EWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQAYLQINSLRAEDTAV YYCAR**IESIGTTYSFDY**WGQGTLVTVSS
6	hBDI-9E8.12 VL (PDGF)	DFQLTQSPSSLSASVGDRVTITC**ERSSGDIGDSYVS**WYQQKPGKAPK NVIY**ADDQRPS**GVPSRFSGSGSGNSASLTISSLQPEDFATYYC**QSYD INIDIV**FGQGTKVEIK
7	hBDI-9E8.9 VH (PDGF)	EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPPGKAL EWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQAVLTITNMDPVDTAT YYCAR**IESIGTTYSFDY**WGQGTTVTVSS
8	hBDI-9E8.9 VL (PDGF)	DFVLTQSPDSLAVSLGERATINC**ERSSGDIGDSYVS**WYQQKPGQPPK NVIY**ADDQRPS**GVPDRFSGSGSGNSASLTISSLQAEDVAVYFC**QSYD INIDIV**FGGGTKVEIK
9	hBDI-9E8.12 VH (PDGF)	EVQLVESGGGLVQPGGSLRLSCAFS**GFSLSTYGMGVG**WIRQAPGKGL EWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQAYLQINSLRAEDTAV YYCAR**IESIGTTYSFDY**WGQGTLVTVSS
10	hBDI-9E8.12 VL (PDGF)	DFQLTQSPSSLSASVGDRVTITC**ERSSGDIGDSYVS**WYQQKPGKAPK NVIY**ADDQRPS**GVPSRFSGSGSGNSASLTISSLQPEDFATYYC**QSYD INIDIV**FGQGTKVEIK
11	hBDI-9E8.4E VH (PDGF)	EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPPGKAL EWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTNMDPVDTAT YYCAR**IESIGTTYSFDY**WGQGTMVTVSS
12	hBDI-9E8.4E VL (PDGF)	EFVLTQSPGTLSLSPGERATLSC**ERSSGDIGESYVS**WYQQKPGQAPR LVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QSYD INIDIV**FGGGTKVEIK
13	hBFU-3E2.1 VH (PDGF)	EVQLVQSGAEVKKPGSSVKVSCKAS**GYTFTESYMY**WVKQAPGQGLEL IG**RIDPEDGSTDYVEKFKN**KATLTADKSTSTAYMELSSLRSEDTAVY FCAR**FGARSYFYPMDA**WGQGTTVTVSS
14	hBFU-3E2.1 VL (PDGF)	ETVLTQSPATLSLSPGERATLSC**RASESVSTLMH**WYQQKPGQQPRLL IY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPEDFAVYFC**QQSWND PWT**FGGGTKVEIK
15	CL-33675 VH (PDGF)	EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPPGKAL EWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTNMDPVDTAT YYCAR**IESSGPKYSFDY**WGQGTMVTVSS
16	CL-33675 VL (PDGF)	EIVLTQSPGTLSLSPGERATLSC**RASSGSIWYSFVS**WYQQKPGQAPR LLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QSYG INIDVV**FGGGTKVEIK
17	hBDB-4G8.3	EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQGLEW MG**WINTETGKPTYADDFKG**RFVFSLDTSVSTAYLQISSLKAEDTAVY

	VH (VEGF)	YCAR**TNYYYRSYIFYFDY**WGQGTMVTVSS
18	hBDB-4G8.3 VL (VEGF)	DTVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPGQAPRLL IY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPEDFAVYFC**QQSWND PFT**FGQGTKLEIK
19	hBDB-4G8.13 VH (VEGF)	EIQLVQSGTEVKKPGESLKISCKAS**GYTFTNYGMY**WVKQMPGKGLEY MG**WINTETGKPTYADDFKG**RFTFSLDKSFNTAFLQWSSLKASDTAMY FCAR**TNYYYRSYIFYFDY**WGQGTMVTVSS
20	hBDB-4G8.13 VL (VEGF)	ETVLTQSPATLSVSPGERATLSC**RASESVSTHMH**WYQQKPGQAPRLL IY**GASNLES**GVPARFSGSGSGTDFTLTISSLQSEDFAVYFC**QQSWND PFT**FGQGTRLEIK
21	hBDB-4G8.14 VH (VEGF)	EIQLVQSGGGVVQPGGSLRLSCAAS**GYTFTNYGMY**WVKQAPGKGLEY MG**WINTETGKPTYADDFKG**RFTFSLDTSKSTAYLQLNSLRAEDTAVY FCAR**TNYYYRSYIFYFDY**WGQGTLVTVSS
22	hBDB-4G8.14 VL (VEGF)	DTVLTQSPSTLSASPGERATISC**RASESVSTHMH**WYQQKPGQAPKLL IY**GASNLES**GVPSRFSGSRSGTDFTLTISSLQPEDFAVYFC**QQSWND PFT**FGQGTKVEIK
23	hBDB-4G8.15 VH (VEGF)	EVQLVESGGGLVQPGGSLRLSCAAS**GYTFTNYGMY**WVKQAPGKGLEY MG**WINTETGKPTYADDFKG**RFTFSLDTSKSTAYLQMNSLRAEDTAVY FCAR**TNYYYRSYIFYFDY**WGQGTLVTVSS
24	hBDB-4G8.15 VL (VEGF)	DTQLTQSPSSLSASVGDRVTISC**RASESVSTHMH**WYQQKPGKAPKLL IY**GASNLES**GVPSRFSGSGSGTDFTLTISSLQPEDFATYFC**QQSWND PFT**FGQGTKVEIK
25	hBEW-9A8.12 VH (VEGF)	EVQLVQSGAEVKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQGLEW MG**WINTETGKPIYADDFKG**RVTMTTDTSTSTAYMELRSLRSDDTAVY YCAR**VDYDGSFWFAY**WGQGTLVTVSS
26	hBEW-9A8.12 VL (VEGF)	DTQLTQSPSSLSASVGDRVTITC**RASESVSTVIH**WYQQKPGKQPKLL IH**GASNLES**GVPSRFSGSGSGTDFTLTISSLQPEDFATYFC**QQHWND PPT**FGQGTKLEIK
27	hBDB-4G8.2 VH (VEGF)	EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQGLEW MG**WINTETGKPTYADDFKG**RFVFSLDTSVSTAYLQISSLKAEDTAVY YCAR**TNYYYRSYIFYFDY**WGQGTMVTVSS
28	hBDB-4G8.2 VL (VEGF)	ATQLTQSPSLSASVGDRVTITC**RASESVSTHMH**WYQQKPGKQPKLLI Y**GASNLES**GVPSRFSGSGSGTDFTLTISSLQPEDFATYFC**QQSWNDP FT**FGQGTKLEIK
29	hBDB-4G8.4 VH (VEGF)	EIQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQGLEY MG**WINTETGKPTYADDFKG**RFVFSLDTSVSTAYLQISSLKAEDTAVY FCAR**TNYYYRSYIFYFDY**WGQGTMVTVSS
30	hBDB-4G8.4 VL (VEGF)	AIQLTQSPSSLSASVGDRVTITC**RASESVSTHMH**WYQQKPGKAPKLL IY**GASNLES**GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC**QQSWND PFT**FGQGTKLEIK
31	hBDB-4G8.5 VH (VEGF)	EIQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQGLEY MG**WINTETGKPTYADDFKG**RFVFSLDTSVSTAYLQISSLKAEDTAVY FCAR**TNYYYRSYIFYFDY**WGQGTMVTVSS
32	hBDB-4G8.5 VL (VEGF)	ATQLTQSPSLSASVGDRVTITC**RASESVSTHMH**WYQQKPGKQPKLLI Y**GASNLES**GVPSRFSGSGSGTDFTLTISSLQPEDFATYFC**QQSWNDP FT**FGQGTKLEIK
33	hBDB-4G8.12 VH (VEGF)	EIQLVQSGAEVKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQGLEY MG**WINTETGKPTYADDFKG**RFTFTLDTSTSTAYMELRSLRSDDTAVY FCAR**TNYYYRSYIFYFDY**WGQGTMVTVSS
34	hBDB-4G8.12 VL (VEGF)	DTVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPGQAPRLL IY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPEDFAVYFC**QQSWND PFT**FGQGTKLEIK
35	hBEW-9E10.1 VH (VEGF)	EIQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVKQAPGQGLEY MG**WIDTETGRPTYADDFKG**RFVFSLDTSVSTAYLQISSLKAEDTAVY FCAR**WSGDTTGIRGPWFAY**WGQGTLVTVSS

36	hBEW-9E10.1 VL (VEGF)	DIRMTQSPSSLSASVGDRVTIEC**LASEDIYSDLA**WYQQKPGKSPKLL IY**NANGLQN**GVPSRFSGSGSGTDYSLTISSLQPEDVATYFC**QQYNYF PGT**FGQGTKLEIK
37	hBEW-9E10.6 VH (VEGF)	EVQLVQSGAEVKKPGSSVKVSCKAS**GYTFTNYGMY**WVRQAPGQGLEW MG**WIDTETGRPTYADDFKG**RFTFTADKSTSTAYMELSSLRSEDTAVY YCAR**WSGDTTGIRGPWFAY**WGQGTLVTVSS
38	hBEW-9E10.6 VL (VEGF)	DIRMTQSPSSLSASVGDRVTITC**LASEDIYSDLA**WYQQKPGKSPKLL IY**NANGLQN**GVPSRFSGSGSGTDYTLTISSLQPEDVATYFC**QQYNYF PGT**FGQGTKLEIK
39	hBEW-1B10.1 VH (VEGF)	EVQLVESGGGLVQPGGSLRLSCAAS**GFSFSKYDMA**WFRQAPGKGLEW VA**SITTSGVGTYYRDSVKG**RFTVSRDNAKSTLYLQMNSLRAEDTAVY YCAR**GYGAMDA**WGQGTTVTVSS
40	hBEW-1B10.1 VL (VEGF)	DIQMTQSPSSLSASVGDRVTITC**KASQDIDDYLS**WYQQKPGKSPKLV IY**AATRLAD**GVPSRFSGSGSGTDYTLTISSLQPEDFATYYC**LQSSST PWT**FGGGTKVEIK
41	hBEW-1E3.4 VH (VEGF)	EIQLVQSGSELKKPGASVKVSCKAS**GYPFTNSGMY**WVKQAPGQGLEY MG**WINTEAGKPTYADDFKG**RFVFSLDTSVSTAYLQISSLKAEDTAVY FCAR**WGYISDNSYGWFDY**WGQGTLVTVSS
42	hBEW-1E3.4 VL (VEGF)	ATQLTQSPSSLSASVGDRVTISC**RASEGVYSYMH**WYQQKPGKQPKLL IY**KASNLAS**GVPSRFSGSGSGTDFTLTISSLQPEDFATYFC**HQNWND PLT**FGQGTKLEIK
43	CL-34565 VH (VEGF)	EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQGLEW MG**WIDTETGDPTYADDFKG**RFVFSLDTSVSTAYLQISSLKAEDTAVY YCAR**TNYYYRNYMFYFDY**WGQGTMVTVSS
44	CL-34565 VL (VEGF)	EIVLTQSPATLSLSPGERATLFC**RASQSVSNHMH**WYQQKPGQAPRLL IY**GASILES**GVPARFSGSGSGTDFTLTISSLEPEDFAVYYC**QQSWYD PIT**FGQGTKLEIK
211	hBDI-5H1.12 VH (PDGF)	EVQLVESGGGLVQPGGSLRLSCAFS**GFSLSTFGMGVG**WIRQAPGKGL EWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQAYLQINSLRAEDTAV YYCAR**ISTGISSYYVMDA**WGQGTLVTVSS
212	hBDI-5H1.12 VL (PDGF)	DFQLTQSPSSLSASVGDRVTITC**ERSSGDIGDTYVS**WYQQKPGKAPK NVIY**GNDQRPS**GVPSRFSGSGSGNSATLTISSLQPEDFATYFC**QSYD SDIDIV**FGQGTKVEIK

[0181] It will be readily apparent to those skilled in the art that other suitable modifications and adaptations of the methods described herein are obvious and may be made using suitable equivalents without departing from the scope of the embodiments disclosed herein. Having now described certain embodiments in detail, the same will be more clearly understood by reference to the following examples, which are included for purposes of illustration only and are not intended to be limiting.

EXAMPLES

Example 1: In vitro Assays Used to Determine the Functional Activity of Anti-VEGF-A Antibodies, Anti-PDGF-BB Antibodies, Anti-VEGFR Antibodies, Anti-PDGFR-B Antibodies, and DVD-Ig Proteins

Example 1.1: Affinity Determination Using BIACORE® Surface Plasmon Resonance Technology for Antigen Binding

[0182] The BIACORE® surface plasmon resonance assay (Biacore, Inc., Piscataway, NJ) determines the affinity of antibodies with kinetic measurements of on-rate and off-rate constants. Binding of anti-VEGF-A antibodies, anti-PDGF-BB antibodies, anti-VEGFR antibodies, anti-PDGFR-B antibodies, or anti-VEGF-A/anti-PDGF-BB DVD-Ig molecules, to a purified recombinant VEGF-A, PDGF-BB, VEGFR extracellular domain (ECD), PDGFR-B ECD or their Fc fusion proteins was determined by surface plasmon resonance-based measurements with a Biacore® instrument (either a Biacore 2000, Biacore 3000, or Biacore T100; GE Healthcare, Piscataway, NJ) using running buffer HBS-EPB (10 mM HEPES [pH 7.4], 150 mM NaCl, 3 mM EDTA, 0.1 mg/ml BSA and 0.005% surfactant P20) at 25°C. For example, approximately 9000 RU of goat anti-human Fc specific polyclonal antibody (Thermo Fisher Scientific Inc., Rockford, IL) diluted in 10 mM sodium acetate (pH 4.5) is directly immobilized across a CM5 research grade biosensor chip using a standard amine coupling kit according to manufacturer's instructions and procedures at 25 μg/ml. Unreacted moieties on the biosensor surface were blocked with ethanolamine. For kinetic analysis, rate equations derived from the 1:1 Langmuir binding model were fitted simultaneously to multiple antigen injections (using global fit analysis) with the use of Scrubber 2 (BioLogic Software), Biacore Biaevaluation 4.0.1 software or Biacore T100 Evaluation software. Purified antibodies or DVD-Ig molecules were diluted in running buffer for capture across goat anti-human Fc reaction surfaces. Antibodies or DVD-Ig molecules to be captured as a ligand (1 μg/ml) were injected over reaction matrices at a flow rate of 10 μl/minute. During the assay, all measurements were referenced against the capture surface alone (i.e., with no captured antibody or DVD-Ig molecule). The association and dissociation rate constants, K_{on} ($M^{-1}s^{-1}$) and K_{off} (s^{-1}) were determined under a continuous flow rate of 80 μl/minute. Rate constants were derived by making kinetic binding measurements at different antigen concentrations ranging from 1.23 – 900 nM, as a 3-fold dilution series, and included buffer-only injections (to be used for double referencing). The equilibrium dissociation constant K_D (M) of the reaction between antibodies and the target antigen was then calculated from the kinetic rate constants by the following formula: $K_D = K_{off}/K_{on}$. Binding was recorded as a function of time and kinetic rate constants were calculated. In this assay, on-rates as fast as 10^6 $M^{-1}s^{-1}$ and off-rates as slow as 10^{-6} s^{-1} could be measured.

[0183] In some experiements, the conditions below were used for affinity determination:

[0184] Chip surface: CM5 chip with goat anti human Fc IgG (5000 RU).

[0185] Reference: Goat IgG (capture ~5000 RU).

[0186] Running buffer: HBS-EP, 0.1 mg/ml BSA

[0187] DVD-Ig or mAbs were captured at 1 μg/ml, at 70-200 RU.

[0188] Recombinant ECD proteins were serially diluted 1:5 at 0.016-50nM.

[0189] Association time was 5 min and dissociation time was observed for 10 and 30 min.

[0190] Flow rate was 50ul/min.

[0191] Surface regeneration: two 30s pulses of 10mM Glycine, pH 1.5, at 50μl/min.

Example 1.2: Surface Resonance FcγRIIa, FcγRIIb, FcγRIIIa, and FcRn Binding Assay

[0192] The binding of VEGF/PDGF DVD-Ig molecules to recombinant FcγRs captured via 6xHis-tag was assessed using a Biacore T200 (GE Healthcare) instrument. A CM5 chip (GE Healthcare, Pittsburgh, PA) with mouse anti-6xHis antibodies that were directly immobilized on the chip via amine coupling according to the GE Healthcare protocol to the density of 10000RU (all flow cells) was used for experiments. Human FcγRs were captured on flow cells 2, 3 and 4. Flow cell 1 was used as a reference surface. HBS-EP+ was used as the running buffer. Anti VEGF/PDGF DVD-Igs were injected over all the flow cells at a flow rate of 50μL/minute for 1-2 minutes at concentrations of 31.25; 62.5, 125, 250, 500, 1000, 2000 and 4000 nM, followed by 1-3 minutes of dissociation. The chip surfaces were regenerated with an injection of 10mM glycine pH 1.5 at a flow rate of 100μL/minute over all four flow cells after each cycle.

[0193] For FcRn binding analysis, VEGF/PDGF DVD-Igs were directly immobilized on a CM5 chip by amine coupling according to the manufacturer's (GE Healthcare) protocol to a density of approximately 750 RU. Flow cell 1, where blank immobilization was performed, did not contain DVD-Igs and was used as a reference surface. Human, cynomolgus, mouse, rat and rabbit recombinant FcRns were injected over all the flow cells at a flow rate of 50μL/minute for 1 minute at a concentrations range of from 2.7 to 6000 nM (three fold serial dilution), followed by a 2 minute dissociation time. The surfaces were regenerated with an injection of 10mM HCl at 100μL/minute for 2 seconds followed by an injection of HBS-EP+, pH 7.4, at a flow rate of 50μL/minute for 30 seconds over all four flow cells. Samples were prepared and run in two running buffer systems, pH 6.0 MES-EP+, and pH 7.4 HBS-EP-EP+. Recombinant human FcγRIIIa V158 and rat and mouse FcRn data were fitted to 1:1 kinetic model. Recombinant human FcγRIIa R131 and FcγRIIa H131, FcγRIIIa F158, and recombinant human, cynomolgus

and rabbit FcRn binding data were fitted to a steady state affinity model. Biacore T200 Evaluation Software version 2.0 was used to fit all the data.

Example 1.3: VEGF-A Binding Activity Determined by Capture ELISA

[0194] To identify molecules that could bind $hVEGF_{165}$, a direct binding ELISA was performed. 96-well high binding neutravidin plates (Thermo Scientific cat#15507) were coated with 0.25 µg/mL / 6.51E-9 M biotinylated recombinant human $VEGF_{165}$ (AP PR-1361002, 50 µL/well in D-PBS), and shaken for 1.5 hours at 25°C. During the coating step, supernatant, antibodies, benchmark compounds or DVD-Ig were diluted in 10 % Superblock (Thermo Scientific, cat#37535) and an eight point titration of each sample molecule was performed. Plates were then washed four times with wash buffer (TBS, 0.05% Tween-20). The sample molecule titration was added to the coated plate at 50 µL in duplicate and incubated for one hour at 25°C with shaking. Following incubation, plates were washed four times with wash buffer. The appropriate anti-species-IgG HRP conjugate was diluted in assay diluent (10% Superblock containing 0.05% surfactamps) and added to plates (50 µL) for forty-five minutes at 25°C with shaking. Plates were washed four times with wash buffer and developed with the addition of Enhanced K-blue TMB substrate (Neogen, Lexington, KY cat#308177). The reaction was stopped with 2N sulfuric acid (VWR, Radnor, PA cat#BDH3500-1) and the absorbance was read at 450 nm - 570 nm. An increase in optical density indicates the binding of the test molecule to biotinylated recombinant human $VEGF_{165}$. Data was analyzed using Softmax Pro 4.8 software and IC_{50} values calculated using a sigmoidal dose response (variable slope) fit in GraphPad Prism 5.

Example 1.4: VEGF-A Blocking Activity Determined by Inhibition of VEGF-R2 Interaction with Human $VEGF_{165}$

[0195] To identify molecules that could block the binding of $hVEGF_{165}$ to the hVEGF-R2 (KDR/Flk-1) receptor, a competition ELISA was performed. 96-well Costar high binding plates (#3369) were coated with 0.5 µg/mL / 2.27E-9 M recombinant human VEGF-R2-Fc (R&D Systems cat#357-KD), 50 µL/well in D-PBS), shaken for 2 hours at 25°C and stored overnight at 4°C. Plates were then washed four times with wash buffer (TBS, 0.05% Tween-20) and blocked with Superblock blocking buffer (Thermo Scientific, cat#37535). During the blocking step, supernatant, antibodies, benchmark compounds or DVD-Ig were diluted in 1% Blocker BSA (Thermo Scientific cat#37525) and an eight point titration of each sample molecule was performed. The biotinylated human $VEGF_{165}$ (AP, PR-1361002) was diluted in 1% Blocker BSA at 35 ng/mL. The sample molecule titration was added to the biotinylated human $VEGF_{165}$ (17.5 ng/mL / 4.56E-10 M final concentration) and pre-incubated for 45 minutes at 25°C with shaking. The pre-incubated sample/ $hVEGF_{165}$ complex was added to the coated plate at 50 µL in duplicate and incubated for 30 minutes at 25°C with shaking. Following incubation, plates were

washed four times with wash buffer. Streptavidin-polyHRP-40 (Fitzgerald cat#65r-s104phrp) was diluted in assay diluent (10% Superblock containing 0.05% surfactamps) and added to plates (50 µL) for 45 minutes at 25°C with shaking. Plates were washed four times with wash buffer and developed with the addition of Enhanced K-blue TMB substrate (Neogen cat#308177). The reaction was stopped with 2N sulfuric acid (VWR, cat# BDH3500-1) and the absorbance was read at 450 nm - 570 nm. A decrease in observed optical density indicates the test molecule is blocking the $hVEGF_{165}$ binding to the hVEGF-R2-Fc. Data was analyzed using Softmax Pro 4.8 software and IC_{50} values calculated using a sigmoidal dose response (variable slope) fit in GraphPad Prism 5.

Example 1.5: Mouse VEGF-A Blocking Activity Determined by Inhibition of Mouse VEGF-R2 Interaction with Mouse $VEGF_{164}$

[0196] To identify molecules that could block the binding of $mVEGF_{164}$ to the mVEGF-R2, a competition ELISA was performed. 96-well Costar high binding plates (#3369) were coated with 2 µg/mL anti-human IgG-Fc (Thermo-Scientific, cat 31125) shaken for 2 hours at 25°C and stored overnight at 4°C. Plates were washed four times with wash buffer (TBS, 0.05% Tween-20) and 1 µg/mL / 4.55E-9 M recombinant mouse VEGF-R2-Fc (R&D Systems cat#443-KD) (50 µL/well in D-PBS) was added to wells and incubated for 1.5 hour at 25°C with shaking. Plates were then washed four times with wash buffer (TBS, 0.05% Tween-20) and blocked with Superblock blocking buffer (Thermo Scientific, cat#37535). During the blocking step, hybridoma supernatants were diluted in 1% Blocker BSA (Thermo Scientific cat#37525). The mouse $VEGF_{164}$ (R&D Systems cat# 493-MV-005) was diluted in 1% Blocker BSA to 20 ng/mL. The diluted sample was added to the mouse $VEGF_{164}$ (10 ng/mL / 5.15E-10 M final concentration) and pre-incubated for 45 minutes at 25°C with shaking. The pre-incubated sample/ $mVEGF_{164}$ complex was added to the coated plate at 50 µL and incubated for 30 minutes at 25°C with shaking. Following incubation, plates were washed four times with wash buffer. The detection reagent biotinylated goat anti-$mVEGF_{164}$ (R&D Systems cat#BAF-493) was diluted in assay diluent (10% Superblock containing 0.05% surfactamps) and added to plates for 1 hour at 25°C with shaking. Following incubation, plates were washed four times with wash buffer. Streptavidin-polyHRP-40 (Fitzgerald cat#65r-s104phrp) was diluted in assay diluent and added to plates (50 µL) for 45 minutes at 25°C with shaking. Plates were washed four times with wash buffer and developed with the addition of Enhanced K-blue TMB substrate (Neogen cat#308177). The reaction was stopped with 2N sulfuric acid (VWR, cat# BDH3500-1) and the absorbance was read at 450 nm - 570 nm. A decrease in observed optical density indicates the test molecule is blocking the $mVEGF_{164}$ binding to the mouse VEGF-R2-Fc. Data was analyzed using Softmax Pro 4.8 software and IC_{50} values calculated using a sigmoidal dose response (variable slope) fit in GraphPad Prism 5.

Example 1.6: VEGF-A Blocking Activity Determined by VEGFR2 (Tyr1054) Phosphorylation

[0197] To test candidate molecules for the ability to neutralize hVEGF-A activity, a cell based human VEGF-R2 (KDR/Flk-1) phosphorylation assay was performed. Stably transfected VEGFR2-3T3 cells (AP) were trypsinized, washed in D-PBS and resuspended at 3.5E5 cells/mL in growth media assay (DMEM, 2mM L-glutamine, 100 units/mL penicillin/ 100 µg/mL streptomycin, 0.1 % MEM non-essential amino acids, 1mM sodium pyruvate, 400 µg/mL geneticin and 10% FBS). Cells were plated at 3.5E4 cells/well in 96-well plates (Costar cat#3599) and incubated for 6 hours at 37°C, 5% CO_2. Growth media was removed and cells were washed with D-PBS. Starvation media was added to wells (DMEM, 2mM L-glutamine, 100 units/mL penicillin/100 µg/mL streptomycin and 1mM sodium pyruvate) and cells were incubated for 18 hours at 37°C, 5% CO_2. The following day, the MSD anti-VEGFR2-phospho assay plate (Mesoscale VEGFR2-Tyr1054 phospho-MSD kit cat# K151DJD-2) was blocked with MSD Blocker-A for 1 hour at 25°C with shaking. During blocking, anti-VEGF-A monoclonal antibodies, benchmark compounds or DVD-Ig were serially diluted in growth media and pre-incubated with recombinant human $VEGF_{165}$ (AP, PR-1350437) (50 ng/ml / 1.3E-9 M final concentration), $hVEGF_{111}$ (R&DSystems, cat#5336-VE-10/CF) (50 ng/mL / 1.9E-9 M final concentration) or rabbit $VEGF_{165}$ (AbbVie, PR-1563693.0) (50 ng/mL / 1.24E-9 M final concentration) for 30 minutes at 25°C with shaking. Starvation media was removed from wells and pre-incubated sample added to cells in duplicate (100 µL) for 8 minutes at 37°C, 5% CO_2 Immediately following incubation, plates were transferred to ice where media was removed and cells washed with ice-cold D-PBS. Plates were frozen for 10 minutes at -80°C. Ice-cold lysis buffer (CST cat#9803S) containing 1 mM PMSF was added to cells (50 µL) on ice. Plates were centrifuged at 3000 rpm for 15 minutes at 4°C. The MSD plate was washed four times with wash buffer (TBS, 0.05% Tween-20). The cell lysates were transferred to MSD plate (40 µL) and incubated for 1 hour at 25°C with shaking. Following incubation, the MSD plate was washed four times with wash buffer. The anti-phospho-Tyr1054-IgG-sulfotag reagent was diluted in detection solution (K151DJD-2 components) and 25 µL added to foil covered wells for 1 hour at 25°C with shaking. Plates were washed four times with wash buffer, 150 µL MSD read buffer (K151DJD-2 component) added to wells and plates read on MSD Sector Imager 6000. A decrease in observed signal indicates the test molecule is neutralizing the hVEGF-A mediated activation. Data was analyzed using Graphpad Prism software and IC_{50} values calculated using a sigmoidal dose response (variable slope) fit in GraphPad Prism 5.

Example 1.7: VEGF-A Blocking Activity Determined by Inhibition of Human $VEGF_{165}$ Stimulated VEGFR2-3T3 Cell Proliferation/Survival

[0198] To screen candidate molecules for the ability to neutralize $hVEGF_{165}$ activity, a cell based proliferation assay was performed. Stably transfected VEGFR2-3T3 cells (AP) were trypsinized, washed in D-PBS and resuspended at 8.5E4 cells/mL in assay media (DMEM, 2mM L-glutamine, 100 units/mL penicillin/ 100 µg/mL streptomycin, 0.1 % MEM non-essential amino acids, 1mM sodium pyruvate and 0.1% BSA). Cells were plated at 4,250 cells / well (50 µL) on black 96-well plates and incubated for 24 hours at 37°C, 5% CO_2. The following day, anti-VEGF-A monoclonal antibodies, benchmark compounds or DVD-Ig were serially diluted in assay media and pre-incubated with recombinant human $VEGF_{165}$ (AP, PR-1350437) (40 ng/ml / 1.04E-9 M final concentration in assay well) for 1 hour at 25°C with gentle shaking. The pre-incubated samples were then added to the cells (50 µL) in triplicate and plates were incubated at 37°C, 5% CO2 for 72 hours. Cell survival/proliferation was measured indirectly by assessing ATP levels using an ATPlite kit (Perkin Elmer, Waltham, MA) according to the manufacturer's instructions. A decrease in observed signal indicates the test molecule is neutralizing the $hVEGF_{165}$ induced proliferation. Data was analyzed and IC_{50} values calculated using a sigmoidal dose response (variable slope) fit in GraphPad Prism 5.

Example 1.8: VEGF-A Blocking Activity Determined by Inhibition of Human $VEGF_{111}$ and Human $VEGF_{121}$ Stimulated VEGFR2-3T3 Cell Proliferation/Survival

[0199] To test the ability of candidate molecules to neutralize $hVEGF_{111}$ and $hVEGF_{121}$ activity, a cell based proliferation assay was performed. Stably transfected VEGFR2-3T3 cells (AP) were trypsinized, washed in D-PBS and resuspended at 8.5E4 cells/mL in assay media (DMEM, 2mM L-glutamine, 100 units/mL penicillin/ 100 µg/mL streptomycin, 0.1 % MEM non-essential amino acids, 1mM sodium pyruvate and 0.1% BSA). Cells were plated at 4,250 cells / well (50 µL) on black 96-well plates and incubated for 24 hours at 37°C, 5% CO_2. The following day, anti-VEGF-A monoclonal antibodies, benchmark compounds or DVD-Ig were serially diluted in assay media and pre-incubated with either recombinant human $VEGF_{111}$ (R&D Systems, cat#5336-VE) (10 ng/ml / 3.85E-10 M final concentration) or human $VEGF_{121}$ (R&D Systems, cat#4644-VS) (10 ng/ml / 3.57 E-10 M final concentration in assay well) for 1 hour at 25°C with gentle shaking. The pre-incubated samples were then added to the cells (50 µL) in triplicate and plates were incubated at 37°C, 5% CO2 for 72 hours. Cell survival/proliferation was measured indirectly by assessing ATP levels using an ATPlite kit (Perkin Elmer, Waltham, MA) according to the manufacturer's instructions. A decrease in observed signal indicates the test molecule is neutralizing the $hVEGF_{111}$ or $hVEGF_{121}$ induced proliferation. Data was analyzed and IC_{50} values calculated using a sigmoidal dose response (variable slope) fit in GraphPad Prism 5.

Example 1.9: VEGF-A Blocking Activity Determined by Inhibition of Rabbit $VEGF_{165}$ Stimulated VEGFR2-3T3 Cell Proliferation/Survival

[0200] To screen candidates for the ability to neutralize rabbit$VEGF_{165}$, a cell based proliferation assay was performed. Stably transfected VEGFR2-3T3 cells (AP) were trypsinized, washed in D-PBS and resuspended at 8.5E4 cells/mL in assay media (DMEM, 2mM L-glutamine, 100 units/mL penicillin/ 100 µg/mL streptomycin, 0.1 % MEM non-essential amino acids, 1mM sodium pyruvate and 0.1% BSA). Cells were plated at 4,250 cells / well (50 µL) on black 96-well plates and incubated for 24 hours at 37°C, 5% CO_2. The following day, anti-VEGF-A monoclonal antibodies, benchmark compounds or DVD-Ig were serially diluted in assay media and pre-incubated with recombinant rabbit $VEGF_{165}$ (AbbVie, PR-1563693.0) (40 ng/ml / 9.92E-10M final concentration in assay well) for 1 hour at 25°C with gentle shaking. The pre-incubated samples were then added to the cells (50 µL) in triplicate and plates were incubated at 37°C, 5% CO_2 for 72 hours. Cell survival/proliferation was measured indirectly by assessing ATP levels using an ATPlite kit (Perkin Elmer, Waltham, MA) according to the manufacturer's instructions. A decrease in observed signal indicates the test molecule is neutralizing the rabbit$VEGF_{165}$ induced proliferation. Data was analyzed and IC_{50} values calculated using a sigmoidal dose response (variable slope) fit in GraphPad Prism 5.

Example 1.10: VEGF-A Blocking Activity Determined by Inhibition of Human $VEGF_{165}$ Stimulated Endothelial Cell Proliferation/Survival

[0201] To test for the ability to neutralize h$VEGF_{165}$, a cell based proliferation assay was performed. Human microvascular endothelial cells (Lonza, cat#CC-2516) were maintained in EBM-2 (Lonza cat#CC3156) supplemented with EGM-2V singlequots (Lonza cat#3202). The day of the assay, the cells (passage 2 – 7) were trypsinized, washed in D-PBS and resuspended at 1E5 cells/mL in assay media (M199, 2 mM L-glutamine, 100 units/mL penicillin/ 100 µg/mL streptomycin, 10 mM HEPES and 10% FBS). Cells were plated at 5,000 cells / well (50 µL) on 96-well gelatin coated plates (BD Biocoat cat#354689) and incubated at 37°C, 5% CO_2. The anti-VEGF-A monoclonal antibodies, benchmark compounds or DVD-Ig were serially diluted in assay media and pre-incubated with recombinant human $VEGF_{165}$ (AP, PR-1350437) (5 ng/ml / 1.3E-10 M final concentration in assay well) for 1 hour at 25°C with gentle shaking. The pre-incubated samples were then added to the cells (50 µL) in triplicate and plates were incubated at 37°C, 5% CO_2 for 72 hours. Cell survival/proliferation was measured indirectly by assessing ATP levels using a CellTiter-Glo Luminescent Cell Viability Assay kit (Promega, Madison, WI) according to the manufacturer's instructions. A decrease in observed signal indicates the test molecule is neutralizing the h$VEGF_{165}$ induced proliferation. Data was analyzed and IC_{50} values calculated using a sigmoidal dose response (variable slope) fit in GraphPad Prism 5.

Example 1.11: Generation of naturally derived human VEGF-A and Reactivity to the Anti-VEGF antibodies or Anti-VEGF-A/Anti-PDGF-BB DVD-Ig Proteins

[0202] To identify molecules that could bind naturally derived human VEGF-A, a sandwich ELISA was performed. Native human VEGF-A was obtained from the supernatant of Y-79 cells (ATCC, cat#HTB-18) grown in the presence of dimethyloxalylglycine (Sigma-Aldrich, cat#D3695). The naturally derived material was quantified using the R&D Systems VEGF Duoset kit (cat#DY293B). 96-well Costar high binding plates (#3369)were coated with 13.3E-8 M antibodies, benchmark compounds or DVD-Ig in D-PBS, shaken for 2 hours at 25°C and stored overnight at 4°C. Plates were blocked with Superblock blocking buffer (Thermo Scientific, cat#37535) followed by four washes with wash buffer (TBS, 0.05% Tween-20). The naturally derived human VEGF-A supernatant was serially diluted in assay diluent (1% Blocker BSA; Pierce, cat#37525) for final test concentrations of 2900 ng/mL – 11.88 ng/mL. The dilutions were added to the plates (50 µL) and incubated for 2 hours at 25°C with shaking. Following incubation, plates were washed four times with wash buffer. Detection antibody from the R&D Systems Duoset kit (Part 840163, cat#DY293B) was diluted in assay diluent and added to plates (50 µL) for 2 hours at 25°C with shaking. Plates were then washed four times with wash buffer. The streptavidin-HRP from the R&D Systems Duoset kit (Part 890803, cat#DY293B) wasdiluted in assay diluent and added to plates (50 µL) for 35 minutes at 25°C with shaking. Plates were washed four times with wash buffer and developed with the addition of Enhanced K-blue TMB substrate (Neogen, cat#308177). The reaction was stopped with 2N sulfuric acid (VWR, cat# BDH3500-1) and the absorbance was read at 450 nm - 570 nm. An increase in optical density indicates binding of the test molecule to the naturally derived human VEGF-A. Data was analyzed using Softmax Pro 4.8 software and IC_{50} values calculated using a sigmoidal dose response (variable slope) fit in GraphPad Prism 5.

Example 1.12: PDGF-BB Binding Activity Determined by Capture ELISA

[0203] To identify molecules that could bind hPDGF-BB, a direct binding ELISA was performed. 96-well high binding neutravidin plates (Thermo Scientific cat#15507)were coated with 0.5 µg/mL / 1.99E-8 M recombinant human PDGF-BB-biotin (CST cat#8912BF; labeled at AbbVie, 50 µL/well in D-PBS), shaken for 2 hours at 25°C. During the coating step, supernatants, benchmark compounds or DVD-Ig were diluted in 10% Superblock (Thermo Scientific, cat#37525) and an eight point titration of each sample molecule was performed. Plates were then washed four times with wash buffer (TBS, 0.05% Tween-20). The sample molecule titration was added to the coated plate at 50 µL in duplicate and incubated for one hour at 25°C with shaking. Following incubation, plates were washed four times with wash buffer. The appropriate anti-species-IgG HRP conjugate was in assay diluent (10% Superblock containing 0.05% surfactamps) and added to plates (50 µL) for one hour at 25°C with shaking. Plates

were washed four times with wash buffer and developed with the addition of Enhanced K-blue TMB substrate (Neogen, cat#308177). The reaction was stopped with 2N sulfuric acid (VWR, cat# BDH3500-1) and the absorbance was read at 450 nm - 570 nm. An increase in optical density indicates binding of the test molecule to biotinylated recombinant human PDGF-BB.Data was analyzed using Softmax Pro 4.8 software and IC_{50} values calculated using a sigmoidal dose response (variable slope) fit in GraphPad Prism 5.

Example 1.13: PDGF-BB Blocking Activity Determined by Inhibition of PDGF-Rβ Interaction with Human PDGF-BB

[0204] To identify molecules that could block the binding of hPDGF-BB to the hPDGF-Rβ, a competition ELISA was performed. 96-well Costar high binding plates (#3369) were coated with 0.5 µg/mL / 2.98E-9 M recombinant human PDGF-Rβ-Fc(R&D Systems #385-PR, 50 µL/well in D-PBS), shaken for 2 hours at 25°C and stored overnight at 4°C. Plates were then washed four times with wash buffer (TBS, 0.05% Tween-20) and blocked with Superblock blocking buffer (Thermo Scientific, cat#37535). During the blocking step, supernatants, antibodies, benchmark compounds or DVD-Ig were diluted in assay diluent (10% Superblock containing 0.05% surfactamps) and an eight point titration of each sample molecule was performed. The recombinant human PDGF-BB-biotin (CST cat#8912BF; labeled at AbbVie) was diluted in assay diluent at 20 ng/mL. The sample molecule titration was added to the human PDGF-BB-biotin (10 ng/mL / 3.97E-10 M final concentration) and pre-incubated for 45 minutes at 25°C with shaking. The pre-incubated sample/PDGF-BB complex was added to the coated plate at 50 µL in duplicate and incubated for 35 minutes at 25°C with shaking. Following incubation, plates were washed four times with wash buffer. Detection reagent Streptavidin-polyHRP-40 (Fitzgerald, cat#65r-s104phrp) was diluted in assay diluent and added to plates (50 µL) for 45 minutes at 25°C with shaking. Plates were washed four times with wash buffer and developed with the addition of Enhanced K-blue TMB substrate (Neogen, cat#308177). The reaction was stopped with 2N sulfuric acid (VWR, cat# BDH3500-1) and the absorbance was read at 450 nm - 570 nm. A decrease in observed optical density indicates the test molecule is blocking the hPDGF-BB binding to the human PDGF-Rβ-Fc. Data was analyzed using Softmax Pro 4.8 software and IC_{50} values calculated using a sigmoidal dose response (variable slope) fit in GraphPad Prism 5.

Example 1.14: PDGF-BB Blocking Activity Determined by PDGFRβ (Tyr751) Phosphorylation

[0205] To test candidate molecules for the ability to neutralize hPDGF-BB activity, a cell based PDGF-Rβ phosphorylation assay was performed. Balb-3T3 cells (ATCC cat# CCL-163) were trypsinized, washed in D-PBS and resuspended at 3.5E5 cells/mL in growth media assay (DMEM, 2mM L-glutamine, 100 units/mL penicillin/ 100 µg/mL streptomycin, 0.1 % MEM non-essential amino acids, 1mM sodium pyruvate, and 10% FCS). Cells were plated at

3.5E4 cells/well in 96-well plates (Costar cat#3599) and incubated for 20 hours at 37°C, 5% CO_2. Growth media was removed and cells were washed with D-PBS. Starvation media was added to wells (DMEM, 2mM L-glutamine, 100 units/mL penicillin/100 µg/mL streptomycin and 1mM sodium pyruvate) and cells were incubated for 18 hours at 37°C, 5% CO_2. The following day, the MSD anti-PDGF-Rβ phospho-assay plate (Mesoscale PDGF-Rβ-Tyr751 phospho-MSD kit cat# K150DVD-2) was blocked with MSD Blocker-A for 1 hour at 25°C with shaking. During blocking, anti-PDGF-BB supernatants, monoclonal antibodies, benchmark compounds or DVD-Ig were serially diluted in growth media and pre-incubated with recombinant human PDGF-BB (CST, cat#8912BF) (20 ng/ml / 7.94E-10 M final concentration) and rat PDGF-BB (R&D Systems,cat#520-BB) (70 ng/ml / 1.4E-9 M final concentration) for 30 minutes at 25°C with shaking. Starvation media was removed from wells and pre-incubated sample added to cells in duplicate (100 µL) for 8 minutes at 37°C, 5% CO_2. Immediately following incubation, plates were transferred to ice where media was removed and cells washed with ice-cold D-PBS. Plates were frozen for 10 minutes at -80°C. On ice, ice-cold lysis buffer (CST cat#9803S) containing 1 mM PMSF was added to cells (50 µL). Plates were centrifuged at 3000 rpm for 15 minutes at 4°C. The MSD plate was washed four times with wash buffer (TBS, 0.05% Tween-20). The cell lysates were transferred to MSD plate (40 µL) and incubated 1 hour at 25°C with shaking. Following incubation, the MSD plate was washed four times with wash buffer. The anti-phospho-Tyr751-IgG-sulfotag reagent was diluted in detection solution (K150DVD-2 components) and 25 µl added to foil covered wells for 1 hour at 25°C with shaking. Plates were washed four times with wash buffer, 150 µL MSD read buffer (K150DVD-2 component) added to wells and plates read on MSD Sector Imager 6000. A decrease in observed reporter signal indicates the test molecule is neutralizing the hPDGF-BB mediated activation. Data was analyzed using Graphpad Prism software and IC_{50} values calculated using a sigmoidal dose response (variable slope) fit in GraphPad Prism 5.

Example 1.15: PDGF-BB Blocking Activity Determined by Inhibition of Human PDGF-BB Stimulated NIH-3T3 Cell Proliferation/Survival

[0206] To screen candidate molecules for the ability to neutralize hPDGF-BB activity, a cell based proliferation assay was performed. NIH-3T3 cells (ATCC, cat#CRL-1658) were trypsinized, washed in D-PBS and resuspended at 4.5E4 cells/mL in assay media (DMEM, 2mM L-glutamine, 100 units/mL penicillin/ 100 µg/mL streptomycin, 0.1 % MEM non-essential amino acids, 1mM sodium pyruvate and 0.1% BSA). Cells were plated at 2,250 cells / well (50 µL) on black 96-well plates and incubated for 5 hours at 37°C, 5% CO_2. During cell incubation, anti-PDGF-BB monoclonal antibodies, benchmark compounds or DVD-Ig were serially diluted in assay media and pre-incubated with recombinant human PDGF-BB (CST, cat#8912BF) (1.67 ng/ml / 6.63E-11 M final concentration) for 1 hour at 25°C with gentle

shaking. The pre-incubated samples were then added to the cells (50μL) in triplicate and plates were incubated at 37°C, 5% CO_2 for 44 hours. Cell survival/proliferation was measured indirectly by assessing ATP levels using a CellTiter-Glo Luminescent Cell Viability Assay kit (Promega, Madison, WI) according to the manufacturer's instructions. A decrease in observed signal indicates the test molecule is neutralizing the hPDGF-BB induced proliferation. Data was analyzed and IC_{50} values calculated using a sigmoidal dose response (variable slope) fit in GraphPad Prism 5.

Example 1.16: PDGF-BB Blocking Activity Determined by Inhibition of Cynomolgus PDGF-BB Stimulated NIH-3T3 Cell Proliferation/Survival

[0207] To screen candidate molecules for the ability to neutralize cynomolgus PDGF-BB activity, a cell based proliferation assay was performed. NIH-3T3 cells (ATCC, cat#CRL-1658) were trypsinized, washed in D-PBS and resuspended at 4.5E4 cells/mL in assay media (DMEM, 2mM L-glutamine, 100 units/mL penicillin/ 100 μg/mL streptomycin, 0.1 % MEM non-essential amino acids, 1mM sodium pyruvate and 0.1% BSA). Cells were plated at 2,250 cells / well (50 μL) on black 96-well plates and incubated for 5 hours at 37°C, 5% CO_2. During cell incubation, anti-PDGF-BB monoclonal antibodies, benchmark compounds or DVD-Ig were serially diluted in assay media and pre-incubated with recombinant cynomolgus PDGF-BB (AP, PR-1575400) (4 ng/ml / 1.61E-10 M final concentration in assay well) for 1 hour at 25°C with gentle shaking. The pre-incubated samples were then added to the cells (50μL) in triplicate and plates were incubated at 37°C, 5% CO_2 for 44 hours. Cell survival/proliferation was measured indirectly by assessing ATP levels using a CellTiter-Glo Luminescent Cell Viability Assay kit (Promega, Madison, WI) according to the manufacturer's instructions. A decrease in observed signal indicates the test molecule is neutralizing the cynoPDGF-BB induced proliferation. Data was analyzed and IC_{50} values calculated using a sigmoidal dose response (variable slope) fit in GraphPad Prism 5.

Example 1.17: PDGF-BB Blocking Activity Determined by Inhibition of Murine PDGF-BB Stimulated NIH-3T3 Cell Proliferation/Survival

[0208] To test candidate molecules for the ability to neutralize mouse PDGF-BB activity, a cell based assay was performed. NIH-3T3 cells (ATCC, cat#CRL-1658) were trypsinized, washed in D-PBS and resuspended at 4.5E4 cells/mL in assay media (DMEM, 2mM L-glutamine, 100 units/mL penicillin/ 100 μg/mL streptomycin, 0.1 % MEM non-essential amino acids, 1mM sodium pyruvate and 0.1% BSA). Cells were plated at 2,250 cells / well (50 μL) on black 96-well plates and incubated for 5 hours at 37°C, 5% CO_2. During cell incubation, anti-PDGF-BB monoclonal antibodies, benchmark compounds or DVD-Ig were serially diluted in assay media and pre-incubated with recombinant murine PDGF-BB (Abnova, cat#0309-200-58-S) (2 ng/ml / 8.13E-11 M final concentration) for 1 hour at 25°C with gentle

shaking. The pre-incubated samples were then added to the cells (50 µL) in triplicate and plates were incubated at 37°C, 5% CO_2 for 44 hours. Cell survival/proliferation was measured indirectly by assessing ATP levels using a CellTiter-Glo Luminescent Cell Viability Assay kit (Promega, Madison, WI) according to the manufacturer's instructions. A decrease in observed signal indicates the test molecule is neutralizing the murine PDGF-BB induced proliferation. Data was analyzed and IC_{50} values calculated using a sigmoidal dose response (variable slope) fit in GraphPad Prism 5.

Example 1.18: PDGF-BB Blocking Activity Determined by Inhibition of Rat PDGF-BB Stimulated NIH-3T3 Cell Proliferation/Survival

[0209] To test candidate molecules for the ability to neutralize rat PDGF-BB activity, a cell based assay was performed. NIH-3T3 cells (ATCC, cat#CRL-1658) were trypsinized, washed in D-PBS and resuspended at 4.5E4 cells/mL in assay media (DMEM, 2mM L-glutamine, 100 units/mL penicillin/ 100 µg/mL streptomycin, 0.1 % MEM non-essential amino acids, 1mM sodium pyruvate and 0.1% BSA). Cells were plated at 2,250 cells / well (50 µL) on black 96-well plates and incubated for 5 hours at 37°C, 5% CO_2. During cell incubation, anti-PDGF-BB monoclonal antibodies, benchmark compounds or DVD-Ig were serially diluted in assay media and pre-incubated with recombinant rat PDGF-BB (R&D Systems,cat#520-BB) (2 ng/ml / 8.0E-11 M final concentration) for 1 hour at 25°C with gentle shaking. The pre-incubated samples were then added to the cells (50 µL) in triplicate and plates were incubated at 37°C, 5% CO_2 for 44 hours. Cell survival/proliferation was measured indirectly by assessing ATP levels using a CellTiter-Glo Luminescent Cell Viability Assay kit (Promega, Madison, WI) according to the manufacturer's instructions. A decrease in observed signal indicates the test molecule is neutralizing the rat PDGF-BB induced proliferation. Data was analyzed and IC_{50} values calculated using a sigmoidal dose response (variable slope) fit in GraphPad Prism 5.

Example 1.19: Generation of Naturally Derived Human PDGF-BB and Reactivity to the Anti-PDGF-BB Antibodies or Anti-VEGF-A/Anti-PDGF-BB DVD-Ig Proteins

[0210] The native form of human PDGF was purified from platelets by a modified protocol from Antoniades et al. (Antoniades et al. (1979) Proc. Natl. Acad. Sci. USA 76(4): 1809-1813. In the modified protocol, ten units of platelets (Bioreclamation Inc.) were thawed, washed with 12 ml of Platelet Wash Buffer (HBSS – Gibco #14175 /0.3%BSA/10 mM EDTA) and centrifuged. The platelets were then suspended in 25 ml of Buffer A (20 mM NaHPO4, pH 7.4, 80 mM NaCl in a 50 ml tube). From here the platelet wash (50 ml tube) and the suspended platelets were worked up in parallel using the same protocol.

[0211] Both the suspended platelets and platelets wash tubes were placed into a boiling water bath for 10 minutes, after which the contents of the tubes were cooled on ice. The

supernatant was separated from the pellet by centrifugation. The supernatant was placed aside at 4°C and the pellet was extracted with 30 ml Buffer B (20 mM NaHPO4, pH 7.4, 1M NaCl) by stirring overnight at 4°C. The supernatant was separated from the pellet by centrifugation. The supernatant was placed aside (4°C) and the pellet was extracted with 30 ml Buffer B by stirring overnight at 4°C. This was repeated two more times. All the supernatants were then dialyzed separately against Buffer A. After removal from dialysis, they were all analyzed for protein content and PDGF-BB (ELISA) (See Table 6).

Table 6: Native PDGF Extraction from Human Platelets

Sample	Volume (ml)	PDGF-BB (ng/mL)	Total PDGF-BB (ng)	Protein (mg/mL)	Total Protein (mg)	ng PDGF-BB per mg Protein
Boiled platelet Supernatant	50	4.52	226.18	0.63	31.50	7.18
Pellet						
Extraction 1	35	8.77	306.95	0.31	10.85	28.29
Extraction 2	35	3.79	132.76	0.25	8.58	15.48
Extraction 3	35	1.26	44.03	0.10	3.43	12.83
Extraction 4	37	1.53	56.65	0.19	7.03	8.05
Platelet Wash Boiled Supernatant	27	7.49	202.12	0.64	17.28	11.70
Extracted Pellet	37	10.89	402.75	0.90	33.15	12.15
Total	*256*	*5.36*	*1371.32*	*0.44*	*111.82*	*12.26*

Table 7: Native PDGF Purification from Human Platelets

Platelet Purification	PDGF-BB (ng/mL)	Volume (mL)	Total PDGF-BB (ng)	Total Protein (mg)	Specific Activity ng PDGF/mg Protein	Endotoxin Levels		
						EU/ml	EU/mg protein	EU/μg PDGF
Eluate 1	214.94	6.74	1449	0.443	3266.49	2.36	35.87	10.98
Flow Thru 1	1.17	500	585	110.5	5.29			

[0212] Due to low specific activity (ng PDGF-BB per mg protein), the supernatants were subjected to further purification by CM sepharose. The supernatants were applied (with washing Buffer A) to a 20 ml CM sepharose column (GE Healthcare cat# 17-0719-01) and the PDGF was eluted with Buffer B. Subsequently the eluted protein was dialyzed against Buffer A. From here the protein that was eluted and subsequently dialyzed as well as the flow through were

all analyzed for protein content and PDGF-BB (ELISA). At this point the specific activity (eluate 1) was high enough to be queried in the assay.

[0213] To identify molecules that could bind naturally derived human PDGF-BB, a sandwich ELISA was performed. The native human PDGF-BB was isolated and purified from human platelets (AbbVie, PR-1566692). This material was quantified using the R&D Systems PDGF-BB Duoset kit (cat#DY220). 96-well Costar high binding plates (#3369) were coated with 13.3E-8 M antibodies, benchmark compounds or DVD-Ig in D-PBS, shaken for 2 hours at 25°C and stored overnight at 4°C. Plates were blocked with Superblock blocking buffer (Thermo Scientific, cat#37535) followed by four washes with wash buffer (TBS, 0.05% Tween-20). The native human PDGF-BB was serially diluted in assay diluent (1% Blocker BSA; Pierce, cat#37525) for final test concentrations of 2000 ng/mL – 2.74 ng/mL (5.4E-8 M – 7.5E-11 M). The dilutions were added to the plates (50 µL) and incubated for 2 hours at 25°C with shaking. Following incubation, plates were washed four times with wash buffer. Detection antibody from the R&D Systems Duoset kit (Part 840926, cat#DY220) was diluted in assay diluent and added to plates (50 µL) for 2 hours at 25°C with shaking. Plates were then washed four times with wash buffer. The streptavidin-HRP from the R&D Systems Duoset kit (Part 890803, cat#DY220) was diluted in assay diluent and added to plates (50 µL) for 35 minutes at 25°C with shaking. Plates were washed four times with wash buffer and developed with the addition of Enhanced K-blue TMB substrate (Neogen, cat#308177). The reaction was stopped with 2N sulfuric acid (VWR, cat# BDH3500-1) and the absorbance was read at 450 nm - 570 nm. An increase in optical density indicates binding of the test molecule to the naturally derived human PDGF-BB. Data was analyzed using Softmax Pro 4.8 software and IC_{50} values calculated using a sigmoidal dose response (variable slope) fit in GraphPad Prism 5.

Example 1.20: hVEGF-A Neutralization Potency of Anti-VEGF-A/Anti-PDGF-BB DVD-Ig Proteins When Pre-incubated with hPDGF-BB

[0214] To test candidate molecules for the ability to neutralize hVEGF-A activity in the presence of hPDGF-BB, a cell based VEGF-R2 (KDR/Flk-1) phosphorylation assay was performed. Stably transfected VEGFR2-3T3 cells (AP) were trypsinized, washed in D-PBS and resuspended at 3.5E5 cells/mL in growth media assay (DMEM, 2mM L-glutamine, 100 units/mL penicillin/ 100 µg/mL streptomycin, 0.1 % MEM non-essential amino acids, 1mM sodium pyruvate, 400 µg/mL geneticin and 10% FBS). Cells were plated at 3.5E4 cells/well in 96-well plates (Costar cat#3599) and incubated for 6 hours at 37°C, 5% CO_2 Growth media was removed and cells were washed with D-PBS. Starvation media was added to wells (DMEM, 2mM L-glutamine, 100 units/mL penicillin/100 µg/mL streptomycin and 1mM sodium pyruvate) and cells were incubated for 18 hours at 37°C, 5% CO_2. The following day, the MSD anti-VEGFR2-phospho assay plate (Mesoscale VEGFR2-Tyr1054 phospho-MSD kit, cat#K151DJD-2) was

blocked with MSD Blocker-A for 1 hour at 25°C with shaking. During blocking, anti-VEGF-A monoclonal antibodies, benchmark compounds or DVD-Ig were serially diluted in growth media and pre-incubated with recombinant human PDGF-BB (CST cat#8912BF) (0.992 μg/ml / 3.94E-8 M final concentration) for 30 minutes at 25°C with shaking. Following the first pre-incubation step, recombinant human $VEGF_{165}$ (AP, PR-1350437) was added to the samples for a final concentration of human $VEGF_{165}$ of 50 ng/ml / 1.3E-9 M and of hPDGF-BB of 0.496 μg/ml / 1.97E-8 M final concentration for 30 minutes at 25°C with shaking. Starvation media was removed from wells and pre-incubated sample added to cells in duplicate (100 μL) for 8 minutes at 37°C, 5% CO_2. Immediately following incubation, plates were transferred to ice where media was removed and cells washed with ice-cold D-PBS. Plates were frozen for 10 minutes at -80°C. Ice-cold lysis buffer (CST cat#9803S) containing 1 mM PMSF was added to cells (50 μL) on ice. Plates were centrifuged at 3000 rpm for 15 minutes at 4°C. The MSD plate was washed four times with wash buffer (TBS, 0.05% Tween-20). The cell lysates were transferred to MSD plate (40 μL) and incubated 1 hour at 25°C with shaking. Following incubation, the MSD plate was washed four times with wash buffer. The anti-phospho-Tyr1054-IgG-sulfotag reagent was diluted in detection solution (K151DJD-2 components) and 25 μL added to foil covered wells for 1 hour at 25°C with shaking. Plates were washed four times with wash buffer, 150 μL MSD read buffer (K151DJD-2 component) added to wells and plates read on MSD Sector Imager 6000. A decrease in observed signal indicates the test molecule is neutralizing the $hVEGF_{165}$ mediated activation in the presence of hPDGF-BB. Data was analyzed using Graphpad Prism software and IC_{50} values calculated using a sigmoidal dose response (variable slope) fit in GraphPad Prism 5.

Example 1.21: PDGF Neutralization Potency of Anti-VEGF-A/Anti-PDGF-BB DVD-Ig Proteins When Pre-incubated with VEGF

[0215] To test candidate molecules for the ability to neutralize hPDGF-BB activity in the presence of hVEGF-A, a cell based proliferation assay was performed. NIH-3T3 cells (ATCC, cat#CRL-1658) were trypsinized, washed in D-PBS and resuspended at 4.5E4 cells/mL in assay media (DMEM, 2mM L-glutamine, 100 units/mL penicillin/ 100 μg/mL streptomycin, 0.1 % MEM non-essential amino acids, 1mM sodium pyruvate and 0.1% BSA). Cells were plated at 2,250 cells / well (50 μL) on black 96-well plates and incubated for 5 hours at 37°C, 5% CO_2. During cell incubation, anti-PDGF-BB monoclonal antibodies, benchmark compounds or DVD-Ig were serially diluted in assay media containing $hVEGF_{165}$ (4 μg/mL/104.2 nM). The samples were pre-incubated with recombinant human PDGF-BB in assay media (CST, cat#8912BF) (3.34 ng/ml / 1.33E-10 M final concentration in well) for 1 hour at 25°C with gentle shaking. The final concentrations of ligand in assay wells were $hVEGF_{165}$ 2.6E-8 M and hPDGF-BB 6.63E-11 M. The pre-incubated samples were added to

the cells (50 µL) in triplicate and plates were incubated at 37°C, 5% CO_2 for 44 hours. Cell survival/proliferation was measured indirectly by assessing ATP levels using a CellTiter-Glo Luminescent Cell Viability Assay kit (Promega, Madison, WI) according to the manufacturer's instructions. A decrease in observed signal indicates the test molecule is neutralizing the hPDGF-BB induced proliferation in the presence of $hVEGF_{165}$. Data was analyzed and IC_{50} values calculated using a sigmoidal dose response (variable slope) fit in GraphPad Prism 5.

Example 1.22: Human VEGF-R2 Binding Activity of the Anti-VEGF-R2 Antibodies

[0216] To identify molecules which could bind VEGF-R2 (KDR/Flk-1), a direct binding ELISA was performed. 96-well Costar high binding plates (#3369)were coated with 0.5 µg/mL / 2.27E-9 M recombinant human VEGF-R2-Fc(R&D Systems cat#357-KD), 50 µL/well in D-PBS), shaken for 2 hours at 25°C and stored overnight at 4°C. Plates were then washed four times with wash buffer (TBS, 0.05% Tween-20) and blocked with Superblock blocking buffer (Thermo Scientific, cat#37535). During the blocking step, supernatant, antibodies or benchmark compounds were diluted in 1% Blocker BSA (Thermo Scientific cat#37525) and an eight point titration of each sample molecule was performed. The samples were added to wells and incubated for one hour at 25°C with shaking. Following incubation, plates were washed four times with wash buffer. The appropriate anti-species-IgG HRP conjugate was diluted in assay diluent (10% Superblock containing 0.05% surfactamps) and added to plates (50 µL) for forty-five minutes at 25°C with shaking. Plates were washed four times with wash buffer and developed with the addition of Enhanced K-blue TMB substrate (Neogen cat#308177). The reaction was stopped with 2N sulfuric acid (VWR, cat# BDH3500-1) and the absorbance was read at 450 nm - 570 nm. An increase in observed optical density indicates the test molecule is binding the human VEGF-R2-Fc. Data was analyzed using Softmax Pro 4.8 software and IC_{50} values calculated using a sigmoidal dose response (variable slope) fit in GraphPad Prism 5.

Example 1.23: Human VEGF-R2 Blocking Activity of the Anti-VEGF-R2 Antibodies as Determined by Inhibition of Human VEGF-R2 Interaction with Human $VEGF_{165}$

[0217] To identify molecules which could block the binding of VEGF-R2 (KDR/Flk-1) to $hVEGF_{165}$, a competition ELISA was performed. 96-well Costar high binding plates (#3369)were coated with 0.5 µg/mL / 2.27E-9 M recombinant human VEGF-R2-Fc(R&D Systems cat#357-KD), 50 µL/well in D-PBS), shaken for 2 hours at 25°C and stored overnight at 4°C. Plates were then washed four times with wash buffer (TBS, 0.05% Tween-20) and blocked with Superblock blocking buffer (Thermo Scientific, cat#37535). During the blocking step, supernatant, antibodies or benchmark compounds were diluted in 1% Blocker BSA

(Thermo Scientific cat#37525) and an eight point titration of each sample molecule was performed. The samples were added to wells and incubated for 30 minutes at 25°C with shaking. The biotinylated human $VEGF_{165}$ (AP, PR-1361002) was diluted in 1% BSA at 35 ng/mL. This was added to wells (17.5 ng/mL / 4.56E-10 M final concentration) and incubation was continued for 30 minutes at 25°C with shaking. Following incubation, plates were washed four times with wash buffer. Streptavidin-polyHRP-40 (Fitzgerald cat#65r-s104phrp) was diluted in assay diluent (10% Superblock containing 0.05% surfactamps) and added to plates (50 µL) for 45 minutes at 25°C with shaking. Plates were washed four times with wash buffer and developed with the addition of Enhanced K-blue TMB substrate (Neogen cat#308177). The reaction was stopped with 2N sulfuric acid (VWR, cat# BDH3500-1) and the absorbance was read at 450 nm - 570 nm. A decrease in observed optical density indicates the test molecule is blocking the human VEGF-R2-Fc binding to $hVEGF_{165}$. Data was analyzed using Softmax Pro 4.8 software and IC_{50} values calculated using a sigmoidal dose response (variable slope) fit in GraphPad Prism 5.

Example 1.24: VEGF-A Blocking Activity of the Anti-VEGF-R2 Antibodies as Determined by VEGFR2 (Tyr1054) Phosphorylation

[0218] To test candidate molecules for the ability to neutralize hVEGF-R2 activity, a cell based VEGF-R2 (KDR/Flk-1) phosphorylation assay was performed. Stably transfected VEGFR2-3T3 cells (AP) were trypsinized, washed in D-PBS and resuspended at 3.5E5 cells/mL in growth media assay (DMEM, 2mM L-glutamine, 100 units/mL penicillin/ 100 µg/mL streptomycin, 0.1 % MEM non-essential amino acids, 1mM sodium pyruvate, 400 µg/mL geneticin and 10% FBS). Cells were plated at 3.5E4 cells/well in 96-well plates (Costar cat#3599) and incubated for 6 hours at 37°C, 5% CO_2. Growth media was removed and cells were washed with D-PBS. Starvation media was added to wells (DMEM, 2mM L-glutamine, 100 units/mL penicillin/100 µg/mL streptomycin and 1mM sodium pyruvate) and cells were incubated for 18 hours at 37°C, 5% CO_2. The following day, the MSD anti-VEGR2-phospho assay plate (Mesoscale VEGFR2-Tyr1054 phospho-MSD #kit cat K151DJD-2) was blocked with MSD Blocked with MSD Blocker-A for 1 hour at 25°C with shaking. During blocking, anti-VEGF-R2 supernatant, monoclonal antibodies and benchmark compounds were serially diluted in growth media and pre-incubated with recombinant human VEGFR2-Fc (R&D Systems, cat#357-KD) (500 ng/ml / 2.27E-9 M final concentration) for 30 minutes at 25°C with shaking. Recombinant human $VEGF_{165}$ (AP, PR-1350437) (50 ng/ml / 1.3E-9 M final concentration) was added to the wells and incubation was continued for 30 minutes at 25°C with shaking. Starvation media was removed from wells and pre-incubated sample added to cells in duplicate (100 µL) for 8 minutes at 37°C, 5% CO_2 Immediately following incubation, plates were transferred to ice where media was removed and cells washed with ice-cold D-PBS. Plates were frozen for 10 minutes at -80°C. Ice-cold lysis buffer (CST cat# 9803S) containing 1 mM PMSF was added to cells (50 µL) on ice. Plates were centrifuged at 3000 rpm for 15 minutes at 4°C. The MSD plate

was washed four times with wash buffer (TBS, 0.05% Tween-20). The cell lysates were transferred to MSD plate (40 µL) and incubated 1 hour at 25°C with shaking. Following incubation, the MSD plate was washed four times with wash buffer. The anti-phospho-Tyr1054-IgG-sulfotag reagent was diluted in detection solution (K151DJD-2 components) and 25 µL added to foil covered wells for 1 hour at 25°C with shaking. Plates were washed four times with wash buffer, 150 µL MSD read buffer (K151DJD-2 component) added to wells and plates read on MSD Sector Imager 6000. An increase in observed signal indicates the test molecule is neutralizing the exogeneous hVEGFR2 and allowing for $hVEGF_{165}$ mediated activation. Data was analyzed using Graphpad Prism software and IC_{50} values calculated using a sigmoidal dose response (variable slope) fit in GraphPad Prism 5.

Example 1.25: Mouse VEGF-R2 Blocking Activity of the Anti-VEGF-R2 Antibodies as Determined by Inhibition of Mouse VEGF-R2 Interaction with Mouse $VEGF_{164}$

[0219] To identify molecules which could block the binding of $mVEGF_{164}$ to the mVEGF-R2, a competition ELISA was performed. 96-well Costar high binding plates (#3369) were coated with 1 µg/mL / 4.55E-9 M recombinant mouse VEGF-R2-Fc (R&D Systems cat#443-KD)(50 µL/well in D-PBS) shaken for 2 hours at 25°C and stored overnight at 4°C. Plates were washed four times with wash buffer (TBS, 0.05% Tween-20). Plates were then washed four times with wash buffer (TBS, 0.05% Tween-20) and blocked with Superblock blocking buffer (Thermo Scientific, cat#37535). During the blocking step, hybridoma supernatants and rat IgG were diluted in 1% Blocker BSA (Thermo Scientific cat#37525). The sample was added to the plates (50 µL) and incubated for 45 minutes at 25°C with shaking. The mouse $VEGF_{164}$ (R&D Systems cat# 493-MV-005) was diluted in 1% Blocker BSA to 20 ng/mL and added to wells for a final concentration of 10 ng/mL / 5.15E-10 M final concentration. Incubation was continued for 30 minutes at 25°C with shaking. Following incubation, plates were washed four times with wash buffer. The detection reagent biotinylated goat anti-$mVEGF_{164}$ (R&D Systems cat#BAF-493) was diluted in assay diluent (10% Superblock containing 0.05% surfactamps) and added to plates for 1 hour at 25°C with shaking. Following incubation, plates were washed four times with wash buffer. Streptavidin-polyHRP-40 (Fitzgerald cat#65r-s104phrp) was diluted in assay diluent and added to plates (50 µL) for 45 minutes at 25°C with shaking. Plates were washed four times with wash buffer and developed with the addition of Enhanced K-blue TMB substrate (Neogen cat#308177). The reaction was stopped with 2N sulfuric acid (VWR, cat# BDH3500-1) and the absorbance was read at 450 nm - 570 nm. A decrease in observed optical density indicates the test molecule is blocking the mouse VEGF-R2-Fc binding to the $mVEGF_{164}$. Data was analyzed using Softmax

Pro 4.8 software and IC_{50} values calculated using a sigmoidal dose response (variable slope) fit in GraphPad Prism 5.

Example 1.26: PDGF-Rβ Binding Activity of the Anti-PDGF-Rβ Antibodies

[0220] To identify molecules which bind hPDGF-Rβ, a direct ELISA was performed. 96-well Costar high binding plates (#3369)were coated with 0.5 µg/mL / 2.98E-9 M recombinant human PDGF-Rβ-Fc(R&D Systems #385-PR, 50 µL/well in D-PBS), shaken for 2 hours at 25°C and stored overnight at 4°C. Plates were then washed four times with wash buffer (TBS, 0.05% Tween-20) and blocked with Superblock blocking buffer (Thermo Scientific, cat#37535). During the blocking step, supernatants, antibodies and benchmark compounds were diluted in assay diluent (10% Superblock containing 0.05% surfactamps) and an eight point titration of each sample molecule was performed. The samples were added to wells and incubated for one hour at 25°C with shaking. Following incubation, plates were washed four times with wash buffer. The appropriate anti-species-IgG HRP conjugate was diluted in assay diluent (10% Superblock containing 0.05% surfactamps) and added to plates (50 µL) for forty-five minutes at 25°C with shaking. Plates were washed four times with wash buffer and developed with the addition of Enhanced K-blue TMB substrate (Neogen, cat#308177). The reaction was stopped with 2N sulfuric acid (VWR, cat# BDH3500-1) and the absorbance was read at 450 nm - 570 nm. An increase in observed optical density indicates the test molecule is binding the human PDGF-Rβ-Fc. Data was analyzed using Softmax Pro 4.8 software and IC_{50} values calculated using a sigmoidal dose response (variable slope) fit in GraphPad Prism 5.

Example 1.27: PDGF-Rβ Blocking Activity of the Anti-PDGF-Rβ Antibodies as Determined by Inhibition of PDGF-Rβ Interaction with Human PDGF-BB

[0221] To identify molecules which could block the binding of hPDGF-Rβ to hPDGF-BB, a competition ELISA was performed. 96-well Costar high binding plates (#3369)were coated with 0.5 µg/mL / 2.98E-9 M recombinant human PDGF-Rβ-Fc(R&D Systems #385-PR, 50 µL/well in D-PBS), shaken for 2 hours at 25°C and stored overnight at 4°C. Plates were then washed four times with wash buffer (TBS, 0.05% Tween-20) and blocked with Superblock blocking buffer (Thermo Scientific, cat#37535). During the blocking step, supernatants, antibodies and benchmark compounds were diluted in assay diluent (10% Superblock containing 0.05% surfactamps) and an eight point titration of each sample molecule was performed. The samples were added to wells and incubated for 30 minutes at 25°C with shaking. The recombinant human PDGF-BB-biotin (CST cat#8912BF; labeled at ABC) was diluted in assay diluent at 20 ng/mL. This was added to wells (10 ng/mL / 3.97E-10 M final concentration) and incubation was continued for 35 minutes at 25°C with shaking. Following incubation, plates were washed four times with wash buffer. Detection reagent Streptavidin-polyHRP-40 (Fitzgerald, cat# 65r-s104phrp) was diluted in assay diluent and added

to plates (50 µL) for 45 minutes at 25°C with shaking. Plates were washed four times with wash buffer and developed with the addition of Enhanced K-blue TMB substrate (Neogen, cat#308177). The reaction was stopped with 2N sulfuric acid (VWR, cat# BDH3500-1) and the absorbance was read at 450 nm - 570 nm. A decrease in observed optical density indicates the test molecule is blocking the human PDGF-Rβ-Fc binding to hPDGF-BB. Data was analyzed using Softmax Pro 4.8 software and IC_{50} values calculated using a sigmoidal dose response (variable slope) fit in GraphPad Prism 5.

Example 1.28: PDGF-Rβ Blocking Activity of the Anti-PDGF- Rβ Antibodies as Determined by PDGFRβ (Tyr751) Phosphorylation

[0222] To test candidate molecules for the ability to neutralize hPDGF-Rβ activity, a cell based PDGF-Rβ phosphorylation assay was performed. Balb-3T3 cells (ATCC cat# CCL-163) were trypsinized, washed in D-PBS and resuspended at 3.5E5 cells/mL in growth media assay (DMEM, 2mM L-glutamine, 100 units/mL penicillin/ 100 µg/mL streptomycin, 0.1 % MEM non-essential amino acids, 1mM sodium pyruvate, and 10% FCS). Cells were plated at 3.5E4 cells/well in 96-well plates (Costar cat#3599) and incubated for 20 hours at 37°C, 5% CO_2. Growth media was removed and cells were washed with D-PBS. Starvation media was added to wells (DMEM, 2mM L-glutamine, 100 units/mL penicillin/100 µg/mL streptomycin and 1mM sodium pyruvate) and cells were incubated for 18 hours at 37°C, 5% CO_2. The following day, the MSD anti-PDGFRβ-phospho-assay plate (Mesoscale PDGF-Rβ-Tyr751 phospho-MSD kit cat# K150DVD-2) was blocked with MSD Blocker-A for 1 hour at 25°C with shaking. During blocking, supernatants, antibodies or benchmark compounds were serially diluted in growth media and pre-incubated with 500 ng/mL / 2.98E-9 M hPDGF-Rβ (R&D System, cat 385-PR) for 30 minutes at 25°C. Recombinant human PDGF-BB (CST, cat#8912BF) (20 ng/ml / 7.94E-10 nM final concentration) was added to the wells and incubation was continued for 30 minutes at 25°C with shaking. Starvation media was removed from wells and pre-incubated sample added to cells in duplicate (100 µL) for 8 minutes at 37°C, 5% CO_2 Immediately following incubation, plates were transferred to ice where media was removed and cells washed with ice-cold D-PBS. Plates were frozen for 10 minutes at -80°C. Ice-cold lysis buffer (CST cat#9803S) containing 1 mM PMSF was added to cells (50 µL) on ice. Plates were centrifuged at 3000 rpm for 15 minutes at 4°C. The MSD plate was washed four times with wash buffer (TBS, 0.05% Tween-20). The cell lysates were transferred to MSD plate (40 µL) and incubated 1 hour at 25°C with shaking. Following incubation, the MSD plate was washed four times with wash buffer. The anti-phospho-Tyr751-IgG-sulfotag reagent was diluted in detection solution (K150DVD -2 components) and 25 µL added to foil covered wells for 1 hour at 25°C with shaking. Plates were washed four times with wash buffer, 150 µL MSD read buffer (K150DVD -2 components) added to wells and plates read on MSD Sector Imager 6000. An increase in observed signal indicates the test molecule is

neutralizing the exogeneous hPDGF-Rβ and allowing for hPDGF-BB mediated activation. Data was analyzed using Graphpad Prism software and IC_{50} values calculated using a sigmoidal dose response (variable slope) fit in GraphPad Prism 5.

Example 1.29: Reactivity of Anti-PDGF-BB Antibodies and Anti-VEGF-A/anti-PDGF-BB DVD-Ig Molecules to ECM-associated PDGF-BB

[0223] Both recombinant cell line HEK293 cells over-expressing PDGFBB-RM and HUVEC naturally expressing ECM-associated PDGF-BB cells were used for staining:

[0224] **HEK293 Cell Staining:** PDGFB-RM transient transfected HEK 293 cells and parental HEK293 cells were re-suspended at 1E6 cells/mL in PBS and fixed in 4% paraformaldehyde at RT for 10 minutes, washed with PBS and 2E5 cells/tube were incubated in blocking buffer (10% goat serum in PBS) for one hour on ice. Cells were washed with PBS and incubated with primary antibodies or DVD-Ig molecules at 33nM in antibody dilution buffer (5% goat serum in PBS) for one hour on ice. Cells were washed three times with PBS and incubated with Alexa Fluo 488 conjugated Goat anti-Human IgG (Jackson Immune, code: 109-546-098; lot: 108427) 1 : 400 dilution in antibody dilution buffer, incubated on ice for 45 minutes, cells were washed three times with PBS and cytospin onto glass slides and mounted with mounting media with DAPI. Pictures were taken by fluorescent microscopy.

[0225] **HUVEC Staining:** The anti-VEGF/anti-PDGF DVD-Ig was further assessed for its staining on naturally derived ECM-associated PDGF-BB on HUVEC cells. HUVECs (Lonza, cat#: C2519A lot: 181607) were trypsinized, resuspended at 2E4 cells/mL in culture media (Lonza, EGM2 MV Bulletkit: CC-3202). Cells were plated at 10,000 cells / 500 µl / well in 8-chamber glass slide and incubated for 16 hours at 37°C, 5% CO_2. After incubation, cells were fixed with 200 µl 4% paraformaldehyde at RT for 10 minutes, washed with PBS and incubated in blocking buffer (10% goat serum in PBS) for one hour on ice. Cells were washed with PBS 3X and incubated with primary antibodies or DVD-Ig molecules at 33 nM in antibody dilution buffer (5% goat serum in PBS) for one hour on ice. Cells were washed three times with PBS and incubated with Alexa Fluo 488 conjugated Goat anti-Human IgG (JacksonImmune, code: 109-546-098; lot: 108427) 1 : 400 dilution in antibody dilution buffer, incubate on ice for 45 minutes, cells were washed three times with PBS and mounted with mounting media with DAPI. Pictures were taken by fluorescent microscopy.

A. Example 1.30: Inhibition of Sprouting in HUVEC/MSC Co-culture Sprouting Assay by Anti-VEGF-A/anti-PDGF-BB DVD-Ig Molecules

[0226] In early therapeutic treatment mode, Cytodex-3 beads (Sigma-Aldrich, cat# C3275) were coated with HUVEC cells (Lonza) overnight, and then embedded (100 beads/well) with human mesenchymal stem cells (Lonza, 20,000 cells/well) in fibrin gel in 24-well tissue culture plates. A 1:1 mixture of fresh EGM-2 complete media (Lonza) and fibroblast (Lonza) conditioned EGM-2 media were added on top of the fibrin gel along with 2 ng/mL of recombinant

human HGF. Medium was replaced every 2-3 days till the end of the experiment. After EC sprouts and pericyte covering were formed usually on day 4, anti-VEGF-A (4G8.4), anti-PDGFBB (9E8.) or anti-PDGFBB/VEGF-A DVD-Ig, were added to the culture medium at 10 nM starting. 10 days later cells were fixed in 4% PFA overnight at 4°C. Endothelial cells were stained with anti-PECAM (Abcam, ab32457), followed by fluorescence-conjugated secondary antibody, and pericytes were labeled with anti-αSMA-Cy3 (Sigma, C6198). Cells were then viewed by an inverted fluorescence microscope and 5 × images were captured (Figures 2 and 3).

Example 2: Analytical Methods and Techniques for Physicochemical Property Characterizations of DVD-Ig Proteins

Example 2.1: Size Exclusion Chromatography Technique

[0227] Size exclusion chromatography (SEC) is used to separate proteins based on size. Proteins are carried in an aqueous mobile phase and through a porous stationary phase resin packed in a column. The retention time in the column is a function of the hydrodynamic size of the protein and the size of the pores in the packed resin bed. Smaller molecules can penetrate into smaller pores in the resin and are retained longer than larger molecules. Samples at 1 mg/ml, or diluted with formulation buffer to this concentration, are injected onto the SEC column at a volume of 10 µl. Upon elution from the column, the proteins are detected by UV absorbance. The SEC method uses a TSK gel guard (TOSOH Biosciences, Montgomeryville, PA, cat. no. 08543) and a TSK gel G3000SWxL (TOSOH Biosciences, Montgomeryville, PA, cat. no. 08541). The mobile phase was 100 mM Na_2HPO_4, 100 mM Na_2SO_4, pH 6.8. The flow rate is 0.25 ml/minute. The column temperature is room temperature. The autosampler temperature is 2-8ºC. The total run time is 55 minutes. The detection is based on UV absorbance at 214 nm wavelength, with band width set at 8 nm, using reference wavelength at 360 nm with band width 100 nm. The resulting chromatogram is analysed for the distribution of different size species (aggregate, monomer, and fragment) by the percentage of the total area of the signal.

Example 2.2: Differential Scanning Calorimetry Technique

[0228] The thermal stability of the protein samples was assessed using a differential scanning calorimetry (DSC) instrument. The DSC instrument used was an automated VP-DSC equipment with Capillary Cell (Microcal, GE Healthcare Ltd./Microcal, Buckinghamshire, UK). Unfolding of molecules was studied applying a 1°C/minute scan rate over a 25°C - 95°C temperature range for samples at 1 mg/mL. Additional measurement parameters applied were a fitting period of 16 seconds, a pre-scan wait time of 10 minutes, and measurements were performed in none- feedback mode. For each measurement, 420 µL of sample or blank buffer was filled into the designated receptacle within the DSC instrument. The thermograms obtained

(heat capacity versus temperature) were fitted to a non-two state model to obtain the midpoint temperatures and enthalpies of the different transitions.

Example 2.3: Sample Preparation

[0229] The antibodies and DVD-Ig molecules were initially obtained as a solution and diluted below 10 mg/ml with the formulation buffer. Each sample was then inserted into a separate dialysis cartridge (Slide-a-lyzer cassette, 10,000 MWCO, 3-12 mL capacity, Thermo Scientific, USA, Cat. No. 66810) and dialyzed against 2L of the formulation buffer with continuous stirring via a magnetic stir bar for 18-24 hours. The samples were then retrieved from the cartridge and briefly spun down in a centrifuge and/or passed through 0.45 μm PVDF filters to remove any precipitation or particles. This was followed by up-concentration of the DVD-Ig solutions with centrifuge spin filters (Amicon Ultra 30,000 MWCO Regenerated Cellulose) to reach the desired protein concentration which was confirmed by UV measurements at 280 nm. If the solutions were above the desired concentration, they were diluted to that concentration with the formulation buffer.

Example 2.4: Storage Stability Analysis Method

[0230] The antibodies and DVD-Ig molecule solutions prepared according to Example 2.3 were analyzed for their physical stability during storage at 40°C, 25°C, and/or 5°C. Both 25°C (room temperature) and 5°C (storage temperature) are typical temperatures at which the samples would be subjected either during preparation and storage for manufacture or as part of the final drug product presentation. Storage at 40°C is considered an accelerated stability condition which provides an indication of long-term stability prospects. The samples were aliquoted into low volume containers (< 0.1 ml), tightly sealed, and placed at the designated temperatures (sometimes in a water bath). The samples were then pulled at periodic intervals and a small portion was removed for analysis by SEC (Example 2.1).

Example 2.5: Freeze-Thaw Analysis Method

[0231] The antibody and DVD-Ig molecule solutions prepared according to Example 2.3 were analyzed for their physical stability during freeze/thaw stress. Samples were aliquoted into low volume containers (< 1 ml) and tightly sealed. The samples were then placed at -80°C for at least 6 hours and then thawed at 30°C in a water bath. This was repeated three more times. After the second and fourth thaws, a small portion of each sample was removed for analysis by SEC (Example 2.1).

[0232] DVD-Ig solutions are typically frozen at -80°C for long term storage as well as shipping to remote manufacturing sites. The samples are then thawed in order to complete the drug product manufacturing process. Stability due to freeze-thawing was assessed at low concentration in order to evaluate greater exposure of protein molecules to the denaturing ice-

water interfaces. At higher concentrations, proportionally less protein encounters the ice-water interface, instead interacting with other protein molecules.

Example 2.6: Viscosity Determination Method

[0233] The antibody and DVD-Ig molecule solutions prepared according to Example 2.3 were analyzed for their viscosity at room temperature (~23°C) with a Malvern Viscosizer 200 instrument. The viscosity serves as an indication of the ease of delivery of the sample through a small diameter needle attached to a syringe, a likely drug product presentation. A higher viscosity requires a greater force for delivery, and vice-versa.

Example 2.7: Intact and Reduced Molecular Weight Determination

[0234] The intact molecular weights of the three samples shown in Table 8 were acquired. Each sample was diluted to 1 mg/mL with Milli-Q water. 1.0 µL of the 1 mg/mL sample was injected onto an Agilent 6510 Q-Tof LC/MS system with a C4 MicroTrap column. Table 9 shows the HPLC gradient for intact molecular weight analysis. Buffer A was 0.02% TFA, 0.08% FA in water. Buffer B was 0.02% TFA, 0.08% FA in acetonitrile. The flow rate was 50 µL/minute. The column temperature was set at 60°C. The mass spectrometer was operated at 5 kvolts spray voltage and the scan range was from 600 to 3200 mass to charge ratio. The deglycosylated intact molecular weights of all three samples were measured by Agilent 6510 Q-Tof LC/MS system after the samples were deglycosylated. 100 µL of 1 mg/mL sample was mixed with 5 µL of 10% N-octylglucoside and 2 µL of PNGase F enzyme. The sample was incubated at 37°C for 18 hours. 1.0 µg of the deglycosylated sample was injected onto an Agilent 6510 Q-Tof LC/MS system with a C4 MicroTrap for deglycosylated intact molecular weight analysis.

[0235] The reduced molecular weights of all three samples were obtained. Each sample was diluted to 1 mg/mL with Milli-Q water. 1.0 µL of 1M DTT was added to 100 µL of a 1 mg/mL sample and incubated at 37°C for 30 minutes. 2.0 µL of the reduced sample was injected onto an Agilent 6510 Q-Tof LC/MS system with a diphenyl column. The HPLC gradient for reduced molecular weight analysis is shown in Table 9. The mass spectrometer was operated at 5 kvolts spray voltage and the scan range was from 600 to 3200 mass to charge ratio.

Table 8. VEGF/PDGF DVD-Ig Formulations

Sample ID	Lot	Detailed name	Concentration (mg/mL)	Formulation
PR-1572102	Lot 2211502	hu VEGF 4G8.3-GS-hu PDGF 9E8.4 (germline) [hu IgG1/k] LALA H435A	6.5	30mM histidine, 8% sucrose pH 5.2
PR-1572105	Lot 2211597	hu VEGF 4G8.3-SL-hu PDGF 9E8.4 (germline) [hu IgG1/k] LALA H435A	1.5	30 mM Histidine, 8% Sucrose pH 5.2
PR-1610561	Lot 2213329	hu VEGF 9E10.1-GS-hu PDGF 33675 [hu IgG1/k] LALA H435A	5	30mM Histidine, 8% sucrose, pH 5.2

Table 9. PLC Operating Conditions For Intact And Reduced Molecular Weight

Intact/C4		Reduced/Diphenyl	
Time (min)	% Buffer B	Time (min)	% Buffer B
0	5	0	5
5	5	5	30
5.5	95	30	40
10	95	32	90
10.5	5	37	90
15	5	39	5
		44	5

Example 2.8: Oligosaccharide Profiles Determined By Fc Molecular Weight Measurement

[0236] Samples were partially digested with Lys-C enzyme, reduced and analyzed by LC/MS. Different oligosaccharide species were quantitated based on the peak intensity detected by mass spectrometry and the relative percentage of different oligosaccharide species was reported. Samples were diluted to 1 mg/mL with Milli-Q water. 100 µL of each sample was mixed with 2 µL of 0.005 mg/mL Lys-C enzyme and incubated at 37°C for 30 minutes. 1 µL of 1 M DTT was added and incubated at 37°C for 30 minutes for reduction. 2 µL of sample was injected onto an Agilent 6510 Q-Tof LC/MS system with a diphenyl column and a reduced HPLC gradient was used. The column temperature was set at 60 °C. The mass spectrometer was operated at 5 kvolts spray voltage and the scan range was from 600 to 3200 mass to charge ratio.

Example 2.9: Charge Heterogeneity By Weak Cation Exchange Chromatography And Imaged Isoelectric Focusing (icIEF)

[0237] Charge heterogeneity was studied using a Propac WCX-10 column for weak cation exchange chromatography analysis. Mobile phase A was 20 mM MES, pH 5.5. Mobile phase B was 20 mM MES, 500 mM NaCl, pH 5.5. Each sample was diluted to 1 mg/mL in

mobile phase A. 50 μg of each sample was loaded, and the HPLC gradient is shown in Table 10. The flow rate was 1 mL/minute flow rate and the UV detector was monitored at 280 nm.

Table 10. Gradient Used For Weak Cation Exchange Chromatography

Time (minutes)	Mobile phase B
0	20
5	20
25	40
27	100
32	100
34	20
38	20

[0238] Imaged isoelectric focusing was performed on an iCE instrument from ProteinSimple. All three samples were diluted to 1 mg/mL with Milli-Q water before mixing with amphalyte and other components as shown in Table 11. Each sample was vortexed briefly and centrifuged for 5 minutes at 10k RPM before being transferred to glass inserts for analysis. Each sample was pre-focused at 1500 V for 1 minute and focused at 3000 V for 8 minutes.

Table 11. Sample Preparation for icIEF

Component	Volume (μL)
1% Methyl cellulose	70
Pharmalyte 3-10	4
Pharmalyte 5-8	4
Diluted pI 5.1 marker	8
Diluted pI 8.2 marker	8
1 mg/mL test sample	50
Water	6
8 M Urea	50

Example 3: Generation of Rat Anti-VEGF-A, Anti-VEGFRII, Rat-Anti-PDGF-BB, Anti-PDGFR-B Monoclonal Antibodies by DNA Immunization and Rat Hybridoma Technology

Example 3.1: DNA Immunization, Hybridoma Fusion and Screening

[0239] Genetic immunization enables the development of antibodies against any protein target directly from a cDNA. A cDNA encoding the soluble human VEGFA-165, soluble human PDGF-BB, human VEGFR-II ECD (extracellular domain) or human PDGFR-BB ECD was cloned into a eukaryotic expression vector (Aldevron GmbH, Freiburg, Germany). Wistar rats were immunized by intradermal application of DNA-coated gold-particles using a hand-held device for particle-bombardment ("gene gun"). Antibody-producing splenocytes or lymph node

cells were isolated and fused with fusion partner myeloma cells using polyethylene glycol (PEG) according to standard procedures. To help identify positive antisera and hybridomas, screening is done with the use of either cells transfected with screening vector encoding GPI anchored human VEGF-A165, human PDGF-BB, human VEGFR-II ECD or human PDGFR-BB ECD proteins, soluble recombinant human VEGF-A165 and human PDGF-BB protein or peptides. The tables below are the lists of antibodies generated using the rat DNA immunization approach.

[0240] Anti-VEGF-A antibodies derived from rat hybridomas were characterized for binding, function and cross-reactivity in a panel of assays. Supernatants were tested for the ability to bind $hVEGF_{165}$ (Example 1.3) and block binding of $hVEGF_{165}$ to hVEGFR2 in a competition ELISA format (Example 1.4). Select hybridomas were assessed for cross-reactivity by testing for the ability to block human $VEGF_{111}$ and rabbit $VEGF_{165}$ in a Tyr1054 phosphorylation assay (Example 1.6) and blocking of murine $VEGF_{164}$ binding to mVEGFR2 (Example 1.5). Candidate rat IgG was then examined for potency in the $hVEGF_{165}$ -induced cell proliferation assay (Example 1.7), reactivity to native $hVEGF_{165}$ (Example 1.11) and binding affinity measurement by Biacore analysis (Example 1.1). The data is summarized in Tables 12 and 13 below.

Table 12. A List of Anti-VEGF-A Antibodies Generated Using DNA Immunization and Rat Hybridoma Technology

Hybridoma Clones	Isotype	ELISA huVEGF-A 165 Binding	ELISA huVEGF-A_{121} Binding	Phospho-Tyr1054/ huVEGF-A_{111} Neutral-ization	ELISA Binding to Naturally Derived huVEGF-A	Receptor Competition ELISA huVEGF-A_{165} /huVEGF-R2 (nM)	huVEGF-A_{165} Neutral-ization Potency in hVEGF-R2 Over-expressing Cells (nM)	ELISA Mouse VEGF-A_{164} Binding	ELISA Rat VEGF-A_{164} Binding	Phospho-Tyr1054/ Rabbit VEGF-A_{165} Neutral-ization
BEW-1B4-C4	IgG2b/κ	+	NT	+	+	0.18	0.09	-	NT	+
BEW-1E3-D6	IgG2b/κ	+	NT	+	+	0.62	0.39	-	NT	+
BEW-5C3-E7	IgG2b/κ	+	NT	+	+	0.156	0.88	-	NT	+
BEW-6C2-C8	IgG2b/κ	+	NT	+	+	0.197	< 0.1	-	NT	+
BEW-8E6-E4	IgG2a/κ	+	NT	+	+	0.342	0.41	-	NT	+
BEW-9A8-E2	IgG2a/κ	+	NT	+	+	0.249	0.16	-	NT	+
BEW-9E10-E7	IgG2a/κ	+	NT	+	+	0.274	0.17	-	NT	+
BEW-10H2-B9	IgG2b/κ	+	NT	+	+	0.42	0.42	-	NT	+
BEW-9E3--B9	IgG2a/κ	+	NT	+	+	0.124	< 0.1	-	NT	+
BEW-	IgG2b/	+	NT	+	+	0.207	0.14	-	NT	+

9E7-B4	κ									
BEW-1G1-C2	IgG1/κ	+	NT	+	+	0.584	1.46	-	NT	+
BEW-9C2-D6	IgG2b/κ	+	NT	+	+	0.155	< 0.1	-	NT	+
BEW-9D2-E8	IgG2a/κ	+	NT	+	+	0.127	0.09	-	NT	+
BEW-1B10-B9-C3	IgG2a/κ	+	NT	+	+	0.326	2.8	-	NT	+
BEW-3A1-D10-G9	IgG2b/κ	+	NT	+	+	0.124	0.96	-	NT	+
BED-4G10-C8	IgG2b/κ	+	NT	+	+	0.13	0.38	-	NT	+
BDB-4G8-D4	IgG2b/κ	+	NT	+	+	0.13	0.617	-	NT	+

NT = not tested

Table 13. Biacore Binding of Rat Anti-VEGF Antibodies

Antibody	k_{on} (M-1 s-1)	k_{off} (M-1)	K_D (M)
BDB-4G8-D4	≥1.0 E+07	8.1 E-06	≤8.1 E-13
BDB-4G8-D4	1.4 E+07	1.6 E-05	1.2 E-12
BED-4G10-C8	1.8 E+07	1.1 E-03	6.0 E-11
BEW-1B4-C4	1.8 E+07	1.3 E-04	7.4 E-12
BEW-1B10-B9-C3	4.4 E+06	7.2 E-05	1.6 E-11
BEW-1E3-D6	1.4 E+07	1.4 E-04	1.0 E-11
BEW-1G1-C2	1.6 E+07	3.0 E-05	1.9 E-12
BEW-3A1-D10-G9	1.0 E+07	1.4 E-03	1.4 E-10
BEW-5C3-E7	1.2 E+07	4.8 E-05	3.9 E-12
BEW-6C2-C8	6.9 E+06	8.4 E-05	1.2 E-11
BEW-8E6-E4	6.9 E+06	1.2 E-04	1.7 E-11
BEW-9A8-E2	7.4 E+06	7.1 E-06	9.6 E-13
BEW-9C2-D6	5.5 E+06	≤1.0 E-06	≤1.8 E-13
BEW-9D2-E8	7.0 E+06	9.8 E-05	1.4 E-11
BEW-9E10-E7	1.3 E+07	3.9 E-05	3.1 E-12
BEW-9E3-B9	6.7 E+06	9.5 E-05	1.4 E-11
BEW-9E7-B4	5.9 E+06	2.5 E-05	4.3 E-12
BEW-10H2-B9	2.4 E+07	2.7 E-04	1.1 E-11

[0241] Anti-PDGF-BB antibodies derived from rat hybridomas were characterized for binding, function and cross-reactivity in a panel of assays. Supernatants were tested for the ability to bind hPDGF-BB (Example 1.12) and block binding of hPDGF-BB to hPDGF-R in a competition ELISA format (Example 1.13). Select hybridomas were assessed for the ability to block human and rat PDGF-BB in a Tyr751 phosphorylation assay (Example 1.14). Candidate rat IgG was then examined for potency in the human, mouse and cynomolgus PDGF-BB-induced cell

proliferation assay (Examples 1.15-1.17), reactivity to native hPDGF-BB (Example 1.19) and binding affinity measurement by Biacore analysis (Example 1.1). The data is summarized in Tables 14 and 15 below.

Table 14. A List of Anti-PDGF-BB Antibodies Generated using DNA Immunization and Rat Hybridoma Technology

Hybridoma Clones	Isotype	ELISA huPDGF-BB Binding	ELISA Binding to Naturally Derived huPDGF-BB	Receptor Competition ELISA huPDGF-BB /huPDGFRβ (nM)	Phospho-Tyr751/hPDGF-BB Neutralization (nM)	huPDGF-BB Neutralization Potency (nM) in NIH-3T3 Cells	Phospho-Tyr751 /ratPDGF-BB Neutralization (nM)	mPDGF-BB Neutralization Potency (nM) in NIH-3T3 Cells	cynoPDGF-BB Neutralization Potency (nM) in NIH-3T3 Cells
BDI-9E8-E7	IgG2 b/κ	+	+	1.121	0.629	0.195	0.333	0.026	0.194
BDI-5H1-F6	IgG2 b/κ	+	+	0.528	0.884	0.371	0.319	NT	NT
BDI-7H10-D8	IgG2 b	+	+	>10	>10	>5	>5	NT	NT
BDI-1E1-D5	IgG2 b/κ	+	NT	> 10	1.057	>5	+	NT	NT
BDI-5G2-F9	IgG2 b/λ	+	NT	1.065	0.923	0.741	+	NT	NT
BDI-6A3-A9	IgG2 b/λ	+	NT	3.228	1.618	>5	-	NT	NT
BDI-7F6-D3	IgG2 b	+	NT	>10	>10	>5	-	NT	NT
BDI-10E7-F9	IgG2 b/λ	+	NT	1.035	2.53	>5	-	NT	NT
BDI-8B8-F2	IgG2 b/λ	+	NT	1.086	3.159	>5	-	NT	NT
BFF-5C9-C7-B5	IgG2 b/κ	+	NT	>50	0.753	>5	NT	NT	NT
BFF-7D7-D3-E4	IgG2 b/λ	+	NT	>50	1.745	>10	NT	NT	NT
BFF-7E9-C3-B6	IgG2 b/κ	+	NT	>50	>10	>10	NT	NT	NT
BFF-4G8-B4	IgG2 b/λ	+	NT	>50	1.896	>10	NT	NT	NT
BFF-4E8-E5	IgG2 b/λ	+	NT	>50	0.739	>10	NT	NT	NT
BFU-3E2-B9-B8	IgG2 b/κ	+	NT	>50	0.642	0.247	NT	NT	NT
BFU-11A8-D6-C3	IgG2 b/κ	+	NT	7.095	0.736	0.344	NT	NT	NT
BFU-3H6-D2	IgG2 b	+	NT	2.287	0.639	>10	NT	NT	NT

Table 15. Biacore Binding of Rat Anti-PDGF Antibodies

Antibody	k_{on} (M-1 s-1)	k_{off} (M-1)	K_D (M)
BDI-1E1-D5	≥ 1.0 E+07	3.7 E-04 **	≤ 3.7 E-11 **
BDI-5G2-F9	≥ 1.0 E+07	≤ 1.0 E-06	≤ 1.0 E-13
BDI-5H1-F6	≥ 1.0 E+07	≤ 1.0 E-06	≤ 1.0 E-13
BDI-6A3-A9	≥ 1.0 E+07	6.7 E-03 **	≤ 6.7 E-10 **
BDI-7F6-D3	≥ 1.0 E+07	6.0 E-03	≤ 6.0 E-10

BDI-7H10-D8	≥ 1.0 E+07	≤ 1.3 E-02 **	≤ 1.3 E-09 **
BDI-8B8-F2	≥ 1.0 E+07 *	≤ 1.0 E-06 *	≤ 1.0 E-13 *
BDI-9E8-E7	≥ 1.7 E+07	≤ 1.0 E-06	≤ 5.8 E-14
BDI-9E8-E7	≥ 1.0 E+07	≤ 1.0 E-06	≤ 1.0 E-13
BDI-10E7-F9	≥ 1.0 E+07 *	1.3 E-04 *	≤ 1.3 E-11 *
BFF-4E8-E5	≥ 1.0 E+07	8.3 E-03 ***	≤ 8.3 E-10 ***
BFF-4G4-B8	≥ 1.0 E+07	8.3 E-03 **	≤ 8.3 E-10 **
BFF-5C9-C7-B5	≥ 1.0 E+07	5.8 E-05	≤ 5.8 E-12
BFF-7D7-D3-E4	≥ 1.0 E+07	2.1 E-02 **	≤ 2.1 E-09 **
BFF-7E9-C3-B6	≥ 1.0 E+07	1.2 E-03 **	≤ 1.2 E-10 **
BFU-3E2-B9-B8	≥ 1.0 E+07	1.5 E-06	≤ 1.5 E-13
BFU-3H6-D2	≥ 1.0 E+07	2.7 E-04 **	≤ 2.7 E-11 **
BFU-11A8-D6-C3	2.1 E+07	≤ 1.0 E-06	≤ 4.7 E-14

*Low Ag response

**Heterogeneous off-rate

*** Low Ag response and Heterogeneous off-rate

[0242] Anti-VEGFR2 antibodies derived from rat hybridomas were characterized for binding, function and cross-reactivity in a panel of assays. The subcloned rat antibodies were tested for the ability to bind hVEGFR2 (Example 1.22), block binding of hVEGF-R2 to $hVEGF_{165}$ in a competition ELISA format (Example 1.23), and a $hVEGF_{165}$ Tyr1054 phosphorylation assay (Example 1.24). Candidate molecules were then characterized for species cross-reactivity by testing their ability to block binding of mVEGFR2 to $mVEGF_{164}$ in a competition ELISA format (Example 1.25). The data is summarized in Table 16 below.

Table 16. A List of Anti-VEGFR II Antibodies Generated Using DNA Immunization and Rat Hybridoma Technology

Hybridoma Clones	Isotype	Potency (nM)			
		hVEGFR2-Fc Binding	$hVEGF_{165}$/ hVEGFR2-Fc Competition	$mVEGF_{164}$/ mVEGFR2-Fc Competition	Tyr1054 phospho-assay
BCU-3D6-C9		+	NT	NT	NT
BCU-6B1-G6	IgG2a/κ	+	4.850	1.350	+
BCU-7A6-C2	IgG2b/κ	+	-	-	+

[0243] Anti-PDGF-Rβ antibodies derived from rat hybridomas were characterized for binding and function in a panel of assays. The subcloned rat antibodies were tested for the ability to bind hPDGF-Rβ (Example 1.26). Candidate IgG was also characterized for the ability to block binding of hPDGF-Rβ to hPDGF-BB in a competition ELISA format (Example 1.27) and an hPDGF-BB Tyr751 phosphorylation assay (Example 1.28). The data is summarized in Table 17 below.

Table 17. A List of Anti-PDGFR-B Antibodies Generated Using DNA Immunization and Rat Hybridoma Technology

Hybridoma Clones	Isotype	Potency (nM)		
		hPDGFRβ-Fc Binding	hPDGF-BB/ hPDGFRβ-Fc Competition	hPDGF-BB / Tyr751 phospho-assay
BDE-3C9-G4	IgG2b/κ	+	0.832	4.696
BDE-4F2-D4	IgG2a/κ	+	0.527	+
BDE-8H6-F7		+	+	-

Example 4: Deduction of Variable Region Protein Sequences of Monoclonal Antibodies by DNA Cloning and Sequencing

[0244] Total RNA was extracted from hybridoma cell pellets using RNeasy mini kit (Qiagen, catalog # 74104) using the following protocol. 600 µl of buffer RLT were added to disrupt cells by pipetting up and down several times. The cell lysate was homogenized by passing it 10 times through a 20-gauge needle fitted to an RNase-free syringe. One volume of 70% ethanol was added to the homogenized lysate and mixed well by pipetting. Up to 700 µl at a time of the sample were added to an RNeasy spin column and spun for 15 seconds at 10,000 rpm, discarding flow through. 700 µl of buffer RW1 were added to the column and spun for 15 seconds at 10,000 rpm, discarding flow through. 500 µl of buffer RPE were added to wash the column membrane and spun for 15 seconds at 10,000 rpm, discarding flow through. The same step was repeated one more time, but the column was centrifuged for 2 minutes. Sample was then centrifuged for 1 minute at 10,000 rpm to eliminate any carryover of buffer RPE. RNA was eluted with 30 µl of RNase-free water by centrifuging for 1 minute at 10,000 rpm. Subsequently, 2 µg of total RNA were used to synthesize first-strand cDNA using SuperScript First-Strand Synthesis System for RT-PCR (Invitrogen, catalog # 11904-018) according to following protocol: 2 µg of RNA + 2 µl dNTP + 2 µl Oligo (dT) + DEPC-H_2O (to 20 µl) were incubated at 65°C for 5 minutes, then transferred to ice for at least 1 minute. The sample was then added to the following mixture: 4 µl of 10X RT buffer + 8 µl 25 mM $MgCl_2$ + 4 µl 0.1 M DTT + 2 µl RNase OUT and incubated at 42°C for 2 minutes. Then, 2 µl of SuperScript II RT were added to the sample and incubated at 42°C for 50 minutes. Sample was then incubated at 70°C for 15 minutes and chilled on ice. 2 µl of RNase H were then added and the sample was incubated at 37°C for 20 minutes. cDNA was then used as template for PCR amplification of variable regions of antibodies. PCR was performed using first-strand cDNA, primers from Mouse Ig-Primer Set (Novagen, catalog # 69831-3) and Platinum Super Mix High Fidelity (Invitrogen, catalog # 12532-016). To amplify heavy chain variable regions, PCR samples were assembled as follows: 22.5 µl PCR Super Mix + 0.25 µl reverse primer MuIgG V_H3'-2 + 1 µl cDNA + 1.25 µl of one the forward primers (VH-A, VH-B) or 0.5 µl of one of the forward primers (VH-C, VH-D, VH-E, VH-F). To amplify light

chain variable regions, PCR samples were assembled as follows: 22.5 µl PCR Super Mix + 0.25 µl reverse primer MuIgKV$_L$-3'-1 + 1 µl cDNA + 1.25 µl of one the forward primers (VL-A, VL-B) or 0.5 µl of one of the forward primers (VL-C, VL-D, VL-E, VL-F, VL-G).

[0245] For samples with primers VH-A, VH-B, VL-A and VL-B, the following PCR cycles were used (40-45 cycles, steps 2 through 4):

1-Denature 94°C 2 minutes.

2-Denature 94°C 30 seconds.

3-Anneal 50°C 30 seconds.

4-Extend 68°C 1 minute.

5-Final extension 68°C 5 minutes.

6-Cool 4°C forever

For samples with primers VH-C through VH-F, and VL-C through VL-G, the following PCR cycles were used (40-45 cycles, steps 2 through 4):

1-Denature 94°C 2 minutes.

2-Denature 94°^{0}C 30 seconds.

3-Anneal 60°C 30 seconds.

4-Extend 68°C 1 minute.

5-Final extension 68°C 5 minutes.

6-Cool 4°C forever

[0246] PCR products were run on a 1.2% agarose gel, and bands migrating at the expected size (400-500 bp) were excised for DNA extraction. DNA was purified using QIAquick Gel Extraction Kit (Qiagen, catalog # 28704) according to the following protocol: gel slices were weighed. 3 volumes of buffer QG to 1 volume of gel were added to each gel slice. Samples were incubated at 50°C for 10 minutes until gel slices were completely dissolved, mixing every 2-3 minutes. One gel volume of isopropanol was then added to each sample and mixed. Samples were then applied to QIAquick column and centrifuged for 1 minute at 13000 rpm. To wash, 750 µl of buffer PE were added to samples and spun for 1 minute at 13000 rpm. Columns were then centrifuged for an additional minute at 13,000 rpm to completely remove residual ethanol. DNA was eluted by adding 30 µl of H_2O to each column and by spinning 1 minute at 13,000 rpm. Purified PCR products were then sequenced to identify variable region sequences (see Tables below).

Table 18. VH and VL Amino Acid Sequences of Rat Anti-Human VEGFA Monoclonal Antibodies

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				12345678901234567890123456 7
	BDB-4G8-D4 VH			QIQLVQSGPELKKPGESVKISCKAS**GY TFTNYGMY**WVKQAPGQGLQYMG**WINTE TGKPTYADDFKG**RFVFFLETSASTAYL QINNLKNEDMATYFCAR**TNYYYRSYIF YFDY**WGQGTMVTVSS
	BDB-4G8-D4	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	BDB-4G8-D4	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPTYADDFKG**
	BDB-4G8-D4	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TNYYYRSYIFYFDY**
	BDB-4G8-D4 VL			DTVLTQSPALAVSPGERVSISC**RASES VSTHMH**WYQQKPGQQPKLLIY**GASNLE S**GVPARFSGSGSGTDFTLTIDPVEADD TATYFC**QQSWNDPFT**FGAVTKLELK
	BDB-4G8-D4	CDR-L1	Residues 23-33 of SEQ ID NO.:	**RASESVSTHMH**
	BDB-4G8-D4	CDR-L2	Residues 49-55 of SEQ ID NO.:	**GASNLES**
	BDB-4G8-D4	CDR-L3	Residues 88-96 of SEQ ID NO.:	**QQSWNDPFT**
	BED-4G10-C8 VH			QVQLQQSGTELVKPGSSVKISCKAS**GY TFTSNYMH**WIRQQPGNGLEWIG**WIYPG DGDTNYNHNFNG**KATLTADKSSSTAYM QLSSLTSEDFAVYFCAS**STRAIPGWFT Y**WGQGTLVTVSS
	BED-4G10-C8	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTSNYMH**
	BED-4G10-C8	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WIYPGDGDTNYNHNFNG**
	BED-4G10-C8	CDR-H3	Residues 99-109 of SEQ ID NO.:	**STRAIPGWFTY**
	BED-4G10-C8 VL			DTVLTQSPALAVSPGERVSISC**WASES VSTLMH**WYQQKLGQQPKLLIY**GASNLE S**GVPARFRGSGSGTDFTLTIDPVEADD TATYFC**QQSWSDPYT**FGAGTKLELK
	BED-4G10-C8	CDR-L1	Residues 23-33 of SEQ ID NO.:	**WASESVSTLMH**
	BED-4G10-C8	CDR-L2	Residues 49-55 of SEQ ID NO.:	**GASNLES**
	BED-4G10-C8	CDR-L3	Residues 88-96 of SEQ ID NO.:	**QQSWSDPYT**
	BEW-10H2-B9 VH			QIQLVQSGPELKKPGESVKISCKAS**GY SFTNFGLY**WVKQAPGQGLQYMG**WIDTE TGKPTYADDFRG**RFVFFLETSASTAYL QINNLKNEDMATYFCAR**VYGYPSWYFD F**WGPGTMVTVSS

SEQ ID NO:	Clone	Protein Region	Residues	V Region
	BEW-10H2-B9	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYSFTNFGLY**
	BEW-10H2-B9	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WIDTETGKPTYADDFRG**
	BEW-10H2-B9	CDR-H3	Residues 99-109 of SEQ ID NO.:	**VYGYPSWYFDF**
	BEW-10H2-B9 VL			DIQMTQSPASLSTSLEEIVTITC**QASQ** **DIDNYLS**WYQQKPGKSPQLLIH**SATSL** **AD**GVPSRFSGSRSGTQFSLKIHRLQVE DTGIYYC**LQHFFPPWT**FGGGTKLELK
	BEW-10H2-B9	CDR-L1	Residues 24-34 of SEQ ID NO.:	**QASQDIDNYLS**
	BEW-10H2-B9	CDR-L2	Residues 50-56 of SEQ ID NO.:	**SATSLAD**
	BEW-10H2-B9	CDR-L3	Residues 89-97 of SEQ ID NO.:	**LQHFFPPWT**
	BEW-1B10-B9-C3 VH			EVQLVESGGGLVQPGRSLKLSCAAS**GF** **SFSKYDMA**WFRQTPTKGLEWVA**SITTS** **GVGTYYRDSVKG**RFTVSRDNAKSTLYL QMDSLRSEDTATYYCAR**GYGAMDA**WGQ GTSVTVSS
	BEW-1B10-B9-C3	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GFSFSKYDMA**
	BEW-1B10-B9-C3	CDR-H2	Residues 50-66 of SEQ ID NO.:	**SITTSGVGTYYRDSVKG**
	BEW-1B10-B9-C3	CDR-H3	Residues 99-105 of SEQ ID NO.:	**GYGAMDA**
	BEW-1B10-B9-C3 VL			DIQMTQSPASLSASLEEIVTITC**KASQ** **DIDDYLS**WYQQKPGKSPQLVIY**AATRL** **AD**GVPSRFSGSGSGTQYSLKISRLQVD DSGIYYC**LQSSSTPWT**FGGGTNLELK
	BEW-1B10-B9-C3	CDR-L1	Residues 24-34 of SEQ ID NO.:	**KASQDIDDYLS**
	BEW-1B10-B9-C3	CDR-L2	Residues 50-56 of SEQ ID NO.:	**AATRLAD**
	BEW-1B10-B9-C3	CDR-L3	Residues 89-97 of SEQ ID NO.:	**LQSSSTPWT**
	BEW-1B4-C4 VH			QIQLVQSGPELKKPGESVKISCKAS**GY** **SFTNYGMY**WVKQAPGQGLQYMG**WIDTE** **TGKPTYTDDFKG**RFVFFLETSASTAYL QINNLKNEDMATYFCAR**WSGDTAGIRG** **PWFAY**WGQGTLVTVSS
	BEW-1B4-C4	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYSFTNYGMY**
	BEW-1B4-C4	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WIDTETGKPTYTDDFKG**
	BEW-1B4-C4	CDR-H3	Residues 99-113 of SEQ ID NO.:	**WSGDTAGIRGPWFAY**
	BEW-1B4-C4 VL			DIRMTQSPASLSASLGETVNIEC**LASE** **DIYSDLA**WYQQKPGKSPQLLIY**NANDL**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				QKGVPSRFSGSGSGTQYSLKINSLQSE DVATYFC**QQYNYYPGT**FGAGTKLELK
	BEW-1B4-C4	CDR-L1	Residues 24-34 of SEQ ID NO.:	**LASEDIYSDLA**
	BEW-1B4-C4	CDR-L2	Residues 50-56 of SEQ ID NO.:	**NANDLQK**
	BEW-1B4-C4	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQYNYYPGT**
	BEW-1C6-D2 VH			QIQLVQSGPELKKPGESVKISCKAS**GY** **TFTNYGMY**WVKQAPGQGLQYMG**WINTE** **TGKPTYADDFKG**RFVFFLETSASTAYF QINNLKNEDLATYFCAR**PSDYYDGFWF** **PY**WGQGTLVTVSS
	BEW-1C6-D2	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	BEW-1C6-D2	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPTYADDFKG**
	BEW-1C6-D2	CDR-H3	Residues 99-110 of SEQ ID NO.:	**PSDYYDGFWFPY**
	BEW-1C6-D2 VL			DTALTQSPALAVSPGERVSISC**RASEG** **VNSYMH**WYQQSPGQQPKLLIY**KASNLA** **S**GVPARFSGSGSGTDFTLTIDPVEADD TATYFC**QQSWYDPLT**FGSGTKLEIK
	BEW-1C6-D2	CDR-L1	Residues 23-33 of SEQ ID NO.:	**RASEGVNSYMH**
	BEW-1C6-D2	CDR-L2	Residues 49-55 of SEQ ID NO.:	**KASNLAS**
	BEW-1C6-D2	CDR-L3	Residues 88-96 of SEQ ID NO.:	**QQSWYDPLT**
	BEW-1E3-D6 VH			QIQLVQSGPELKKPGESVKISCKAS**GY** **PFTNSGMY**WVKQAPGQGLQYMG**WINTE** **AGKPTYADDFKG**RFVFFLETSASTAYL QINNLKNEDMATYFCAR**WGYISDNSYG** **WFDY**WGQGTLVTVSS
	BEW-1E3-D6	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYPFTNSGMY**
	BEW-1E3-D6	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTEAGKPTYADDFKG**
	BEW-1E3-D6	CDR-H3	Residues 99-112 of SEQ ID NO.:	**WGYISDNSYGWFDY**
	BEW-1E3-D6 VL			DTVLTQSPALAVSPGERVSISC**RASEG** **VYSYMH**WYQQNPGQQPKLLIY**KASNLA** **S**GVPARFSGSGSGTDFTLTIDPVEADD TATYFC**HQNWNDPLT**FGSGTKLEIK
	BEW-1E3-D6	CDR-L1	Residues 23-33 of SEQ ID NO.:	**RASEGVYSYMH**
	BEW-1E3-D6	CDR-L2	Residues 49-55 of SEQ ID NO.:	**KASNLAS**
	BEW-1E3-D6	CDR-L3	Residues 88-96 of SEQ ID NO.:	**HQNWNDPLT**
	BEW-3A1-D10-			QVQLEQSGAELVKPGTSVKLSCMAS**GY**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
	G9 VH			**TSSSNHMN**WMKQTTGQGLEWIG**IINPG** **SGGTRYNVKFEG**KATLTVDKSSSTAFM QLNSLTPEDSAVYYCAR**AGFPGPFSYY** **AMGA**WGQGTSVTVSS
	BEW-3A1-D10-G9	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTSSSNHMN**
	BEW-3A1-D10-G9	CDR-H2	Residues 50-66 of SEQ ID NO.:	**IINPGSGGTRYNVKFEG**
	BEW-3A1-D10-G9	CDR-H3	Residues 99-112 of SEQ ID NO.:	**AGFPGPFSYYAMGA**
	BEW-3A1-D10-G9 VL			DIQMTQSPPVLSASVGDRVTLSC**KASQ** **NIHNNLD**WYQQKHGEAPKLLIF**YTNNL** **QT**GIPSRFSGSGSGTDYTLTISSLQPE DVATYYC**YQYNSGYT**FGAGTKLELK
	BEW-3A1-D10-G9	CDR-L1	Residues 24-34 of SEQ ID NO.:	**KASQNIHNNLD**
	BEW-3A1-D10-G9	CDR-L2	Residues 50-56 of SEQ ID NO.:	**YTNNLQT**
	BEW-3A1-D10-G9	CDR-L3	Residues 89-96 of SEQ ID NO.:	**YQYNSGYT**
	BEW-5C3-E7 VH			QIQLVQSGPELKKPGESVKISCKAS**GY** **TFTNYGVY**WVKQAPGQGLQYMG**WINTE** **TGKPTYADDFKG**RFVFFLETSTNTAYL QINNLKNEDMATFFCAR**ARQLDWFVY**W GQGTLVTVSS
	BEW-5C3-E7	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGVY**
	BEW-5C3-E7	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPTYADDFKG**
	BEW-5C3-E7	CDR-H3	Residues 99-107 of SEQ ID NO.:	**ARQLDWFVY**
	BEW-5C3-E7 VL			DTVLTQSPALTVSPGERVSISC**RARES** **LTTSLC**WFQQKPGQQPKLLIY**GASKLE** **S**GVPARFSGSGSGTDFTLTIDPVEADD TATYFC**QQSWYDPPT**FGGGTKLELK
	BEW-5C3-E7	CDR-L1	Residues 23-33 of SEQ ID NO.:	**RARESLTTSLC**
	BEW-5C3-E7	CDR-L2	Residues 49-55 of SEQ ID NO.:	**GASKLES**
	BEW-5C3-E7	CDR-L3	Residues 88-96 of SEQ ID NO.:	**QQSWYDPPT**
	BEW-6C2-C8 VH			EVQLVESGGGLVQPGSSLKLSCAAS**GF** **TFSYYGMH**WIRQAPKKGLEWMA**LIYYD** **SSKMYYADSVKG**RFTISRDNSKNTLYL EMNSLRSEDTAMYYCAA**GGTAPVY**WGQ GVMVTVSS
	BEW-6C2-C8	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GFTFSYYGMH**
	BEW-6C2-C8	CDR-H2	Residues 50-66 of SEQ ID NO.:	**LIYYDSSKMYYADSVKG**
	BEW-6C2-C8	CDR-H3	Residues 99-	**GGTAPVY**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
			105 of SEQ ID NO.:	
	BEW-6C2-C8 VL			NIQLTQSPSLLSASVGDRVTLSC**KGSQ** **NIANYLA**WYQQKLGEAPKLLIY**NTDSL** **QT**GIPSRFSGSGSGTDYTLTISSLQPE DVATYFC**YQSNNGYT**FGAGTKLELR
	BEW-6C2-C8	CDR-L1	Residues 24-34 of SEQ ID NO.:	**KGSQNIANYLA**
	BEW-6C2-C8	CDR-L2	Residues 50-56 of SEQ ID NO.:	**NTDSLQT**
	BEW-6C2-C8	CDR-L3	Residues 89-96 of SEQ ID NO.:	**YQSNNGYT**
	BEW-8E6-E4 VH			QIQLVQSGPELKKPGESVKISCKAS**GY** **TFTDYAMH**WVKQAPGKVLKWMG**WINTF** **TGKPTYIDDFKG**RFVFSLEASASTANL QISDLKNEDTATYFCAR**GNYYSGYWYF** **DF**WGPGTMVTMSS
	BEW-8E6-E4	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTDYAMH**
	BEW-8E6-E4	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTFTGKPTYIDDFKG**
	BEW-8E6-E4	CDR-H3	Residues 99-110 of SEQ ID NO.:	**GNYYSGYWYFDF**
	BEW-8E6-E4 VL			DIQMTQSPASLSASLGETISIEC**RASE** **DISSNLA**WYQQKSGKSPQLLIF**AANRL** **QD**GVPSRFSGSGSGTQFSLKISGMQPE DEGDYFC**LQGSKFYT**FGAGTKLELK
	BEW-8E6-E4	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASEDISSNLA**
	BEW-8E6-E4	CDR-L2	Residues 50-56 of SEQ ID NO.:	**AANRLQD**
	BEW-8E6-E4	CDR-L3	Residues 89-96 of SEQ ID NO.:	**LQGSKFYT**
	BEW-9A8-E2 VH			QIQLVQSGPELKKPGESVKISCKAS**GY** **TFTNYGMY**WVKQAPGQGLQYMG**WINTE** **TGKPIYADDFKG**RFVFFLETSASTAYL QINNLKNEDMATFFCAR**VDYDGSFWFA** **Y**WGQGTLVTVSS
	BEW-9A8-E2	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	BEW-9A8-E2	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPIYADDFKG**
	BEW-9A8-E2	CDR-H3	Residues 99-109 of SEQ ID NO.:	**VDYDGSFWFAY**
	BEW-9A8-E2 VL			DTVLTQSPALAVSPGERVSISC**RASES** **VSTVIH**WYQQKPGQQPKLLIH**GASNLE** **S**GVPARFSGSGSGTDFTLTIDPVEADD TATYFC**QQHWNDPPT**FGAGTKLEMK
	BEW-9A8-E2	CDR-L1	Residues 23-33 of SEQ ID NO.:	**RASESVSTVIH**
	BEW-9A8-E2	CDR-L2	Residues 49-55	**GASNLES**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
			of SEQ ID NO.:	
	BEW-9A8-E2	CDR-L3	Residues 88-96 of SEQ ID NO.:	**QQHWNDPPT**
	BEW-9C2-D6 VH			QIQLVQSGPELKKPGESVKVSCKAS**GY TFTNYGIH**WVKQAPGQGLQYVG**WINTE TGRPTYADDFKG**RFVFFLETSASTAYL QINNLKNEDMATYFCAR**PLYYGYAHYF DY**WGQGVMVTVSS
	BEW-9C2-D6	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGIH**
	BEW-9C2-D6	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGRPTYADDFKG**
	BEW-9C2-D6	CDR-H3	Residues 99-110 of SEQ ID NO.:	**PLYYGYAHYFDY**
	BEW-9C2-D6 VL			DIQMTQSPASLSASLEEIVTITC**QASQ DIGNWLA**WYQQKPGKSPQLLIY**GATSL AD**GVPSRFSGSRSGTQYSLKISRLQVE DIGIYYC**QQASSVTYT**FGAGTKLELK
	BEW-9C2-D6	CDR-L1	Residues 24-34 of SEQ ID NO.:	**QASQDIGNWLA**
	BEW-9C2-D6	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GATSLAD**
	BEW-9C2-D6	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQASSVTYT**
	BEW-9D2-E8 VH			QIQLVQSGPELKKPGESVKISCKAS**GY TFTNYGMY**WVKLAPGQGLQYLG**WINTE TGKPTYADDFKG**RFVFFLETSASTAYL QINNLRNEDMATYFCAR**PSDYYDGFWF AY**WGQGTLVTVSS
	BEW-9D2-E8	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	BEW-9D2-E8	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPTYADDFKG**
	BEW-9D2-E8	CDR-H3	Residues 99-110 of SEQ ID NO.:	**PSDYYDGFWFAY**
	BEW-9D2-E8 VL			DTVLTQSPALTVSPGERVSISC**RASEW VNSYMH**WYQQNPGQQPKLLIY**KASNLA S**GVPARFSGSGSGTDFTLTLDPVEADD TATYFC**QQSWNDPLT**FGSGTKLEIK
	BEW-9D2-E8	CDR-L1	Residues 23-33 of SEQ ID NO.:	**RASEWVNSYMH**
	BEW-9D2-E8	CDR-L2	Residues 49-55 of SEQ ID NO.:	**KASNLAS**
	BEW-9D2-E8	CDR-L3	Residues 88-96 of SEQ ID NO.:	**QQSWNDPLT**
	BEW-9E10-E7 VH			QIQLLQSGPELKKPGESVKISCKAS**GY TFTNYGMY**WVKQAPGQGLQYMG**WIDTE TGRPTYADDFKG**RFVFFLETSASTAYL QINNLKNEDMATYFCAR**WSGDTTGIRG PWFAY**WGQGTLVTVSS

SEQ ID NO:	Clone	Protein Region	Residues	V Region
	BEW-9E10-E7	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	BEW-9E10-E7	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WIDTETGRPTYADDFKG**
	BEW-9E10-E7	CDR-H3	Residues 99-113 of SEQ ID NO.:	**WSGDTTGIRGPWFAY**
	BEW-9E10-E7 VL			DIRMTQSPASLSASLGETVNIEC**LASE** **DIYSDLA**WYQQKPGRSPQLLIY**NANGL** **QN**GVPSRFGGSGSGTQYSLKINSLQSE DVATYFC**QQYNYFPGT**FGAGTKLELK
	BEW-9E10-E7	CDR-L1	Residues 24-34 of SEQ ID NO.:	**LASEDIYSDLA**
	BEW-9E10-E7	CDR-L2	Residues 50-56 of SEQ ID NO.:	**NANGLQN**
	BEW-9E10-E7	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQYNYFPGT**
	BEW-9E3-B9 VH			QIQLVQSGPELKKPGESVKISCKAS**GY** **TFTNYGMY**WVKQAPGQGLQYMG**WINTE** **TGKPTYADDFKG**RFVFFLETSASTAFL QINNLKNEDMATYFCAR**PSDYYDGFWF** **PY**WGQGALVTVSS
	BEW-9E3-B9	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	BEW-9E3-B9	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPTYADDFKG**
	BEW-9E3-B9	CDR-H3	Residues 99-110 of SEQ ID NO.:	**PSDYYDGFWFPY**
	BEW-9E3-B9 VL			DTILTQSPALAVSPGERISISC**RASEG** **VNSYMH**WYQQNPGQQPKLLIY**KASNLA** **S**GVPARFSGSGSGTDFTLTIDPVEADD TATYFC**QQSWNDPLT**FGSGTKLEIK
	BEW-9E3-B9	CDR-L1	Residues 23-33 of SEQ ID NO.:	**RASEGVNSYMH**
	BEW-9E3-B9	CDR-L2	Residues 49-55 of SEQ ID NO.:	**KASNLAS**
	BEW-9E3-B9	CDR-L3	Residues 88-96 of SEQ ID NO.:	**QQSWNDPLT**
	BEW-9E7-B4 VH			QIQLVQSGPELKKPGESVKISCKAS**GY** **TFTNYGMY**WVKQAPGQGLQYMG**WIDTE** **TGKPTYADDFKG**RFVFFLETSASTAYL QINNLRNEDMATYFCAR**WGYTSDYYYG** **WFPD**WGQGTLVTVST
	BEW-9E7-B4	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	BEW-9E7-B4	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WIDTETGKPTYADDFKG**
	BEW-9E7-B4	CDR-H3	Residues 99-112 of SEQ ID NO.:	**WGYTSDYYYGWFPD**
	BEW-9E7-B4 VL			DTVLTQSPALAVSPGERVSISC**RASEG** **VNSYMH**WYQQNPGQQPKLLIY**KASNLA**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				SGVPARFSGSGSGTDFTLNIHPVEADD TATYFC**QQNWNVPLT**FGSGTKLEIK
	BEW-9E7-B4	CDR-L1	Residues 23-33 of SEQ ID NO.:	**RASEGVNSYMH**
	BEW-9E7-B4	CDR-L2	Residues 49-55 of SEQ ID NO.:	**KASNLAS**
	BEW-9E7-B4	CDR-L3	Residues 88-96 of SEQ ID NO.:	**QQNWNVPLT**

Table 19. VH and VL Amino Acid Sequences of Rat Anti-Human PDGF-BB Monoclonal Antibodies

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				123456789012345678901234 56
	BDI-1E1-D5 VH			EVKLQQSGDELVRPGASVKMSCKAS**GY TFTDYVMH**WVKQSPGQGLEWIG**TIIPL IDTTSYNQKFKG**KATLTADKSSNTAYM ELSRLTSEDSAVYYCAR**TSPYYYSSYD VMDA**WGQGASVTVSS
	BDI-1E1-D5	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTDYVMH**
	BDI-1E1-D5	CDR-H2	Residues 50-66 of SEQ ID NO.:	**TIIPLIDTTSYNQKFKG**
	BDI-1E1-D5	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TSPYYYSSYDVMDA**
	BDI-1E1-D5 VL			NIQLTQSPSLLSASVGDRVTLSC**KGSQ NINNYLA**WYQQKLGEAPKLLIY**KTNNL QT**GIPSRFSGCGSGTDYTLTISSLHSE DLATYYC**YQYDNGYT**FGAGTKLELK
	BDI-1E1-D5	CDR-L1	Residues 24-34 of SEQ ID NO.:	**KGSQNINNYLA**
	BDI-1E1-D5	CDR-L2	Residues 50-56 of SEQ ID NO.:	**KTNNLQT**
	BDI-1E1-D5	CDR-L3	Residues 89-96 of SEQ ID NO.:	**YQYDNGYT**
	BDI-5G2-F9 VH			QVTLKESGPGILQPSQTLSLTCTFS**GF SLSTFGMGVG**WIRQPSGKGLEWLA**NIW WDDDKYYNPSLKN**RLTISKDTSNSQAF LEITNVDTADTATYYCAR**ISTGISSYY VMDA**WGQGASVTVSS
	BDI-5G2-F9	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTFGMGVG**
	BDI-5G2-F9	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	BDI-5G2-F9	CDR-H3	Residues 100-112 of SEQ ID NO.:	**ISTGISSYYVMDA**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
	BDI-5G2-F9 VL			QFTLTQPKSVSGSLRSTITIPC**ERSSG** **DIGDTYVS**WYQQHLGRPPINVIY**GNDQ** **RPS**EVSDRFSGSIDSSSNSASLTITNL QMDDEADYFC**QSYDSDIDIV**FGGGTKL TVL
	BDI-5G2-F9	CDR-L1	Residues 23-35 of SEQ ID NO.:	**ERSSGDIGDTYVS**
	BDI-5G2-F9	CDR-L2	Residues 51-57 of SEQ ID NO.:	**GNDQRPS**
	BDI-5G2-F9	CDR-L3	Residues 92-101 of SEQ ID NO.:	**QSYDSDIDIV**
	BDI-5H1-F6 VH			QVTLKESGPGILQPSQTLSLTCTFS**GF** **SLSTFGMGVG**WIRQPSGKGLEWLA**NIW** **WDDDKYYNPSLKN**RLTISKDTSNSQAF LEITNVDTADTATYYCAR**ISTGISSYY** **VMDA**WGQGASVTVSS
	BDI-5H1-F6	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTFGMGVG**
	BDI-5H1-F6	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	BDI-5H1-F6	CDR-H3	Residues 100-112 of SEQ ID NO.:	**ISTGISSYYVMDA**
	BDI-5H1-F6 VL			QFTLTQPKSVSGSLRSTITIPC**ERSSG** **DIGDTYVS**WYQQHLGRPPINVIY**GNDQ** **RPS**EVSDRFSGSIDSSSNSASLTITNL QMDDEADYFC**QSYDSDIDIV**FGGGTKL TVL
	BDI-5H1-F6	CDR-L1	Residues 23-35 of SEQ ID NO.:	**ERSSGDIGDTYVS**
	BDI-5H1-F6	CDR-L2	Residues 51-57 of SEQ ID NO.:	**GNDQRPS**
	BDI-5H1-F6	CDR-L3	Residues 92-101 of SEQ ID NO.:	**QSYDSDIDIV**
	BDI-6A3-A9 VH			EVQLVESGGGLVQPGRSLKFSCAAS**GF** **SFSDSAMA**WVRQAPKKGLEWVA**TIIYD** **GSGTYYRDSVKG**RFTISRDNAKSTLYL QMDSLRSEDTATYYCAR**LGFNYGNYGY** **YVMDA**WGQGASVTVSS
	BDI-6A3-A9	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GFSFSDSAMA**
	BDI-6A3-A9	CDR-H2	Residues 50-66 of SEQ ID NO.:	**TIIYDGSGTYYRDSVKG**
	BDI-6A3-A9	CDR-H3	Residues 99-113 of SEQ ID NO.:	**LGFNYGNYGYYVMDA**
	BDI-6A3-A9 VL			QFTLTQPKSVSGSLRNTITIPC**ERSSG** **DIGDSYVS**WYQQHLGRPPINVIF**ADDQ**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				RPSEVSDRFSGSIDSSSNSASLTITNL QMDDEADYFC**QSYDSNIDINIV**FGGGT KLTVL
	BDI-6A3-A9	CDR-L1	Residues 23-35 of SEQ ID NO.:	**ERSSGDIGDSYVS**
	BDI-6A3-A9	CDR-L2	Residues 51-57 of SEQ ID NO.:	**ADDQRPS**
	BDI-6A3-A9	CDR-L3	Residues 92-103 of SEQ ID NO.:	**QSYDSNIDINIV**
	BDI-7H10-D8 VH			EVKLQQSGDELVRPGASVKMSCKAS**GY TFTDYAMH**WVKQSPGQGLEWIG**TIIPL IDTTSYNQKFKG**KATLTADTSSNTAYM ELSRLTSEDSAVYYCAR**DWDNNWGYFD Y**WGQGVMVTVSS
	BDI-7H10-D8	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTDYAMH**
	BDI-7H10-D8	CDR-H2	Residues 50-66 of SEQ ID NO.:	**TIIPLIDTTSYNQKFKG**
	BDI-7H10-D8	CDR-H3	Residues 99-109 of SEQ ID NO.:	**DWDNNWGYFDY**
	BDI-7H10-D8 VL			DVVLTQTPVSLSVTLGDQASISC**RSSQ SLEYSDGYTYLE**WYLQKPGQSPQLLIY **GVSNRFS**GVPDRFIGSGSGTDFTLKIS RVEPEDLGVYYC**FQATHDPLT**FGSGTK LEIK
	BDI-7H10-D8	CDR-L1	Residues 24-39 of SEQ ID NO.:	**RSSQSLEYSDGYTYLE**
	BDI-7H10-D8	CDR-L2	Residues 55-61 of SEQ ID NO.:	**GVSNRFS**
	BDI-7H10-D8	CDR-L3	Residues 94-102 of SEQ ID NO.:	**FQATHDPLT**
	BDI-9E8-E7 VH			QVTLKESGPGILQPSQTLSLTCTFS**GF SLSTYGMGVG**WIRQPSGKGLEWLA**NIW WDDDKYYNPSLKN**RLTISKDTSNNQAF LKITNVDTADTATYYCAR**IESIGTTYS FDY**WGQGVMVTVSS
	BDI-9E8-E7	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTYGMGVG**
	BDI-9E8-E7	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	BDI-9E8-E7	CDR-H3	Residues 100-111 of SEQ ID NO.:	**IESIGTTYSFDY**
	BDI-9E8-E7 VL			QFTLTQPKSVSGSLRSTITIPC**ERSSG DIGDSYVS**WYQQHLGRPPINVIY**ADDQ RPS**EVSDRFSGSIDSSSNSASLTITNL QMDDEADYFC**QSYDINIDIV**FGGGTKL

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				TVL
	BDI-9E8-E7	CDR-L1	Residues 23-35 of SEQ ID NO.:	**ERSSGDIGDSYVS**
	BDI-9E8-E7	CDR-L2	Residues 51-57 of SEQ ID NO.:	**ADDQRPS**
	BDI-9E8-E7	CDR-L3	Residues 92-101 of SEQ ID NO.:	**QSYDINIDIV**
	BFU-11A8-D6-C3 VH			EVQLQQSGPELQRPGASVKLSCKAS**GY TFTESYIY**WVKQRPEQSLELIG**RIDPE DGSTDYVEKFKN**KATLTADTSSNTAYM QLSSLTSEDTATYFCAR**FGARSYFYPM DA**WGQGTSVTVSS
	BFU-11A8-D6-C3	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTESYIY**
	BFU-11A8-D6-C3	CDR-H2	Residues 50-66 of SEQ ID NO.:	**RIDPEDGSTDYVEKFKN**
	BFU-11A8-D6-C3	CDR-H3	Residues 99-110 of SEQ ID NO.:	**FGARSYFYPMDA**
	BFU-11A8-D6-C3 VL			DTVLTQSPTLAVSPGERVSIPC**RASES VSTLMH**WYQQKPGQQPRLLIY**GASNLE S**GVPARFSGSGSGTDFTLTIDPVEADD TATYFC**QQSWNDPWT**FGGGTKLELK
	BFU-11A8-D6-C3	CDR-L1	Residues 23-33 of SEQ ID NO.:	**RASESVSTLMH**
	BFU-11A8-D6-C3	CDR-L2	Residues 49-55 of SEQ ID NO.:	**GASNLES**
	BFU-11A8-D6-C3	CDR-L3	Residues 88-96 of SEQ ID NO.:	**QQSWNDPWT**
	BFU-3E2-B9-B8 VH			EVQLQQSGPELQRPGASVKLSCKAS**GY TFTESYMY**WVKQRPEQSLELIG**RIDPE DGSTDYVEKFKN**KATLTADTSSNTAYM QLSSLTSEDSATYFCAR**FGARSYFYPM DA**WGQGTSVTVSS
	BFU-3E2-B9-B8	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTESYMY**
	BFU-3E2-B9-B8	CDR-H2	Residues 50-66 of SEQ ID NO.:	**RIDPEDGSTDYVEKFKN**
	BFU-3E2-B9-B8	CDR-H3	Residues 99-110 of SEQ ID NO.:	**FGARSYFYPMDA**
	BFU-3E2-B9-B8 VL			DTVLTQPPALAVSPGERVSISC**RASES VSTLMH**WYQQKPGQQPRLLIY**GASNLE S**GVPARFSGSGSGTDFTLTIDPVEADD TATYFC**QQSWNDPWT**FGGGTKLELK
	BFU-3E2-B9-B8	CDR-L1	Residues 23-33 of SEQ ID NO.:	**RASESVSTLMH**
	BFU-3E2-B9-B8	CDR-L2	Residues 49-55 of SEQ ID NO.:	**GASNLES**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
	BFU-3E2-B9-B8	CDR-L3	Residues 88-96 of SEQ ID NO.:	**QQSWNDPWT**

Table 20. VH and VL Amino Acid Sequences of Rat Anti-Human VEGFR II Monoclonal Antibodies

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				123456789012345678901234 56
	BCU-3D6-C9 VH			QIQLVQSGPELKKPGESVKISCKAS**EY TFTDYAIH**WVKQAPGKGLKWMG**WINTY TGKPTYADDFKG**RFVFSLEASASTANL QISNLKNEDTATYFCAR**DYGGYGERRD YFDY**WGQGVMVTVSS
	BCU-3D6-C9	CDR-H1	Residues 26-35 of SEQ ID NO.:	**EYTFTDYAIH**
	BCU-3D6-C9	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTYTGKPTYADDFKG**
	BCU-3D6-C9	CDR-H3	Residues 99-112 of SEQ ID NO.:	**DYGGYGERRDYFDY**
	BCU-3D6-C9 VL			DIQMTQSPASLSASLGETVTIEC**RVSE DIYNGLA**WYQQKPGKSPQFLIY**NANRL HT**GVPSRFSGSGSGTQFSLKINSLQSE DVANYFC**QQYYDYPLT**FGSATKLEIK
	BCU-3D6-C9	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RVSEDIYNGLA**
	BCU-3D6-C9	CDR-L2	Residues 50-56 of SEQ ID NO.:	**NANRLHT**
	BCU-3D6-C9	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQYYDYPLT**
	BCU-6B1-G6 VH			QIQLVQSGPELKKPGESVKISCKAS**GY TFTNYGMY**WVKQAPGQALQFMG**WINTE TGQPTYADDFKG**RFVFFLETSASTAYL QINNLKNEDMATYFCAR**LGNNYGIWFA Y**WGQGTLVTVSS
	BCU-6B1-G6	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	BCU-6B1-G6	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGQPTYADDFKG**
	BCU-6B1-G6	CDR-H3	Residues 99-109 of SEQ ID NO.:	**LGNNYGIWFAY**
	BCU-6B1-G6 VL			DIQMTQSPASLSASLGETVTIEC**RASD DLYSTLA**WYQQKPGDSPQLLIF**DANRL AA**GVPSRFSGSGSGTQYSLKINSLQSE DVASYFC**QQYNKFPWT**FGGGTKLELK
	BCU-6B1-G6	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASDDLYSTLA**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
	BCU-6B1-G6	CDR-L2	Residues 50-56 of SEQ ID NO.:	**DANRLAA**
	BCU-6B1-G6	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQYNKFPWT**
	BCU-7A6-C2 VH			EVQLVESGGGLVQPRGSLKLSCAAS**GF DFNSYGMS**WVRQAPGKGLDLVA**DISSK SYNYATYYADSVKD**RFTISRDDSQSMV YLQMDNLKTEDTALYYCTE**SLELGGAY** WGQGTLVTVSS
	BCU-7A6-C2	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GFDFNSYGMS**
	BCU-7A6-C2	CDR-H2	Residues 50-68 of SEQ ID NO.:	**DISSKSYNYATYYADSVKD**
	BCU-7A6-C2	CDR-H3	Residues 101-108 of SEQ ID NO.:	**SLELGGAY**
	BCU-7A6-C2 VL			DIQMTQSPPSLSASLGDEVTITC**QASQ NINKFIA**WYQQKPGKAPRLLIR**YTSTL KS**GTPSRFSGSGSGRDYSFSISNVESE DIASYYC**LQYDSLPWT**FGGGTKLELK
	BCU-7A6-C2	CDR-L1	Residues 24-34 of SEQ ID NO.:	**QASQNINKFIA**
	BCU-7A6-C2	CDR-L2	Residues 50-56 of SEQ ID NO.:	**YTSTLKS**
	BCU-7A6-C2	CDR-L3	Residues 89-97 of SEQ ID NO.:	**LQYDSLPWT**

Table 21. VH and VL Amino Acid Sequences of Rat Anti-Human PDGFR-B Monoclonal Antibodies

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				123456789012345678901234 56
	BDE-3C9-G4 VH			EVQLVESGGGLVQPGRSLKLSCAAS**G FTFSNYGMA**WVRQAPTQGLEWVA**SIT NSGGNTYYRDSVKG**RFTISRDSAKNT QYLQMDSLRSEDTATYFCAR**HTPGAN YFDY**WGQGLMVTVSS
	BDE-3C9-G4	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GFTFSNYGMA**
	BDE-3C9-G4	CDR-H2	Residues 50-66 of SEQ ID NO.:	**SITNSGGNTYYRDSVKG**
	BDE-3C9-G4	CDR-H3	Residues 99-108 of SEQ ID NO.:	**HTPGANYFDY**
	BDE-3C9-G4 VL			DIQMTQSPPSLSASLGEKVTITC**QAS QSIKNYIA**WYQLKPGTAPRLLMR**YTS TLES**GTPSRFSGSGSGRDYSFSISNV ESEDIASYYC**VQYANLYT**FGGGTKLE LK

SEQ ID NO:	Clone	Protein Region	Residues	V Region
	BDE-3C9-G4	CDR-L1	Residues 24-34 of SEQ ID NO.:	**QASQSIKNYIA**
	BDE-3C9-G4	CDR-L2	Residues 50-56 of SEQ ID NO.:	**YTSTLES**
	BDE-3C9-G4	CDR-L3	Residues 89-96 of SEQ ID NO.:	**VQYANLYT**
	BDE-4F2-D4 VH			QVQLKESGPGLMQPSQTLSLTCTVS**G** **FSLTNYGVS**WVRQFPGKGLEWIA**AIS** **SGGSTYYNSALKS**RLSISRDTSRSQV FLKMNSLLTEDTAFYFCTR**VYYGSNY** **FDY**WGPGVMVTVSS
	BDE-4F2-D4	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GFSLTNYGVS**
	BDE-4F2-D4	CDR-H2	Residues 50-65 of SEQ ID NO.:	**AISSGGSTYYNSALKS**
	BDE-4F2-D4	CDR-H3	Residues 98-107 of SEQ ID NO.:	**VYYGSNYFDY**
	BDE-4F2-D4 VL			DIVMTQTPSSQAVSAGEKVTMSC**KSS** **QSLLYGGDQKNFLA**WYQQKPGQSPKL LIY**LASTRES**GVPDRFIGSGSGTDFT LTISSVQAEDLADYYC**QQHYGYPFT**F GSGTKLEIK
	BDE-4F2-D4	CDR-L1	Residues 24-40 of SEQ ID NO.:	**KSSQSLLYGGDQKNFLA**
	BDE-4F2-D4	CDR-L2	Residues 56-62 of SEQ ID NO.:	**LASTRES**
	BDE-4F2-D4	CDR-L3	Residues 95-103 of SEQ ID NO.:	**QQHYGYPFT**
	BDE-8H6-F7 VH			EVQLVESGGGLVQPGSSLKLSCLAS**G** **FTFSNYNMY**WIRQAPKKGLEWIA**LIF** **YDNNNKYYADSVKG**RFTISRDNSKNT LYLEMNSLRSEDTAMYYCLR**DSGPFS** **Y**WGQGTLVTVSS
	BDE-8H6-F7	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GFTFSNYNMY**
	BDE-8H6-F7	CDR-H2	Residues 50-66 of SEQ ID NO.:	**LIFYDNNNKYYADSVKG**
	BDE-8H6-F7	CDR-H3	Residues 99-105 of SEQ ID NO.:	**DSGPFSY**
	BDE-8H6-F7 VL			DIQMTQSPPSLSASLGDKVTINC**QAG** **QNIKKYIA**WYQQEPGKVPRLLIR**YTS** **KLES**DTPSRFSGSGSGRDYSFSISNV ESEDIASYYC**LQYDNLPWT**FGGGTKL ELK
	BDE-8H6-F7	CDR-L1	Residues 24-34 of SEQ ID NO.:	**QAGQNIKKYIA**
	BDE-8H6-F7	CDR-L2	Residues 50-56 of SEQ ID NO.:	**YTSKLES**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
	BDE-8H6-F7	CDR-L3	Residues 89-97 of SEQ ID NO.:	LQYDNLPWT

Example 5: Generation of Chimeric Antibodies

[0247] The variable domains of the heavy and light chain of the rat mAbs were cloned in-frame to mutant human IgG1 (L234, 235A) heavy-chain and kappa light-chain constant regions, respectively. The activities of the resulting chimeric antibodies were confirmed in ELISA-based binding and competition assays or Biacore binding assay, and were comparable to their parental rat mAbs.

[0248] Chimeric anti-VEGF-A antibodies were characterized for binding, function and cross-reactivity in a panel of assays. Potency for all chimeric molecules was characterized in the $hVEGF_{165}$ -induced cell proliferation assay (Example 1.7). Binding affinity of these molecules to $hVEGF_{165}$ was measured by Biacore analysis (Example 1.1). Select chimeric molecules were tested for the ability to block binding of $hVEGF_{165}$ to hVEGF-R2 in a competition ELISA format (Example 1.4) and a $hVEGF_{111}$ Tyr1054 phosphorylation assay (Example 1.6). Candidate molecules were then examined for potency in the HMVEC-d $hVEGF_{165}$-induced proliferation assay (Example 1.10) and species cross-reactivity in the $rabVEGF_{165}$ -induced cell proliferation assay (Example 1.9). The data is summarized in Tables 22 and 23 below.

Table 22. Characterization of Chimeric Anti-Human VEGF-A Monoclonal Antibodies

Chimeric Clones	ELISA huVEGF-A_{165} Binding	Receptor Competition ELISA huVEGF-A_{165} /huVEGFR2 (nM)	Phospho-Tyr1054/ huVEGF-A_{111} Neutralization (nM)	huVEGF-A_{165} Neutralization Potency in hVEGFR2 Overexpressing Cells (nM)	rabbitVEGF-A_{165} Neutralization Potency in hVEGFR2 Overexpressing Cells (nM)	huVEGF-A_{165} Neutralization Potency in HMVEC-d cells (nM)
chBEW-1B4	NT	NT	NT	1.428	NT	NT
chBEW-1B4 half-body	NT	NT	NT	1.669	NT	NT
chBEW-1E3	NT	NT	NT	0.657	NT	NT
chBEW-1E3 half-body	NT	NT	NT	3.752	NT	NT
chBEW-5C3	NT	NT	NT	0.244	NT	NT
chBEW-5C3 half-body	NT	NT	NT	2.264	NT	NT
chBEW-6C2	NT	0.148	0.435	>10	0.58	0.031
chBEW-6C2 half-body	NT	NT	NT	>10	NT	NT
chBEW-8E6	NT	NT	NT	0.499	NT	NT
chBEW-8E6 half-body	NT	NT	NT	>10	NT	NT
chBEW-9A8	NT	0.097	0.260	0.416	0.510	0.026
chBEW-9A82 half-body	NT	NT	NT	1.584	NT	NT

chBEW-9E10	NT	NT	NT	0.448	NT	NT
chBEW-9E10 half-body	NT	NT	NT	0.598	NT	NT
chBEW-10H2	NT	NT	NT	0.912	NT	NT
chBEW-10H2-B9 half-body	NT	NT	NT	2.562	NT	NT
chBEW-9C2	NT	NT	NT	2.090	NT	NT
chBEW-9C2 half-body	NT	NT	NT	2.740	NT	NT
chBEW-9D2	NT	NT	NT	1.556	0.740	2.150
chBEW-9D2 half-body	NT	NT	NT	>10	NT	NT
chBEW-1B10	NT	NT	NT	0.377	NT	NT
chBEW-3A1	NT	NT	NT	0.680	NT	NT
chBEW-3A1 half-body	NT	NT	NT	>10	NT	NT
chBDB-4G8	NT	0.157	0.575	0.687	NT	0.195
chBEW-1C6 half-body	NT	NT	NT	3.595	NT	NT

NT – Not tested

Table 23. Biacore Binding of Rat and Rat-Human Chimera Anti-VEGF

Antibody	k_{on} (M-1 s-1)	k_{off} (M-1)	K_D (M)
chBDB-4G8	1.7 E+07	2.4 E-05	1.9 E-12
chBDB-4G8	1.2 E+07	4.7 E-05	3.8 E-12
chBED-4G10-C8	1.0 E+07	5.9 E-03	5.9 E-10
chBEW-1B4-C4	1.1 E+07	1.2 E-04	1.1 E-11
chBEW-1B10-B9-C3	5.5 E+06	5.2 E-05	9.4 E-12
chBEW-1E3-D6	7.2 E+06	8.0 E-05	1.1 E-11
chBEW-3A1-D10-G9	3.5 E+07	8.0 E-04	2.3 E-11
chBEW-5C3-E7	6.8 E+06	8.2 E-05	1.2 E-11
chBEW-6C2	4.9 E+06	4.3 E-05	8.8 E-12
chBEW-8E6-E4	6.2 E+06	1.0 E-04	1.6 E-11
chBEW-9A8	8.9 E+06	≤1.0 E-06	≤1.1 E-13
chBEW-10H2-B9	2.8 E+07	3.5 E-04	1.3 E-11

[0249] Chimeric anti-PDGF-BB antibodies were characterized for binding, function and cross-reactivity in a panel of assays. The chimeric molecules were first tested for the ability to bind hPDGF-BB in a direct binding ELISA (Example 1.12). Binding affinity of these molecules to hPDGF-BB was then measured by Biacore analysis (Example 1.1). Functional characterization of these molecules included testing of the ability to block binding of hPDGF-BB to hPDGF-Rβ in a competition ELISA format (Example 1.13) and an hPDGFRβ Tyr751 phosphorylation assay (Example 1.14). Potency was further characterized in the hPDGF-BB - induced cell proliferation assay (Example 1.15). Candidate molecules were advanced and cross-reactivity was determined for mouse and rat/rabbit PDGF-BB in the cell-based proliferation assay (Examples 1.17-1.18). The data is summarized in Tables 24 and 25 below.

Table 24. Characterization of Chimeric Anti-Human PDGF-BB Monoclonal Antibodies

Chimeric Molecule	ELISA huPDGF-BB Binding	Receptor Competition ELISA huPDGF-BB /huPDGFR	Phospho-Tyr751/hPDGF-BB Neutralization (nM)	huPDGF-BB Neutralization Potency (nM) in NIH-3T3 Cells	ratPDGF-BB Neutralization Potency (nM) in NIH-3T3 Cells B (nM)	mPDGF-BB Neutralization Potency (nM) in NIH-3T3 Cells
chBDI-9E8	0.38	0.791	0.388	0.058	0.075	0.08
chBDI-9E8 half-body	NT	NT	NT	1.84	NT	NT
chBDI-5H1	0.12	1.039	1.602	0.275	0.17	NT
chBDI-5H1 half-body	NT	NT	NT	>10	NT	NT
chBDI-7H10	>10	10.1	2.476	>10	NT	NT
chBDI-5G2	NT	1.08	NT	0.181	0.118	NT
chBDI-1E1	NT	0.417	NT	>5	NT	NT
chBDI-1E1 half body	NT	NT	NT	>10	NT	NT
chBDI-8B8	NT	0.179	NT	>10	NT	NT
chBFU-3E2	NT	NT	NT	0.099	NT	NT
chBFU-3E2 half-body	NT	NT	NT	2.494	NT	NT
chBFU-11A8	NT	NT	NT	0.086	NT	NT
chBFU-11A8 half-body	NT	NT	NT	>10	NT	NT

NT – Not tested

Table 25. Biacore Binding Of Rat And Rat-Human Chimera Anti-PDGF

Antibody	k_{on} (M-1 s-1)	k_{off} (M-1)	K_D (M)
BFU-11A8-D6-C3	2.1 E+07	≤ 1.0 E-06	≤ 4.7 E-14
chBDI-5H1	≥ 1.0 E+07	1.5 E-04	≤ 1.5 E-11
chBDI-9E8	≥ 1.0 E+07	1.2 E-04	≤ 1.2 E-11
chBFU-3E2-B9-B8	≥ 1.0 E+07	1.9 E-04	≤ 1.9 E-11
chBFU-11A8-D6-C3	≥ 1.0 E+07	1.5 E-04	≤ 1.5 E-11

[0250] Chimeric anti-VEGFR2 antibodies were tested for the ability to block binding of VEGFR2 to $hVEGF_{165}$ in a competition ELISA format, as described in Example 1.22. The data is summarized in Table 26.

Table 26. Characterization of Chimeric Anti-Human VEGFR II Monoclonal Antibodies

Chimeric Molecules	$hVEGF_{165}$/ hVEGFR2-Fc Competition
chBCU-6B1-G6	0.498
chBCU-7A6-C2	NT

Example 6: Humanization of Rat Monoclonal Antibodies

[0251] Below are the humanization designs for the rat monoclonal antibodies, followed by summaries of amino acid sequences and characterization of selected humanized antibodies.

Example 6.1: Humanization of PDGF-BB Antibodies

Example 6.1.1: Humanization Method

[0252] Antibody humanization is achieved by grafting CDRs of the rodent antibody onto a "similar" human framework (acceptor) and incorporating minimal number of key framework residues (back-mutation) from the rodent antibody that are selected to maintain the original CDR conformation in order to minimize the immunogenicity while retaining the optimal antigen binding.

Example 6.1.2: Human Germline Sequence Selections For Constructing CDR-Grafted, Humanized PDGF Antibodies

[0253] By applying the aforementioned method, the CDR sequences of VH and VL chains of monoclonal antibodies BDI-5H1-F6, BDI-9E8-E7, BDI-7H10-D8, BDI-1E1-D5, BDI-6A3-A9, BFU-3E2 and BFU-11A8 were grafted onto different human heavy and light chain acceptor sequences.

Example 6.1.2.1: BDI-5H1-F6

[0254] Based on the alignments with the VH and VL sequences of monoclonal antibody BDI-5H1-F6 of the present invention, the following known human sequences are selected:

1. IGHV2-70*01 and IGHJ6*01 for constructing heavy chain acceptor sequences
2. IGHV2-70*04 and IGHJ6*01 as alternative acceptor sequence for constructing heavy chain
3. IGHV3-66*01 and IGHJ1 *01as alternative acceptor sequence for constructing heavy chain
4. IGLV6-57*01 and IGJL2*01 for constructing light chain acceptor sequences

5. IGKV3-20*01 and IGJK4*01 as alternative acceptor sequences for constructing light chain
6. IGKV4-1*01 and IGJK4*01 as alternative acceptor sequences for constructing light chain
7. IGKV1-39*01 and IGJK1*01 as alternative acceptor sequences for constructing light chain

[0255] By grafting the corresponding VH and VL CDRs of BDI-5H1-F6 into said acceptor sequences, the CDR-grafted, humanized, and modified VH and VL sequences were prepared.

Example 6.1.2.2: BDI-9E8-E7

[0256] Based on the alignments with the VH and VL sequences of monoclonal antibody BDI-9E8-E7 of the present invention, the following known human sequences are selected:

1. IGHV2-70*01 and IGHJ3*01 for constructing heavy chain acceptor sequences
2. IGHV2-70*04 and IGHJ6*01 as alternative acceptor sequence for constructing heavy chain
3. IGHV3-66*01 and IGHJ1 *01as alternative acceptor sequence for constructing heavy chain
4. IGLV6-57*01 and IGJL2*01 for constructing light chain acceptor sequences
5. IGKV3-20*01 and IGJK4*01 as alternative acceptor for constructing light chain sequences
6. IGKV4-1*01 and IGJK4*01 as alternative acceptor sequences for constructing light chain
7. IGKV1-39*01 and IGJK1*01 as alternative acceptor sequences for constructing light chain

[0257] By grafting the corresponding VH and VL CDRs of BDI-9E8-E7 into said acceptor sequences, the CDR-grafted, humanized, and modified VH and VL sequences were prepared.

Example 6.1.2.3: BDI-7H10-D8

[0258] Based on the alignments with the VH and VL sequences of monoclonal antibody BDI-7H10-D8 of the present invention, the following known human sequences are selected:

1. IGHV1-69*01 and IGHJ3*01 for constructing heavy chain acceptor sequences

2. IGKV2-29*02 and IGK2*01 for constructing light chain acceptor sequences

[0259] By grafting the corresponding VH and VL CDRs of BDI-7H10-D8 into said acceptor sequences, the CDR-grafted, humanized, and modified VH and VL sequences were prepared.

Example 6.1.2.4: BDI-1E1-D5

[0260] Based on the alignments with the VH and VL sequences of monoclonal antibody BDI-1E1-D5 of the present invention the following known human sequences are selected:

1. IGHV1-69*06 and IGHJ6*01 for constructing heavy chain acceptor sequences
2. IGKV1D-13*01 and IGKJ2*01 for constructing light chain acceptor sequences
3. IGKV3-11*01 and IGKJ2*01 as alternative acceptor sequence for constructing light chain

[0261] By grafting the corresponding VH and VL CDRs of BDI-1E1-D5 into said acceptor sequences, the CDR-grafted, humanized, and modified VH and VL sequences were prepared.

Example 6.1.2.5: BDI-6A3-A9

[0262] Based on the alignments with the VH and VL sequences of monoclonal antibody BDI-6A3-A9 of the present invention the following known human sequences are selected:

1. IGHV3-7*01 and IGHJ6*01 for constructing heavy chain acceptor sequences
2. IGHV1-3*01 and IGHJ6*01 as alternative acceptor sequence for constructing heavy chain
3. IGLV6-57*01 and IGJL2*01 for constructing light chain acceptor sequences

[0263] By grafting the corresponding VH and VL CDRs of BDI-6A3-A9 into said acceptor sequences, the CDR-grafted, humanized, and modified VH and VL sequences were prepared.

Example 6.1.2.6: BFU-3E2

[0264] Based on the alignments with the VH and VL sequences of monoclonal antibody BFU-3E2 of the present invention, the following known human sequences are selected:

1. IGHV1-69*01 and IGHJ6*01 for constructing heavy chain acceptor sequences
2. IGKV3-11*01 and IGKJ4*01 for constructing light chain acceptor sequences

3. IGKV1-13*01 and IGKJ4*01 as alternative acceptor sequence for constructing light chain

[0265] By grafting the corresponding VH and VL CDRs of BFU-3E2 into said acceptor sequences, the CDR-grafted, humanized, and modified VH and VL sequences were prepared.

Example 6.1.2.7: BFU-11A8

[0266] Based on the alignments with the VH and VL sequences of monoclonal antibody BFU-11A8 of the present invention, the following known human sequences are selected:

1. IGHV1-69*01 and IGHJ6*01 for constructing heavy chain acceptor sequences
2. IGKV3-11*01 and IGKJ4*01 for constructing light chain acceptor sequences
3. IGKV1-5*01 and IGKJ4*01 as alternative acceptor sequence for constructing light chain

[0267] By grafting the corresponding VH and VL CDRs of BFU-11A8 into said acceptor sequences, the CDR-grafted, humanized, and modified VH and VL sequences were prepared.

Example 6.1.3: Introducing Potential Framework Back-Mutations In CDR-Grafted Antibodies

[0268] To generate humanized antibody with potential framework back-mutations, the mutations were identified and introduced into the CDR-grafted antibody sequences by *de novo* synthesis of the variable domain, or mutagenic oligonucleotide primers and polymerase chain reactions, or by methods well known in the art. Different combinations of back mutations and other mutations are constructed for each of the CDR-grafts as follows. Residue numbers for these mutations are based on the Kabat numbering system.

BDI-5H1-F6

[0269] When IGHV2-70*01 and IGHJ6*01 selected as BDI-5H1-F6 heavy chain acceptor sequences, one or more of the following residues could be back-mutated as follows: Q1→E, A44→G, K75→N, V78→A, M82→I with or without N65→T (CDR change).

[0270] When IGHV2-70*04 and IGHJ6*01 selected as BDI-5H1-F6 heavy chain acceptor sequences, one or more of the following residues could be back-mutated as follows: Q→1E, K5→R, K75→N, N76→S, V78→A and M82→I.

[0271] When IGHV3-66*01 and IGHJ1*01 selected as BDI-5H1-F6 heavy chain acceptor sequences, one or more of the following residues could be back-mutated as follows: A24→F, V37→I, V48→L, S49→A, F67→L, R71→K, N73→T, T77→Q, L78→A, and M82→I.

[0272] When IGLV6-57*01 and IGJL2*01 selected as BDI-5H1-F6 light chain acceptor sequences, one or more of the following residues could be back-mutated as follows: N1→Q, S22→P, S43→P, T46→N, G57→E, P59→S, and Y87→F.

[0273] When IGKV3-20*01 and IGJK4*01 selected as BDI-5H1-F6 light chain acceptor sequences, one or more of the following residues could be back-mutated as follows: I2→F, A43→P, L46→N, L47→V, I58→V, G66→I, G68→S, T69→N, F71→A, Y87→F and with or without two residues insertion D66a, S66b and deletion of T10.

[0274] When IGKV4-1*01 and IGJK4*01 selected as BDI-5H1-F6 light chain acceptor sequences, one or more of the following residues could be back-mutated as follows: I2→F, M4→L, L46→N, L47→V, T69→N, D70→S, F71→A, Y87→F.

[0275] When IGKV1-39*01 and IGJK1*01 selected as BDI-5H1-F6 light chain acceptor sequences, one or more of the following residues could be back-mutated as follows: I2→F, M4→L, L46→N, L47→V, T69→N, D70→S, F71→A, and Y87→F.

BDI-9E8-E7

[0276] When IGHV2-70*01 and IGHJ6*01 selected as BDI-9E8-E7 heavy chain acceptor sequences, one or more of following residues could be back-mutated as follows: Q1→E, A44→G, V78→A M82→I with or without N65→T (CDR change).

[0277] When IGHV2-70*04 and IGHJ6*01 selected as BDI-9E8-E7 heavy chain acceptor sequences, one or more of the following residues could be back-mutated as follows: Q1→E, K5→R, V78→A, and M82→I.

[0278] When IGHV3-66*01 and IGHJ1*01 selected as BDI-9E8-E7 heavy chain acceptor sequences, one or more of the following residues could be back-mutated as follows: A24→F, V37→I, V48→L, S49→A, F67→L, R71→K, N73→T, T77→Q, L78→A, and M82→I.

[0279] When IGLV6-57*01 and IGJL2*01 selected as BDI-9E8-E7 light chain acceptor sequences, one or more of the following residues could be back-mutated as follows: S43→P, T46→N and Y87→F.

[0280] When IGKV3-20*01 and IGJK4*01 selected as BDI-9E8-E7 light chain acceptor sequences, one or more of the following residues could be back-mutated as follows: I2→F, A43→P, L46→N, L47→V, I58→V, G66→I, T69→N, F71→A, Y87→F and W/WO two residues insertion (D66a, S66b) and deletion of T10.

[0281] When IGKV4-1*01 and IGJK4*01 selected as BDI-9E8-E7 light chain acceptor sequences, one or more of the following residues could be back mutated as follows: I2→F, M4→L, L46→N, L47→V, T69→N, D70→S, F71→A, T72→S, and Y87→F.

[0282] When IGKV1-39*01 and IGJK1*01 selected as BDI-9E8-E7 light chain acceptor sequences, one or more of the following residues could be back mutated as follows: I2→F, M4→L, L46→N, L47→V, T69→N, D70→S, F71→A, and T72→S.

BDI-7H10-D8

[0283] When IGHV1-69*01and IGHJ3*01 selected as BDI-7H10-D8 heavy chain acceptor sequences, one or more of following residues could be back-mutated as follows: Q1→E, M48→I, V67→A, I69→L, E73→T, S76→N, with or without CDR changes Y27→G and T30→S.

[0284] When IGKV2-29*02 and IGKJ2*01 selected as BDI-7H10-D8 light chain acceptor sequences, one or more of following residues could be back-mutated as follows: I2→V and M4→L.

BDI-1E1-D5

[0285] When IGHV1-69*06 and IGHJ6*01 selected as BDI-1E1-D5 heavy chain acceptor sequence, one or more of the following residues could be back-mutated as follows: Q1→E M48→I, V67→A, I69→L and S76→N.

[0286] When IGKV1D-13*01 and IGKJ2*01 selected as BDI-1E1-D5 light chain acceptor sequences, one or more of the following residues could be back-mutated as follows: V58→I and F71→Y.

[0287] When IGKV3-11*01 and IGKJ2*01 selected as BDI-1E1-D5 light chain acceptor sequences, one or more of the following residues could be back-mutated as follows: F71→Y and V85→T.

BDI-6A3-A9

[0288] When IGHV3-7*01 and IGHJ6*01 selected as BDI-6A3-A9 heavy chain acceptor sequences, one or more of the following residues could be back-mutated as follows: S28→T, R60→V, N76→S.

[0289] When IGHV1-3*01 and IGHJ6*01 selected as BDI-6A3-A9 heavy chains acceptor sequences, one or more of following residues could be back-mutated as follows: Q1→E, R44→G, M48→V, G49→A, V67→F, T73→N, A78→L and M80→L.

[0290] When IGLV6-57*01 and IGJL2*01 selected as BDI-6A3-A9 light chain acceptor sequences, one or more of the following residues could be back-mutated as follows: S43→P, T46→N, Y49→F and Y87→F.

BFU-3E2

[0291] When IGHV1-69*01 and IGHJ6*01 selected as BFU-3E2 heavy chain acceptor sequences, one or more of the following residues could be back-mutated as follows: R38-->K, G44-->S, W47-->L, M48-->I, R66-->K, V67-->A, I69-->L, S76-->N, Y91-->F.

[0292] When IGKV3-11*01 and IGKJ4*01 selected as BFU-3E2 light chain acceptor sequences, one or more of the following could be back-mutated as follows: I2-->T, A43-->Q, I58-->V, Y87-->F.

[0293] When IGKV1-13*01 and IGKJ4*01 selected as BFU-3E2 light chain acceptor sequences, one or more of the following residues could be back-mutated as follows: I2-->T, T22-->S, A43-->Q, K45-->R, Y87-->F.

BFU-11A8

[0294] When IGHV1-69*01 and IGHJ6*01 selected as BFU-11A8 heavy chain acceptor sequences, one or more of the following residues could be back-mutated as follows: R38-->K,W47-->L, M48-->I, R66-->K, V67-->A, I69-->L, S76-->N, and Y91-->F.

[0295] When IGKV3-11*01 and IGKJ4*01 selected as BFU-11A8 light chain acceptor sequences, one or more of the following residues could be back-mutated as follows: I2-->T, S22-->P, A43-->Q, I58-->V, Y87-->F.

[0296] When IGKV1-5*01 and IGKJ4*01 selected as BFU-11A8 light chain acceptor sequences, one or more of the following residues could be back-mutated as follows: I2-->T, M4-->L, T22-->P, A43-->Q, Y87-->F.

Example 6.1.4: Generation of Humanized Antibodies To PDGF Containing Framework Back-Mutations In CDR-Grafted Antibodies

[0297] The following humanized variable regions of the murine monoclonal PDGF antibodies were cloned into IgG expression vectors for functional characterization.

Example 6.1.4.1: BDI-5H1-F6

Table 1.4.1. Sequences of Humanized BDI-5H1-F6 Variable Regions

	Protein region	Sequence
		123456789**0**123456789**0**123456789**0**
	hBDI-5H1-F6VH.1z	QVTLRESGPALVKPTQTLTLTCTFS**GFSLS TFGMGVG**WIRQPPGKALEWLA**NIWWDDDKY YNPSLKN**RLTISKDTSKNQVVLTMTNMDPV DTATYYCAR**ISTGISSYYVMDA**WGQGTTVT VSS
	hBDI-5H1-F6VH.1	EVTLRESGPALVKPTQTLTLTCTFS**GFSLS TFGMGVG**WIRQPPGKALEWLA**NIWWDDDKY YNPSLKN**RLTISKDTSKNQVVLTMTNMDPV DTATYYCAR**ISTGISSYYVMDA**WGQGTTVT VSS
	hBDI-5H1-F6VH.1a	EVTLRESGPALVKPTQTLTLTCTFS**GFSLS TFGMGVG**WIRQPPGKGLEWLA**NIWWDDDKY YNPSLKN**RLTISKDTSNNQAVLTITNMDPV DTATYYCAR**ISTGISSYYVMDA**WGQGTTVT VSS
	hBDI-5H1-F6VH.1b	EVTLRESGPALVKPTQTLTLTCTFS**GFSLS TFGMGVG**WIRQPPGKGLEWLA**NIWWDDDKY YNPSLKN**RLTISKDTSKNQVVLTITNMDPV DTATYYCAR**ISTGISSYYVMDA**WGQGTTVT VSS
	hBDI-5H1-F6VH.1c	EVTLRESGPALVKPTQTLTLTCTFS**GFSLS TFGMGVG**WIRQPPGKGLEWLA**NIWWDDDKY YNPSLKT**RLTISKDTSKNQVVLTITNMDPV DTATYYCAR**ISTGISSYYVMDA**WGQGTTVT VSS
	hBDI-5H1-F6VH.2z	QVTLKESGPALVKPTQTLTLTCTFS**GFSLS TFGMGVG**WIRQPPGKALEWLA**NIWWDDDKY YNPSLKN**RLTISKDTSKNQVVLTMTNMDPV DTATYYCAR**ISTGISSYYVMDA**WGQGTTVT VSS
	hBDI-5H1-F6VH.2	EVTLKESGPALVKPTQTLTLTCTFS**GFSLS TFGMGVG**WIRQPPGKALEWLA**NIWWDDDKY YNPSLKN**RLTISKDTSKNQVVLTMTNMDPV DTATYYCAR**ISTGISSYYVMDA**WGQGTTVT VSS
	hBDI-5H1-F6VH.2a	EVTLKESGPALVKPTQTLTLTCTFS**GFSLS TFGMGVG**WIRQPPGKGLEWLA**NIWWDDDKY YNPSLKN**RLTISKDTSNSQAVLTITNMDPV DTATYYCAR**ISTGISSYYVMDA**WGQGTTVT VSS
	hBDI-5H1-F6VH.2b	EVTLKESGPALVKPTQTLTLTCTFS**GFSLS TFGMGVG**WIRQPPGKALEWLA**NIWWDDDKY YNPSLKN**RLTISKDTSKNQAVLTITNMDPV DTATYYCAR**ISTGISSYYVMDA**WGQGTTVT VSS

	Protein region	Sequence
		123456789**0**123456789**0**1234567890
	hBDI-5H1-F6VH.2c	EVTLRESGPALVKPTQTLTLTCTFS**GFSLS TFGMGVG**WIRQPPGKALEWLA**NIWWDDDKY YNPSLKN**RLTISKDTSKNQAVLTITNMDPV DTATYYCAR**ISTGISSYYVMDA**WGQGTTVT VSS
	hBDI-5H1-F6VH.v7	EVQLVESGGGLVQPGGSLRLSCAFS**GFSLS TFGMGVG**WIRQAPGKGLEWLA**NIWWDDDKY YNPSLKN**RLTISKDTSKNQAYLQINSLRAE DTAVYYCAR**ISTGISSYYVMDA**WGQGTLVT VSS
	hBDI-5H1-F6VL.1	NFMLTQPHSVSESPGKTVTISC**ERSSGDIG DTYVS**WYQQRPGSSPTTVIY**GNDQRPS**GVP DRFSGSIDSSSNSASLTISGLKTEDEADYY C**QSYDSDIDIV**FGGGTKLTVL
	hBDI-5H1-F6VL.1a	NFMLTQPHSVSESPGKTVTISC**ERSSGDIG DTYVS**WYQQRPGSPPTNVIY**GNDQRPS**GVP DRFSGSIDSSSNSASLTISGLKTEDEADYF C**QSYDSDIDIV**FGGGTKLTVL
	hBDI-5H1-F6VL.1b	QFMLTQPHSVSESPGKTVTIPC**ERSSGDIG DTYVS**WYQQRPGSPPTNVIY**GNDQRPS**EVS DRFSGSIDSSSNSASLTISGLKTEDEADYF C**QSYDSDIDIV**FGGGTKLTVL
	hBDI-5H1-F6VL.1c	QFMLTQPHSVSESPGKTVTISC**ERSSGDIG DTYVS**WYQQRPGSSPTTVIY**GNDQRPS**GVP DRFSGSIDSSSNSASLTISGLKTEDEADYF C**QSYDSDIDIV**FGGGTKLTVL
	hBDI-5H1-F6VL.2	EIVLTQSPGTLSLSPGERATLSC**ERSSGDI GDTYVS**WYQQKPGQAPRLLIY**GNDQRPS**GI PDRFSGSGSGTDFTLTISRLEPEDFAVYYC **QSYDSDIDIV**FGGGTKVEIK
	hBDI-5H1-F6L.2a	EFVLTQSPGLSLSPGERATLSC**ERSSGDIG DTYVS**WYQQKPGQPPRNVIY**GNDQRPS**GVP DRFSGSIDSSSNDATLTISRLEPEDFAVYF C**QSYDSDIDIV**FGGGTKVEIK
	hBDI-5H1-F6L.2b	EFVLTQSPGTLSLSPGERATLSC**ERSSGDI GDTYVS**WYQQKPGQAPRLVIY**GNDQRPS**GI PDRFSGSGSGTDFTLTISRLEPEDFAVYYC **QSYDSDIDIV**FGGGTKVEIK
	hBDI-5H1-F6L.2c	EFVLTQSPGTLSLSPGERATLSC**ERSSGDI GDTYVS**WYQQKPGQPPRNVIY**GNDQRPS**GV PDRFSGSGSGTDFTLTISRLEPEDFAVYFC **QSYDSDIDIV**FGGGTKVEIK
	hBDI-5H1-F6VL.v6	DFVLTQSPDSLAVSLGERATINC**ERSSGDI GDTYVS**WYQQKPGQPPKNVIY**GNDQRPS**GV PDRFSGSGSGNSATLTISSLQAEDVAVYFC **QSYDSDIDIV**FGGGTKVEIK

	Protein region	Sequence
		123456789**0**123456789**0**1234567890
	hBDI-5H1-F6VL.v7	DFQLTQSPSSLSASVGDRVTITC**ERSSGDI** **GDTYVS**WYQQKPGKAPKNVIY**GNDQRPS**GV PSRFSGSGSGNSATLTISSLQPEDFATYFC **QSYDSDIDIV**FGQGTKVEIK

- **hBDI-5H1-F6VH.1z** is a CDR-grafted, humanized BDI-5H1-F6 VH containing IGHV2-70*01 and IGHJ6 framework sequences.
- **hBDI-5H1-F6VH.1** is based on .1z with a Q1E change to prevent pyroglutamate formation.
- **hBDI-5H1-F6VH.1a** is a humanized design based on .1 and contains four proposed framework back-mutations (A44G, K75N, V78A and M82I).
- **hBDI-5H1-F6VH.1b** is an intermediate design between .1 and .1a and only has two proposed framework back-mutations (A44G and M82I).
- **hBDI-5H1-F6VH.1c** is based on .1b with additional one CDR germlining change N65T to improve identity to human germline sequence.
- **hBDI-5H1-F6VH.2z** is a CDR-grafted, humanized BDI-5H1-F6 VH containing IGHV2-70*04 and IGHJ6 framework sequences.
- **hBDI-5H1-F6VH.2** is based on .2z with Q1E change to prevent pyroglutamate formation.
- **hBDI-5H1-F6VH.2a** (hBDI-5H1-F6VH.1d) is based on .2 and contains four proposed framework back-mutations (K75N, N76S, V78A and M82I).
- **hBDI-5H1-F6VH.2b** (hBDI-5H1-F6VH.v2) is an intermediate design between .2 and .2a and only has two proposed framework back-mutations (V78A and M82I).
- **hBDI-5H1-F6VH.2c** (hBDI-5H1-F6VH.v6) is based on .2 and contains three proposed framework back-mutations (K5R, V78A, M82I).
- **hBDI-5H1-F6VH.v7** is a humanized BDI-5H1-F6 VH containing IGHV3-66*01 and IGHJ1 framework sequences with ten proposed framework back-mutations (A24F, V37I, V48L, S49A, F67L, R71K, N73T, T77Q, L78A, and M82I**).**

- **hBDI-5H1-F6VL.1** is a CDR-grafted humanized BDI-5H1-F6 VL containing IGLV6-57*01 and IGJL2*01 framework sequences.
- **hBDI-5H1-F6VL.1a** is a humanized design based on .1 with 3 proposed framework back-mutations (S43P, T46N and Y87F).
- **hBDI-5H1-F6VL.1b** is a humanized design based on .1 with 7 proposed framework back-mutations (N1Q, S22P, S43P, T46N, G57E, P59S, Y87F).
- **hBDI-5H1-F6VL.1c** is an intermediate design between .1 and .1b with 2 back-mutations (N1Q and Y87F).
- **hBDI-5H1-F6VL.2** is a CDR-grafted humanized BDI-5H1-F6 VL containing IGKV3-20*01 and IGJK4*01 framework sequences.
- **hBDI-5H1-F6VL.2a** is a humanized design based on .2 with 10 proposed framework back-mutations (I2F, A43P, L46N, L47V, I58V, G66I, G68S, T69N, F71A, Y87F) and one residue deletion (T10) and two residues insertion (D66a and S66b).
- **hBDI-5H1-F6VL.2b** is based on .2a only with 2 proposed framework back-mutations (I2F, L47V) and without residues deletion (T10) and insertion (D66a, S66b).
- **hBDI-5H1-F6VL.2c** is a humanized design on .2 with 6 proposed framework back-mutations (I2F, A43P, L46N, L47V, I58V, Y87F) and without residues deletion (T10) and insertion (D66a, S66b).
- **hBDI-5H1-F6VL.v6** is a humanized BDI-5H1-F6 VL containing IGKV4-1*01 and IGJK4*01 framework sequences with eight proposed framework back-mutations (I2F, M4L, L46N, L47V, T69N, D70S, F71A, Y87F).
- **hBDI-5H1-F6VL.v7** is a humanized BDI-5H1-F6 VL containing IGKV1-39*01 and IGJK1*01 framework sequences with eight proposed framework back-mutations (I2F, M4L, L46N, L47V, T69N, D70S, F71A, and Y87F).

Example 6.1.4.2: BDI-9E8-E7

Table 1.4.2. Sequences of Humanized BDI-9E8-E7 Variable Regions

	Protein region	Sequence
		123456789**0**123456789**0**123456789**0**
	hBDI-9E8-E7VH.1z	QVTLRESGPALVKPTQTLTLTCTFS**GFSLS TYGMGVG**WIRQPPGKALEWLA**NIWWDDDKY YNPSLKN**RLTISKDTSKNQVVLTMTNMDPV DTATYYCAR**IESIGTTYSFDY**WGQGTMVTV SS
	hBDI-9E8-E7VH.1	EVTLRESGPALVKPTQTLTLTCTFS**GFSLS TYGMGVG**WIRQPPGKALEWLA**NIWWDDDKY YNPSLKN**RLTISKDTSKNQVVLTMTNMDPV DTATYYCAR**IESIGTTYSFDY**WGQGTMVTV SS
	hBDI-9E8-E7VH.1a	EVTLRESGPALVKPTQTLTLTCTFS**GFSLS TYGMGVG**WIRQPPGKGLEWLA**NIWWDDDKY YNPSLKN**RLTISKDTSKNQAVLTITNMDPV DTATYYCAR**IESIGTTYSFDY**WGQGTMVTV SS
	hBDI-9E8-E7VH.1b	EVTLRESGPALVKPTQTLTLTCTFS**GFSLS TYGMGVG**WIRQPPGKGLEWLA**NIWWDDDKY YNPSLKN**RLTISKDTSKNQVVLTITNMDPV DTATYYCAR**IESIGTTYSFDY**WGQGTMVTV SS
	hBDI-9E8-E7VH.1c	EVTLRESGPALVKPTQTLTLTCTFS**GFSLS TYGMGVG**WIRQPPGKGLEWLA**NIWWDDDKY YNPSLKT**RLTISKDTSKNQVVLTITNMDPV DTATYYCAR**IESIGTTYSFDY**WGQGTMVTV SS
	hBDI-9E8-E7VH.v6	EVTLRESGPALVKPTQTLTLTCTFS**GFSLS TYGMGVG**WIRQPPGKALEWLA**NIWWDDDKY YNPSLKN**RLTISKDTSKNQAVLTITNMDPV DTATYYCAR**IESIGTTYSFDY**WGQGTTVTV SS
	hBDI-9E8-E7VH.v7	EVQLVESGGGLVQPGGSLRLSCAFS**GFSLS TYGMGVG**WIRQAPGKGLEWLA**NIWWDDDKY YNPSLKN**RLTISKDTSKNQAYLQINSLRAE DTAVYYCAR**IESIGTTYSFDY**WGQGTLVTV SS
	hBDI-9E8-E7VL.1	NFMLTQPHSVSESPGKTVTISC**ERSSGDIG DSYVS**WYQQRPGSSPTTVIY**ADDQRPS**GVP DRFSGSIDSSSNSASLTISGLKTEDEADYY C**QSYDINIDIV**FGGGTKLTVL
	hBDI-9E8-E7VL.1a	NFMLTQPHSVSESPGKTVTISC**ERSSGDIG DSYVS**WYQQRPGSPPTNVIY**ADDQRPS**GVP DRFSGSIDSSSNSASLTISGLKTEDEADYF C**QSYDINIDIV**FGGGTKLTVL

	Protein region	Sequence
		123456789**0**123456789**0**1234567890
	hBDI-9E8-E7VL.2	EIVLTQSPGTLSLSPGERATLSC**ERSSGDI** **GDSYVS**WYQQKPGQAPRLLIY**ADDQRPS**GI PDRFSGSGSGTDFTLTISRLEPEDFAVYYC **QSYDINIDIV**FGGGTKVEIK
	hBDI-9E8-E7VL.2a	EFVLTQSPGLSLSPGERATLSC**ERSSGDIG** **DSYVS**WYQQKPGQPPRNVIY**ADDQRPS**GVP DRFSGSIDSSGNDATLTISRLEPEDFAVYF C**QSYDINIDIV**FGGGTKVEIK
	hBDI-9E8-E7VL.2b	EFVLTQSPGTLSLSPGERATLSC**ERSSGDI** **GDSYVS**WYQQKPGQAPRLVIY**ADDQRPS**GI PDRFSGSGSGTDFTLTISRLEPEDFAVYYC **QSYDINIDIV**FGGGTKVEIK
	hBDI-9E8-E7VL.v6	DFVLTQSPDSLAVSLGERATINC**ERSSGDI** **GDSYVS**WYQQKPGQPPKNVIY**ADDQRPS**GV PDRFSGSGSGNSASLTISSLQAEDVAVYFC **QSYDINIDIV**FGGGTKVEIK
	hBDI-9E8-E7VL.v7	DFQLTQSPSSLSASVGDRVTITC**ERSSGDI** **GDSYVS**WYQQKPGKAPKNVIY**ADDQRPS**GV PSRFSGSGSGNSASLTISSLQPEDFATYYC **QSYDINIDIV**FGQGTKVEIK

- **hBDI-9E8-E7VH.1z** is a CDR-grafted, humanized BDI-9E8-E7 VH containing IGHV2-70*01 and IGHJ3*01 framework sequences.
- **hBDI-9E8-E7VH.1** is based on .1z with a Q1E change to prevent pyroglutamate formation.
- **hBDI-9E8-E7VH.1a** is a humanized design based on .1 and contains three proposed framework back-mutations (A44G, V78A and M82I).
- **hBDI-9E8-E7VH.1b** is an intermediate design between .1 and .1a and only has two proposed framework back-mutations (A44G and M82I).
- **hBDI-9E8-E7VH.1c** is based on .1b with additional one CDR germlining change N65T to improve identity to human germline sequence.
- **hBDI-9E8-E7VH.v6** is a humanized BDI-9E8-E7 VH containing IGHV2-70*04 and IGHJ6 framework sequences with four proposed framework back-mutations (Q1E, K5R, V78A, and M82I).
- **hBDI-9E8-E7VH.v7** is a humanized BDI-9E8-E7 VH containing IGHV3-66*01 and IGHJ1 framework sequences with ten proposed framework back-mutations (A24F, V37I, V48L, S49A, F67L, R71K, N73T, T77Q, L78A, and M82I **).**

- **hBDI-9E8-E7VL.1** is a CDR-grafted humanized BDI-9E8-E7 VL containing IGLV6-57*01 and IGJL2*01 framework sequences.
- **hBDI-9E8-E7VL.1a** is a humanized design based on .1 with three proposed framework back-mutations (S43P, T46N and Y87F).
- **hBDI-9E8-E7VL.2** is a CDR-grafted humanized BDI-9E8-E7 VL containing IGKV3-20*01 and IGJK4*01 framework sequences.
- **hBDI-9E8-E7VL.2a** is a humanized design based on .2 with 9 proposed framework back-mutations (I2F, A43P, L46N, L47V, I58V, G66I, T69N, F71A, Y87F) and one residue deletion (T10) and two residues insertion (D66a and S66b).
- **hBDI-9E8-E7VL.2b** is based on .2a only with 2 proposed framework back-mutations (I2F, L47V) and without residues deletion (T10) and insertion (D66a, S66b).
- **hBDI-9E8-E7VL.v6** is a humanized BDI-9E8-E7 VL containing IGKV4-1*01 and IGJK4*01 framework sequences with nine proposed framework back-mutations: (I2F, M4L, L46N, L47V, T69N, D70S, F71A, T72S, and Y87F).
- **hBDI-9E8-E7VL.v7** is a humanized BDI-9E8-E7 VL containing IGKV1-39*01 and IGJK1*01 framework sequences with eight proposed framework back-mutations: I2F, M4L, L46N, L47V, T69N, D70S, F71A, and T72S.

Example 6.1.4.3: BDI-7H10-D8

Table 1.4.3. Sequences of Humanized BDI-7H10-D8 Variable Regions

	Protein region	Sequence
		123456789**0**123456789**0**1234567890
	hBDI-7H10-D8VH.1z	QVQLVQSGAEVKKPGSSVKVSCKAS**GYTFT** **DYAMH**WVRQAPGQGLEWMG**TIIPLIDTTSY** **NQKFKG**RVTITADESTSTAYMELSSLRSED TAVYYCAR**DWDNNWGYFDY**WGQGTMVTVSS
	hBDI-7H10-D8VH.1	EVQLVQSGAEVKKPGSSVKVSCKAS**GYTFT** **DYAMH**WVRQAPGQGLEWMG**TIIPLIDTTSY** **NQKFKG**RVTITADESTSTAYMELSSLRSED TAVYYCAR**DWDNNWGYFDY**WGQGTMVTVSS
	hBDI-7H10-D8VH.1a	EVQLVQSGAEVKKPGSSVKVSCKAS**GYTFT** **DYAMH**WVRQAPGQGLEWIG**TIIPLIDTTSY** **NQKFKG**RATLTADTSTNTAYMELSSLRSED TAVYYCAR**DWDNNWGYFDY**WGQGTMVTVSS

	Protein region	Sequence
		123456789**0**123456789**0**1234567890
	hBDI-7H10-D8VH.1b	EVQLVQSGAEVKKPGSSVKVSCKAS**GYTFT** **DYAMH**WVRQAPGQGLEWIG**TIIPLIDTTSY** **NQKFKG**RVTITADESTSTAYMELSSLRSED TAVYYCAR**DWDNNWGYFDY**WGQGTMVTVSS
	hBDI-7H10-D8VH.1c	EVQLVQSGAEVKKPGSSVKVSCKAS**GGTFS** **DYAMH**WVRQAPGQGLEWIG**TIIPLIDTTSY** **NQKFKG**RVTITADESTSTAYMELSSLRSED TAVYYCAR**DWDNNWGYFDY**WGQGTMVTVSS
	hBDI-7H10-D8VL.1	DIVMTQTPLSLSVTPGQPASISC**RSSQSLE** **YSDGYTYLE**WYLQKPGQSPQLLIY**GVSNRF** **S**GVPDRFSGSGSGTDFTLKISRVEAEDVGV YYC**FQATHDPLT**FGQGTKLEIK
	hBDI-7H10-D8VL.1a	DVVLTQTPLSLSVTPGQPASISC**RSSQSLE** **YSDGYTYLE**WYLQKPGQSPQLLIY**GVSNRF** **S**GVPDRFSGSGSGTDFTLKISRVEAEDVGV YYC**FQATHDPLT**FGQGTKLEIK
	hBDI-7H10-D8VL.1b	DVVMTQTPLSLSVTPGQPASISC**RSSQSLE** **YSDGYTYLE**WYLQKPGQSPQLLIY**GVSNRF** **S**GVPDRFSGSGSGTDFTLKISRVEAEDVGV YYC**FQATHDPLT**FGQGTKLEIK

- **hBDI-7H10-D8VH.1z** is a CDR-grafted, humanized BDI-7H10-D8 VH containing IGHV1-69*01 and IGHJ3 framework sequences.
- **hBDI-7H10-D8VH.1** is based on .1z with a Q1E change to prevent pyroglutamate formation.
- **hBDI-7H10-D8VH.1a** is a humanized design based on .1 and contains five proposed framework back-mutations (M48I, V67A, I69L, E73T and S76N).
- **hBDI-7H10-D8VH.1b** is an intermediate design between .1 and .1a and only has one proposed framework back-mutation M48I.
- **hBDI-7H10-D8VH.1c** is based on .1b with two additional CDR germlining changes Y27G and T30S.
- **hBDI-7H10-D8VL.1** is a CDR-grafted humanized BDI-7H10-D8 VL containing IGKV2-29*02 and IGKJ2 framework sequences.
- **hBDI-7H10-D8VL.1a** is a humanized design based on .1 with 2 proposed framework back-mutations I2V and M4L.
- **hBDI-7H10-D8VL.1b** is an intermediate design between .1 and .1a with only one proposed framework back-mutation I2V.

Example 6.1.4.4: BDI-1E1-D5

Table 1.4.4. Sequences of Humanized BDI-1E1-D5 Variable Regions

	Protein region	Sequence
		123456789**0**123456789**0**1234567890
	hBDI-1E1-D5VH.1z	QVQLVQSGAEVKKPGSSVKVSCKAS**GYTFT DYVMH**WVRQAPGQGLEWMG**TIIPLIDTTSY NQKFKG**RVTITADKSTSTAYMELSSLRSED TAVYYCAR**TSPYYYSSYDVMDA**WGQGTTVT VSS
	hBDI-1E1-D5VH.1	EVQLVQSGAEVKKPGSSVKVSCKAS**GYTFT DYVMH**WVRQAPGQGLEWMG**TIIPLIDTTSY NQKFKG**RVTITADKSTSTAYMELSSLRSED TAVYYCAR**TSPYYYSSYDVMDA**WGQGTTVT VSS
	hBDI-1E1-D5VH.1a	EVQLVQSGAEVKKPGSSVKVSCKAS**GYTFT DYVMH**WVRQAPGQGLEWIG**TIIPLIDTTSY NQKFKG**RATLTADKSTNTAYMELSSLRSED TAVYYCAR**TSPYYYSSYDVMDA**WGQGTTVT VSS
	hBDI-1E1-D5VH.1b	EVQLVQSGAEVKKPGSSVKVSCKAS**GYTFT DYVMH**WVRQAPGQGLEWIG**TIIPLIDTTSY NQKFKG**RVTITADKSTSTAYMELSSLRSED TAVYYCAR**TSPYYYSSYDVMDA**WGQGTTVT VSS
	hBDI-1E1-D5VL.1	AIQLTQSPSSLSASVGDRVTITC**KGSQNIN NYLA**WYQQKPGKAPKLLIY**KTNNLQT**GVPS RFSGSGSGTDFTLTISSLQPEDFATYYC**YQ YDNGYT**FGQGTKLEIK
	hBDI-1E1-D5VL.1a	AIQLTQSPSSLSASVGDRVTITC**KGSQNIN NYLA**WYQQKPGKAPKLLIY**KTNNLQT**GIPS RFSGSGSGTDYTLTISSLQPEDFATYYC**YQ YDNGYT**FGQGTKLEIK
	hBDI-1E1-D5VL.2	EIVLTQSPATLSLSPGERATLSC**KGSQNIN NYLA**WYQQKPGQAPRLLIY**KTNNLQT**GIPA RFSGSGSGTDFTLTISSLEPEDFAVYYC**YQ YDNGYT**FGQGTKLEIK
	hBDI-1E1-D5VL.2a	EIVLTQSPATLSLSPGERATLSC**KGSQNIN NYLA**WYQQKPGQAPRLLIY**KTNNLQT**GIPA RFSGSGSGTDYTLTISSLEPEDFATYYC**YQ YDNGYT**FGQGTKLEIK

- **hBDI-1E1-D5VH.1z** is a CDR-grafted, humanized BDI-1E1-D5 VH containing IGHV1-69*06 and JH6 framework sequences.
- **hBDI-1E1-D5VH.1** is based on .1z with a Q1E change to prevent pyroglutamate formation.

- **hBDI-1E1-D5VH.1a** is a humanized design based on .1 and contains four proposed framework back-mutations (M48I, V67A, I69L and S76N).
- **hBDI-1E1-D5VH.1b** is an intermediate design between .1 and .1a and only has one back-mutations M48I. This design eliminates Carter residue back-mutations.
- **hBDI-1E1-D5VL.1** is a CDR-grafted humanized BDI-1E1-D5 VL containing IGKV1D-13*01 and Jk2 framework sequences.
- **hBDI-1E1-D5VL.1a** is a humanized design based on .1 with 2 proposed framework back-mutations (V58I and F71Y).
- **hBDI-1E1-D5VL.2** is a CDR-grafted humanized BDI-1E1-D5 VL containing IGKV3-11*01 and Jk2 framework sequences.
- **hBDI-1E1-D5VL.2a** is a humanized design based on .2 with 2 proposed framework back-mutations (F71Y and V85T).

Example 6.1.4.5: BDI-6A3-A9

Table 1.4.5. Sequences of Humanized BDI-6A3-A9 Variable Regions

	Protein region	Sequence
		123456789**0**123456789**0**123456789**0**
	hBDI-6A3-A9VH.1	EVQLVESGGGLVQPGGSLRLSCAAS**GFSFS DSAMA**WVRQAPGKGLEWVA**TIIYDGSGTYY RDSVKG**RFTISRDNAKNSLYLQMNSLRAED TAVYYCAR**LGFNYGNYGYYVMDA**WGQGTTV TVSS
	hBDI-6A3-A9VH.1a	EVQLVESGGGLVQPGGSLRLSCAAS**GFSFS DSAMA**WVRQAPGKGLEWVA**TIIYDGSGTYY RDSVKG**RFTISRDNAKSSLYLQMNSLRAED TAVYYCAR**LGFNYGNYGYYVMDA**WGQGTTV TVSS
	hBDI-6A3-A9VH.1b	EVQLVESGGGLVQPGGSLRLSCAAS**GFTFS DSAMA**WVRQAPGKGLEWVA**TIIYDGSGTYY VDSVKG**RFTISRDNAKNSLYLQMNSLRAED TAVYYCAR**LGFNYGNYGYYVMDA**WGQGTTV TVSS
	hBDI-6A3-A9VH.2z	QVQLVQSGAEVKKPGASVKVSCKAS**GFSFS DSAMA**WVRQAPGQRLEWMG**TIIYDGSGTYY RDSVKG**RVTITRDTSASTAYMELSSLRSED TAVYYCAR**LGFNYGNYGYYVMDA**WGQGTTV TVSS

	Protein region	Sequence
		123456789**0**123456789**0**1234567890
	hBDI-6A3-A9VH.2	EVQLVQSGAEVKKPGASVKVSCKAS**GFSFS DSAMA**WVRQAPGQRLEWMG**TIIYDGSGTYY RDSVKG**RVTITRDTSASTAYMELSSLRSED TAVYYCAR**LGFNYGNYGYYVMDA**WGQGTTV TVSS
	hBDI-6A3-A9VH.2a	EVQLVQSGAEVKKPGASVKVSCKAS**GFSFS DSAMA**WVRQAPGQGLEWVA**TIIYDGSGTYY RDSVKG**RFTITRDNSASTLYLELSSLRSED TAVYYCAR**LGFNYGNYGYYVMDA**WGQGTTV TVSS
	hBDI-6A3-A9VH.2b	EVQLVQSGAEVKKPGASVKVSCKAS**GFSFS DSAMA**WVRQAPGQGLEWVG**TIIYDGSGTYY RDSVKG**RVTITRDTSASTAYLELSSLRSED TAVYYCAR**LGFNYGNYGYYVMDA**WGQGTTV TVSS
	hBDI-6A3-A9VL.1	NFMLTQPHSVSESPGKTVTISC**ERSSGDIG DSYVS**WYQQRPGSSPTTVIY**ADDQRPS**GVP DRFSGSIDSSSNSASLTISGLKTEDEADYY C**QSYDSNIDINIV**FGGGTKLTVL
	hBDI-6A3-A9VL.1a	NFMLTQPHSVSESPGKTVTISC**ERSSGDIG DSYVS**WYQQRPGSPPTNVIF**ADDQRPS**GVP DRFSGSIDSSSNSASLTISGLKTEDEADYF C**QSYDSNIDINIV**FGGGTKLTVL
	hBDI-6A3-A9VL.1b	NFMLTQPHSVSESPGKTVTISC**ERSSGDIG DSYVS**WYQQRPGSSPTTVIF**ADDQRPS**GVP DRFSGSIDSSSNSASLTISGLKTEDEADYY C**QSYDSNIDINIV**FGGGTKLTVL

- **hBDI-6A3-A9VH.1** is a CDR-grafted, humanized BDI-6A3-A9 VH containing IGHV3-7*01 and JH6 framework sequences.
- **hBDI-6A3-A9VH.1a** is a humanized design based on .1 and contains one proposed framework back-mutation N76S.
- **hBDI-6A3-A9VH.1b** is based on .1 with additional two CDR germlining changes S28T and R60V to improve identity to human germline sequence.
- **hBDI-6A3-A9VH.2z** is a CDR-grafted, humanized BDI-6A3-A9 VH containing IGHV1-3*01 and JH6 framework sequences.
- **hBDI-6A3-A9VH.2** is based on .2z with a Q1E change to prevent pyroglutamate formation.
- **hBDI-6A3-A9VH.2a** is a humanized design based on .2 and contains seven proposed framework back-mutations R44G, M48V, G49A, V67F, T73N, A78L and M80L.

- **hBDI-6A3-A9VH.2b** is an intermediate design between .2 and .2a with only three proposed framework back-mutations R44G, M48V and M80L.
- **hBDI-6A3-A9VL.1** is a CDR-grafted humanized BDI-6A3-A9 VL containing IGLV6-57*01 and JL2 framework sequences.
- **hBDI-6A3-A9VL.1a** is a humanized design based on .1 with 4 proposed framework back-mutations (S43P, T46N, Y49F and Y87F).
- **hBDI-6A3-A9VL.1b** is an intermediate design between .1 and .1a with only 1 proposed framework back-mutation Y49F.

Example 6.1.4.6: BFU-3E2

Table 1.4.6. Sequences of Humanized BFU-3E2 Variable Regions

	Protein region	Sequence
		123456789**0**123456789**0**123456789**0**
	hBFU-3E2VH.1z	QVQLVQSGAEVKKPGSSVKVSCKAS**GYTFT ESYMY**WVRQAPGQGLEWMG**RIDPEDGSTDY VEKFKN**RVTITADESTSTAYMELSSLRSED TAVYYCAR**FGARSYFYPMDA**WGQGTTVTVS S**
	hBFU-3E2VH.1	EVQLVQSGAEVKKPGSSVKVSCKAS**GYTFT ESYMY**WVRQAPGQGLEWMG**RIDPEDGSTDY VEKFKN**RVTITADESTSTAYMELSSLRSED TAVYYCAR**FGARSYFYPMDA**WGQGTTVTVS S**
	hBFU-3E2VH.1a	EVQLVQSGAEVKKPGSSVKVSCKAS**GYTFT ESYMY**WVKQAPGQGLELIG**RIDPEDGSTDY VEKFKN**KATLTADKSTSTAYMELSSLRSED TAVYFCAR**FGARSYFYPMDA**WGQGTTVTVS S**
	hBFU-3E2VH.1b	EVQLVQSGAEVKKPGSSVKVSCKAS**GYTFT ESYMY**WVRQAPGQGLELIG**RIDPEDGSTDY VEKFKN**RVTLTADESTSTAYMELSSLRSED TAVYYCAR**FGARSYFYPMDA**WGQGTTVTVS S**
	hBFU-3E2VH.1c	EVQLVQSGAEVKKPGSSVKVSCKAS**GYTFT ESYMY**WVRQAPGQGLELIG**RIDPEDGSTDY VEKFKN**RVTITADESTSTAYMELSSLRSED TAVYYCAR**FGARSYFYPMDA**WGQGTTVTVS S**

	Protein region	Sequence
		123456789**0**123456789**0**1234567890
	hBFU-3E2VH.1d	EVQLVQSGAEVKKPGSSVKVSCKAS**GYTFT ESYMY**WVKQAPGQSLELIG**RIDPEDGSTDY VEKFKN**KATLTADESTNTAYMELSSLRSED TAVYFCAR**FGARSYFYPMDA**WGQGTTVTVS S
	hBFU-3E2VL.1	EIVLTQSPATLSLSPGERATLSC**RASESVS TLMH**WYQQKPGQAPRLLIY**GASNLES**GIPA RFSGSGSGTDFTLTISSLEPEDFAVYYC**QQ SWNDPWT**FGGGTKVEIK
	hBFU-3E2VL.1a	ETVLTQSPATLSLSPGERATLSC**RASESVS TLMH**WYQQKPGQQPRLLIY**GASNLES**GVPA RFSGSGSGTDFTLTISSLEPEDFAVYFC**QQ SWNDPWT**FGGGTKVEIK
	hBFU-3E2VL.1b	ETVLTQSPATLSLSPGERATLSC**RASESVS TLMH**WYQQKPGQAPRLLIY**GASNLES**GVPA RFSGSGSGTDFTLTISSLEPEDFAVYFC**QQ SWNDPWT**FGGGTKVEIK
	hBFU-3E2VL.1c	ETVLTQSPATLSLSPGERATLSC**RASESVS TLMH**WYQQKPGQAPRLLIY**GASNLES**GIPA RFSGSGSGTDFTLTISSLEPEDFAVYYC**QQ SWNDPWT**FGGGTKVEIK
	hBFU-3E2VL.2	AIQLTQSPSSLSASVGDRVTITC**RASESVS TLMH**WYQQKPGKAPKLLIY**GASNLES**GVPS RFSGSGSGTDFTLTISSLQPEDFATYYC**QQ SWNDPWT**FGGGTKVEIK
	hBFU-3E2VL.2a	ATQLTQSPSSLSASVGDRVTISC**RASESVS TLMH**WYQQKPGKQPRLLIY**GASNLES**GVPS RFSGSGSGTDFTLTISSLQPEDFATYFC**QQ SWNDPWT**FGGGTKVEIK
	hBFU-3E2VL.2b	ATQLTQSPSSLSASVGDRVTITC**RASESVS TLMH**WYQQKPGKAPRLLIY**GASNLES**GVPS RFSGSGSGTDFTLTISSLQPEDFATYFC**QQ SWNDPWT**FGGGTKVEIK
	hBFU-3E2VL.2c	ATQLTQSPSSLSASVGDRVTITC**RASESVS TLMH**WYQQKPGKAPRLLIY**GASNLES**GVPS RFSGSGSGTDFTLTISSLQPEDFATYYC**QQ SWNDPWT**FGGGTKVEIK

- **hBFU-3E2VH.1z** is a CDR-grafted, humanized BFU-3E2 VH containing IGHV1-69*01 and IGHJ6*01 framework sequences.
- **hBFU-3E2VH.1** is based on .1z with a Q1E change to prevent pyroglutamate formation.
- **hBFU-3E2VH.1a** is a humanized design based on .1 and contains 7 proposed framework back-mutations (R38K, W47L, M48I, R66K, V67A, I69L, Y91F).

- **hBFU-3E2VH.1b** is an intermediate design between .1 and .1a and contains 3 proposed framework back-mutations (W47L, M48I, I69L).
- **hBFU-3E2VH.1c** is an intermediate design between .1 and .1a and contains 2 proposed framework back-mutations (W47L, M48I.)
- **hBFU-3E2VH.1d** is a humanized design based on .1 and contains 9 proposed framework back-mutations (R38K, G44S, W47L, M48I, R66K, V67A, I69L, S76N, Y91F)
- **hBFU-3E2VL.1** is a CDR-grafted, humanized BFU-3E2 VL containing IGKV3-11*01 and IGKJ4*01 framework sequences.
- **hBFU-3E2VL.1a** is a humanized design based on .1 and contains 4 proposed framework back-mutations (I2T, A43Q, I58V, Y87F).
- **hBFU-3E2VL.1b** is an intermediate design between .1 and 1a. It contains 3 proposed framework back-mutations (I2T, I58V, Y87F).
- **hBFU-3E2VL.1c** is a design based on .1b and contains 1 proposed framework back-mutations: I2T.
- **hBFU-3E2VL.2** is a CDR-grafted, humanized BFU-3E2 VL containing IGKV1-13*01 and IGKJ4*01 framework sequences.
- **hBFU-3E2VL.2a** is a humanized design based on .2 and contains 5 proposed framework back-mutations (I2T, T22S, A43Q, K45R, Y87F).
- **hBFU-3E2VL.2b** is an intermediate design between .2 and 2a. It contains 3 proposed framework back-mutations (I2T, K45R, Y87F).
- **hBFU-3E2VL.2c** is a design based on .2b and contains 2 proposed framework back-mutations (I2T, K45R).

Example 6.1.4.7: BFU-11A8

Table 1.4.7. Sequences of Humanized BFU-11A8 Variable Regions

	Protein region	Sequence
		123456789**0**123456789**0**123456789**0**
	hBFU-11A8VH.1z	QVQLVQSGAEVKKPGSSVKVSCKAS**GYTFT ESYIY**WVRQAPGQGLEWMG**RIDPEDGSTDY VEKFKN**RVTITADESTSTAYMELSSLRSED TAVYYCAR**FGARSYFYPMDA**WGQGTTVTVS S**
	hBFU-11A8VH.1	EVQLVQSGAEVKKPGSSVKVSCKAS**GYTFT ESYIY**WVRQAPGQGLEWMG**RIDPEDGSTDY VEKFKN**RVTITADESTSTAYMELSSLRSED TAVYYCAR**FGARSYFYPMDA**WGQGTTVTVS S**
	hBFU-11A8VH.1a	EVQLVQSGAEVKKPGSSVKVSCKAS**GYTFT ESYIY**WVKQAPGQGLELIG**RIDPEDGSTDY VEKFKN**KATLTADESTNTAYMELSSLRSED TAVYFCAR**FGARSYFYPMDA**WGQGTTVTVS S**
	hBFU-11A8VH.1b	EVQLVQSGAEVKKPGSSVKVSCKAS**GYTFT ESYIY**WVRQAPGQGLELIG**RIDPEDGSTDY VEKFKN**RVTLTADESTNTAYMELSSLRSED TAVYYCAR**FGARSYFYPMDA**WGQGTTVTVS S**
	hBFU-11A8VH.1c	EVQLVQSGAEVKKPGSSVKVSCKAS**GYTFT ESYIY**WVRQAPGQGLELIG**RIDPEDGSTDY VEKFKN**RVTITADESTSTAYMELSSLRSED TAVYYCAR**FGARSYFYPMDA**WGQGTTVTVS S**
	hBFU-11A8VL.1	EIVLTQSPATLSLSPGERATLSC**RASESVS TLMH**WYQQKPGQAPRLLIY**GASNLES**GIPA RFSGSGSGTDFTLTISSLEPEDFAVYYC**QQ SWNDPWT**FGGGTKVEIK
	hBFU-11A8VL.1a	ETVLTQSPATLSLSPGERATLPC**RASESVS TLMH**WYQQKPGQQPRLLIY**GASNLES**GVPA RFSGSGSGTDFTLTISSLEPEDFAVYFC**QQ SWNDPWT**FGGGTKVEIK
	hBFU-11A8VL.1b	ETVLTQSPATLSLSPGERATLSC**RASESVS TLMH**WYQQKPGQAPRLLIY**GASNLES**GVPA RFSGSGSGTDFTLTISSLEPEDFAVYFC**QQ SWNDPWT**FGGGTKVEIK
	hBFU-11A8VL.1c	ETVLTQSPATLSLSPGERATLSC**RASESVS TLMH**WYQQKPGQAPRLLIY**GASNLES**GIPA RFSGSGSGTDFTLTISSLEPEDFAVYYC**QQ SWNDPWT**FGGGTKVEIK
	hBFU-11A8VL.2	DIQMTQSPSTLSASVGDRVTITC**RASESVS TLMH**WYQQKPGKAPKLLIY**GASNLES**GVPS RFSGSGSGTEFTLTISSLQPDDFATYYC**QQ SWNDPWT**FGGGTKVEIK

	Protein region	Sequence
		123456789**0**123456789**0**1234567890
	hBFU-11A8VL.2a	DTQLTQSPSTLSASVGDRVTIPC**RASESVS** **TLMH**WYQQKPGKQPKLLIY**GASNLES**GVPS RFSGSGSGTEFTLTISSLQPDDFATYFC**QQ** **SWNDPWT**FGGGTKVEIK
	hBFU-11A8VL.2b	DTQLTQSPSTLSASVGDRVTITC**RASESVS** **TLMH**WYQQKPGKAPKLLIY**GASNLES**GVPS RFSGSGSGTEFTLTISSLQPDDFATYFC**QQ** **SWNDPWT**FGGGTKVEIK
	hBFU-11A8VL.2c	DTQMTQSPSTLSASVGDRVTITC**RASESVS** **TLMH**WYQQKPGKAPKLLIY**GASNLES**GVPS RFSGSGSGTEFTLTISSLQPDDFATYYC**QQ** **SWNDPWT**FGGGTKVEIK

- **hBFU-11A8VH.1z** is a CDR-grafted, humanized BFU-11A8 VH containing IGHV1-69*01 and IGHJ6*01 framework sequences.
- **hBFU-11A8VH.1** is based on .1z with a Q1E change to prevent pyroglutamate formation.
- **hBFU-11A8VH.1a** is a humanized design based on .1 and contains 8 proposed framework back-mutations: R38K, W47L, M48I, R66K, V67A, I69L, S76N, Y91F.
- **hBFU-11A8VH.1b** is an intermediate design between .1 and .1a and contains 4 proposed framework back-mutations: W47L, M48I, I69L, S76N.
- **hBFU-11A8VH.1c** is a design based on .1b and contains 2 proposed framework back-mutations: W47L, M48I.
- **hBFU-11A8VL.1** is a CDR-grafted, humanized BFU-11A8 VL containing IGKV3-11*01 and IGKJ4*01 framework sequences.
- **hBFU-11A8VL.1a** is a humanized design based on .1 and contains 5 proposed framework back-mutations: I2T, S22P, A43Q, I58V, Y87F.
- **hBFU-11A8VL.1b** is an intermediate design between .1 and 1a. It contains 3 proposed framework back-mutations: I2T, I58V, Y87F.
- **hBFU-11A8VL.1c** is a design based on .1b and contains 1 proposed framework back-mutations: I2T.
- **hBFU-11A8VL.2** is a CDR-grafted, humanized BFU-11A8 VL containing IGKV1-5*01 and IGKJ4*01 framework sequences.

- **hBFU-11A8VL.2a** is a humanized design based on .2 and contains 5 proposed framework back-mutations: I2T, M4L, T22P, A43Q, Y87F.
- **hBFU-11A8VL.2b** is an intermediate design between .2 and 2a. It contains 3 proposed framework back-mutations: I2T, M4L, Y87F.
- **hBFU-11A8VL.2c** is a design based on .2b and contains 1 proposed framework back-mutations: I2T.

Example 6.2: Humanization Of VEGF Antibodies

Example 6.2.1: Humanization Method

[0298] Antibody humanization is achieved by grafting CDRs of the rodent antibody onto a "similar" human framework (acceptor) and incorporating minimal number of key framework residues (back-mutation) from the rodent antibody that are selected to maintain the original CDR conformation in order to minimize the immunogenicity while retaining the optimal antigen binding.

Example 6.2.2: Human Germline Sequence Selections For Constructing CDR-Grafted, Humanized VEGF Antibodies

[0299] By applying the aforementioned method, the CDR sequences of VH and VL chains of monoclonal antibodies BDB-4G8-D4, BEW-9A8-E2, BEW-6C2-C8, BEW-9D2-E8, BEW-9E3-B9, BEW-5C3, BEW-9E10, BEW-1B10, and BEW-1E3 were grafted onto different human heavy and light chain acceptor sequences.

Example 6.2.2.1: BDB-4G8-D4

[0300] Based on the alignments with the VH and VL sequences of monoclonal antibody BDB-4G8-D4 of the present invention, the following known human sequences are selected:

1. IGHV7-4-1*02 and IGHJ3*01 for constructing heavy chain acceptor sequences
2. IGHV1-18*01 and IGHJ3*01 as backup acceptor sequences for constructing heavy chain
3. IGHV5-51*01 and IGHJ3*01 as backup acceptor sequences for constructing heavy chain
4. IGHV3-66*01 and IGHJ1*01 as backup acceptor sequences for constructing heavy chain
5. IGKV1D-13*01 and IGKJ2*01 for constructing light chain acceptor sequences
6. IGKV3-11*01 and IGKJ2*01 as alternative acceptor sequences for constructing light chain
7. IGKV3-15*01 and IGKJ5*01 as alternative acceptor sequences for constructing light chain

8. IGKV3-15*01 and IGKJ1*01 as alternative acceptor sequences for constructing light chain
9. IGKV1-39*01 and IGKJ1*01 as alternative acceptor sequences for constructing light chain.

[0301] By grafting the corresponding VH and VL CDRs of BDB-4G8-D4 into said acceptor sequences, the CDR-grafted, humanized, and modified VH and VL sequences were prepared.

Example 6.2.2.2: BEW-9A8-E2

[0302] Based on the alignments with the VH and VL sequences of monoclonal antibody BEW-9A8-E2 of the present invention the following known human sequences are selected:

1. IGHV7-81*01 and IGHJ1*01 for constructing heavy chain acceptor sequences
2. IGHV1-18*01 and IGHJ1*01 as alternative acceptor sequence for constructing heavy chain
3. IGHV7-4-1*01 and IGHJ1*01 as alternative acceptor sequence for constructing heavy chain
4. IGKV6-21*01 and IGKJ2*01 for constructing light chain acceptor sequences
5. IGKV1-39*01 and IGKJ2*01 as alternative acceptor sequence for constructing light chain
6. IGKV3-11*01 and IGKJ2*01 as alternative acceptor sequence for constructing light chain
7. IGKV1-13*01 and IGKJ2*01 as alternative acceptor sequence for constructing light chain

[0303] By grafting the corresponding VH and VL CDRs of BEW-9A8-E2 into said acceptor sequences, the CDR-grafted, humanized, and modified VH and VL sequences were prepared.

Example 6.2.2.3: BEW-6C2-C8

[0304] Based on the alignments with the VH and VL sequences of monoclonal antibody BEW-6C2-C8 of the present invention the following known human sequences are selected:

1. IGHV3-7*01 and IGHJ3*01 for constructing heavy chain acceptor sequences
2. IGKV3-11*01 and IGKJ2*01 for constructing light chain acceptor sequences

3. IGKV1-39*01 and IGKJ2*01 as alternative acceptor sequence for constructing light chain

[0305] By grafting the corresponding VH and VL CDRs of BEW-6C2-C8 into said acceptor sequences, the CDR-grafted, humanized, and modified VH and VL sequences were prepared.

Example 6.2.2.4: BEW-9D2-E8

[0306] Based on the alignments with the VH and VL sequences of monoclonal antibody BEW-9D2-E8 of the present invention the following known human sequences are selected:

1. IGHV7-81*01 and IGHJ4*01 for constructing heavy chain acceptor sequences
2. IGHV1-18*01 and IGHJ4*01 as alternative acceptor sequence for constructing heavy chain
3. IGKV3-11*01 and IGKJ2*01 for constructing light chain acceptor sequences
4. IGKV1-39*01 and IGKJ2*01 as alternative acceptor sequence for constructing light chain

[0307] By grafting the corresponding VH and VL CDRs of BEW-9D2-E8 into said acceptor sequences, the CDR-grafted, humanized, and modified VH and VL sequences were prepared.

Example 6.2.2.5: BEW-9E3-B9

[0308] Based on the alignments with the VH and VL sequences of monoclonal antibody BEW-9E3-B9 of the present invention the following known human sequences are selected:

1. IGHV7-81*01 and IGHJ4*01 for constructing heavy chain acceptor sequences
2. IGHV1-18*01 and IGHJ4*01 as alternative acceptor sequence for constructing heavy chain
3. IGKV3-11*01 and IGKJ2*01 for constructing light chain acceptor sequences
4. IGKV1-39*01 and IGKJ2*01 as alternative acceptor sequence for constructing light chain

[0309] By grafting the corresponding VH and VL CDRs of BEW-9E3-B9 into said acceptor sequences, the CDR-grafted, humanized, and modified VH and VL sequences were prepared.

Example 6.2.2.6: BEW-5C3

[0310] Based on the alignments with the VH and VL sequences of monoclonal antibody BEW-5C3 of the present invention, the following known human sequences are selected:

1. IGHV7-4-1*01 and IGHJ1*01 for constructing heavy chain acceptor sequences
2. IGHV1-69*06 and IGHJ1*01 as alternative acceptor for constructing heavy chain
3. IGKV3-11*01 and IGKJ4*01 for constructing light chain acceptor sequences
4. IGKV1-13*01 and IGKJ4*01 as alternative acceptor for constructing light chain

[0311] By grafting the corresponding VH and VL CDRs of BEW-5C3 into said acceptor sequences, the CDR-grafted, humanized, and modified VH and VL sequences were prepared.

Example 6.2.2.7: BEW-9E10

[0312] Based on the alignments with the VH and VL sequences of monoclonal antibody BEW-9E10 of the present invention, the following known human sequences are selected:

1. IGHV7-4-1*01 and IGHJ1*01 for constructing heavy chain acceptor sequences
2. IGHV1-69*06 and IGHJ1*01 as alternative acceptor for constructing heavy chain
3. IGKV1-27*01 and IGKJ2*01 for constructing light chain acceptor sequences

[0313] By grafting the corresponding VH and VL CDRs of BEW-9E10 into said acceptor sequences, the CDR-grafted, humanized, and modified VH and VL sequences were prepared.

Example 6.2.2.8: BEW-1B10

[0314] Based on the alignments with the VH and VL sequences of monoclonal antibody BEW-1B10 of the present invention, the following known human sequences are selected:

1. IGHV3-7*01 and IGHJ6*01 for constructing heavy chain acceptor sequences
2. IGKV1-39*01 and IGKJ4*01 for constructing light chain acceptor sequences

[0315] By grafting the corresponding VH and VL CDRs of BEW-1B10 into said acceptor sequences, the CDR-grafted, humanized, and modified VH and VL sequences were prepared.

Example 6.2.2.9: BEW-1E3

[0316] Based on the alignments with the VH and VL sequences of monoclonal antibody BEW-1E3 of the present invention, the following known human sequences are selected:

1. IGHV7-4-1*01(0-1) and IGHJ1*01 for constructing heavy chain acceptor sequences
2. IGHV1-18*01 and IGHJ1*01 as alternative acceptor for constructing heavy chain
3. IGKV3-11*01 and IGKJ2*01 for constructing light chain acceptor sequences
4. IGKV1-13*01 and IGKJ2*01 as alternative acceptor for constructing light chain

[0317] By grafting the corresponding VH and VL CDRs of BEW-1E3 into said acceptor sequences, the CDR-grafted, humanized, and modified VH and VL sequences were prepared.

Example 6.2.3: Introducing Potential Framework Back-Mutations In CDR-Grafted Antibodies

[0318] To generate humanized antibody with potential framework back-mutations, the mutations were identified and introduced into the CDR-grafted antibody sequences by *de novo* synthesis of the variable domain, or mutagenic oligonucleotide primers and polymerase chain reactions, or by methods well known in the art. Different combinations of back mutations and other mutations are constructed for each of the CDR-grafts as follows. Residue numbers for these mutations are based on the Kabat numbering system.

Example 6.2.3.1: BDB-4G8-D4

[0319] When IGHV7-4-1*02 and IGHJ3*01 selected as BDB-4G8-D4 heavy chain acceptor sequences, one or more of the following residues could be back-mutated as follows: Q1→, V2→I, W47→Y, and Y91→F.

[0320] When IGHV1-18*01 and IGHJ3*01 selected as BDB-4G8-D4 heavy chain acceptor sequences, one or more of the following residues could be back-mutated as follows: Q1→E, V2→I, W47→Y, V67→F, M69→F, T71→L and Y91→F.

[0321] When IGHV5-51*01 and IGHJ3*01 selected as BDB-4G8-D4 heavy chain acceptor sequences, one or more following residues could be back-mutated as follows: V2→I, A9→T, G24→A, R38→K, W47→Y, Q66→R, V67→F, I69→F, A71→L, I75→F, S76→N, Y79→F and Y91→F.

[0322] When IGHV3-66*01 and IGHJ1*01 selected as BDB-4G8-D4 heavy chain acceptor sequences, one or more following residues could be back-mutated as follows: V2→I,

E6→Q, L11→V, R38→K, W47→Y, V48→M, S49→G, I69→F, R71→L, N73→T, N76→S, L78→A, M82→L and Y91→F.

[0323] When IGKV1D-13*01 and IGKJ2*01 selected as BDB-4G8-D4 light chain acceptor sequences, one or more of the following residues could be back-mutated as follows: I2→T, A43→Q and Y87→F with or without one residue deletion (S10).

[0324] When IGKV3-11*01 and IGKJ2*01 selected as BDB-4G8-D4 light chain acceptor sequences, one or more of the following residues could be back-mutated as follows: E1→D, I2→T, I58→V, and Y87→F.

[0325] When IGKV3-15*01 and IGKJ5*01 or IGKJ5*01 selected as BDB-4G8-D4 light chain acceptor sequences, one or more of the following residues could be back-mutated as follows: E1→D, I2→T, M4→L, A9→S, L13→A, L21→I, R45→K, I58→V, A60→S, G66→R, E70→D, E79→Q and Y87→F.

[0326] When IGKV1-39*01 and IGKJ1*01 selected as BDB-4G8-D4 light chain acceptor sequences, one or more of the following residues could be back- mutated as follows: I2→T, M4→L, T22→S, and Y87→F.

Example 6.2.3.2: BEW-9A8-E2

[0327] When IGHV7-81*01 and IGHJ1*01 selected as BEW-9A8-E2 heavy chain acceptor sequences, one or more of the following residues could be back-mutated as follows: Q1→E V2→I, P38→K, W47→Y, M71→L, Y90→F and Y91→F with or without CDR change T28→S.

[0328] When IGHV1-18*01 and IGHJ1*01 selected as BEW-9A8-E2 heavy chain acceptor sequences, one or more of the following residues could be back-mutated as follows: Q1→E, V2→I, R38→K, W47→Y, V67→F, M69→F, T71→L, Y90→F and Y91→F.

[0329] When IGHV7-4-1*01 and IGHJ1*01 selected as BEW-9A8-E2 heavy chain acceptor sequences, one or more of the following residues could be back-mutated as follows: Q1→E, V2→I, R38→K, W47→Y, Y90→F, Y91→F.

[0330] When IGKV6-21*01 and IGKJ2*01 selected as BEW-9A8-E2 light chain accepter sequences, one or more of the following residues could be back-mutated as follows: I2→T, S43→Q, K49→H and Y87→F. Additional mutations include the following: F10 deletion.

[0331] When IGKV1-39*01 and IGKJ2*01 selected as BEW-9A8-E2 light chain accepter sequemces, one or more of the following residues could be back-mutated as follows: I2→T, M4→L, A43→Q, Y49→H and Y87→F. Additional mutations include the following: S10 deletion.

[0332] When IGKV3-11*01 and IGKJ2*01 selected as BEW-9A8-E2 light chain acceptor sequences, one or more of the following residues could be back-mutated as follows: I2→T, Y49→H, I58→V, V85→T, and Y87→F.

[0333] When IGKV1-13*01 and IGKJ2*01 selected as BEW-9A8-E2 light chain acceptor sequences, one or more of the following residues could be back-mutated as follows: I2→T, T22→S, Y49→H, Y87→F.

Example 6.2.3.3: BEW-6C2-C8

[0334] When IGHV3-7*01 and IGHJ3*01 selected as BEW-6C2-C8 heavy chain acceptor sequences, one or more of the following residues could be back-mutated as follows: V37→I, V48→M and R94→A.

[0335] When IGKV3-11*01 and IGKJ2*01 selected as BEW-6C2-C8 light chain acceptor sequences, one or more of the following residues could be back-mutated as follows: F71→Y and Y87→F.

[0336] When IGKV1-39*01 and IGKJ2*01 selected as BEW-6C2-C8 light chain acceptor sequence, one or more of the following residues could be back-mutated as follows: M4→L, V58→I, F71→Y and Y87→F.

Example 6.2.3.4: BEW-9D2-E8

[0337] When IGHV7-81*01 and IGHJ4*01 selected as BEW-9D2-E8 heavy chain acceptor sequences, one or more of the following residues could be back-mutated as follows: Q1→E, V2→I, P38→K, Q39→L, W47→Y, M48→L, M71→L and Y91→F with or without CDR change T28→S.

[0338] When IGHV1-18*01 and IGHJ4*01 selected as BEW-9D2-E8 heavy chain acceptor sequences, one or more of the following residues could be back-mutated as follows: Q1→E, V2→I, R38→K, Q39→L, W47→Y, M48→L, V67→F, M69→F, T71→L, M80→L and Y91→F.

[0339] When IGKV3-11*01 and IGKJ2*01 selected as BEW-9D2-E8 light chain acceptor sequences, one or more of the following residues could be back-mutated as follows: I2→T, A43→Q, I58→V and Y87→F. Additional mutations include the following: T10 deletion.

[0340] When IGKV1-39*01 and IGKJ2*01 selected as BEW-9D2-E8 light chain acceptor sequences, one or more of the following residues could be back-mutated as follows: I2→T, M4→L, A43→Q and Y87→F. Additional mutations include the following: T10 deletion.

Example 6.2.3.5: BEW-9E3-B9

[0341] When IGHV7-81*01 and IGHJ4*01 selected as BEW-9E3-B9 heavy chain acceptor sequences, one or more of the following residues could be back-mutated as follows: Q1E, V2→I, W47→Y, M71→L and Y91→F with or without CDR change T28→S.

[0342] When IGHV1-18*01 and IGHJ4*01 selected as BEW-9E3-B9 heavy chain acceptor sequences, one or more of the following residues could be back-mutated as follows: Q1→E, V2→I, W47→Y, V67→F, M69→F, T71→L and Y91→F.

[0343] When IGKV3-11*01 and IGKJ2*01 selected as BEW-9E3-B9 light chain acceptor sequences, one or more of the following residues could be back-mutated as follows: I2→T, A43→Q, I58→V and Y87→F. Additional mutations include the following: S10 deletion.

[0344] When IGKV1-39*01 and IGKJ2*01 selected as BEW-9E3-B9 light chain acceptor sequences, one or more of the following residues could be back-mutated as follows: I2→T, M4→L, A43→Q and Y87→F. Additional mutations include the following: S10 deletion.

Example 6.2.3.6: BEW-5C3

[0345] When IGHV7-4-1*01 and IGHJ1*01 selected as BEW-5C3 heavy chain accepter sequences, one or more of the following residues could be back-mutated as follows: V2→I, R38→K, W47→Y, Y90→F, Y91→F.

[0346] When IGHV1-69*01 and IGHJ1*01 selected as BEW-5C3 heavy chain accepter sequences, one or more of the following residues could be back-mutated as follows: V67→F, I69→F, A71→L. Additional mutations include the following: V2→I, R38→K, W47→Y, T68→V, M80→L, Y90→F, Y91→F.

[0347] When IGKV3-11*01 and IGKJ4*01 selected as BEW-5C3 light chain accepter sequences, one or more of the following residues could be back-mutated as follows: E1→D, I2→T, Y36→F, Y87→F. Additional mutations include the following: A43→Q, I58→V, C34→S (CDR change).

[0348] When IGKV1-13*01 and IGKJ4*01 selected as BEW-5C3 light chain accepter sequences, one or more of the following residues could be back-mutated as follows: A1→D, I2→T, T22→S, Y36→F, A43→Q, Y87→F with CDR change C34→S.

Example 6.2.3.7: BEW-9E10

[0349] When IGHV7-4-1*01 and IGHJ1*01 selected as BEW-9E10 heavy chain acceptor sequences, one or more of the following residues could be back-mutated as follows: V2→I, R38→K, W47→Y, Y91→F.

[0350] When IGHV1-69*06 and IGHJ1*01 selected as BEW-9E10 heavy chain acceptor sequences, one or more of the following residues could be back-mutated as follows: V67→F, I69→F. Additional mutations include the following: V2→I, R38→K, W47→Y, Y91→F.

[0351] When IGKV1-27*01 and IGKJ2*01 selected as BEW-9E10 light chain acceptor sequences, one or more of the following residues could be back-mutated as follows: Q3→R, V43→S, F71→Y, Y87→F. Additional mutations include the following: T22→E, T72→S.

Example 6.2.3.8: BEW-1B10

[0352] When IGHV3-7*01 and IGHJ6*01 selected as BEW-1B10 heavy chain acceptor sequences, one or more of the following residues could be back-mutated as follows: V37→F, I69→V. Additional mutations include the following: N76→S, S77→T.

[0353] When IGKV1-39*01 and IGKJ4*01 selected as BEW-1B10 light chain acceptor sequences, one or more of the following residues could be back-mutated as follows: A43→S, F71→Y. Additional mutations include the following: L47→V.

Example 6.2.3.9: BEW-1E3

[0354] When IGHV7-4-1*01 and IGHJ1*01 selected as BEW-1E3 heavy chain acceptor sequences, one or more of the following residues could be back-mutated as follows: V2→I, R38→K, W47→Y, Y91→F.

[0355] When IGHV1-18*01 and IGHJ1*01 selected as BEW-1E3 heavy chain acceptor sequences, one or more of the following residues could be back-mutated as follows: V67→F, M69→F, T71→L. Additional mutations include the following: V2→I, R38→K, W47→Y, Y91→F.

[0356] When IGKV3-11*01 and IGKJ2*01 selected as BEW-1E3 light chain acceptor sequences, one or more of the following residues could be back-mutated as follows: I58→V, Y87→F. Additional mutations include the following: I2→T, A43→Q.

[0357] When IGKV1-13*01 and IGKJ2*01 selected as BEW-1E3 light chain acceptor sequences, one or more of the following residues could be back-mutated as follows: Y87→F. Additional mutations include the following: I2→T, T22→S, A43→Q.

Example 6.2.4: Generation Of Humanized Antibodies To VEGF Containing Framework Back-Mutations In CDR-Grafted Antibodies

[0358] The following humanized variable regions of the murine monoclonal VEGF antibodies were cloned into IgG expression vectors for functional characterization.

Example 6.2.4.1: BDB-4G8-D4

Table 2.4.1. Sequences of Humanized BDB-4G8-D4 Variable Regions

SEQ ID NO:	Protein region	Sequence
		123456789**0**123456789**0**123456789**0**
	hBDB-4G8-D4VH.1z	QVQLVQSGSELKKPGASVKVSCKAS**GYTFT NYGMY**WVRQAPGQGLEWMG**WINTETGKPTY ADDFKG**RFVFSLDTSVSTAYLQISSLKAED TAVYYCAR**TNYYYRSYIFYFDY**WGQGTMVT VSS
	hBDB-4G8-D4VH.1	EVQLVQSGSELKKPGASVKVSCKAS**GYTFT NYGMY**WVRQAPGQGLEWMG**WINTETGKPTY ADDFKG**RFVFSLDTSVSTAYLQISSLKAED TAVYYCAR**TNYYYRSYIFYFDY**WGQGTMVT VSS
	hBDB-4G8-D4VH.1a	EIQLVQSGSELKKPGASVKVSCKAS**GYTFT NYGMY**WVRQAPGQGLEYMG**WINTETGKPTY ADDFKG**RFVFSLDTSVSTAYLQISSLKAED TAVYFCAR**TNYYYRSYIFYFDY**WGQGTMVT VSS
	hBDB-4G8-D4VH.1b	EVQLVQSGSELKKPGASVKVSCKAS**GYTFT NYGMY**WVRQAPGQGLEYMG**WINTETGKPTY ADDFKG**RFVFSLDTSVSTAYLQISSLKAED TAVYYCAR**TNYYYRSYIFYFDY**WGQGTMVT VSS
	hBDB-4G8-D4VH.2z	QVQLVQSGAEVKKPGASVKVSCKAS**GYTFT NYGMY**WVRQAPGQGLEWMG**WINTETGKPTY ADDFKG**RVTMTTDTSTSTAYMELRSLRSDD TAVYYCAR**TNYYYRSYIFYFDY**WGQGTMVT VSS
	hBDB-4G8-D4VH.2	EVQLVQSGAEVKKPGASVKVSCKAS**GYTFT NYGMY**WVRQAPGQGLEWMG**WINTETGKPTY ADDFKG**RVTMTTDTSTSTAYMELRSLRSDD TAVYYCAR**TNYYYRSYIFYFDY**WGQGTMVT VSS
	hBDB-4G8-D4VH.2a	EIQLVQSGAEVKKPGASVKVSCKAS**GYTFT NYGMY**WVRQAPGQGLEYMG**WINTETGKPTY ADDFKG**RFTFTLDTSTSTAYMELRSLRSDD TAVYFCAR**TNYYYRSYIFYFDY**WGQGTMVT VSS
	hBDB-4G8-D4VH.2b	EVQLVQSGAEVKKPGASVKVSCKAS**GYTFT NYGMY**WVRQAPGQGLEYMG**WINTETGKPTY ADDFKG**RVTMTLDTSTSTAYMELRSLRSDD TAVYYCAR**TNYYYRSYIFYFDY**WGQGTMVT VSS
	hBDB-4G8-D4VH.v3	EIQLVQSGTEVKKPGESLKISCKAS**GYTFT NYGMY**WVKQMPGKGLEYMG**WINTETGKPTY ADDFKG**RFTFSLDKSFNTAFLQWSSLKASD TAMYFCAR**TNYYYRSYIFYFDY**WGQGTMVT VSS
	hBDB-4G8-D4VH.v4	EIQLVQSGGGVVQPGGSLRLSCAAS**GYTFT NYGMY**WVKQAPGKGLEYMG**WINTETGKPTY ADDFKG**RFTFSLDTSKSTAYLQLNSLRAED TAVYFCAR**TNYYYRSYIFYFDY**WGQGTLVT VSS

SEQ ID NO:	Protein region	Sequence
		123456789**0**123456789**0**1234567890
	hBDB-4G8-D4VH.v5	EVQLVESGGGLVQPGGSLRLSCAAS**GYTFT NYGMY**WVKQAPGKGLEYMG**WINTETGKPTY ADDFKG**RFTFSLDTSKSTAYLQMNSLRAED TAVYFCAR**TNYYYRSYIFYFDY**WGQGTLVT VSS
	hBDB-4G8-D4VL.1	AIQLTQSPSSLSASVGDRVTITC**RASESVS THMH**WYQQKPGKAPKLLIY**GASNLES**GVPS RFSGSGSGTDFTLTISSLQPEDFATYYC**QQ SWNDPFT**FGQGTKLEIK
	hBDB-4G8-D4VL.1a	ATQLTQSPSLSASVGDRVTITC**RASESVST HMH**WYQQKPGKQPKLLIY**GASNLES**GVPSR FSGSGSGTDFTLTISSLQPEDFATYFC**QQS WNDPFT**FGQGTKLEIK
	hBDB-4G8-D4VL.1b	ATQLTQSPSLSASVGDRVTITC**RASESVST HMH**WYQQKPGKAPKLLIY**GASNLES**GVPSR FSGSGSGTDFTLTISSLQPEDFATYYC**QQS WNDPFT**FGQGTKLEIK
	hBDB-4G8-D4VL.1c	ATQLTQSPSSLSASVGDRVTITC**RASESVS THMH**WYQQKPGKAPKLLIY**GASNLES**GVPS RFSGSGSGTDFTLTISSLQPEDFATYYC**QQ SWNDPFT**FGQGTKLEIK
	hBDB-4G8-D4VL.v2	DTVLTQSPATLSLSPGERATLSC**RASESVS THMH**WYQQKPGQAPRLLIY**GASNLES**GVPA RFSGSGSGTDFTLTISSLEPEDFAVYFC**QQ SWNDPFT**FGQGTKLEIK
	hBDB-4G8-D4VL.v3	ETVLTQSPATLSVSPGERATLSC**RASESVS THMH**WYQQKPGQAPRLLIY**GASNLES**GVPA RFSGSGSGTDFTLTISSLQSEDFAVYFC**QQ SWNDPFT**FGQGTRLEIK
	hBDB-4G8-D4VL.v4	DTVLTQSPSTLSASPGERATISC**RASESVS THMH**WYQQKPGQAPKLLIY**GASNLES**GVPS RFSGSRSGTDFTLTISSLQPEDFAVYFC**QQ SWNDPFT**FGQGTKVEIK
	hBDB-4G8-D4VL.v5	DTQLTQSPSSLSASVGDRVTISC**RASESVS THMH**WYQQKPGKAPKLLIY**GASNLES**GVPS RFSGSGSGTDFTLTISSLQPEDFATYFC**QQ SWNDPFT**FGQGTKVEIK

- **hBDB-4G8-D4VH.1z** is a CDR-grafted, humanized BDB-4G8-D4 VH containing IGHV7-4-1*02 and IGHJ3*01 framework sequences.
- **hBDB-4G8-D4VH.1** is based on .1z with a Q1E change to prevent pyroglutamate formation.
- **hBDB-4G8-D4VH.1a** is a humanized design based on .1 and contains three proposed framework back-mutations (V2I, W47Y and Y91F).
- **hBDB-4G8-D4VH.1b** is an intermediate design between .1 and .1a and only has one back-mutations W47Y.
- **hBDB-4G8-D4VH.2z** is a CDR-grafted, humanized BDB-4G8-D4 VH containing IGHV1-18*01 and IGHJ3*01 framework sequences.

- **hBDB-4G8-D4VH.2** is based on .2z with a Q1E change to prevent pyroglutamate formation.
- **hBDB-4G8-D4VH.2a** is a humanized design based on .2 and contains six proposed framework back-mutations (V2I, W47Y, V67F, M69F, T71L and Y91F).
- **hBDB-4G8-D4VH.2b** is an intermediate design between .2 and .2a and only has two proposed framework back-mutations (W47Y and T71L).
- **hBDB-4G8-D4VH.v3** is a humanized BDB-4G8-D4 VH containing IGHV5-51*01 and IGHJ3*01 framework sequences with thirteen proposed framework back-mutations (V2I, A9T, G24A, R38K, W47Y, Q66R, V67F, I69F, A71L, I75F, S76N, Y79F and Y91F).
- **hBDB-4G8-D4VH.v4** is a humanized BDB-4G8-D4 VH containing IGHV3-66*01 and IGHJ1*01 framework sequences with thirteen proposed framework back-mutations (V2I, E6Q, L11V, W47Y, V48M, S49G, I69F, R71L, N73T, N76S, L78A, M82L and Y91F).
- **hBDB-4G8-D4VH.v5** is a humanized BDB-4G8-D4 containing IGHV3-66*01 and IGHJ1*01 framework sequences with ten proposed framework back-mutations (R38K, W47Y, V48M, S49G, I69F, R71L, N73T, N76S, L78A and Y91F).
- **hBDB-4G8-D4VL.1** is a CDR-grafted humanized BDB-4G8-D4 VL containing IGKV1D-13*01 and IGKJ2*01 framework sequences.
- **hBDB-4G8-D4VL.1a** is a humanized design based on .1 with 3 proposed framework back-mutations (I2T, A43Q and Y87F) and one residue deletion (S10).
- **hBDB-4G8-D4VL.1b** is an intermediate design between .1 and .1a with only one proposed framework back-mutation I2T.
- **hBDB-4G8-D4VL.1c** is a humanized design based on .1b with one residue insertion (S10).
- **hBDB-4G8-D4VL.v2** is a humanized BDB-4G8-D4 VL containing IGKV3-11*01 and IGKJ2*01 framework sequences with four proposed framework back-mutations (E1D, I2T, I58V, and Y87F).
- **hBDB-4G8-D4VL.v3** is a humanized BDB-4G8-D4 VL design containing IGKV3-15*01 and IGKJ5*01 framework sequences with five proposed framework back-mutations (I2T, M4L, I58V, E70D, and Y87F).
- **hBDB-4G8-D4VL.v4** is a humanized BDB-4G8-D4 VL containing IGKV3-15*01 and IGKJ1*01 framework sequences with eleven proposed framework back-mutations (E1D, I2T, A9S, L13A, L21I, R45K, I58V, A60S, G66R, E79Q, and Y87F).

- **hBDB-4G8-D4VL.v5** is a humanized BDB-4G8-D4 VL containing IGKV1-39*01 and IGKJ1*01 framework sequences with four proposed framework back-mutations (I2T, M4L, T22S, and Y87F).

Example 6.2.4.2: BEW-9A8-E2

Table 2.4.2. Sequences of Humanized BEW-9A8-E2 Variable Regions

	Protein region	Sequence
		123456789**0**123456789**0**123456789**0**
	hBEW-9A8-E2VH.1z	QVQLVQSGHEVKQPGASVKVSCKAS**GYTFT** **NYGMY**WVPQAPGQGLEWMG**WINTETGKPIY** **ADDFKG**RFVFSMDTSASTAYLQISSLKAED MAMYYCAR**VDYDGSFWFAY**WGQGTLVTVSS
	hBEW-9A8-E2VH.1	EVQLVQSGHEVKQPGASVKVSCKAS**GYTFT** **NYGMY**WVPQAPGQGLEWMG**WINTETGKPIY** **ADDFKG**RFVFSMDTSASTAYLQISSLKAED MAMYYCAR**VDYDGSFWFAY**WGQGTLVTVSS
	hBEW-9A8-E2VH.1a	EIQLVQSGHEVKQPGASVKVSCKAS**GYTFT** **NYGMY**WVKQAPGQGLEYMG**WINTETGKPIY** **ADDFKG**RFVFSLDTSASTAYLQISSLKAED MAMFFCAR**VDYDGSFWFAY**WGQGTLVTVSS
	hBEW-9A8-E2VH.1b	EVQLVQSGHEVKQPGASVKVSCKAS**GYTFT** **NYGMY**WVPQAPGQGLEYMG**WINTETGKPIY** **ADDFKG**RFVFSLDTSASTAYLQISSLKAED MAMFYCAR**VDYDGSFWFAY**WGQGTLVTVSS
	hBEW-9A8-E2VH.1c	EVQLVQSGHEVKQPGASVKVSCKAS**GYSFT** **NYGMY**WVPQAPGQGLEYMG**WINTETGKPIY** **ADDFKG**RFVFSLDTSASTAYLQISSLKAED MAMFYCAR**VDYDGSFWFAY**WGQGTLVTVSS
	hBEW-9A8-E2VH.2z	QVQLVQSGAEVKKPGASVKVSCKAS**GYTFT** **NYGMY**WVRQAPGQGLEWMG**WINTETGKPIY** **ADDFKG**RVTMTTDTSTSTAYMELRSLRSDD TAVYYCAR**VDYDGSFWFAY**WGQGTLVTVSS
	hBEW-9A8-E2VH.2	EVQLVQSGAEVKKPGASVKVSCKAS**GYTFT** **NYGMY**WVRQAPGQGLEWMG**WINTETGKPIY** **ADDFKG**RVTMTTDTSTSTAYMELRSLRSDD TAVYYCAR**VDYDGSFWFAY**WGQGTLVTVSS
	hBEW-9A8-E2VH.2a	EIQLVQSGAEVKKPGASVKVSCKAS**GYTFT** **NYGMY**WVKQAPGQGLEYMG**WINTETGKPIY** **ADDFKG**RFTFTLDTSTSTAYMELRSLRSDD TAVFFCAR**VDYDGSFWFAY**WGQGTLVTVSS
	hBEW-9A8-E2VH.2b	EVQLVQSGAEVKKPGASVKVSCKAS**GYTFT** **NYGMY**WVRQAPGQGLEYMG**WINTETGKPIY** **ADDFKG**RVTMTLDTSTSTAYMELRSLRSDD TAVFYCAR**VDYDGSFWFAY**WGQGTLVTVSS

	Protein region	Sequence
		123456789**0**123456789**0**1234567890
	hBEW-9A8-E2VH.2c	EIQLVQSGAEVKKPGASVKVSCKAS**GYTFT** **NYGMY**WVKQAPGQGLEYMG**WINTETGKPIY** **ADDFKG**RFTFTLDTSTSTAYMELRSLRSDD TAVYYCAR**VDYDGSFWFAY**WGQGTLVTVSS
	hBEW-9A8-E2VH.2d	EIQLVQSGAEVKKPGASVKVSCKAS**GYTFT** **NYGMY**WVRQAPGQGLEWMG**WINTETGKPIY** **ADDFKG**RFTFTLDTSTSTAYMELRSLRSDD TAVYYCAR**VDYDGSFWFAY**WGQGTLVTVSS
	hBEW-9A8-E2VH.3z	QVQLVQSGSELKKPGASVKVSCKAS**GYTFT** **NYGMY**WVRQAPGQGLEWMG**WINTETGKPIY** **ADDFKG**RFVFSLDTSVSTAYLQISSLKAED TAVYYCAR**VDYDGSFWFAY**WGQGTLVTVSS
	hBEW-9A8-E2VH.3	EVQLVQSGSELKKPGASVKVSCKAS**GYTFT** **NYGMY**WVRQAPGQGLEWMG**WINTETGKPIY** **ADDFKG**RFVFSLDTSVSTAYLQISSLKAED TAVYYCAR**VDYDGSFWFAY**WGQGTLVTVSS
	hBEW-9A8-E2VH.3a	EIQLVQSGSELKKPGASVKVSCKAS**GYTFT** **NYGMY**WVKQAPGQGLEYMG**WINTETGKPIY** **ADDFKG**RFVFSLDTSVSTAYLQISSLKAED TAVYYCAR**VDYDGSFWFAY**WGQGTLVTVSS
	hBEW-9A8-E2VH.3b	EIQLVQSGSELKKPGASVKVSCKAS**GYTFT** **NYGMY**WVRQAPGQGLEWMG**WINTETGKPIY** **ADDFKG**RFVFSLDTSVSTAYLQISSLKAED TAVYYCAR**VDYDGSFWFAY**WGQGTLVTVSS
	hBEW-9A8-E2VH.3c	EIQLVQSGSELKKPGASVKVSCKAS**GYTFT** **NYGMY**WVKQAPGQGLEYMG**WINTETGKPIY** **ADDFKG**RFVFSLDTSVSTAYLQISSLKAED TAVFFCAR**VDYDGSFWFAY**WGQGTLVTVSS
	hBEW-9A8-E2VL.1	EIVLTQSPDFQSVTPKEKVTITC**RASESVS** **TVIH**WYQQKPDQSPKLLIK**GASNLES**GVPS RFSGSGSGTDFTLTINSLEAEDAATYYC**QQ** **HWNDPPT**FGQGTKLEIK
	hBEW-9A8-E2VL.1a	ETVLTQSPDFQSVTPKEKVTITC**RASESVS** **TVIH**WYQQKPDQQPKLLIH**GASNLES**GVPS RFSGSGSGTDFTLTINSLEAEDAATYFC**QQ** **HWNDPPT**FGQGTKLEIK
	hBEW-9A8-E2VL.1b	ETVLTQSPDFQSVTPKEKVTITC**RASESVS** **TVIH**WYQQKPDQSPKLLIH**GASNLES**GVPS RFSGSGSGTDFTLTINSLEAEDAATYYC**QQ** **HWNDPPT**FGQGTKLEIK
	hBEW-9A8-E2VL.1c	ETVLTQSPDQSVTPKEKVTITC**RASESVST** **VIH**WYQQKPDQSPKLLIH**GASNLES**GVPSR FSGSGSGTDFTLTINSLEAEDAATYYC**QQH** **WNDPPT**FGQGTKLEIK
	hBEW-9A8-E2VL.2	DIQMTQSPSSLSASVGDRVTITC**RASESVS** **TVIH**WYQQKPGKAPKLLIY**GASNLES**GVPS RFSGSGSGTDFTLTISSLQPEDFATYYC**QQ** **HWNDPPT**FGQGTKLEIK

	Protein region	Sequence
		123456789**0**123456789**0**1234567890
	hBEW-9A8-E2VL.2a	DTQLTQSPSSLSASVGDRVTITC**RASESVS** **TVIH**WYQQKPGKQPKLLIH**GASNLES**GVPS RFSGSGSGTDFTLTISSLQPEDFATYFC**QQ** **HWNDPPT**FGQGTKLEIK
	hBEW-9A8-E2VL.2b	DTQMTQSPSSLSASVGDRVTITC**RASESVS** **TVIH**WYQQKPGKAPKLLIH**GASNLES**GVPS RFSGSGSGTDFTLTISSLQPEDFATYYC**QQ** **HWNDPPT**FGQGTKLEIK
	hBEW-9A8-E2VL.2c	DTQMTQSPSLSASVGDRVTITC**RASESVST** **VIH**WYQQKPGKAPKLLIH**GASNLES**GVPSR FSGSGSGTDFTLTISSLQPEDFATYYC**QQH** **WNDPPT**FGQGTKLEIK
	hBEW-9A8-E2VL.3	EIVLTQSPATLSLSPGERATLSC**RASESVS** **TVIH**WYQQKPGQAPRLLIY**GASNLES**GIPA RFSGSGSGTDFTLTISSLEPEDFAVYYC**QQ** **HWNDPPT**FGQGTKLEIK
	hBEW-9A8-E2VL.3a	ETVLTQSPATLSLSPGERATLSC**RASESVS** **TVIH**WYQQKPGQAPRLLIH**GASNLES**GVPA RFSGSGSGTDFTLTISSLEPEDFATYFC**QQ** **HWNDPPT**FGQGTKLEIK
	hBEW-9A8-E2VL.3b	ETVLTQSPATLSLSPGERATLSC**RASESVS** **TVIH**WYQQKPGQAPRLLIY**GASNLES**GIPA RFSGSGSGTDFTLTISSLEPEDFAVYFC**QQ** **HWNDPPT**FGQGTKLEIK
	hBEW-9A8-E2VL.3c	ETVLTQSPATLSLSPGERATLSC**RASESVS** **TVIH**WYQQKPGQAPRLLIY**GASNLES**GIPA RFSGSGSGTDFTLTISSLEPEDFAVYYC**QQ** **HWNDPPT**FGQGTKLEIK
	hBEW-9A8-E2VL.4	AIQLTQSPSSLSASVGDRVTITC**RASESVS** **TVIH**WYQQKPGKAPKLLIY**GASNLES**GVPS RFSGSGSGTDFTLTISSLQPEDFATYYC**QQ** **HWNDPPT**FGQGTKLEIK
	hBEW-9A8-E2VL.4a	ATQLTQSPSSLSASVGDRVTISC**RASESVS** **TVIH**WYQQKPGKAPKLLIH**GASNLES**GVPS RFSGSGSGTDFTLTISSLQPEDFATYFC**QQ** **HWNDPPT**FGQGTKLEIK
	hBEW-9A8-E2VL.4b	ATQLTQSPSSLSASVGDRVTITC**RASESVS** **TVIH**WYQQKPGKAPKLLIY**GASNLES**GVPS RFSGSGSGTDFTLTISSLQPEDFATYFC**QQ** **HWNDPPT**FGQGTKLEIK
	hBEW-9A8-E2VL.4c	ATQLTQSPSSLSASVGDRVTITC**RASESVS** **TVIH**WYQQKPGKAPKLLIY**GASNLES**GVPS RFSGSGSGTDFTLTISSLQPEDFATYYC**QQ** **HWNDPPT**FGQGTKLEIK

- **hBEW-9A8-E2VH.1z** is a CDR-grafted, humanized BEW-9A8-E2 VH containing IGHV7-81*01 and IGHJ1*01 framework sequences.

- **hBEW-9A8-E2VH.1** is based on .1z with a Q1E change to prevent pyroglutamate formation.
- **hBEW-9A8-E2VH.1a** is a humanized design based on .1 and contains six proposed framework back-mutations (V2I, P38K, W47Y, M71L, Y90F and Y91F).
- **hBEW-9A8-E2VH.1b** is an intermediate design between .1 and .1a and only has three proposed framework back-mutations (W47Y, M71L and Y90F).
- **hBEW-9A8-E2VH.1c** is based on .1b with additional one CDR germlining change T28S to improve identity to human germline sequence.
- **hBEW-9A8-E2VH.2z** is a CDR-grafted, humanized BEW-9A8-E2 VH containing IGHV1-18*01 and IGHJ1*01 framework sequences.
- **hBEW-9A8-E2VH.2** is based on .2z with a Q1E change to prevent pyroglutamate formation.
- **hBEW-9A8-E2VH.2a** is a humanized design based on .2 and contains eight proposed framework back-mutations (V2I, R38K, W47Y, V67F, M69F, T71L, Y90F and Y91F).
- **hBEW-9A8-E2VH.2b** is an intermediate design between .2 and .2a and contains three back-mutations (W47Y, M71L and Y90F).
- **hBEW-9A8-E2VH.2c** (hBEW-9A8VH.4a) is an intermediate design between .2 and .2a and contains six proposed framework back-mutations (V2I, R38K, W47Y, V67F, M69F, and T71L).
- **hBEW-9A8-E2VH.2d** (hBEW-9A8VH.4b) is an intermediate design between .2 and .2a contains four proposed framework back-mutations (V2I, V67F, M69F, and T71L).
- **hBEW-9A8VH.3z** is a CDR-grafted, humanized BEW-9A8 VH containing IGHV7-4-1*01 and IGHJ1*01 framework sequences.
- **hBEW-9A8VH.3** is based on .3z with a Q1E change to prevent pyroglutamate formation.
- **hBEW-9A8VH.3a** is a humanized design based on .3 and contains 3 proposed framework back-mutations (V2I, R38K, W47Y).
- **hBEW-9A8VH.3b** is an intermediate design between .3 and .3a and contains 1 proposed framework back-mutations: V2I.
- **hBEW-9A8VH.3c** is a humanized design based on .3 and contains 5 proposed framework back-mutations (V2I, R38K, W47Y, Y90F, Y91F).
- **hBEW-9A8-E2VL.1** is a CDR-grafted humanized BEW-9A8-E2 VL containing IGKV6-21*01 and IGKJ2*01 framework sequences.

- **hBEW-9A8-E2VL.1a** is a humanized design based on .1 with four proposed framework back-mutations (I2T, S43Q, K49H and Y87F).
- **hBEW-9A8-E2VL.1b** is an intermediate design between .1 and .1a with only two proposed framework back-mutation (I2T and K49H).
- **hBEW-9A8-E2VL.1c** is based on .1b with one residue deletion of F10.
- **hBEW-9A8-E2VL.2** is a CDR-grafted humanized BEW-9A8-E2 VL containing IGKV1-39*01 and IGKJ2*01 framework sequences.
- **hBEW-9A8-E2VL.2a** is a humanized design based on .2 with five proposed framework back-mutations (I2T, M4L, A43Q, Y49H and Y87F).
- **hBEW-9A8-E2VL.2b** is an intermediate design between .1 and .1a with only two proposed framework back-mutation (I2T and Y49H).
- **hBEW-9A8-E2VL.2c** is based on .2b with one residue deletion of S10.
- **hBEW-9A8VL.3** is a CDR-grafted, humanized BEW-9A8 VL containing IGKV3-11*01 and IGKJ2*01 framework sequences.
- **hBEW-9A8VL.3a** is a humanized design based on .3 and contains 5 proposed framework back-mutations: (I2T, Y49H, I58V, V85T, Y87F).
- **hBEW-9A8VL.3b** is an intermediate design between .3 and 3a. It contains 2 proposed framework back-mutations: (I2T, Y87F).
- **hBEW-9A8VL.3c** is a design based on .3b and contains 1 proposed framework back-mutations: I2T.
- **hBEW-9A8VL.4** is a CDR-grafted, humanized BEW-9A8 VL containing IGKV1-13*01 and IGKJ2*01 framework sequences.
- **hBEW-9A8VL.4a** is a humanized design based on .4 and contains 4 proposed framework back-mutations: I2T, T22S, Y49H, Y87F.
- **hBEW-9A8VL.4b** is an intermediate design between .4 and 4a. It contains 2 proposed framework back-mutations: I2T, Y87F.
- **hBEW-9A8VL.4c** is a design based on .4b and eliminated Carter residue back-mutations. It contains 1 proposed framework back-mutations: I2T.

Example 6.2.4.3: BEW-6C2-C8

Table 2.4.3. Sequences of Humanized BEW-6C2-C8 Variable Regions

	Protein region	Sequence
		123456789**0**123456789**0**123456789**0**
	hBEW-6C2-C8VH.1	EVQLVESGGGLVQPGGSLRLSCAAS**GFTFS** **YYGMH**WVRQAPGKGLEWVA**LIYYDSSKMYY** **ADSVKG**RFTISRDNAKNSLYLQMNSLRAED TAVYYCAR**GGTAPVY**WGQGTMVTVSS
	hBEW-6C2-C8VH.1a	EVQLVESGGGLVQPGGSLRLSCAAS**GFTFS** **YYGMH**WIRQAPGKGLEWMA**LIYYDSSKMYY** **ADSVKG**RFTISRDNAKNSLYLQMNSLRAED TAVYYCAA**GGTAPVY**WGQGTMVTVSS
	hBEW-6C2-C8VH.1b	EVQLVESGGGLVQPGGSLRLSCAAS**GFTFS** **YYGMH**WVRQAPGKGLEWMA**LIYYDSSKMYY** **ADSVKG**RFTISRDNAKNSLYLQMNSLRAED TAVYYCAA**GGTAPVY**WGQGTMVTVSS
	hBEW-6C2-C8VL.1	EIVLTQSPATLSLSPGERATLSC**KGSQNIA** **NYLA**WYQQKPGQAPRLLIY**NTDSLQT**GIPA RFSGSGSGTDFTLTISSLEPEDFAVYYC**YQ** **SNNGYT**FGQGTKLEIK
	hBEW-6C2-C8VL.1a	EIVLTQSPATLSLSPGERATLSC**KGSQNIA** **NYLA**WYQQKPGQAPRLLIY**NTDSLQT**GIPA RFSGSGSGTDYTLTISSLEPEDFAVYFC**YQ** **SNNGYT**FGQGTKLEIK
	hBEW-6C2-C8VL.2	DIQMTQSPSSLSASVGDRVTITC**KGSQNIA** **NYLA**WYQQKPGKAPKLLIY**NTDSLQT**GVPS RFSGSGSGTDFTLTISSLQPEDFATYYC**YQ** **SNNGYT**FGQGTKLEIK
	hBEW-6C2-C8VL.2a	DIQLTQSPSSLSASVGDRVTITC**KGSQNIA** **NYLA**WYQQKPGKAPKLLIY**NTDSLQT**GIPS RFSGSGSGTDYTLTISSLQPEDFATYFC**YQ** **SNNGYT**FGQGTKLEIK

- **hBEW-6C2-C8VH.1** is a CDR-grafted, humanized BEW-6C2-C8 VH containing IGHV3-7*01 and IGHJ3*01 framework sequences.
- **hBEW-6C2-C8VH.1a** is a humanized design based on .1 and contains three proposed framework back-mutations V37I, V48M and R94A.
- **hBEW-6C2-C8VH.1b** is an intermediate design between .1 and .1a and only has two back-mutations V48M and R94A. This design eliminates Carter residue back-mutations.
- **hBEW-6C2-C8VL.1** is a CDR-grafted humanized BEW-6C2-C8 VL containing IGKV3-11*01 and IGKJ2*01 framework sequences.

- **hBEW-6C2-C8VL.1a** is a humanized design based on .1 with 2 proposed framework back-mutations (F71Y and Y87F).
- **hBEW-6C2-C8VL.2** is a CDR-grafted humanized BEW-6C2-C8 VL containing IGKV1-39*01 and IGKJ2*01 framework sequences.
- **hBEW-6C2-C8VL.2a** is a humanized design based on .2 with 4 proposed framework back-mutations (M4L, V58I, F71Y and Y87F).

Example 6.2.4.4: BEW-9D2-E8

Table 2.4.4. Sequences of Humanized BEW-9D2-E8 Variable Regions

	Protein region	Sequence
		123456789**0**123456789**0**123456789**0**
	hBEW-9D2-E8VH.1z	QVQLVQSGHEVKQPGASVKVSCKAS**GYTFT NYGMY**WVPQAPGQGLEWMG**WINTETGKPTY ADDFKG**RFVFSMDTSASTAYLQISSLKAED MAMYYCAR**PSDYYDGFWFAY**WGQGTLVTVS S
	hBEW-9D2-E8VH.1	EVQLVQSGHEVKQPGASVKVSCKAS**GYTFT NYGMY**WVPQAPGQGLEWMG**WINTETGKPTY ADDFKG**RFVFSMDTSASTAYLQISSLKAED MAMYYCAR**PSDYYDGFWFAY**WGQGTLVTVS S
	hBEW-9D2-E8VH.1a	EIQLVQSGHEVKQPGASVKVSCKAS**GYTFT NYGMY**WVKLAPGQGLEYLG**WINTETGKPTY ADDFKG**RFVFSLDTSASTAYLQISSLKAED MAMYFCAR**PSDYYDGFWFAY**WGQGTLVTVS S
	hBEW-9D2-E8VH.1b	EVQLVQSGHEVKQPGASVKVSCKAS**GYTFT NYGMY**WVKQAPGQGLEYLG**WINTETGKPTY ADDFKG**RFVFSLDTSASTAYLQISSLKAED MAMYYCAR**PSDYYDGFWFAY**WGQGTLVTVS S
	hBEW-9D2-E8VH.1c	EVQLVQSGHEVKQPGASVKVSCKAS**GYSFT NYGMY**WVKQAPGQGLEYLG**WINTETGKPTY ADDFKG**RFVFSLDTSASTAYLQISSLKAED MAMYYCAR**PSDYYDGFWFAY**WGQGTLVTVS S
	hBEW-9D2-E8VH.2z	QVQLVQSGAEVKKPGASVKVSCKAS**GYTFT NYGMY**WVRQAPGQGLEWMG**WINTETGKPTY ADDFKG**RVTMTTDTSTSTAYMELRSLRSDD TAVYYCAR**PSDYYDGFWFAY**WGQGTLVTVS S

	Protein region	Sequence
		123456789**0**123456789**0**1234567890
	hBEW-9D2-E8VH.2	EVQLVQSGAEVKKPGASVKVSCKAS**GYTFT NYGMY**WVRQAPGQGLEWMG**WINTETGKPTY ADDFKG**RVTMTTDTSTSTAYMELRSLRSDD TAVYYCAR**PSDYYDGFWFAY**WGQGTLVTVS S
	hBEW-9D2-E8VH.2a	EIQLVQSGAEVKKPGASVKVSCKAS**GYTFT NYGMY**WVKLAPGQGLEYLG**WINTETGKPTY ADDFKG**RFTFTLDTSTSTAYLELRSLRSDD TAVYFCAR**PSDYYDGFWFAY**WGQGTLVTVS S
	hBEW-9D2-E8VH.2b	EVQLVQSGAEVKKPGASVKVSCKAS**GYTFT NYGMY**WVKQAPGQGLEYLG**WINTETGKPTY ADDFKG**RVTMTLDTSTSTAYLELRSLRSDD TAVYYCAR**PSDYYDGFWFAY**WGQGTLVTVS S
	hBEW-9D2-E8VL.1	EIVLTQSPATLSLSPGERATLSC**RASEWVN SYMH**WYQQKPGQAPRLLIY**KASNLAS**GIPA RFSGSGSGTDFTLTISSLEPEDFAVYYC**QQ SWNDPLT**FGQGTKLEIK
	hBEW-9D2-E8VL.1a	ETVLTQSPATLSLSPGERATLSC**RASEWVN SYMH**WYQQKPGQQPRLLIY**KASNLAS**GVPA RFSGSGSGTDFTLTISSLEPEDFAVYFC**QQ SWNDPLT**FGQGTKLEIK
	hBEW-9D2-E8VL.1b	ETVLTQSPATLSLSPGERATLSC**RASEWVN SYMH**WYQQKPGQAPRLLIY**KASNLAS**GIPA RFSGSGSGTDFTLTISSLEPEDFAVYYC**QQ SWNDPLT**FGQGTKLEIK
	hBEW-9D2-E8VL.2	DIQMTQSPSSLSASVGDRVTITC**RASEWVN SYMH**WYQQKPGKAPKLLIY**KASNLAS**GVPS RFSGSGSGTDFTLTISSLQPEDFATYYC**QQ SWNDPLT**FGQGTKLEIK
	hBEW-9D2-E8VL.2a	DTQLTQSPSSLSASVGDRVTITC**RASEWVN SYMH**WYQQKPGKQPKLLIY**KASNLAS**GVPS RFSGSGSGTDFTLTISSLQPEDFATYFC**QQ SWNDPLT**FGQGTKLEIK
	hBEW-9D2-E8VL.2b	DTQMTQSPSSLSASVGDRVTITC**RASEWVN SYMH**WYQQKPGKAPKLLIY**KASNLAS**GVPS RFSGSGSGTDFTLTISSLQPEDFATYYC**QQ SWNDPLT**FGQGTKLEIK

- **hBEW-9D2-E8VH.1z** is a CDR-grafted, humanized BEW-9D2-E8 VH containing IGHV7-81*01 and IGHJ4*01 framework sequences.
- **hBEW-9D2-E8VH.1** is based on .1z with a Q1E change to prevent pyroglutamate formation.

- **hBEW-9D2-E8VH.1a** is a humanized design based on .1 and contains seven proposed framework back-mutations (V2I, P38K, Q39L, W47Y, M48L, M71L and Y91F).
- **hBEW-9D2-E8VH.1b** is an intermediate design between .1 and .1a and only has four proposed framework back-mutations (P38K, W47Y, M48L, M71L).
- **BEW-9D2-E8VH.1c** is based on .1b with additional one CDR germlining change T28S to improve identity to human germline sequence.
- **hBEW-9D2-E8VH.2z** is a CDR-grafted, humanized BEW-9D2-E8 VH containing IGHV1-18*01 and IGHJ4*01 framework sequences.
- **hBEW-9D2-E8VH.2** is based on .2z with a Q1E change to prevent pyroglutamate formation.
- **hBEW-9D2-E8VH.2a** is a humanized design based on .2 and contains ten proposed framework back-mutations (V2I, R38K, Q39L, W47Y, M48L, V67F, M69F, T71L, M80L and Y91F).
- **hBEW-9D2-E8VH.2b** is an intermediate design between .2 and .2a and only has five proposed framework back-mutations (R38K, W47Y, M48L, T71L and M80L).
- **hBEW-9D2-E8VL.1** is a CDR-grafted humanized BEW-9D2-E8 VL containing IGKV3-11*01 and IGKJ2*01 framework sequences.
- **hBEW-9D2-E8VL.1a** is a humanized design based on .1 with four proposed framework back-mutations (I2T, A43Q, I58V and Y87F).
- **hBEW-9D2-E8VL.1b** is an intermediate design between .1 and .1a with one proposed framework back-mutation I2V.
- **hBEW-9D2-E8VL.2** is a CDR-grafted humanized BEW-9D2-E8 VL containing IGKV1-39*01 and IGKJ2*01 framework sequences.
- **hBEW-9D2-E8VL.2a** is a humanized design based on .2 with four proposed framework back-mutations (I2T, M4L, A43Q and Y87F).
- **hBEW-9D2-E8VL.2b** is an intermediate design between .2 and .2a with one proposed framework back-mutation I2V.

Example 6.2.4.5 BEW-9E3-B9

Table 2.4.5. Sequences of Humanized BEW-9E3-B9 Variable Regions

	Protein region	Sequence
		123456789**0**123456789**0**123456789**0**
	hBEW-9E3-B9VH.1z	QVQLVQSGHEVKQPGASVKVSCKAS**GYTFT NYGMY**WVPQAPGQGLEWMG**WINTETGKPTY ADDFKG**RFVFSMDTSASTAYLQISSLKAED MAMYYCAR**PSDYYDGFWFPY**WGQGTLVTVS S
	hBEW-9E3-B9VH.1	EVQLVQSGHEVKQPGASVKVSCKAS**GYTFT NYGMY**WVPQAPGQGLEWMG**WINTETGKPTY ADDFKG**RFVFSMDTSASTAYLQISSLKAED MAMYYCAR**PSDYYDGFWFPY**WGQGTLVTVS S
	hBEW-9E3-B9VH.1a	EIQLVQSGHEVKQPGASVKVSCKAS**GYTFT NYGMY**WVPQAPGQGLEYMG**WINTETGKPTY ADDFKG**RFVFSLDTSASTAYLQISSLKAED MAMYFCAR**PSDYYDGFWFPY**WGQGTLVTVS S
	hBEW-9E3-B9VH.1b	EVQLVQSGHEVKQPGASVKVSCKAS**GYTFT NYGMY**WVPQAPGQGLEYMG**WINTETGKPTY ADDFKG**RFVFSLDTSASTAYLQISSLKAED MAMYYCAR**PSDYYDGFWFPY**WGQGTLVTVS S
	hBEW-9E3-B9VH.1c	EVQLVQSGHEVKQPGASVKVSCKAS**GYSFT NYGMY**WVPQAPGQGLEYMG**WINTETGKPTY ADDFKG**RFVFSLDTSASTAYLQISSLKAED MAMYYCAR**PSDYYDGFWFPY**WGQGTLVTVS S
	hBEW-9E3-B9VH.2z	QVQLVQSGAEVKKPGASVKVSCKAS**GYTFT NYGMY**WVRQAPGQGLEWMG**WINTETGKPTY ADDFKG**RVTMTTDTSTSTAYMELRSLRSDD TAVYYCAR**PSDYYDGFWFPY**WGQGTLVTVS S
	hBEW-9E3-B9VH.2	EVQLVQSGAEVKKPGASVKVSCKAS**GYTFT NYGMY**WVRQAPGQGLEWMG**WINTETGKPTY ADDFKG**RVTMTTDTSTSTAYMELRSLRSDD TAVYYCAR**PSDYYDGFWFPY**WGQGTLVTVS S
	hBEW-9E3-B9VH.2a	EIQLVQSGAEVKKPGASVKVSCKAS**GYTFT NYGMY**WVRQAPGQGLEYMG**WINTETGKPTY ADDFKG**RFTFTLDTSTSTAYMELRSLRSDD TAVYFCAR**PSDYYDGFWFPY**WGQGTLVTVS S
	hBEW-9E3-B9VH.2b	EVQLVQSGAEVKKPGASVKVSCKAS**GYTFT NYGMY**WVRQAPGQGLEYMG**WINTETGKPTY ADDFKG**RVTMTLDTSTSTAYMELRSLRSDD TAVYYCAR**PSDYYDGFWFPY**WGQGTLVTVS S

	Protein region	Sequence
		123456789**0**123456789**0**1234567890
	hBEW-9E3-B9VL.1	EIVLTQSPATLSLSPGERATLSC**RASEGVN** **SYMH**WYQQKPGQAPRLLIY**KASNLAS**GIPA RFSGSGSGTDFTLTISSLEPEDFAVYYC**QQ** **SWNDPLT**FGQGTKLEIK
	hBEW-9E3-B9VL.1a	ETVLTQSPATLSLSPGERATLSC**RASEGVN** **SYMH**WYQQKPGQQPRLLIY**KASNLAS**GVPA RFSGSGSGTDFTLTISSLEPEDFAVYFC**QQ** **SWNDPLT**FGQGTKLEIK
	hBEW-9E3-B9VL.1b	ETVLTQSPATLSLSPGERATLSC**RASEGVN** **SYMH**WYQQKPGQAPRLLIY**KASNLAS**GIPA RFSGSGSGTDFTLTISSLEPEDFAVYYC**QQ** **SWNDPLT**FGQGTKLEIK
	hBEW-9E3-B9VL.2	DIQMTQSPSSLSASVGDRVTITC**RASEGVN** **SYMH**WYQQKPGKAPKLLIY**KASNLAS**GVPS RFSGSGSGTDFTLTISSLQPEDFATYYC**QQ** **SWNDPLT**FGQGTKLEIK
	hBEW-9E3-B9VL.2a	DTQLTQSPSSLSASVGDRVTITC**RASEGVN** **SYMH**WYQQKPGKQPKLLIY**KASNLAS**GVPS RFSGSGSGTDFTLTISSLQPEDFATYFC**QQ** **SWNDPLT**FGQGTKLEIK
	hBEW-9E3-B9VL.2b	DTQMTQSPSSLSASVGDRVTITC**RASEGVN** **SYMH**WYQQKPGKAPKLLIY**KASNLAS**GVPS RFSGSGSGTDFTLTISSLQPEDFATYYC**QQ** **SWNDPLT**FGQGTKLEIK

- **hBEW-9E3-B9VH.1z** is a CDR-grafted, humanized BEW-9E3-B9 VH containing IGHV7-81*01 and IGHJ4*01 framework sequences.
- **hBEW-9E3-B9VH.1** is based on .1z with a Q1E change to prevent pyroglutamate formation.
- **hBEW-9E3-B9VH.1a** is a humanized design based on .1 and contains four proposed framework back-mutations (V2I, W47Y, M71L and Y91F).
- **hBEW-9E3-B9VH.1b** is an intermediate design between .1 and .1a and only has two back-mutations (W47Y and M71L).
- **hBEW-9E3-B9VH.1c** is based on .1b with additional one CDR germlining change T28S to improve identity to human germline sequence.
- **hBEW-9E3-B9VH.2z** is a CDR-grafted, humanized BEW-9E3-B9 VH containing IGHV1-18*01 and IGHJ4*01 framework sequences.

- **hBEW-9E3-B9VH.2** is based on .2z with a Q1E change to prevent pyroglutamate formation.
- **hBEW-9E3-B9VH.2a** is a humanized design based on .2 and contains six proposed framework back-mutations (V2I, W47Y, V67F, M69F, T71L and Y91F).
- **hBEW-9E3-B9VH.2b** is an intermediate design between .2 and .2a and only has two back-mutations W47Y and T71L.
- **hBEW-9E3-B9VL.1** is a CDR-grafted humanized BEW-9E3-B9 VL containing IGKV3-11*01 and IGKJ2*01 framework sequences.
- **hBEW-9E3-B9VL.1a** is a humanized design based on .1 with four proposed framework back-mutations (I2T, A43Q, I58V and Y87F).
- **hBEW-9E3-B9VL.1b** is an intermediate design between .1 and .1a with 1 proposed framework back-mutation I2T.
- **hBEW-9E3-B9VL.2** is a CDR-grafted humanized BEW-9E3-B9 VL containing IGKV1-39*01 and IGKJ2*01 framework sequences.
- **hBEW-9E3-B9VL.2a** is a humanized design based on .1 with four proposed framework back-mutations (I2T, M4L, A43Q and Y87F).
- **hBEW-9E3-B9VL.2b** is an intermediate design between .1 and .1a with 1 proposed framework back-mutation I2T.

Example 6.2.4.6: BEW-5C3

Table 2.4.6. Sequences of Humanized BEW-5C3 Variable Regions

SEQ ID NO:	Protein region	Sequence
		123456789**0**123456789**0**123456789**0**
	hBEW-5C3VH.1z	QVQLVQSGSELKKPGASVKVSCKAS**GYTFT** **NYGVY**WVRQAPGQGLEWMG**WINTETGKPTY** **ADDFKG**RFVFSLDTSVSTAYLQISSLKAED TAVYYCAR**ARQLDWFVY**WGQGTLVTVSS
	hBEW-5C3VH.1	EVQLVQSGSELKKPGASVKVSCKAS**GYTFT** **NYGVY**WVRQAPGQGLEWMG**WINTETGKPTY** **ADDFKG**RFVFSLDTSVSTAYLQISSLKAED TAVYYCAR**ARQLDWFVY**WGQGTLVTVSS
	hBEW-5C3VH.1a	EIQLVQSGSELKKPGASVKVSCKAS**GYTFT** **NYGVY**WVKQAPGQGLEYMG**WINTETGKPTY** **ADDFKG**RFVFSLDTSVSTAYLQISSLKAED TAVYYCAR**ARQLDWFVY**WGQGTLVTVSS
	hBEW-5C3VH.1b	EIQLVQSGSELKKPGASVKVSCKAS**GYTFT** **NYGVY**WVKQAPGQGLEYMG**WINTETGKPTY** **ADDFKG**RFVFSLDTSVSTAYLQISSLKAED TAVFFCAR**ARQLDWFVY**WGQGTLVTVSS
	hBEW-5C3VH.2z	QVQLVQSGAEVKKPGSSVKVSCKAS**GYTFT** **NYGVY**WVRQAPGQGLEWMG**WINTETGKPTY** **ADDFKG**RVTITADKSTSTAYMELSSLRSED TAVYYCAR**ARQLDWFVY**WGQGTLVTVSS

SEQ ID NO:	Protein region	Sequence
		123456789**0**123456789**0**1234567890
	hBEW-5C3VH.2	EVQLVQSGAEVKKPGSSVKVSCKAS**GYTFT** **NYGVY**WVRQAPGQGLEWMG**WINTETGKPTY** **ADDFKG**RVTITADKSTSTAYMELSSLRSED TAVYYCAR**ARQLDWFVY**WGQGTLVTVSS
	hBEW-5C3VH.2a	EIQLVQSGAEVKKPGSSVKVSCKAS**GYTFT** **NYGVY**WVKQAPGQGLEYMG**WINTETGKPTY** **ADDFKG**RFTFTLDKSTSTAYMELSSLRSED TAVYFCAR**ARQLDWFVY**WGQGTLVTVSS
	hBEW-5C3VH.2b	EVQLVQSGAEVKKPGSSVKVSCKAS**GYTFT** **NYGVY**WVRQAPGQGLEWMG**WINTETGKPTY** **ADDFKG**RFTFTLDKSTSTAYMELSSLRSED TAVYYCAR**ARQLDWFVY**WGQGTLVTVSS
	hBEW-5C3VH.2C	EIQLVQSGAEVKKPGSSVKVSCKAS**GYTFT** **NYGVY**WVKQAPGQGLEYMG**WINTETGKPTY** **ADDFKG**RFVFTLDKSTSTAYLELSSLRSED TAVFFCAR**ARQLDWFVY**WGQGTLVTVSS
	hBEW-5C3VL.1	EIVLTQSPATLSLSPGERATLSC**RARESLT** **TSLC**WYQQKPGQAPRLLIY**GASKLES**GIPA RFSGSGSGTDFTLTISSLEPEDFAVYYC**QQ** **SWYDPPT**FGGGTKVEIK
	hBEW-5C3VL.1a	DTVLTQSPATLSLSPGERATLSC**RARESLT** **TSLS**WFQQKPGQQPRLLIY**GASKLES**GVPA RFSGSGSGTDFTLTISSLEPEDFAVYFC**QQ** **SWYDPPT**FGGGTKVEIK
	hBEW-5C3VL.1b	DTVLTQSPATLSLSPGERATLSC**RARESLT** **TSLS**WFQQKPGQAPRLLIY**GASKLES**GIPA RFSGSGSGTDFTLTISSLEPEDFAVYFC**QQ** **SWYDPPT**FGGGTKVEIK
	hBEW-5C3VL.1c	DTVLTQSPATLSLSPGERATLSC**RARESLT** **TSLS**WYQQKPGQAPRLLIYgasklesGIPA RFSGSGSGTDFTLTISSLEPEDFAVYYC**QQ** **SWYDPPT**FGGGTKVEIK
	hBEW-5C3VL.2	AIQLTQSPSSLSASVGDRVTITC**RARESLT** **TSLS**WYQQKPGKAPKLLIY**GASKLES**GVPS RFSGSGSGTDFTLTISSLQPEDFATYYC**QQ** **SWYDPPT**FGGGTKVEIK
	hBEW-5C3VL.2a	DTQLTQSPSSLSASVGDRVTISC**RARESLT** **TSLS**WFQQKPGKQPKLLIY**GASKLES**GVPS RFSGSGSGTDFTLTISSLQPEDFATYFC**QQ** **SWYDPPT**FGGGTKVEIK
	hBEW-5C3VL.2b	DTQLTQSPSSLSASVGDRVTITC**RARESLT** **TSLS**WFQQKPGKAPKLLIY**GASKLES**GVPS RFSGSGSGTDFTLTISSLQPEDFATYFC**QQ** **SWYDPPT**FGGGTKVEIK
	hBEW-5C3VL.2c	DTQLTQSPSSLSASVGDRVTITC**RARESLT** **TSLS**WYQQKPGKAPKLLIY**GASKLES**GVPS RFSGSGSGTDFTLTISSLQPEDFATYYC**QQ** **SWYDPPT**FGGGTKVEIK

- **hBEW-5C3VH.1z** is a CDR-grafted, humanized BEW-5C3 VH containing IGHV7-4-1*01 and IGHJ1*01 framework sequences.
- **hBEW-5C3VH.1** is based on .1z with a Q1E change to prevent pyroglutamate formation.

- **hBEW-5C3VH.1a** is a humanized design based on .1 and contains three proposed framework back-mutations (V2I, R38K, W47Y).
- **hBEW-5C3VH.1b** is a humanized design based on .1 and contains five proposed framework back-mutations (V2I, R38K, W47Y, Y90F, Y91F).
- **hBEW-5C3VH.2z** is a CDR-grafted, humanized BEW-5C3 VH containing IGHV1-69*06 and IGHJ1*01 framework sequences.
- **hBEW-5C3VH.2** is based on .2z with a Q1E change to prevent pyroglutamate formation.
- **hBEW-5C3VH.2a** is a humanized design based on .2 and contains seven proposed framework back-mutations (V2I, R38K, W47Y, V67F, I69F, A71L, Y91F).
- **hBEW-5C3VH.2b** is an intermediate design between .2 and .2a and contains three proposed framework back-mutations (V67F, I69F, A71L).
- **hBEW-5C3VH.2c** is a humanized design based on .2 and contains ten proposed framework back-mutations (V2I, R38K, W47Y, V67F, T68V, I69F, A71L, M80L, Y90F, Y91F).
- **hBEW-5C3VL.1** is a CDR-grafted, humanized BEW-5C3 VL containing IGKV3-11*01 and IGKJ4*01 framework sequences.
- **hBEW-5C3VL.1a** is a humanized design based on .1 and contains six proposed framework back-mutations (E1D, I2T, Y36F, A43Q, I58V, Y87F).
- **hBEW-5C3VL.1b** is an intermediate design between .1 and 1a. It contains four proposed framework back-mutations (E1D, I2T, Y36F, Y87F).
- **hBEW-5C3VL.1c** is a design based on .1b and contains two proposed framework back-mutations (E1D, I2T)
- **hBEW-5C3VL.2** is a CDR-grafted, humanized BEW-5C3 VL containing IGKV1-13*01 and IGKJ4*01 framework sequences.
- **hBEW-5C3VL.2a** is a humanized design based on .2 and contains six proposed framework back-mutations (A1D, I2T, T22S, Y36F, A43Q, Y87F).
- **hBEW-5C3VL.2b** is an intermediate design between .2 and 2a. It contains four proposed framework back-mutations (A1D, I2T, Y36F, Y87F).
- **hBEW-5C3VL.2c** is a design based on .2b and contains two proposed framework back-mutations (A1D, I2T)

Example 6.2.4.7: BEW-9E10

Table 2.4.7. Sequences of Humanized BEW-9E10 Variable Regions

SEQ ID NO:	Protein region	Sequence
		123456789**0**123456789**0**1234567890
	hBEW-9E10VH.1z	QVQLVQSGSELKKPGASVKVSCKAS**GYTFT NYGMY**WVRQAPGQGLEWMG**WIDTETGRPTY ADDFKG**RFVFSLDTSVSTAYLQISSLKAED TAVYYCAR**WSGDTTGIRGPWFAY**WGQGTLV TVSS
	hBEW-9E10VH.1	EVQLVQSGSELKKPGASVKVSCKAS**GYTFT NYGMY**WVRQAPGQGLEWMG**WIDTETGRPTY ADDFKG**RFVFSLDTSVSTAYLQISSLKAED TAVYYCAR**WSGDTTGIRGPWFAY**WGQGTLV TVSS
	hBEW-9E10VH.1a	EIQLVQSGSELKKPGASVKVSCKAS**GYTFT NYGMY**WVKQAPGQGLEYMG**WIDTETGRPTY ADDFKG**RFVFSLDTSVSTAYLQISSLKAED TAVYFCAR**WSGDTTGIRGPWFAY**WGQGTLV TVSS
	hBEW-9E10VH.2z	QVQLVQSGAEVKKPGSSVKVSCKAS**GYTFT NYGMY**WVRQAPGQGLEWMG**WIDTETGRPTY ADDFKG**RVTITADKSTSTAYMELSSLRSED TAVYYCAR**WSGDTTGIRGPWFAY**WGQGTLV TVSS
	hBEW-9E10VH.2	EVQLVQSGAEVKKPGSSVKVSCKAS**GYTFT NYGMY**WVRQAPGQGLEWMG**WIDTETGRPTY ADDFKG**RVTITADKSTSTAYMELSSLRSED TAVYYCAR**WSGDTTGIRGPWFAY**WGQGTLV TVSS
	hBEW-9E10VH.2a	EIQLVQSGAEVKKPGSSVKVSCKAS**GYTFT NYGMY**WVKQAPGQGLEYMG**WIDTETGRPTY ADDFKG**RFTFTADKSTSTAYMELSSLRSED TAVYFCAR**WSGDTTGIRGPWFAY**WGQGTLV TVSS
	hBEW-9E10VH.2b	EVQLVQSGAEVKKPGSSVKVSCKAS**GYTFT NYGMY**WVRQAPGQGLEWMG**WIDTETGRPTY ADDFKG**RFTFTADKSTSTAYMELSSLRSED TAVYYCAR**WSGDTTGIRGPWFAY**WGQGTLV TVSS
	hBEW-9E10VL.1	DIQMTQSPSSLSASVGDRVTITC**LASEDIY SDLA**WYQQKPGKVPKLLIY**NANGLQN**GVPS RFSGSGSGTDFTLTISSLQPEDVATYYC**QQ YNYFPGT**FGQGTKLEIK
	hBEW-9E10VL.1a	DIRMTQSPSSLSASVGDRVTIEC**LASEDIY SDLA**WYQQKPGKSPKLLIY**NANGLQN**GVPS RFSGSGSGTDYSLTISSLQPEDVATYFC**QQ YNYFPGT**FGQGTKLEIK
	hBEW-9E10VL.1b	DIRMTQSPSSLSASVGDRVTITC**LASEDIY SDLA**WYQQKPGKSPKLLIY**NANGLQN**GVPS RFSGSGSGTDYTLTISSLQPEDVATYFC**QQ YNYFPGT**FGQGTKLEIK

- **hBEW-9E10VH.1z** is a CDR-grafted, humanized BEW-9E10 VH containing IGHV7-4-1*01 and IGHJ1*01 framework sequences.

- **hBEW-9E10VH.1** is based on .1z with a Q1E change to prevent pyroglutamate formation.
- **hBEW-9E10VH.1a** is a humanized design based on .1 and contains four proposed framework back-mutations (V2I, R38K, W47Y, Y91F).
- **hBEW-9E10VH.2z** is a CDR-grafted, humanized BEW-9E10 VH containing IGHV1-69*06 and IGHJ1*01 framework sequences.
- **hBEW-9E10VH.2** is based on .2z with a Q1E change to prevent pyroglutamate formation.
- **hBEW-9E10VH.2a** is a humanized design based on .2 and contains six proposed framework back-mutations (V2I, R38K, W47Y, V67F, I69F, Y91F).
- **hBEW-9E10VH.2b** is an intermediate design between .2 and .2a and contains two proposed framework back-mutations: (V67F, I69F).
- **hBEW-9E10VL.1** is a CDR-grafted, humanized BEW-9E10 VL containing IGKV1-27*01 and IGKJ2*01 framework sequences.
- **hBEW-9E10VL.1a** is a humanized design based on .1 and contains six proposed framework back-mutations (Q3R, T22E, V43S, F71Y, T72S, Y87F).
- **hBEW-9E10VL.1b** is an intermediate design between .1 and 1a. It contains four proposed framework back-mutations (Q3R, V43S, F71Y, Y87F).

Example 6.2.4.8: BEW-1B10

Table 2.4.8. Sequences of Humanized BEW-1B10 Variable Regions

SEQ ID NO:	Protein region	Sequence
		123456789**0**123456789**0**123456789**0**
	hBEW-1B10VH.1	EVQLVESGGGLVQPGGSLRLSCAAS**GFSFS KYDMA**WVRQAPGKGLEWVA**SITTSGVGTYY RDSVKG**RFTISRDNAKNSLYLQMNSLRAED TAVYYCAR**GYGAMDA**WGQGTTVTVSS
	hBEW-1B10VH.1a	EVQLVESGGGLVQPGGSLRLSCAAS**GFSFS KYDMA**WFRQAPGKGLEWVA**SITTSGVGTYY RDSVKG**RFTVSRDNAKSTLYLQMNSLRAED TAVYYCAR**GYGAMDA**WGQGTTVTVSS
	hBEW-1B10VH.1b	EVQLVESGGGLVQPGGSLRLSCAAS**GFSFS KYDMA**WFRQAPGKGLEWVA**SITTSGVGTYY RDSVKG**RFTVSRDNAKNSLYLQMNSLRAED TAVYYCAR**GYGAMDA**WGQGTTVTVSS
	hBEW-1B10VL.1	DIQMTQSPSSLSASVGDRVTITC**KASQDID DYLS**WYQQKPGKAPKLLIY**AATRLAD**GVPS RFSGSGSGTDFTLTISSLQPEDFATYYC**LQ SSSTPWT**FGGGTKVEIK
	hBEW-1B10VL.1a	DIQMTQSPSSLSASVGDRVTITC**KASQDID DYLS**WYQQKPGKSPKLVIY**AATRLAD**GVPS RFSGSGSGTDYTLTISSLQPEDFATYYC**LQ SSSTPWT**FGGGTKVEIK

SEQ ID NO:	Protein region	Sequence
		123456789**0**123456789**0**1234567890
	hBEW-1B10VL.1b	DIQMTQSPSSLSASVGDRVTITC**KASQDID DYLS**WYQQKPGKSPKLLIY**AATRLAD**GVPS RFSGSGSGTDYTLTISSLQPEDFATYYC**LQ SSSTPWT**FGGGTKVEIK

- **hBEW-1B10VH.1** is a CDR-grafted, humanized BEW-1B10 VH containing IGHV3-7*01 and IGHJ6*01 framework sequences.
- **hBEW-1B10VH.1a** is a humanized design based on .1 and contains four proposed framework back-mutations (V37F, I69V, N76S, S77T).
- **hBEW-1B10VH.1b** is an intermediate design between .1 and .1a and contains two proposed framework back-mutations: (V37F, I69V).
- **hBEW-9E10VH.1z** is a CDR-grafted, humanized BEW-9E10 VH containing IGHV7-4-1*01 and IGHJ1*01 framework sequences.
- **hBEW-9E10VH.1** is based on .1z with a Q1E change to prevent pyroglutamate formation.
- **hBEW-1B10VL.1** is a CDR-grafted, humanized BEW-1B10 VL containing IGKV1-39*01 and IGKJ4*01 framework sequences.
- **hBEW-1B10VL.1a** is a humanized design based on .1 and contains three proposed framework back-mutations: (A43S, L47V, F71Y).
- **hBEW-1B10VL.1b** is an intermediate design between .1 and 1a. It contains two proposed framework back-mutations (A43S, F71Y).

Example 6.2.4.9: BEW-1E3

Table 2.4.9. Sequences of Humanized BEW-1E3 Variable Regions

SEQ ID NO:	Protein region	Sequence
		123456789**0**123456789**0**1234567890
	hBEW-1E3VH.1z	QVQLVQSGSELKKPGASVKVSCKAS**GYPFT NSGMY**WVRQAPGQGLEWMG**WINTEAGKPTY ADDFKG**RFVFSLDTSVSTAYLQISSLKAED TAVYYCAR**WGYISDNSYGWFDY**WGQGTLVT VSS
	hBEW-1E3VH.1	EVQLVQSGSELKKPGASVKVSCKAS**GYPFT NSGMY**WVRQAPGQGLEWMG**WINTEAGKPTY ADDFKG**RFVFSLDTSVSTAYLQISSLKAED TAVYYCAR**WGYISDNSYGWFDY**WGQGTLVT VSS

SEQ ID NO:	Protein region	Sequence
		123456789**0**123456789**0**1234567890
	hBEW-1E3VH.1a	EIQLVQSGSELKKPGASVKVSCKAS**GYPFT NSGMY**WVKQAPGQGLEYMG**WINTEAGKPTY ADDFKG**RFVFSLDTSVSTAYLQISSLKAED TAVYFCAR**WGYISDNSYGWFDY**WGQGTLVT VSS
	hBEW-1E3VH.2z	QVQLVQSGAEVKKPGASVKVSCKAS**GYPFT NSGMY**WVRQAPGQGLEWMG**WINTEAGKPTY ADDFKG**RVTMTTDTSTSTAYMELRSLRSDD TAVYYCAR**WGYISDNSYGWFDY**WGQGTLVT VSS
	hBEW-1E3VH.2	EVQLVQSGAEVKKPGASVKVSCKAS**GYPFT NSGMY**WVRQAPGQGLEWMG**WINTEAGKPTY ADDFKG**RVTMTTDTSTSTAYMELRSLRSDD TAVYYCAR**WGYISDNSYGWFDY**WGQGTLVT VSS
	hBEW-1E3VH.2a	EIQLVQSGAEVKKPGASVKVSCKAS**GYPFT NSGMY**WVKQAPGQGLEYMG**WINTEAGKPTY ADDFKG**RFTFTLDTSTSTAYLEIRSLRSDD TAVYFCAR**WGYISDNSYGWFDY**WGQGTLVT VSS
	hBEW-1E3VH.2b	EVQLVQSGAEVKKPGASVKVSCKAS**GYPFT NSGMY**WVRQAPGQGLEWMG**WINTEAGKPTY ADDFKG**RFTFTLDTSTSTAYLEIRSLRSDD TAVYYCAR**WGYISDNSYGWFDY**WGQGTLVT VSS
	hBEW-1E3VL.1	EIVLTQSPATLSLSPGERATLSC**RASEGVY SYMH**WYQQKPGQAPRLLIY**KASNLAS**GIPA RFSGSGSGTDFTLTISSLEPEDFAVYYC**HQ NWNDPLT**FGQGTKLEIK
	hBEW-1E3VL.1a	ETVLTQSPATLSLSPGERATLSC**RASEGVY SYMH**WYQQKPGQQPRLLIY**KASNLAS**GVPA RFSGSGSGTDFTLTISSLEPEDFAVYFC**HQ NWNDPLT**FGQGTKLEIK
	hBEW-1E3VL.1b	EIVLTQSPATLSLSPGERATLSC**RASEGVY SYMH**WYQQKPGQAPRLLIY**KASNLAS**GVPA RFSGSGSGTDFTLTISSLEPEDFAVYFC**HQ NWNDPLT**FGQGTKLEIK
	hBEW-1E3VL.2	AIQLTQSPSSLSASVGDRVTITC**RASEGVY SYMH**WYQQKPGKAPKLLIY**KASNLAS**GVPS RFSGSGSGTDFTLTISSLQPEDFATYYC**HQ NWNDPLT**FGQGTKLEIK
	hBEW-1E3VL.2a	ATQLTQSPSSLSASVGDRVTISC**RASEGVY SYMH**WYQQKPGKQPKLLIY**KASNLAS**GVPS RFSGSGSGTDFTLTISSLQPEDFATYFC**HQ NWNDPLT**FGQGTKLEIK
	hBEW-1E3VL.2b	AIQLTQSPSSLSASVGDRVTITC**RASEGVY SYMH**WYQQKPGKAPKLLIY**KASNLAS**GVPS RFSGSGSGTDFTLTISSLQPEDFATYFC**HQ NWNDPLT**FGQGTKLEIK

- **hBEW-1E3VH.1z** is a CDR-grafted, humanized BEW-1E3 VH containing IGHV7-4-1*01 and IGHJ1*01 framework sequences.
- **hBEW-1E3VH.1** is based on .1z with a Q1E change to prevent pyroglutamate formation.

- **hBEW-1E3VH.1a** is a humanized design based on .1 and contains four proposed framework back-mutations (V2I, R38K, W47Y, Y91F).
- **hBEW-1E3VH.2z** is a CDR-grafted, humanized BEW-1E3 VH containing IGHV1-18*01 and IGHJ1*01 framework sequences.
- **hBEW-1E3VH.2** is based on .2z with a Q1E change to prevent pyroglutamate formation.
- **hBEW-1E3VH.2a** is a humanized design based on .2 and contains seven proposed framework back-mutations (V2I, R38K, W47Y, V67F, M69F, T71L, Y91F).
- **hBEW-1E3VH.2b** is an intermediate design between .2 and .2a and contains three proposed framework back-mutations (V67F, M69F, T71L).
- **hBEW-1E3VL.1** is a CDR-grafted, humanized BEW-1E3 VL containing IGKV3-11*01 and IGKJ2*01 framework sequences.
- **hBEW-1E3VL.1a** is a humanized design based on .1 and contains four proposed framework back-mutations (I2T, A43Q, I58V, Y87F).
- **hBEW-1E3VL.1b** is an intermediate design between .1 and 1a. It contains two proposed framework back-mutations (I58V, Y87F).
- **hBEW-1E3VL.2** is a CDR-grafted, humanized BEW-1E3 VL containing IGKV1-13*01 and IGKJ2*01 framework sequences.
- **hBEW-1E3VL.2a** is a humanized design based on .2 and contains four proposed framework back-mutations (I2T, T22S, A43Q, Y87F).
- **hBEW-1E3VL.2b** is an intermediate design between .2 and 2a. It contains one proposed framework back-mutations Y87F.

Example 6.3: Humanization of VEGFRII Antibodies

Example 6.3.1: Humanization Method

[0359] Antibody humanization is achieved by grafting CDRs of the rodent antibody onto a "similar" human framework (acceptor) and incorporating minimal number of key framework residues (back-mutation) from the rodent antibody that are selected to maintain the original CDR conformation in order to minimize the immunogenicity while retaining the optimal antigen binding.

Example 6.3.2: Human Germline Sequence Selections For Constructing CDR-Grafted, Humanized VEGFRII Antibodies

[0360] By applying the aforementioned method, the CDR sequences of VH and VL chains of monoclonal antibody BCU-6B1-G6 were grafted onto different human heavy and light chain acceptor sequences.

Example 6.3.2.1: BCU-6B1-G6

[0361] Based on the alignments with the VH and VL sequences of monoclonal antibody BCU-6B1-G6 of the present invention, the following known human sequences are selected:

1. IGHV7-4-1*01 and IGHJ1*01 for constructing heavy chain acceptor sequences
2. IGHV1-18*01 and IGHJ1*01 as alternative acceptor for constructing heavy chain
3. IGKV1-27*01 and IGKJ4*01 for constructing light chain acceptor sequences

[0362] By grafting the corresponding VH and VL CDRs of BCU-6B1-G6 into said acceptor sequences, the CDR-grafted, humanized, and modified VH and VL sequences were prepared.

Example 6.3.3: Introducing Potential Framework Back-Mutations In CDR-Grafted Antibodies

[0363] To generate humanized antibody with potential framework back-mutations, the mutations were identified and introduced into the CDR-grafted antibody sequences by *de novo* synthesis of the variable domain, or mutagenic oligonucleotide primers and polymerase chain reactions, or by methods well known in the art. Different combinations of back mutations and other mutations are constructed for each of the CDR-grafts as follows. Residue numbers for these mutations are based on the Kabat numbering system.

Example 6.3.3.1: BCU-6B1-G6

[0364] When IGHV7-4-1*01 and IGHJ1*01 selected as BCU-6B1-G6 heavy chain acceptor sequence, one or more of the following residues could back-mutated as follows: W47→F. Additional mutations include the following: R38→K, Y91→F.

[0365] When IGHV1-18*01 and IGHJ1*01 selected as BCU-6B1-G6 heavy chain acceptor sequence, one or more of the following residues could back-mutated as follows: W47→F, V67→F, M69→F, T71→L. Additional mutations include the following: R38→K, Y91→F.

[0366] When IGKV1-27*01 and IGKJ4*01 selected as BCU-6B1-G6 light chain acceptor sequence, one or more of the following residues could back-mutated as follows: V43→S, Y49→F, F71→Y, Y87→F. Additional mutations include the following: T22→E, T72→S.

Example 6.3.4: Generation Of Humanized Antibodies To VEGFRII Containing Framework Back-Mutations In CDR-Grafted Antibodies

[0367] The following humanized variable regions of the murine monoclonal VEGFRII antibodies were cloned into IgG expression vectors for functional characterization.

Example 6.3.4.1: BCU-6B1-G6

Table 3.4.1. Sequences of Humanized BCU-6B1-G6 Variable Regions

	Protein region	Sequence
		123456789**0**123456789**0**123456789**0**
	hBCU-6B1-G6VH.1z	QVQLVQSGSELKKPGASVKVSCKAS**GYTFT** **NYGMY**WVRQAPGQGLEWMG**WINTETGQPTY** **ADDFKG**RFVFSLDTSVSTAYLQISSLKAED TAVYYCAR**LGNNYGIWFAY**WGQGTLVTVSS
	hBCU-6B1-G6VH.1	EVQLVQSGSELKKPGASVKVSCKAS**GYTFT** **NYGMY**WVRQAPGQGLEWMG**WINTETGQPTY** **ADDFKG**RFVFSLDTSVSTAYLQISSLKAED TAVYYCAR**LGNNYGIWFAY**WGQGTLVTVSS
	hBCU-6B1-G6VH.1a	EVQLVQSGSELKKPGASVKVSCKAS**GYTFT** **NYGMY**WVKQAPGQGLEFMG**WINTETGQPTY** **ADDFKG**RFVFSLDTSVSTAYLQISSLKAED TAVYFCAR**LGNNYGIWFAY**WGQGTLVTVSS
	hBCU-6B1-G6VH.1b	EVQLVQSGSELKKPGASVKVSCKAS**GYTFT** **NYGMY**WVRQAPGQGLEFMG**WINTETGQPTY** **ADDFKG**RFVFSLDTSVSTAYLQISSLKAED TAVYYCAR**LGNNYGIWFAY**WGQGTLVTVSS
	hBCU-6B1-G6VH.2z	QVQLVQSGAEVKKPGASVKVSCKAS**GYTFT** **NYGMY**WVRQAPGQGLEWMG**WINTETGQPTY** **ADDFKG**RVTMTTDTSTSTAYMELRSLRSDD TAVYYCAR**LGNNYGIWFAY**WGQGTLVTVSS
	hBCU-6B1-G6VH.2	EVQLVQSGAEVKKPGASVKVSCKAS**GYTFT** **NYGMY**WVRQAPGQGLEWMG**WINTETGQPTY** **ADDFKG**RVTMTTDTSTSTAYMELRSLRSDD TAVYYCAR**LGNNYGIWFAY**WGQGTLVTVSS
	hBCU-6B1-G6VH.2a	EVQLVQSGAEVKKPGASVKVSCKAS**GYTFT** **NYGMY**WVKQAPGQGLEFMG**WINTETGQPTY** **ADDFKG**RFTFTLDTSTSTAYMELRSLRSDD TAVYFCAR**LGNNYGIWFAY**WGQGTLVTVSS
	hBCU-6B1-G6VH.2b	EVQLVQSGAEVKKPGASVKVSCKAS**GYTFT** **NYGMY**WVRQAPGQGLEFMG**WINTETGQPTY** **ADDFKG**RFTFTLDTSTSTAYMELRSLRSDD TAVYYCAR**LGNNYGIWFAY**WGQGTLVTVSS
	hBCU-6B1-G6VL.1	DIQMTQSPSSLSASVGDRVTITC**RASDDLY** **STLA**WYQQKPGKVPKLLIY**DANRLAA**GVPS RFSGSGSGTDFTLTISSLQPEDVATYYC**QQ** **YNKFPWT**FGGGTKVEIK
	hBCU-6B1-G6VL.1a	DIQMTQSPSSLSASVGDRVTIEC**RASDDLY** **STLA**WYQQKPGKSPKLLIF**DANRLAA**GVPS RFSGSGSGTDYSLTISSLQPEDVATYFC**QQ** **YNKFPWT**FGGGTKVEIK
	hBCU-6B1-G6VL.1b	DIQMTQSPSSLSASVGDRVTITC**RASDDLY** **STLA**WYQQKPGKSPKLLIF**DANRLAA**GVPS RFSGSGSGTDYTLTISSLQPEDVATYFC**QQ** **YNKFPWT**FGGGTKVEIK

- **hBCU-6B1-G6VH.1z** is a CDR-grafted, humanized BCU-6B1-G6 VH containing IGHV7-4-1*01 and IGHJ1*01 framework sequences.
- **hBCU-6B1-G6VH.1** is based on .1z with a Q1E change to prevent pyroglutamate formation.
- **hBCU-6B1-G6VH.1a** is a humanized design based on .1 and contains 3 proposed framework back-mutations: (R38K, W47F, Y91F).
- **hBCU-6B1-G6VH.1b** is an intermediate design between .1 and .1a and contains 1 proposed framework back-mutations: W47F
- **hBCU-6B1-G6VH.2z** is a CDR-grafted, humanized BCU-6B1-G6 VH containing IGHV1-18*01 and IGHJ1*01 framework sequences.
- **hBCU-6B1-G6VH.2** is based on .2z with a Q1E change to prevent pyroglutamate formation.
- **hBCU-6B1-G6VH.2a** is a humanized design based on .2 and contains six proposed framework back-mutations (R38K, W47F, V67F, M69F, T71L, Y91F).
- **hBCU-6B1-G6VH.2b** is an intermediate design between .2 and .2a and contains four proposed framework back-mutations: W47F, V67F, M69F, T71L.
- **hBCU-6B1-G6VL.1** is a CDR-grafted, humanized BCU-6B1-G6 VL containing IGKV1-27*01 and IGKJ4*01 framework sequences.
- **hBCU-6B1-G6VL.1a** is a humanized design based on .1 and contains six proposed framework back-mutations (T22E, V43S, Y49F, F71Y, T72S, Y87F).
- **hBCU-6B1-G6VL.1b** is an intermediate design between .1 and 1a. It contains four proposed framework back-mutations (V43S, Y49F, F71Y, Y87F).

Example 6.4: Humanization of PDGFRB Antibodies

Example 6.4.1: Humanization Method

[0368] Antibody humanization is achieved by grafting CDRs of the rodent antibody onto a "similar" human framework (acceptor) and incorporating minimal number of key framework residues (back-mutation) from the rodent antibody that are selected to maintain the original CDR conformation in order to minimize the immunogenicity while retaining the optimal antigen binding.

Example 6.4.2: Human Germline Sequence Selections For Constructing CDR-Grafted, Humanized PDGFRB Antibodies

[0369] By applying the aforementioned method, the CDR sequences of VH and VL chains of monoclonal antibody BDE-3C9-G4 was grafted onto different human heavy and light chain acceptor sequences.

Example 6.4.2.1: BDE-3C9-G4

[0370] Based on the alignments with the VH and VL sequences of monoclonal antibody BDE-3C9-G4 of the present invention, the following known human sequences are selected:

1. IGHV3-7*01 and IGHJ3*01 for constructing heavy chain acceptor sequences
2. IGKV1-33*01 and IGKJ4*01 for constructing light chain acceptor sequences

[0371] By grafting the corresponding VH and VL CDRs of BDE-3C9-G4 into said acceptor sequences, the CDR-grafted, humanized, and modified VH and VL sequences were prepared.

Example 6.4.3: Introducing Potential Framework Back-Mutations In CDR-Grafted Antibodies

[0372] To generate humanized antibody with potential framework back-mutations, the mutations were identified and introduced into the CDR-grafted antibody sequences by *de novo* synthesis of the variable domain, or mutagenic oligonucleotide primers and polymerase chain reactions, or by methods well known in the art. Different combinations of back mutations and other mutations are constructed for each of the CDR-grafts as follows. Residue numbers for these mutations are based on the Kabat numbering system.

Example 6.4.3.1: BDE-3C9-G4

[0373] When IGHV3-7*01 and IGHJ3*01 selected as BDE-3C9-G4 heavy chain acceptor sequence, one or more of the following residues could back-mutated as follows: S77→T, L78→Q, Y91→F.

[0374] When IGKV1-33*01 and IGKJ4*01 selected as BDE-3C9-G4 light chain acceptor sequence, one or more of the following residues could back-mutated as follows: Q38→L, K45→R, I48→M, Y49→R, T69→R, F71→Y. Additional mutations include the following: V58→T.

Example 6.4.4: Generation Of Humanized Antibodies To PDGFRB Containing Framework Back-Mutations In CDR-Grafted Antibodies

[0375] The following humanized variable regions of the murine monoclonal PDGFRB antibodies were cloned into IgG expression vectors for functional characterization.

Example 6.4.4.1: BDE-3C9-G4

Table 4.4.1. Sequences of Humanized BDE-3C9-G4 Variable Regions

	Protein region	Sequence
		123456789**0**123456789**0**123456789**0**
	hBDE-3C9-G4VH.1	EVQLVESGGGLVQPGGSLRLSCAAS**GFTFS** **NYGMA**WVRQAPGKGLEWVA**SITNSGGNTYY** **RDSVKG**RFTISRDNAKNSLYLQMNSLRAED TAVYYCAR**HTPGANYFDY**WGQGTMVTVSS
	hBDE-3C9-G4VH.1a	EVQLVESGGGLVQPGGSLRLSCAAS**GFTFS** **NYGMA**WVRQAPGKGLEWVA**SITNSGGNTYY** **RDSVKG**RFTISRDNAKNTQYLQMNSLRAED TAVYFCAR**HTPGANYFDY**WGQGTMVTVSS
	hBDE-3C9-G4VL.1	DIQMTQSPSSLSASVGDRVTITC**QASQSIK** **NYIA**WYQQKPGKAPKLLIY**YTSTLES**GVPS RFSGSGSGTDFTFTISSLQPEDIATYYC**VQ** **YANLYT**FGGGTKVEIK
	hBDE-3C9-G4VL.1a	DIQMTQSPSSLSASVGDRVTITC**QASQSIK** **NYIA**WYQLKPGKAPRLLMR**YTSTLES**GTPS RFSGSGSGRDYTFTISSLQPEDIATYYC**VQ** **YANLYT**FGGGTKVEIK
	hBDE-3C9-G4VL.1b	DIQMTQSPSSLSASVGDRVTITC**QASQSIK** **NYIA**WYQQKPGKAPRLLIR**YTSTLES**GVPS RFSGSGSGRDYTFTISSLQPEDIATYYC**VQ** **YANLYT**FGGGTKVEIK

- **hBDE-3C9-G4VH.1** is a CDR-grafted, humanized BDE-3C9-G4 VH containing IGHV3-7*01 and IGHJ3*01 framework sequences.
- **hBDE-3C9-G4VH.1a** is a humanized design based on .1 and contains three proposed framework back-mutations (S77T, L78Q, Y91F).
- **hBDE-3C9-G4VL.1** is a CDR-grafted, humanized BDE-3C9-G4 VL containing IGKV1-33*01 and IGKJ4*01 framework sequences.
- **hBDE-3C9-G4VL.1a** is a humanized design based on .1 and contains seven proposed framework back-mutations (Q38L, K45R, I48M, Y49R, V58T, T69R, F71Y).

- **hBDE-3C9-G4VL.1b** is an intermediate design between .1 and 1a. It contains four proposed framework back-mutations (K45R, Y49R, T69R, F71Y).

Summary of VH and VL Amino Acid Sequences of Humanized Rat Anti-human VEGF-A and Humanized Rat Anti-human PDGF-BB Monoclonal Antibodies

Table 27. VH and VL Amino Acid Sequences of Humanized Rat Anti-Human VEGF-A Monoclonal Antibodies (CDRs in bold)

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				12345678901234567890123456789O
	hBDB-4G8.1 VH			EVQLVQSGSELKKPGASVKVSCKAS**G YTFTNYGMY**WVRQAPGQGLEWMG**WIN TETGKPTYADDFKG**RFVFSLDTSVST AYLQISSLKAEDTAVYYCAR**TNYYYR SYIFYFDY**WGQGTMVTVSS
	hBDB-4G8.1	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBDB-4G8.1	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPTYADDFKG**
	hBDB-4G8.1	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TNYYYRSYIFYFDY**
	hBDB-4G8.1 VL			AIQLTQSPSSLSASVGDRVTITC**RAS ESVSTHMH**WYQQKPGKAPKLLIY**GAS NLES**GVPSRFSGSGSGTDFTLTISSL QPEDFATYYC**QQSWNDPFT**FGQGTKL EIK
	hBDB-4G8.1	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASESVSTHMH**
	hBDB-4G8.1	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	hBDB-4G8.1	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQSWNDPFT**
	hBDB-4G8.10 VH			EIQLVQSGAEVKKPGASVKVSCKAS**G YTFTNYGMY**WVRQAPGQGLEYMG**WIN TETGKPTYADDFKG**RFTFTLDTSTST AYMELRSLRSDDTAVYFCAR**TNYYYR SYIFYFDY**WGQGTMVTVSS
	hBDB-4G8.10	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBDB-4G8.10	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPTYADDFKG**
	hBDB-4G8.10	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TNYYYRSYIFYFDY**
	hBDB-4G8.10 VL			AIQLTQSPSSLSASVGDRVTITC**RAS ESVSTHMH**WYQQKPGKAPKLLIY**GAS NLES**GVPSRFSGSGSGTDFTLTISSL QPEDFATYYC**QQSWNDPFT**FGQGTKL EIK
	hBDB-4G8.10	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASESVSTHMH**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
	hBDB-4G8.10	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	hBDB-4G8.10	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQSWNDPFT**
	hBDB-4G8.11 VH			EIQLVQSGAEVKKPGASVKVSCKAS**G YTFTNYGMY**WVRQAPGQGLEYMG**WIN TETGKPTYADDFKG**RFTFTLDTSTST AYMELRSLRSDDTAVYFCAR**TNYYYR SYIFYFDY**WGQGTMVTVSS
	hBDB-4G8.11	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBDB-4G8.11	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPTYADDFKG**
	hBDB-4G8.11	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TNYYYRSYIFYFDY**
	hBDB-4G8.11 VL			ATQLTQSPSLSASVGDRVTITC**RASE SVSTHMH**WYQQKPGKQPKLLIY**GASN LES**GVPSRFSGSGSGTDFTLTISSLQ PEDFATYFC**QQSWNDPFT**FGQGTKLE IK
	hBDB-4G8.11	CDR-L1	Residues 23-33 of SEQ ID NO.:	**RASESVSTHMH**
	hBDB-4G8.11	CDR-L2	Residues 49-55 of SEQ ID NO.:	**GASNLES**
	hBDB-4G8.11	CDR-L3	Residues 88-96 of SEQ ID NO.:	**QQSWNDPFT**
	hBDB-4G8.12 VH			EIQLVQSGAEVKKPGASVKVSCKAS**G YTFTNYGMY**WVRQAPGQGLEYMG**WIN TETGKPTYADDFKG**RFTFTLDTSTST AYMELRSLRSDDTAVYFCAR**TNYYYR SYIFYFDY**WGQGTMVTVSS
	hBDB-4G8.12	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBDB-4G8.12	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPTYADDFKG**
	hBDB-4G8.12	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TNYYYRSYIFYFDY**
	hBDB-4G8.12 VL			DTVLTQSPATLSLSPGERATLSC**RAS ESVSTHMH**WYQQKPGQAPRLLIY**GAS NLES**GVPARFSGSGSGTDFTLTISSL EPEDFAVYFC**QQSWNDPFT**FGQGTKL EIK
	hBDB-4G8.12	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASESVSTHMH**
	hBDB-4G8.12	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	hBDB-4G8.12	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQSWNDPFT**
	hBDB-4G8.13 VH			EIQLVQSGTEVKKPGESLKISCKAS**G YTFTNYGMY**WVKQMPGKGLEYMG**WIN TETGKPTYADDFKG**RFTFSLDKSFNT

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				AFLQWSSLKASDTAMYFCAR**TNYYYR SYIFYFDY**WGQGTMVTVSS
	hBDB-4G8.13	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBDB-4G8.13	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPTYADDFKG**
	hBDB-4G8.13	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TNYYYRSYIFYFDY**
	hBDB-4G8.13 VL			ETVLTQSPATLSVSPGERATLSC**RAS ESVSTHMH**WYQQKPGQAPRLLIY**GAS NLES**GVPARFSGSGSGTDFTLTISSL QSEDFAVYFC**QQSWNDPFT**FGQGTRL EIK
	hBDB-4G8.13	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASESVSTHMH**
	hBDB-4G8.13	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	hBDB-4G8.13	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQSWNDPFT**
	hBDB-4G8.14 VH			EIQLVQSGGGVVQPGGSLRLSCAAS**G YTFTNYGMY**WVKQAPGKGLEYMG**WIN TETGKPTYADDFKG**RFTFSLDTSKST AYLQLNSLRAEDTAVYFCAR**TNYYYR SYIFYFDY**WGQGTLVTVSS
	hBDB-4G8.14	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBDB-4G8.14	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPTYADDFKG**
	hBDB-4G8.14	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TNYYYRSYIFYFDY**
	hBDB-4G8.14 VL			DTVLTQSPSTLSASPGERATISC**RAS ESVSTHMH**WYQQKPGQAPKLLIY**GAS NLES**GVPSRFSGSRSGTDFTLTISSL QPEDFAVYFC**QQSWNDPFT**FGQGTKV EIK
	hBDB-4G8.14	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASESVSTHMH**
	hBDB-4G8.14	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	hBDB-4G8.14	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQSWNDPFT**
	hBDB-4G8.15 VH			EVQLVESGGGLVQPGGSLRLSCAAS**G YTFTNYGMY**WVKQAPGKGLEYMG**WIN TETGKPTYADDFKG**RFTFSLDTSKST AYLQMNSLRAEDTAVYFCAR**TNYYYR SYIFYFDY**WGQGTLVTVSS
	hBDB-4G8.15	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBDB-4G8.15	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPTYADDFKG**
	hBDB-4G8.15	CDR-H3	Residues 99-	**TNYYYRSYIFYFDY**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
			112 of SEQ ID NO.:	
	hBDB-4G8.15 VL			DTQLTQSPSSLSASVGDRVTISC**RAS ESVSTHMH**WYQQKPGKAPKLLIY**GAS NLES**GVPSRFSGSGSGTDFTLTISSL QPEDFATYFC**QQSWNDPFT**FGQGTKV EIK
	hBDB-4G8.15	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASESVSTHMH**
	hBDB-4G8.15	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	hBDB-4G8.15	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQSWNDPFT**
	hBDB-4G8.2 VH			EVQLVQSGSELKKPGASVKVSCKAS**G YTFTNYGMY**WVRQAPGQGLEWMG**WIN TETGKPTYADDFKG**RFVFSLDTSVST AYLQISSLKAEDTAVYYCAR**TNYYYR SYIFYFDY**WGQGTMVTVSS
	hBDB-4G8.2	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBDB-4G8.2	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPTYADDFKG**
	hBDB-4G8.2	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TNYYYRSYIFYFDY**
	hBDB-4G8.2 VL			ATQLTQSPSLSASVGDRVTITC**RASE SVSTHMH**WYQQKPGKQPKLLIY**GASN LES**GVPSRFSGSGSGTDFTLTISSLQ PEDFATYFC**QQSWNDPFT**FGQGTKLE IK
	hBDB-4G8.2	CDR-L1	Residues 23-33 of SEQ ID NO.:	**RASESVSTHMH**
	hBDB-4G8.2	CDR-L2	Residues 49-55 of SEQ ID NO.:	**GASNLES**
	hBDB-4G8.2	CDR-L3	Residues 88-96 of SEQ ID NO.:	**QQSWNDPFT**
	hBDB-4G8.3 VH			EVQLVQSGSELKKPGASVKVSCKAS**G YTFTNYGMY**WVRQAPGQGLEWMG**WIN TETGKPTYADDFKG**RFVFSLDTSVST AYLQISSLKAEDTAVYYCAR**TNYYYR SYIFYFDY**WGQGTMVTVSS
	hBDB-4G8.3	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBDB-4G8.3	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPTYADDFKG**
	hBDB-4G8.3	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TNYYYRSYIFYFDY**
	hBDB-4G8.3 VL			DTVLTQSPATLSLSPGERATLSC**RAS ESVSTHMH**WYQQKPGQAPRLLIY**GAS NLES**GVPARFSGSGSGTDFTLTISSL EPEDFAVYFC**QQSWNDPFT**FGQGTKL EIK

SEQ ID NO:	Clone	Protein Region	Residues	V Region
	hBDB-4G8.3	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASESVSTHMH**
	hBDB-4G8.3	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	hBDB-4G8.3	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQSWNDPFT**
	hBDB-4G8.4 VH			EIQLVQSGSELKKPGASVKVSCKAS**G** **YTFTNYGMY**WVRQAPGQGLEYMG**WIN** **TETGKPTYADDFKG**RFVFSLDTSVST AYLQISSLKAEDTAVYFCAR**TNYYYR** **SYIFYFDY**WGQGTMVTVSS
	hBDB-4G8.4	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBDB-4G8.4	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPTYADDFKG**
	hBDB-4G8.4	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TNYYYRSYIFYFDY**
	hBDB-4G8.4 VL			AIQLTQSPSSLSASVGDRVTITC**RAS** **ESVSTHMH**WYQQKPGKAPKLLIY**GAS** **NLES**GVPSRFSGSGSGTDFTLTISSL QPEDFATYYC**QQSWNDPFT**FGQGTKL EIK
	hBDB-4G8.4	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASESVSTHMH**
	hBDB-4G8.4	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	hBDB-4G8.4	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQSWNDPFT**
	hBDB-4G8.5 VH			EIQLVQSGSELKKPGASVKVSCKAS**G** **YTFTNYGMY**WVRQAPGQGLEYMG**WIN** **TETGKPTYADDFKG**RFVFSLDTSVST AYLQISSLKAEDTAVYFCAR**TNYYYR** **SYIFYFDY**WGQGTMVTVSS
	hBDB-4G8.5	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBDB-4G8.5	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPTYADDFKG**
	hBDB-4G8.5	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TNYYYRSYIFYFDY**
	hBDB-4G8.5 VL			ATQLTQSPSLSASVGDRVTITC**RASE** **SVSTHMH**WYQQKPGKQPKLLIY**GASN** **LES**GVPSRFSGSGSGTDFTLTISSLQ PEDFATYFC**QQSWNDPFT**FGQGTKLE IK
	hBDB-4G8.5	CDR-L1	Residues 23-33 of SEQ ID NO.:	**RASESVSTHMH**
	hBDB-4G8.5	CDR-L2	Residues 49-55 of SEQ ID NO.:	**GASNLES**
	hBDB-4G8.5	CDR-L3	Residues 88-96 of SEQ ID NO.:	**QQSWNDPFT**
	hBDB-4G8.6 VH			EIQLVQSGSELKKPGASVKVSCKAS**G**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				YTFTNYGMYWVRQAPGQGLEYMG**WIN** **TETGKPTYADDFKG**RFVFSLDTSVST AYLQISSLKAEDTAVYFCAR**TNYYYR** **SYIFYFDY**WGQGTMVTVSS
	hBDB-4G8.6	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBDB-4G8.6	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPTYADDFKG**
	hBDB-4G8.6	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TNYYYRSYIFYFDY**
	hBDB-4G8.6 VL			DTVLTQSPATLSLSPGERATLSC**RAS** **ESVSTHMH**WYQQKPGQAPRLLIY**GAS** **NLES**GVPARFSGSGSGTDFTLTISSL EPEDFAVYFC**QQSWNDPFT**FGQGTKL EIK
	hBDB-4G8.6	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASESVSTHMH**
	hBDB-4G8.6	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	hBDB-4G8.6	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQSWNDPFT**
	hBDB-4G8.7 VH			EVQLVQSGAEVKKPGASVKVSCKAS**G** **YTFTNYGMY**WVRQAPGQGLEWMG**WIN** **TETGKPTYADDFKG**RVTMTTDTSTST AYMELRSLRSDDTAVYYCAR**TNYYYR** **SYIFYFDY**WGQGTMVTVSS
	hBDB-4G8.7	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBDB-4G8.7	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPTYADDFKG**
	hBDB-4G8.7	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TNYYYRSYIFYFDY**
	hBDB-4G8.7 VL			AIQLTQSPSSLSASVGDRVTITC**RAS** **ESVSTHMH**WYQQKPGKAPKLLIY**GAS** **NLES**GVPSRFSGSGSGTDFTLTISSL QPEDFATYYC**QQSWNDPFT**FGQGTKL EIK
	hBDB-4G8.7	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASESVSTHMH**
	hBDB-4G8.7	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	hBDB-4G8.7	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQSWNDPFT**
	hBDB-4G8.8 VH			EVQLVQSGAEVKKPGASVKVSCKAS**G** **YTFTNYGMY**WVRQAPGQGLEWMG**WIN** **TETGKPTYADDFKG**RVTMTTDTSTST AYMELRSLRSDDTAVYYCAR**TNYYYR** **SYIFYFDY**WGQGTMVTVSS
	hBDB-4G8.8	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBDB-4G8.8	CDR-H2	Residues 50-66	**WINTETGKPTYADDFKG**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
			of SEQ ID NO.:	
	hBDB-4G8.8	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TNYYYRSYIFYFDY**
	hBDB-4G8.8 VL			ATQLTQSPSLSASVGDRVTITC**RASE SVSTHMH**WYQQKPGKQPKLLIY**GASN LES**GVPSRFSGSGSGTDFTLTISSLQ PEDFATYFC**QQSWNDPFT**FGQGTKLE IK
	hBDB-4G8.8	CDR-L1	Residues 23-33 of SEQ ID NO.:	**RASESVSTHMH**
	hBDB-4G8.8	CDR-L2	Residues 49-55 of SEQ ID NO.:	**GASNLES**
	hBDB-4G8.8	CDR-L3	Residues 88-96 of SEQ ID NO.:	**QQSWNDPFT**
	hBDB-4G8.9 VH			EVQLVQSGAEVKKPGASVKVSCKAS**G YTFTNYGMY**WVRQAPGQGLEWMG**WIN TETGKPTYADDFKG**RVTMTTDTSTST AYMELRSLRSDDTAVYYCAR**TNYYYR SYIFYFDY**WGQGTMVTVSS
	hBDB-4G8.9	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBDB-4G8.9	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPTYADDFKG**
	hBDB-4G8.9	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TNYYYRSYIFYFDY**
	hBDB-4G8.9 VL			DTVLTQSPATLSLSPGERATLSC**RAS ESVSTHMH**WYQQKPGQAPRLLIY**GAS NLES**GVPARFSGSGSGTDFTLTISSL EPEDFAVYFC**QQSWNDPFT**FGQGTKL EIK
	hBDB-4G8.9	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASESVSTHMH**
	hBDB-4G8.9	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	hBDB-4G8.9	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQSWNDPFT**
	hBEW-1B10.1 VH			EVQLVESGGGLVQPGGSLRLSCAAS**G FSFSKYDMA**WFRQAPGKGLEWVA**SIT TSGVGTYYRDSVKG**RFTVSRDNAKST LYLQMNSLRAEDTAVYYCAR**GYGAMD A**WGQGTTVTVSS
	hBEW-1B10.1	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GFSFSKYDMA**
	hBEW-1B10.1	CDR-H2	Residues 50-66 of SEQ ID NO.:	**SITTSGVGTYYRDSVKG**
	hBEW-1B10.1	CDR-H3	Residues 99-105 of SEQ ID NO.:	**GYGAMDA**
	hBEW-1B10.1 VL			DIQMTQSPSSLSASVGDRVTITC**KAS QDIDDYLS**WYQQKPGKSPKLVIY**AAT RLAD**GVPSRFSGSGSGTDYTLTISSL

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				QPEDFATYYC**LQSSSTPWT**FGGGTKV EIK
	hBEW-1B10.1	CDR-L1	Residues 24-34 of SEQ ID NO.:	**KASQDIDDYLS**
	hBEW-1B10.1	CDR-L2	Residues 50-56 of SEQ ID NO.:	**AATRLAD**
	hBEW-1B10.1	CDR-L3	Residues 89-97 of SEQ ID NO.:	**LQSSSTPWT**
	hBEW-1B10.2 VH			EVQLVESGGGLVQPGGSLRLSCAAS**G FSFSKYDMA**WFRQAPGKGLEWVA**SIT TSGVGTYYRDSVKG**RFTVSRDNAKNS LYLQMNSLRAEDTAVYYCAR**GYGAMD A**WGQGTTVTVSS
	hBEW-1B10.2	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GFSFSKYDMA**
	hBEW-1B10.2	CDR-H2	Residues 50-66 of SEQ ID NO.:	**SITTSGVGTYYRDSVKG**
	hBEW-1B10.2	CDR-H3	Residues 99-105 of SEQ ID NO.:	**GYGAMDA**
	hBEW-1B10.2 VL			DIQMTQSPSSLSASVGDRVTITC**KAS QDIDDYLS**WYQQKPGKSPKLVIY**AAT RLAD**GVPSRFSGSGSGTDYTLTISSL QPEDFATYYC**LQSSSTPWT**FGGGTKV EIK
	hBEW-1B10.2	CDR-L1	Residues 24-34 of SEQ ID NO.:	**KASQDIDDYLS**
	hBEW-1B10.2	CDR-L2	Residues 50-56 of SEQ ID NO.:	**AATRLAD**
	hBEW-1B10.2	CDR-L3	Residues 89-97 of SEQ ID NO.:	**LQSSSTPWT**
	hBEW-1E3.1 VH			EIQLVQSGSELKKPGASVKVSCKAS**G YPFTNSGMY**WVKQAPGQGLEYMG**WIN TEAGKPTYADDFKG**RFVFSLDTSVST AYLQISSLKAEDTAVYFCAR**WGYISD NSYGWFDY**WGQGTLVTVSS
	hBEW-1E3.1	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYPFTNSGMY**
	hBEW-1E3.1	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTEAGKPTYADDFKG**
	hBEW-1E3.1	CDR-H3	Residues 99-112 of SEQ ID NO.:	**WGYISDNSYGWFDY**
	hBEW-1E3.1 VL			ETVLTQSPATLSLSPGERATLSC**RAS EGVYSYMH**WYQQKPGQQPRLLIY**KAS NLAS**GVPARFSGSGSGTDFTLTISSL EPEDFAVYFC**HQNWNDPLT**FGQGTKL EIK
	hBEW-1E3.1	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASEGVYSYMH**
	hBEW-1E3.1	CDR-L2	Residues 50-56 of SEQ ID NO.:	**KASNLAS**
	hBEW-1E3.1	CDR-L3	Residues 89-97	**HQNWNDPLT**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
			of SEQ ID NO.:	
	hBEW-1E3.2 VH			EIQLVQSGAEVKKPGASVKVSCKAS**G** **YPFTNSGMY**WVKQAPGQGLEYMG**WIN** **TEAGKPTYADDFKG**RFTFTLDTSTST AYLEIRSLRSDDTAVYFCAR**WGYISD** **NSYGWFDY**WGQGTLVTVSS
	hBEW-1E3.2	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYPFTNSGMY**
	hBEW-1E3.2	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTEAGKPTYADDFKG**
	hBEW-1E3.2	CDR-H3	Residues 99-112 of SEQ ID NO.:	**WGYISDNSYGWFDY**
	hBEW-1E3.2 VL			ETVLTQSPATLSLSPGERATLSC**RAS** **EGVYSYMH**WYQQKPGQQPRLLIY**KAS** **NLAS**GVPARFSGSGSGTDFTLTISSL EPEDFAVYFC**HQNWNDPLT**FGQGTKL EIK
	hBEW-1E3.2	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASEGVYSYMH**
	hBEW-1E3.2	CDR-L2	Residues 50-56 of SEQ ID NO.:	**KASNLAS**
	hBEW-1E3.2	CDR-L3	Residues 89-97 of SEQ ID NO.:	**HQNWNDPLT**
	hBEW-1E3.3 VH			EVQLVQSGAEVKKPGASVKVSCKAS**G** **YPFTNSGMY**WVRQAPGQGLEWMG**WIN** **TEAGKPTYADDFKG**RFTFTLDTSTST AYLEIRSLRSDDTAVYYCAR**WGYISD** **NSYGWFDY**WGQGTLVTVSS
	hBEW-1E3.3	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYPFTNSGMY**
	hBEW-1E3.3	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTEAGKPTYADDFKG**
	hBEW-1E3.3	CDR-H3	Residues 99-112 of SEQ ID NO.:	**WGYISDNSYGWFDY**
	hBEW-1E3.3 VL			ETVLTQSPATLSLSPGERATLSC**RAS** **EGVYSYMH**WYQQKPGQQPRLLIY**KAS** **NLAS**GVPARFSGSGSGTDFTLTISSL EPEDFAVYFC**HQNWNDPLT**FGQGTKL EIK
	hBEW-1E3.3	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASEGVYSYMH**
	hBEW-1E3.3	CDR-L2	Residues 50-56 of SEQ ID NO.:	**KASNLAS**
	hBEW-1E3.3	CDR-L3	Residues 89-97 of SEQ ID NO.:	**HQNWNDPLT**
	hBEW-1E3.4 VH			EIQLVQSGSELKKPGASVKVSCKAS**G** **YPFTNSGMY**WVKQAPGQGLEYMG**WIN** **TEAGKPTYADDFKG**RFVFSLDTSVST AYLQISSLKAEDTAVYFCAR**WGYISD** **NSYGWFDY**WGQGTLVTVSS

SEQ ID NO:	Clone	Protein Region	Residues	V Region
	hBEW-1E3.4	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYPFTNSGMY**
	hBEW-1E3.4	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTEAGKPTYADDFKG**
	hBEW-1E3.4	CDR-H3	Residues 99-112 of SEQ ID NO.:	**WGYISDNSYGWFDY**
	hBEW-1E3.4 VL			ATQLTQSPSSLSASVGDRVTISC**RAS** **EGVYSYMH**WYQQKPGKQPKLLIY**KAS** **NLAS**GVPSRFSGSGSGTDFTLTISSL QPEDFATYFC**HQNWNDPLT**FGQGTKL EIK
	hBEW-1E3.4	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASEGVYSYMH**
	hBEW-1E3.4	CDR-L2	Residues 50-56 of SEQ ID NO.:	**KASNLAS**
	hBEW-1E3.4	CDR-L3	Residues 89-97 of SEQ ID NO.:	**HQNWNDPLT**
	hBEW-1E3.5 VH			EIQLVQSGAEVKKPGASVKVSCKAS**G** **YPFTNSGMY**WVKQAPGQGLEYMG**WIN** **TEAGKPTYADDFKG**RFTFTLDTSTST AYLEIRSLRSDDTAVYFCAR**WGYISD** **NSYGWFDY**WGQGTLVTVSS
	hBEW-1E3.5	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYPFTNSGMY**
	hBEW-1E3.5	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTEAGKPTYADDFKG**
	hBEW-1E3.5	CDR-H3	Residues 99-112 of SEQ ID NO.:	**WGYISDNSYGWFDY**
	hBEW-1E3.5 VL			ATQLTQSPSSLSASVGDRVTISC**RAS** **EGVYSYMH**WYQQKPGKQPKLLIY**KAS** **NLAS**GVPSRFSGSGSGTDFTLTISSL QPEDFATYFC**HQNWNDPLT**FGQGTKL EIK
	hBEW-1E3.5	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASEGVYSYMH**
	hBEW-1E3.5	CDR-L2	Residues 50-56 of SEQ ID NO.:	**KASNLAS**
	hBEW-1E3.5	CDR-L3	Residues 89-97 of SEQ ID NO.:	**HQNWNDPLT**
	hBEW-5C3.1 VH			EIQLVQSGSELKKPGASVKVSCKAS**G** **YTFTNYGVY**WVKQAPGQGLEYMG**WIN** **TETGKPTYADDFKG**RFVFSLDTSVST AYLQISSLKAEDTAVYYCAR**ARQLDW** **FVY**WGQGTLVTVSS
	hBEW-5C3.1	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGVY**
	hBEW-5C3.1	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPTYADDFKG**
	hBEW-5C3.1	CDR-H3	Residues 99-107 of SEQ ID NO.:	**ARQLDWFVY**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
	hBEW-5C3.1 VL			DTVLTQSPATLSLSPGERATLSC**RAR** **ESLTTSLS**WFQQKPGQQPRLLIY**GAS** **KLES**GVPARFSGSGSGTDFTLTISSL EPEDFAVYFC**QQSWYDPPT**FGGGTKV EIK
	hBEW-5C3.1	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RARESLTTSLS**
	hBEW-5C3.1	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASKLES**
	hBEW-5C3.1	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQSWYDPPT**
	hBEW-5C3.2 VH			EIQLVQSGAEVKKPGSSVKVSCKAS**G** **YTFTNYGVY**WVKQAPGQGLEYMG**WIN** **TETGKPTYADDFKG**RFTFTLDKSTST AYMELSSLRSEDTAVYFCAR**ARQLDW** **FVY**WGQGTLVTVSS
	hBEW-5C3.2	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGVY**
	hBEW-5C3.2	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPTYADDFKG**
	hBEW-5C3.2	CDR-H3	Residues 99-107 of SEQ ID NO.:	**ARQLDWFVY**
	hBEW-5C3.2 VL			DTVLTQSPATLSLSPGERATLSC**RAR** **ESLTTSLS**WFQQKPGQQPRLLIY**GAS** **KLES**GVPARFSGSGSGTDFTLTISSL EPEDFAVYFC**QQSWYDPPT**FGGGTKV EIK
	hBEW-5C3.2	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RARESLTTSLS**
	hBEW-5C3.2	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASKLES**
	hBEW-5C3.2	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQSWYDPPT**
	hBEW-5C3.3 VH			EVQLVQSGAEVKKPGSSVKVSCKAS**G** **YTFTNYGVY**WVRQAPGQGLEWMG**WIN** **TETGKPTYADDFKG**RFTFTLDKSTST AYMELSSLRSEDTAVYYCAR**ARQLDW** **FVY**WGQGTLVTVSS
	hBEW-5C3.3	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGVY**
	hBEW-5C3.3	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPTYADDFKG**
	hBEW-5C3.3	CDR-H3	Residues 99-107 of SEQ ID NO.:	**ARQLDWFVY**
	hBEW-5C3.3 VL			DTVLTQSPATLSLSPGERATLSC**RAR** **ESLTTSLS**WFQQKPGQQPRLLIY**GAS** **KLES**GVPARFSGSGSGTDFTLTISSL EPEDFAVYFC**QQSWYDPPT**FGGGTKV EIK
	hBEW-5C3.3	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RARESLTTSLS**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
	hBEW-5C3.3	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASKLES**
	hBEW-5C3.3	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQSWYDPPT**
	hBEW-5C3.4 VH			EIQLVQSGSELKKPGASVKVSCKAS**G YTFTNYGVY**WVKQAPGQGLEYMG**WIN TETGKPTYADDFKG**RFVFSLDTSVST AYLQISSLKAEDTAVYYCAR**ARQLDW FVY**WGQGTLVTVSS
	hBEW-5C3.4	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGVY**
	hBEW-5C3.4	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPTYADDFKG**
	hBEW-5C3.4	CDR-H3	Residues 99-107 of SEQ ID NO.:	**ARQLDWFVY**
	hBEW-5C3.4 VL			DTQLTQSPSSLSASVGDRVTISC**RAR ESLTTSLS**WFQQKPGKQPKLLIY**GAS KLES**GVPSRFSGSGSGTDFTLTISSL QPEDFATYFC**QQSWYDPPT**FGGGTKV EIK
	hBEW-5C3.4	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RARESLTTSLS**
	hBEW-5C3.4	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASKLES**
	hBEW-5C3.4	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQSWYDPPT**
	hBEW-5C3.5 VH			EIQLVQSGAEVKKPGSSVKVSCKAS**G YTFTNYGVY**WVKQAPGQGLEYMG**WIN TETGKPTYADDFKG**RFTFTLDKSTST AYMELSSLRSEDTAVYFCAR**ARQLDW FVY**WGQGTLVTVSS
	hBEW-5C3.5	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGVY**
	hBEW-5C3.5	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPTYADDFKG**
	hBEW-5C3.5	CDR-H3	Residues 99-107 of SEQ ID NO.:	**ARQLDWFVY**
	hBEW-5C3.5 VL			DTQLTQSPSSLSASVGDRVTISC**RAR ESLTTSLS**WFQQKPGKQPKLLIY**GAS KLES**GVPSRFSGSGSGTDFTLTISSL QPEDFATYFC**QQSWYDPPT**FGGGTKV EIK
	hBEW-5C3.5	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RARESLTTSLS**
	hBEW-5C3.5	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASKLES**
	hBEW-5C3.5	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQSWYDPPT**
	hBEW-5C3.6 VH			EVQLVQSGAEVKKPGSSVKVSCKAS**G YTFTNYGVY**WVRQAPGQGLEWMG**WIN TETGKPTYADDFKG**RFTFTLDKSTST

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				AYMELSSLRSEDTAVYYCAR**ARQLDW FVY**WGQGTLVTVSS
	hBEW-5C3.6	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGVY**
	hBEW-5C3.6	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPTYADDFKG**
	hBEW-5C3.6	CDR-H3	Residues 99-107 of SEQ ID NO.:	**ARQLDWFVY**
	hBEW-5C3.6 VL			DTQLTQSPSSLSASVGDRVTISC**RAR ESLTTSLS**WFQQKPGKQPKLLIY**GAS KLES**GVPSRFSGSGSGTDFTLTISSL QPEDFATYFC**QQSWYDPPT**FGGGTKV EIK
	hBEW-5C3.6	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RARESLTTSLS**
	hBEW-5C3.6	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASKLES**
	hBEW-5C3.6	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQSWYDPPT**
	hBEW-6C2.1 VH			EVQLVESGGGLVQPGGSLRLSCAAS**G FTFSYYGMH**WVRQAPGKGLEWVA**LIY YDSSKMYYADSVKG**RFTISRDNAKNS LYLQMNSLRAEDTAVYYCAR**GGTAPV Y**WGQGTMVTVSS
	hBEW-6C2.1	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GFTFSYYGMH**
	hBEW-6C2.1	CDR-H2	Residues 50-66 of SEQ ID NO.:	**LIYYDSSKMYYADSVKG**
	hBEW-6C2.1	CDR-H3	Residues 99-105 of SEQ ID NO.:	**GGTAPVY**
	hBEW-6C2.1 VL			EIVLTQSPATLSLSPGERATLSC**KGS QNIANYLA**WYQQKPGQAPRLLIY**NTD SLQT**GIPARFSGSGSGTDFTLTISSL EPEDFAVYYC**YQSNNGYT**FGQGTKLE IK
	hBEW-6C2.1	CDR-L1	Residues 24-34 of SEQ ID NO.:	**KGSQNIANYLA**
	hBEW-6C2.1	CDR-L2	Residues 50-56 of SEQ ID NO.:	**NTDSLQT**
	hBEW-6C2.1	CDR-L3	Residues 89-96 of SEQ ID NO.:	**YQSNNGYT**
	hBEW-6C2.2 VH			EVQLVESGGGLVQPGGSLRLSCAAS**G FTFSYYGMH**WVRQAPGKGLEWVA**LIY YDSSKMYYADSVKG**RFTISRDNAKNS LYLQMNSLRAEDTAVYYCAR**GGTAPV Y**WGQGTMVTVSS
	hBEW-6C2.2	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GFTFSYYGMH**
	hBEW-6C2.2	CDR-H2	Residues 50-66 of SEQ ID NO.:	**LIYYDSSKMYYADSVKG**
	hBEW-6C2.2	CDR-H3	Residues 99-	**GGTAPVY**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
			105 of SEQ ID NO.:	
	hBEW-6C2.2 VL			EIVLTQSPATLSLSPGERATLSC**KGS** **QNIANYLA**WYQQKPGQAPRLLIY**NTD** **SLQT**GIPARFSGSGSGTDYTLTISSL EPEDFAVYFC**YQSNNGYT**FGQGTKLE IK
	hBEW-6C2.2	CDR-L1	Residues 24-34 of SEQ ID NO.:	**KGSQNIANYLA**
	hBEW-6C2.2	CDR-L2	Residues 50-56 of SEQ ID NO.:	**NTDSLQT**
	hBEW-6C2.2	CDR-L3	Residues 89-96 of SEQ ID NO.:	**YQSNNGYT**
	hBEW-6C2.3 VH			EVQLVESGGGLVQPGGSLRLSCAAS**G** **FTFSYYGMH**WVRQAPGKGLEWVA**LIY** **YDSSKMYYADSVKG**RFTISRDNAKNS LYLQMNSLRAEDTAVYYCAR**GGTAPV** **Y**WGQGTMVTVSS
	hBEW-6C2.3	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GFTFSYYGMH**
	hBEW-6C2.3	CDR-H2	Residues 50-66 of SEQ ID NO.:	**LIYYDSSKMYYADSVKG**
	hBEW-6C2.3	CDR-H3	Residues 99-105 of SEQ ID NO.:	**GGTAPVY**
	hBEW-6C2.3 VL			DIQMTQSPSSLSASVGDRVTITC**KGS** **QNIANYLA**WYQQKPGKAPKLLIY**NTD** **SLQT**GVPSRFSGSGSGTDFTLTISSL QPEDFATYYC**YQSNNGYT**FGQGTKLE IK
	hBEW-6C2.3	CDR-L1	Residues 24-34 of SEQ ID NO.:	**KGSQNIANYLA**
	hBEW-6C2.3	CDR-L2	Residues 50-56 of SEQ ID NO.:	**NTDSLQT**
	hBEW-6C2.3	CDR-L3	Residues 89-96 of SEQ ID NO.:	**YQSNNGYT**
	hBEW-6C2.4 VH			EVQLVESGGGLVQPGGSLRLSCAAS**G** **FTFSYYGMH**WVRQAPGKGLEWVA**LIY** **YDSSKMYYADSVKG**RFTISRDNAKNS LYLQMNSLRAEDTAVYYCAR**GGTAPV** **Y**WGQGTMVTVSS
	hBEW-6C2.4	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GFTFSYYGMH**
	hBEW-6C2.4	CDR-H2	Residues 50-66 of SEQ ID NO.:	**LIYYDSSKMYYADSVKG**
	hBEW-6C2.4	CDR-H3	Residues 99-105 of SEQ ID NO.:	**GGTAPVY**
	hBEW-6C2.4 VL			DIQLTQSPSSLSASVGDRVTITC**KGS** **QNIANYLA**WYQQKPGKAPKLLIY**NTD** **SLQT**GIPSRFSGSGSGTDYTLTISSL QPEDFATYFC**YQSNNGYT**FGQGTKLE IK

SEQ ID NO:	Clone	Protein Region	Residues	V Region
	hBEW-6C2.4	CDR-L1	Residues 24-34 of SEQ ID NO.:	**KGSQNIANYLA**
	hBEW-6C2.4	CDR-L2	Residues 50-56 of SEQ ID NO.:	**NTDSLQT**
	hBEW-6C2.4	CDR-L3	Residues 89-96 of SEQ ID NO.:	**YQSNNGYT**
	hBEW-6C2.5 VH			EVQLVESGGGLVQPGGSLRLSCAAS**G** **FTFSYYGMH**WIRQAPGKGLEWMA**LIY** **YDSSKMYYADSVKG**RFTISRDNAKNS LYLQMNSLRAEDTAVYYCAA**GGTAPV** **Y**WGQGTMVTVSS
	hBEW-6C2.5	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GFTFSYYGMH**
	hBEW-6C2.5	CDR-H2	Residues 50-66 of SEQ ID NO.:	**LIYYDSSKMYYADSVKG**
	hBEW-6C2.5	CDR-H3	Residues 99-105 of SEQ ID NO.:	**GGTAPVY**
	hBEW-6C2.5 VL			EIVLTQSPATLSLSPGERATLSC**KGS** **QNIANYLA**WYQQKPGQAPRLLIY**NTD** **SLQT**GIPARFSGSGSGTDFTLTISSL EPEDFAVYYC**YQSNNGYT**FGQGTKLE IK
	hBEW-6C2.5	CDR-L1	Residues 24-34 of SEQ ID NO.:	**KGSQNIANYLA**
	hBEW-6C2.5	CDR-L2	Residues 50-56 of SEQ ID NO.:	**NTDSLQT**
	hBEW-6C2.5	CDR-L3	Residues 89-96 of SEQ ID NO.:	**YQSNNGYT**
	hBEW-6C2.6 VH			EVQLVESGGGLVQPGGSLRLSCAAS**G** **FTFSYYGMH**WIRQAPGKGLEWMA**LIY** **YDSSKMYYADSVKG**RFTISRDNAKNS LYLQMNSLRAEDTAVYYCAA**GGTAPV** **Y**WGQGTMVTVSS
	hBEW-6C2.6	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GFTFSYYGMH**
	hBEW-6C2.6	CDR-H2	Residues 50-66 of SEQ ID NO.:	**LIYYDSSKMYYADSVKG**
	hBEW-6C2.6	CDR-H3	Residues 99-105 of SEQ ID NO.:	**GGTAPVY**
	hBEW-6C2.6 VL			EIVLTQSPATLSLSPGERATLSC**KGS** **QNIANYLA**WYQQKPGQAPRLLIY**NTD** **SLQT**GIPARFSGSGSGTDYTLTISSL EPEDFAVYFC**YQSNNGYT**FGQGTKLE IK
	hBEW-6C2.6	CDR-L1	Residues 24-34 of SEQ ID NO.:	**KGSQNIANYLA**
	hBEW-6C2.6	CDR-L2	Residues 50-56 of SEQ ID NO.:	**NTDSLQT**
	hBEW-6C2.6	CDR-L3	Residues 89-96 of SEQ ID NO.:	**YQSNNGYT**
	hBEW-6C2.7 VH			EVQLVESGGGLVQPGGSLRLSCAAS**G**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				FTFSYYGMHWIRQAPGKGLEWMA**LIY** **YDSSKMYYADSVKG**RFTISRDNAKNS LYLQMNSLRAEDTAVYYCAA**GGTAPV** **Y**WGQGTMVTVSS
	hBEW-6C2.7	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GFTFSYYGMH**
	hBEW-6C2.7	CDR-H2	Residues 50-66 of SEQ ID NO.:	**LIYYDSSKMYYADSVKG**
	hBEW-6C2.7	CDR-H3	Residues 99-105 of SEQ ID NO.:	**GGTAPVY**
	hBEW-6C2.7 VL			DIQMTQSPSSLSASVGDRVTITC**KGS** **QNIANYLA**WYQQKPGKAPKLLIY**NTD** **SLQT**GVPSRFSGSGSGTDFTLTISSL QPEDFATYYC**YQSNNGYT**FGQGTKLE IK
	hBEW-6C2.7	CDR-L1	Residues 24-34 of SEQ ID NO.:	**KGSQNIANYLA**
	hBEW-6C2.7	CDR-L2	Residues 50-56 of SEQ ID NO.:	**NTDSLQT**
	hBEW-6C2.7	CDR-L3	Residues 89-96 of SEQ ID NO.:	**YQSNNGYT**
	hBEW-6C2.8 VH			EVQLVESGGGLVQPGGSLRLSCAAS**G** **FTFSYYGMH**WIRQAPGKGLEWMA**LIY** **YDSSKMYYADSVKG**RFTISRDNAKNS LYLQMNSLRAEDTAVYYCAA**GGTAPV** **Y**WGQGTMVTVSS
	hBEW-6C2.8	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GFTFSYYGMH**
	hBEW-6C2.8	CDR-H2	Residues 50-66 of SEQ ID NO.:	**LIYYDSSKMYYADSVKG**
	hBEW-6C2.8	CDR-H3	Residues 99-105 of SEQ ID NO.:	**GGTAPVY**
	hBEW-6C2.8 VL			DIQLTQSPSSLSASVGDRVTITC**KGS** **QNIANYLA**WYQQKPGKAPKLLIY**NTD** **SLQT**GIPSRFSGSGSGTDYTLTISSL QPEDFATYFC**YQSNNGYT**FGQGTKLE IK
	hBEW-6C2.8	CDR-L1	Residues 24-34 of SEQ ID NO.:	**KGSQNIANYLA**
	hBEW-6C2.8	CDR-L2	Residues 50-56 of SEQ ID NO.:	**NTDSLQT**
	hBEW-6C2.8	CDR-L3	Residues 89-96 of SEQ ID NO.:	**YQSNNGYT**
	hBEW-9A8.1 VH			EVQLVQSGHEVKQPGASVKVSCKAS**G** **YTFTNYGMY**WVPQAPGQGLEWMG**WIN** **TETGKPIYADDFKG**RFVFSMDTSAST AYLQISSLKAEDMAMYYCAR**VDYDGS** **FWFAY**WGQGTLVTVSS
	hBEW-9A8.1	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBEW-9A8.1	CDR-H2	Residues 50-66	**WINTETGKPIYADDFKG**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
			of SEQ ID NO.:	
	hBEW-9A8.1	CDR-H3	Residues 99-109 of SEQ ID NO.:	**VDYDGSFWFAY**
	hBEW-9A8.1 VL			EIVLTQSPDFQSVTPKEKVTITC**RAS** **ESVSTVIH**WYQQKPDQSPKLLIK**GAS** **NLES**GVPSRFSGSGSGTDFTLTINSL EAEDAATYYC**QQHWNDPPT**FGQGTKL EIK
	hBEW-9A8.1	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASESVSTVIH**
	hBEW-9A8.1	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	hBEW-9A8.1	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQHWNDPPT**
	hBEW-9A8.10 VH			EVQLVQSGAEVKKPGASVKVSCKAS**G** **YTFTNYGMY**WVRQAPGQGLEWMG**WIN** **TETGKPIYADDFKG**RVTMTTDTSTST AYMELRSLRSDDTAVYYCAR**VDYDGS** **FWFAY**WGQGTLVTVSS
	hBEW-9A8.10	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBEW-9A8.10	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPIYADDFKG**
	hBEW-9A8.10	CDR-H3	Residues 99-109 of SEQ ID NO.:	**VDYDGSFWFAY**
	hBEW-9A8.10 VL			ETVLTQSPDFQSVTPKEKVTITC**RAS** **ESVSTVIH**WYQQKPDQQPKLLIH**GAS** **NLES**GVPSRFSGSGSGTDFTLTINSL EAEDAATYFC**QQHWNDPPT**FGQGTKL EIK
	hBEW-9A8.10	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASESVSTVIH**
	hBEW-9A8.10	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	hBEW-9A8.10	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQHWNDPPT**
	hBEW-9A8.11 VH			EVQLVQSGAEVKKPGASVKVSCKAS**G** **YTFTNYGMY**WVRQAPGQGLEWMG**WIN** **TETGKPIYADDFKG**RVTMTTDTSTST AYMELRSLRSDDTAVYYCAR**VDYDGS** **FWFAY**WGQGTLVTVSS
	hBEW-9A8.11	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBEW-9A8.11	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPIYADDFKG**
	hBEW-9A8.11	CDR-H3	Residues 99-109 of SEQ ID NO.:	**VDYDGSFWFAY**
	hBEW-9A8.11 VL			DIQMTQSPSSLSASVGDRVTITC**RAS** **ESVSTVIH**WYQQKPGKAPKLLIY**GAS** **NLES**GVPSRFSGSGSGTDFTLTISSL

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				QPEDFATYYC**QQHWNDPPT**FGQGTKL EIK
	hBEW-9A8.11	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASESVSTVIH**
	hBEW-9A8.11	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	hBEW-9A8.11	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQHWNDPPT**
	hBEW-9A8.12 VH			EVQLVQSGAEVKKPGASVKVSCKAS**G YTFTNYGMY**WVRQAPGQGLEWMG**WIN TETGKPIYADDFKG**RVTMTTDTSTST AYMELRSLRSDDTAVYYCAR**VDYDGS FWFAY**WGQGTLVTVSS
	hBEW-9A8.12	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBEW-9A8.12	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPIYADDFKG**
	hBEW-9A8.12	CDR-H3	Residues 99-109 of SEQ ID NO.:	**VDYDGSFWFAY**
	hBEW-9A8.12 VL			DTQLTQSPSSLSASVGDRVTITC**RAS ESVSTVIH**WYQQKPGKQPKLLIH**GAS NLES**GVPSRFSGSGSGTDFTLTISSL QPEDFATYFC**QQHWNDPPT**FGQGTKL EIK
	hBEW-9A8.12	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASESVSTVIH**
	hBEW-9A8.12	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	hBEW-9A8.12	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQHWNDPPT**
	hBEW-9A8.13 VH			EIQLVQSGAEVKKPGASVKVSCKAS**G YTFTNYGMY**WVKQAPGQGLEYMG**WIN TETGKPIYADDFKG**RFTFTLDTSTST AYMELRSLRSDDTAVFFCAR**VDYDGS FWFAY**WGQGTLVTVSS
	hBEW-9A8.13	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBEW-9A8.13	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPIYADDFKG**
	hBEW-9A8.13	CDR-H3	Residues 99-109 of SEQ ID NO.:	**VDYDGSFWFAY**
	hBEW-9A8.13 VL			EIVLTQSPDFQSVTPKEKVTITC**RAS ESVSTVIH**WYQQKPDQSPKLLIK**GAS NLES**GVPSRFSGSGSGTDFTLTINSL EAEDAATYYC**QQHWNDPPT**FGQGTKL EIK
	hBEW-9A8.13	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASESVSTVIH**
	hBEW-9A8.13	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	hBEW-9A8.13	CDR-L3	Residues 89-97	**QQHWNDPPT**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
			of SEQ ID NO.:	
	hBEW-9A8.14 VH			EIQLVQSGAEVKKPGASVKVSCKAS**G** **YTFTNYGMY**WVKQAPGQGLEYMG**WIN** **TETGKPIYADDFKG**RFTFTLDTSTST AYMELRSLRSDDTAVFFCAR**VDYDGS** **FWFAY**WGQGTLVTVSS
	hBEW-9A8.14	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBEW-9A8.14	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPIYADDFKG**
	hBEW-9A8.14	CDR-H3	Residues 99-109 of SEQ ID NO.:	**VDYDGSFWFAY**
	hBEW-9A8.14 VL			ETVLTQSPDFQSVTPKEKVTITC**RAS** **ESVSTVIH**WYQQKPDQQPKLLIH**GAS** **NLES**GVPSRFSGSGSGTDFTLTINSL EAEDAATYFC**QQHWNDPPT**FGQGTKL EIK
	hBEW-9A8.14	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASESVSTVIH**
	hBEW-9A8.14	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	hBEW-9A8.14	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQHWNDPPT**
	hBEW-9A8.15 VH			EIQLVQSGAEVKKPGASVKVSCKAS**G** **YTFTNYGMY**WVKQAPGQGLEYMG**WIN** **TETGKPIYADDFKG**RFTFTLDTSTST AYMELRSLRSDDTAVFFCAR**VDYDGS** **FWFAY**WGQGTLVTVSS
	hBEW-9A8.15	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBEW-9A8.15	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPIYADDFKG**
	hBEW-9A8.15	CDR-H3	Residues 99-109 of SEQ ID NO.:	**VDYDGSFWFAY**
	hBEW-9A8.15 VL			DIQMTQSPSSLSASVGDRVTITC**RAS** **ESVSTVIH**WYQQKPGKAPKLLIY**GAS** **NLES**GVPSRFSGSGSGTDFTLTISSL QPEDFATYYC**QQHWNDPPT**FGQGTKL EIK
	hBEW-9A8.15	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASESVSTVIH**
	hBEW-9A8.15	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	hBEW-9A8.15	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQHWNDPPT**
	hBEW-9A8.16 VH			EIQLVQSGAEVKKPGASVKVSCKAS**G** **YTFTNYGMY**WVKQAPGQGLEYMG**WIN** **TETGKPIYADDFKG**RFTFTLDTSTST AYMELRSLRSDDTAVFFCAR**VDYDGS** **FWFAY**WGQGTLVTVSS

SEQ ID NO:	Clone	Protein Region	Residues	V Region
	hBEW-9A8.16	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBEW-9A8.16	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPIYADDFKG**
	hBEW-9A8.16	CDR-H3	Residues 99-109 of SEQ ID NO.:	**VDYDGSFWFAY**
	hBEW-9A8.16 VL			DTQLTQSPSSLSASVGDRVTITC**RAS** **ESVSTVIH**WYQQKPGKQPKLLIH**GAS** **NLES**GVPSRFSGSGSGTDFTLTISSL QPEDFATYFC**QQHWNDPPT**FGQGTKL EIK
	hBEW-9A8.16	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASESVSTVIH**
	hBEW-9A8.16	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	hBEW-9A8.16	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQHWNDPPT**
	hBEW-9A8.17 VH			EIQLVQSGSELKKPGASVKVSCKAS**G** **YTFTNYGMY**WVKQAPGQGLEYMG**WIN** **TETGKPIYADDFKG**RFVFSLDTSVST AYLQISSLKAEDTAVYYCAR**VDYDGS** **FWFAY**WGQGTLVTVSS
	hBEW-9A8.17	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBEW-9A8.17	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPIYADDFKG**
	hBEW-9A8.17	CDR-H3	Residues 99-109 of SEQ ID NO.:	**VDYDGSFWFAY**
	hBEW-9A8.17 VL			ETVLTQSPATLSLSPGERATLSC**RAS** **ESVSTVIH**WYQQKPGQQPRLLIH**GAS** **NLES**GVPARFSGSGSGTDFTLTISSL EPEDFAVYFC**QQHWNDPPT**FGQGTKL EIK
	hBEW-9A8.17	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASESVSTVIH**
	hBEW-9A8.17	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	hBEW-9A8.17	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQHWNDPPT**
	hBEW-9A8.2 VH			EVQLVQSGHEVKQPGASVKVSCKAS**G** **YTFTNYGMY**WVPQAPGQGLEWMG**WIN** **TETGKPIYADDFKG**RFVFSMDTSAST AYLQISSLKAEDMAMYYCAR**VDYDGS** **FWFAY**WGQGTLVTVSS
	hBEW-9A8.2	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBEW-9A8.2	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPIYADDFKG**
	hBEW-9A8.2	CDR-H3	Residues 99-109 of SEQ ID NO.:	**VDYDGSFWFAY**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
	hBEW-9A8.2 VL			ETVLTQSPDFQSVTPKEKVTITC**RAS** **ESVSTVIH**WYQQKPDQQPKLLIH**GAS** **NLES**GVPSRFSGSGSGTDFTLTINSL EAEDAATYFC**QQHWNDPPT**FGQGTKL EIK
	hBEW-9A8.2	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASESVSTVIH**
	hBEW-9A8.2	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	hBEW-9A8.2	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQHWNDPPT**
	hBEW-9A8.20 VH			EIQLVQSGAEVKKPGASVKVSCKAS**G** **YTFTNYGMY**WVKQAPGQGLEYMG**WIN** **TETGKPIYADDFKG**RFTFTLDTSTST AYMELRSLRSDDTAVYYCAR**VDYDGS** **FWFAY**WGQGTLVTVSS
	hBEW-9A8.20	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBEW-9A8.20	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPIYADDFKG**
	hBEW-9A8.20	CDR-H3	Residues 99-109 of SEQ ID NO.:	**VDYDGSFWFAY**
	hBEW-9A8.20 VL			ETVLTQSPATLSLSPGERATLSC**RAS** **ESVSTVIH**WYQQKPGQQPRLLIH**GAS** **NLES**GVPARFSGSGSGTDFTLTISSL EPEDFAVYFC**QQHWNDPPT**FGQGTKL EIK
	hBEW-9A8.20	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASESVSTVIH**
	hBEW-9A8.20	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	hBEW-9A8.20	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQHWNDPPT**
	hBEW-9A8.21 VH			EIQLVQSGAEVKKPGASVKVSCKAS**G** **YTFTNYGMY**WVRQAPGQGLEWMG**WIN** **TETGKPIYADDFKG**RFTFTLDTSTST AYMELRSLRSDDTAVYYCAR**VDYDGS** **FWFAY**WGQGTLVTVSS
	hBEW-9A8.21	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBEW-9A8.21	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPIYADDFKG**
	hBEW-9A8.21	CDR-H3	Residues 99-109 of SEQ ID NO.:	**VDYDGSFWFAY**
	hBEW-9A8.21 VL			ETVLTQSPATLSLSPGERATLSC**RAS** **ESVSTVIH**WYQQKPGQQPRLLIH**GAS** **NLES**GVPARFSGSGSGTDFTLTISSL EPEDFAVYFC**QQHWNDPPT**FGQGTKL EIK
	hBEW-9A8.21	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASESVSTVIH**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
	hBEW-9A8.21	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	hBEW-9A8.21	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQHWNDPPT**
	hBEW-9A8.3 VH			EVQLVQSGHEVKQPGASVKVSCKAS**G** **YTFTNYGMY**WVPQAPGQGLEWMG**WIN** **TETGKPIYADDFKG**RFVFSMDTSAST AYLQISSLKAEDMAMYYCAR**VDYDGS** **FWFAY**WGQGTLVTVSS
	hBEW-9A8.3	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBEW-9A8.3	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPIYADDFKG**
	hBEW-9A8.3	CDR-H3	Residues 99-109 of SEQ ID NO.:	**VDYDGSFWFAY**
	hBEW-9A8.3 VL			DIQMTQSPSSLSASVGDRVTITC**RAS** **ESVSTVIH**WYQQKPGKAPKLLIY**GAS** **NLES**GVPSRFSGSGSGTDFTLTISSL QPEDFATYYC**QQHWNDPPT**FGQGTKL EIK
	hBEW-9A8.3	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASESVSTVIH**
	hBEW-9A8.3	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	hBEW-9A8.3	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQHWNDPPT**
	hBEW-9A8.4 VH			EVQLVQSGHEVKQPGASVKVSCKAS**G** **YTFTNYGMY**WVPQAPGQGLEWMG**WIN** **TETGKPIYADDFKG**RFVFSMDTSAST AYLQISSLKAEDMAMYYCAR**VDYDGS** **FWFAY**WGQGTLVTVSS
	hBEW-9A8.4	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBEW-9A8.4	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPIYADDFKG**
	hBEW-9A8.4	CDR-H3	Residues 99-109 of SEQ ID NO.:	**VDYDGSFWFAY**
	hBEW-9A8.4 VL			DTQLTQSPSSLSASVGDRVTITC**RAS** **ESVSTVIH**WYQQKPGKQPKLLIH**GAS** **NLES**GVPSRFSGSGSGTDFTLTISSL QPEDFATYFC**QQHWNDPPT**FGQGTKL EIK
	hBEW-9A8.4	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASESVSTVIH**
	hBEW-9A8.4	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	hBEW-9A8.4	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQHWNDPPT**
	hBEW-9A8.5 VH			EIQLVQSGHEVKQPGASVKVSCKAS**G** **YTFTNYGMY**WVKQAPGQGLEYMG**WIN** **TETGKPIYADDFKG**RFVFSLDTSAST

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				AYLQISSLKAEDMAMFFCAR**VDYDGS FWFAY**WGQGTLVTVSS
	hBEW-9A8.5	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBEW-9A8.5	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPIYADDFKG**
	hBEW-9A8.5	CDR-H3	Residues 99-109 of SEQ ID NO.:	**VDYDGSFWFAY**
	hBEW-9A8.5 VL			EIVLTQSPDFQSVTPKEKVTITC**RAS ESVSTVIH**WYQQKPDQSPKLLIK**GAS NLES**GVPSRFSGSGSGTDFTLTINSL EAEDAATYYC**QQHWNDPPT**FGQGTKL EIK
	hBEW-9A8.5	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASESVSTVIH**
	hBEW-9A8.5	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	hBEW-9A8.5	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQHWNDPPT**
	hBEW-9A8.6 VH			EIQLVQSGHEVKQPGASVKVSCKAS**G YTFTNYGMY**WVKQAPGQGLEYMG**WIN TETGKPIYADDFKG**RFVFSLDTSAST AYLQISSLKAEDMAMFFCAR**VDYDGS FWFAY**WGQGTLVTVSS
	hBEW-9A8.6	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBEW-9A8.6	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPIYADDFKG**
	hBEW-9A8.6	CDR-H3	Residues 99-109 of SEQ ID NO.:	**VDYDGSFWFAY**
	hBEW-9A8.6 VL			ETVLTQSPDFQSVTPKEKVTITC**RAS ESVSTVIH**WYQQKPDQQPKLLIH**GAS NLES**GVPSRFSGSGSGTDFTLTINSL EAEDAATYFC**QQHWNDPPT**FGQGTKL EIK
	hBEW-9A8.6	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASESVSTVIH**
	hBEW-9A8.6	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	hBEW-9A8.6	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQHWNDPPT**
	hBEW-9A8.7 VH			EIQLVQSGHEVKQPGASVKVSCKAS**G YTFTNYGMY**WVKQAPGQGLEYMG**WIN TETGKPIYADDFKG**RFVFSLDTSAST AYLQISSLKAEDMAMFFCAR**VDYDGS FWFAY**WGQGTLVTVSS
	hBEW-9A8.7	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBEW-9A8.7	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPIYADDFKG**
	hBEW-9A8.7	CDR-H3	Residues 99-	**VDYDGSFWFAY**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
			109 of SEQ ID NO.:	
	hBEW-9A8.7 VL			DIQMTQSPSSLSASVGDRVTITC**RAS** **ESVSTVIH**WYQQKPGKAPKLLIY**GAS** **NLES**GVPSRFSGSGSGTDFTLTISSL QPEDFATYYC**QQHWNDPPT**FGQGTKL EIK
	hBEW-9A8.7	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASESVSTVIH**
	hBEW-9A8.7	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	hBEW-9A8.7	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQHWNDPPT**
	hBEW-9A8.8 VH			EIQLVQSGHEVKQPGASVKVSCKAS**G** **YTFTNYGMY**WVKQAPGQGLEYMG**WIN** **TETGKPIYADDFKG**RFVFSLDTSAST AYLQISSLKAEDMAMFFCAR**VDYDGS** **FWFAY**WGQGTLVTVSS
	hBEW-9A8.8	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBEW-9A8.8	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPIYADDFKG**
	hBEW-9A8.8	CDR-H3	Residues 99-109 of SEQ ID NO.:	**VDYDGSFWFAY**
	hBEW-9A8.8 VL			DTQLTQSPSSLSASVGDRVTITC**RAS** **ESVSTVIH**WYQQKPGKQPKLLIH**GAS** **NLES**GVPSRFSGSGSGTDFTLTISSL QPEDFATYFC**QQHWNDPPT**FGQGTKL EIK
	hBEW-9A8.8	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASESVSTVIH**
	hBEW-9A8.8	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	hBEW-9A8.8	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQHWNDPPT**
	hBEW-9A8.9 VH			EVQLVQSGAEVKKPGASVKVSCKAS**G** **YTFTNYGMY**WVRQAPGQGLEWMG**WIN** **TETGKPIYADDFKG**RVTMTTDTSTST AYMELRSLRSDDTAVYYCAR**VDYDGS** **FWFAY**WGQGTLVTVSS
	hBEW-9A8.9	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBEW-9A8.9	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGKPIYADDFKG**
	hBEW-9A8.9	CDR-H3	Residues 99-109 of SEQ ID NO.:	**VDYDGSFWFAY**
	hBEW-9A8.9 VL			EIVLTQSPDFQSVTPKEKVTITC**RAS** **ESVSTVIH**WYQQKPDQSPKLLIK**GAS** **NLES**GVPSRFSGSGSGTDFTLTINSL EAEDAATYYC**QQHWNDPPT**FGQGTKL EIK

SEQ ID NO:	Clone	Protein Region	Residues	V Region
	hBEW-9A8.9	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASESVSTVIH**
	hBEW-9A8.9	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	hBEW-9A8.9	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQHWNDPPT**
	hBEW-9E10.1 VH			EIQLVQSGSELKKPGASVKVSCKAS**G** **YTFTNYGMY**WVKQAPGQGLEYMG**WID** **TETGRPTYADDFKG**RFVFSLDTSVST AYLQISSLKAEDTAVYFCAR**WSGDTT** **GIRGPWFAY**WGQGTLVTVSS
	hBEW-9E10.1	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBEW-9E10.1	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WIDTETGRPTYADDFKG**
	hBEW-9E10.1	CDR-H3	Residues 99-113 of SEQ ID NO.:	**WSGDTTGIRGPWFAY**
	hBEW-9E10.1 VL			DIRMTQSPSSLSASVGDRVTIEC**LAS** **EDIYSDLA**WYQQKPGKSPKLLIY**NAN** **GLQN**GVPSRFSGSGSGTDYSLTISSL QPEDVATYFC**QQYNYFPGT**FGQGTKL EIK
	hBEW-9E10.1	CDR-L1	Residues 24-34 of SEQ ID NO.:	**LASEDIYSDLA**
	hBEW-9E10.1	CDR-L2	Residues 50-56 of SEQ ID NO.:	**NANGLQN**
	hBEW-9E10.1	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQYNYFPGT**
	hBEW-9E10.2 VH			EIQLVQSGAEVKKPGSSVKVSCKAS**G** **YTFTNYGMY**WVKQAPGQGLEYMG**WID** **TETGRPTYADDFKG**RFTFTADKSTST AYMELSSLRSEDTAVYFCAR**WSGDTT** **GIRGPWFAY**WGQGTLVTVSS
	hBEW-9E10.2	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBEW-9E10.2	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WIDTETGRPTYADDFKG**
	hBEW-9E10.2	CDR-H3	Residues 99-113 of SEQ ID NO.:	**WSGDTTGIRGPWFAY**
	hBEW-9E10.2 VL			DIRMTQSPSSLSASVGDRVTIEC**LAS** **EDIYSDLA**WYQQKPGKSPKLLIY**NAN** **GLQN**GVPSRFSGSGSGTDYSLTISSL QPEDVATYFC**QQYNYFPGT**FGQGTKL EIK
	hBEW-9E10.2	CDR-L1	Residues 24-34 of SEQ ID NO.:	**LASEDIYSDLA**
	hBEW-9E10.2	CDR-L2	Residues 50-56 of SEQ ID NO.:	**NANGLQN**
	hBEW-9E10.2	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQYNYFPGT**
	hBEW-9E10.3 VH			EVQLVQSGAEVKKPGSSVKVSCKAS**G**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				YTFTNYGMYWVRQAPGQGLEWMG**WID** **TETGRPTYADDFKG**RFTFTADKSTST AYMELSSLRSEDTAVYYCAR**WSGDTT** **GIRGPWFAY**WGQGTLVTVSS
	hBEW-9E10.3	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBEW-9E10.3	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WIDTETGRPTYADDFKG**
	hBEW-9E10.3	CDR-H3	Residues 99-113 of SEQ ID NO.:	**WSGDTTGIRGPWFAY**
	hBEW-9E10.3 VL			DIRMTQSPSSLSASVGDRVTIEC**LAS** **EDIYSDLA**WYQQKPGKSPKLLIY**NAN** **GLQN**GVPSRFSGSGSGTDYSLTISSL QPEDVATYFC**QQYNYFPGT**FGQGTKL EIK
	hBEW-9E10.3	CDR-L1	Residues 24-34 of SEQ ID NO.:	**LASEDIYSDLA**
	hBEW-9E10.3	CDR-L2	Residues 50-56 of SEQ ID NO.:	**NANGLQN**
	hBEW-9E10.3	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQYNYFPGT**
	hBEW-9E10.4 VH			EIQLVQSGSELKKPGASVKVSCKAS**G** **YTFTNYGMY**WVKQAPGQGLEYMG**WID** **TETGRPTYADDFKG**RFVFSLDTSVST AYLQISSLKAEDTAVYFCAR**WSGDTT** **GIRGPWFAY**WGQGTLVTVSS
	hBEW-9E10.4	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBEW-9E10.4	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WIDTETGRPTYADDFKG**
	hBEW-9E10.4	CDR-H3	Residues 99-113 of SEQ ID NO.:	**WSGDTTGIRGPWFAY**
	hBEW-9E10.4 VL			DIRMTQSPSSLSASVGDRVTITC**LAS** **EDIYSDLA**WYQQKPGKSPKLLIY**NAN** **GLQN**GVPSRFSGSGSGTDYTLTISSL QPEDVATYFC**QQYNYFPGT**FGQGTKL EIK
	hBEW-9E10.4	CDR-L1	Residues 24-34 of SEQ ID NO.:	**LASEDIYSDLA**
	hBEW-9E10.4	CDR-L2	Residues 50-56 of SEQ ID NO.:	**NANGLQN**
	hBEW-9E10.4	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQYNYFPGT**
	hBEW-9E10.5 VH			EIQLVQSGAEVKKPGSSVKVSCKAS**G** **YTFTNYGMY**WVKQAPGQGLEYMG**WID** **TETGRPTYADDFKG**RFTFTADKSTST AYMELSSLRSEDTAVYFCAR**WSGDTT** **GIRGPWFAY**WGQGTLVTVSS
	hBEW-9E10.5	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBEW-9E10.5	CDR-H2	Residues 50-66	**WIDTETGRPTYADDFKG**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
			of SEQ ID NO.:	
	hBEW-9E10.5	CDR-H3	Residues 99-113 of SEQ ID NO.:	**WSGDTTGIRGPWFAY**
	hBEW-9E10.5 VL			DIRMTQSPSSLSASVGDRVTITC**LAS** **EDIYSDLA**WYQQKPGKSPKLLIY**NAN** **GLQN**GVPSRFSGSGSGTDYTLTISSL QPEDVATYFC**QQYNYFPGT**FGQGTKL EIK
	hBEW-9E10.5	CDR-L1	Residues 24-34 of SEQ ID NO.:	**LASEDIYSDLA**
	hBEW-9E10.5	CDR-L2	Residues 50-56 of SEQ ID NO.:	**NANGLQN**
	hBEW-9E10.5	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQYNYFPGT**
	hBEW-9E10.6 VH			EVQLVQSGAEVKKPGSSVKVSCKAS**G** **YTFTNYGMY**WVRQAPGQGLEWMG**WID** **TETGRPTYADDFKG**RFTFTADKSTST AYMELSSLRSEDTAVYYCAR**WSGDTT** **GIRGPWFAY**WGQGTLVTVSS
	hBEW-9E10.6	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBEW-9E10.6	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WIDTETGRPTYADDFKG**
	hBEW-9E10.6	CDR-H3	Residues 99-113 of SEQ ID NO.:	**WSGDTTGIRGPWFAY**
	hBEW-9E10.6 VL			DIRMTQSPSSLSASVGDRVTITC**LAS** **EDIYSDLA**WYQQKPGKSPKLLIY**NAN** **GLQN**GVPSRFSGSGSGTDYTLTISSL QPEDVATYFC**QQYNYFPGT**FGQGTKL EIK
	hBEW-9E10.6	CDR-L1	Residues 24-34 of SEQ ID NO.:	**LASEDIYSDLA**
	hBEW-9E10.6	CDR-L2	Residues 50-56 of SEQ ID NO.:	**NANGLQN**
	hBEW-9E10.6	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQYNYFPGT**
	AB014 VH			EVQLVESGGGLVQPGGSLR LSCAAS**GYTFTNYGMN**WVR QAPGKGLEWVG**WINTYTGE** **PTYAADFKR**RFTFSLDTSK STAYLQMNSLRAEDTAVYY CAK**YPHYYGSSHWYFDV**WG QGTLVTVSS
	AB014	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMN**
	AB014	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTYTGEPTYAADFKR**
	AB014	CDR-H3	Residues 99-112 of SEQ ID NO.:	**YPHYYGSSHWYFDV**
	AB014 VL			DIQMTQSPSSLSASVGDRV

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				TITC**SASQDISNYLN**WYQQ KPGKAPKVLIY**FTSSLHS**G VPSRFSGSGSGTDFTLTIS SLQPEDFATYYC**QQYSTVP** **WT**FGQGTKVEIK
	AB014	CDR-L1	Residues 24-34 of SEQ ID NO.:	**SASQDISNYLN**
	AB014	CDR-L2	Residues 50-56 of SEQ ID NO.:	**FTSSLHS**
	AB014	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQYSTVPWT**

Table 28. VH and VL Amino Acid Sequences of Humanized Versions of Rat Anti-Human PDGF-BB Monoclonal Antibodies (CDRs in bold)

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				12345678901234567890123456789 0
	hBDI-1E1.1 VH			EVQLVQSGAEVKKPGSSVKVSCKAS**GY** **TFTDYVMH**WVRQAPGQGLEWMG**TIIPL** **IDTTSYNQKFKG**RVTITADKSTSTAYM ELSSLRSEDTAVYYCAR**TSPYYYSSYD** **VMDA**WGQGTTVTVSS
	hBDI-1E1.1	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTDYVMH**
	hBDI-1E1.1	CDR-H2	Residues 50-66 of SEQ ID NO.:	**TIIPLIDTTSYNQKFKG**
	hBDI-1E1.1	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TSPYYYSSYDVMDA**
	hBDI-1E1.1 VL			AIQLTQSPSSLSASVGDRVTITC**KGSQ** **NINNYLA**WYQQKPGKAPKLLIY**KTNNL** **QT**GVPSRFSGSGSGTDFTLTISSLQPE DFATYYC**YQYDNGYT**FGQGTKLEIK
	hBDI-1E1.1	CDR-L1	Residues 24-34 of SEQ ID NO.:	**KGSQNINNYLA**
	hBDI-1E1.1	CDR-L2	Residues 50-56 of SEQ ID NO.:	**KTNNLQT**
	hBDI-1E1.1	CDR-L3	Residues 89-96 of SEQ ID NO.:	**YQYDNGYT**
	hBDI-1E1.10 VH			EVQLVQSGAEVKKPGSSVKVSCKAS**GY** **TFTDYVMH**WVRQAPGQGLEWIG**TIIPL** **IDTTSYNQKFKG**RVTITADKSTSTAYM ELSSLRSEDTAVYYCAR**TSPYYYSSYD** **VMDA**WGQGTTVTVSS
	hBDI-1E1.10	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTDYVMH**
	hBDI-1E1.10	CDR-H2	Residues 50-66 of SEQ ID NO.:	**TIIPLIDTTSYNQKFKG**
	hBDI-1E1.10	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TSPYYYSSYDVMDA**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
	hBDI-1E1.10 VL			AIQLTQSPSSLSASVGDRVTITC**KGSQ** **NINNYLA**WYQQKPGKAPKLLIY**KTNNL** **QT**GIPSRFSGSGSGTDYTLTISSLQPE DFATYYC**YQYDNGYT**FGQGTKLEIK
	hBDI-1E1.10	CDR-L1	Residues 24-34 of SEQ ID NO.:	**KGSQNINNYLA**
	hBDI-1E1.10	CDR-L2	Residues 50-56 of SEQ ID NO.:	**KTNNLQT**
	hBDI-1E1.10	CDR-L3	Residues 89-96 of SEQ ID NO.:	**YQYDNGYT**
	hBDI-1E1.11 VH			EVQLVQSGAEVKKPGSSVKVSCKAS**GY** **TFTDYVMH**WVRQAPGQGLEWIG**TIIPL** **IDTTSYNQKFKG**RVTITADKSTSTAYM ELSSLRSEDTAVYYCAR**TSPYYYSSYD** **VMDA**WGQGTTVTVSS
	hBDI-1E1.11	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTDYVMH**
	hBDI-1E1.11	CDR-H2	Residues 50-66 of SEQ ID NO.:	**TIIPLIDTTSYNQKFKG**
	hBDI-1E1.11	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TSPYYYSSYDVMDA**
	hBDI-1E1.11 VL			EIVLTQSPATLSLSPGERATLSC**KGSQ** **NINNYLA**WYQQKPGQAPRLLIY**KTNNL** **QT**GIPARFSGSGSGTDFTLTISSLEPE DFAVYYC**YQYDNGYT**FGQGTKLEIK
	hBDI-1E1.11	CDR-L1	Residues 24-34 of SEQ ID NO.:	**KGSQNINNYLA**
	hBDI-1E1.11	CDR-L2	Residues 50-56 of SEQ ID NO.:	**KTNNLQT**
	hBDI-1E1.11	CDR-L3	Residues 89-96 of SEQ ID NO.:	**YQYDNGYT**
	hBDI-1E1.12 VH			EVQLVQSGAEVKKPGSSVKVSCKAS**GY** **TFTDYVMH**WVRQAPGQGLEWIG**TIIPL** **IDTTSYNQKFKG**RVTITADKSTSTAYM ELSSLRSEDTAVYYCAR**TSPYYYSSYD** **VMDA**WGQGTTVTVSS
	hBDI-1E1.12	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTDYVMH**
	hBDI-1E1.12	CDR-H2	Residues 50-66 of SEQ ID NO.:	**TIIPLIDTTSYNQKFKG**
	hBDI-1E1.12	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TSPYYYSSYDVMDA**
	hBDI-1E1.12 VL			EIVLTQSPATLSLSPGERATLSC**KGSQ** **NINNYLA**WYQQKPGQAPRLLIY**KTNNL** **QT**GIPARFSGSGSGTDYTLTISSLEPE DFATYYC**YQYDNGYT**FGQGTKLEIK
	hBDI-1E1.12	CDR-L1	Residues 24-34 of SEQ ID NO.:	**KGSQNINNYLA**
	hBDI-1E1.12	CDR-L2	Residues 50-56 of SEQ ID NO.:	**KTNNLQT**
	hBDI-1E1.12	CDR-L3	Residues 89-96	**YQYDNGYT**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
			of SEQ ID NO.:	
	hBDI-1E1.2 VH			EVQLVQSGAEVKKPGSSVKVSCKAS**GY** **TFTDYVMH**WVRQAPGQGLEWMG**TIIPL** **IDTTSYNQKFKG**RVTITADKSTSTAYM ELSSLRSEDTAVYYCAR**TSPYYYSSYD** **VMDA**WGQGTTVTVSS
	hBDI-1E1.2	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTDYVMH**
	hBDI-1E1.2	CDR-H2	Residues 50-66 of SEQ ID NO.:	**TIIPLIDTTSYNQKFKG**
	hBDI-1E1.2	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TSPYYYSSYDVMDA**
	hBDI-1E1.2 VL			AIQLTQSPSSLSASVGDRVTITC**KGSQ** **NINNYLA**WYQQKPGKAPKLLIY**KTNNL** **QT**GIPSRFSGSGSGTDYTLTISSLQPE DFATYYC**YQYDNGYT**FGQGTKLEIK
	hBDI-1E1.2	CDR-L1	Residues 24-34 of SEQ ID NO.:	**KGSQNINNYLA**
	hBDI-1E1.2	CDR-L2	Residues 50-56 of SEQ ID NO.:	**KTNNLQT**
	hBDI-1E1.2	CDR-L3	Residues 89-96 of SEQ ID NO.:	**YQYDNGYT**
	hBDI-1E1.3 VH			EVQLVQSGAEVKKPGSSVKVSCKAS**GY** **TFTDYVMH**WVRQAPGQGLEWMG**TIIPL** **IDTTSYNQKFKG**RVTITADKSTSTAYM ELSSLRSEDTAVYYCAR**TSPYYYSSYD** **VMDA**WGQGTTVTVSS
	hBDI-1E1.3	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTDYVMH**
	hBDI-1E1.3	CDR-H2	Residues 50-66 of SEQ ID NO.:	**TIIPLIDTTSYNQKFKG**
	hBDI-1E1.3	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TSPYYYSSYDVMDA**
	hBDI-1E1.3 VL			EIVLTQSPATLSLSPGERATLSC**KGSQ** **NINNYLA**WYQQKPGQAPRLLIY**KTNNL** **QT**GIPARFSGSGSGTDFTLTISSLEPE DFAVYYC**YQYDNGYT**FGQGTKLEIK
	hBDI-1E1.3	CDR-L1	Residues 24-34 of SEQ ID NO.:	**KGSQNINNYLA**
	hBDI-1E1.3	CDR-L2	Residues 50-56 of SEQ ID NO.:	**KTNNLQT**
	hBDI-1E1.3	CDR-L3	Residues 89-96 of SEQ ID NO.:	**YQYDNGYT**
	hBDI-1E1.4 VH			EVQLVQSGAEVKKPGSSVKVSCKAS**GY** **TFTDYVMH**WVRQAPGQGLEWMG**TIIPL** **IDTTSYNQKFKG**RVTITADKSTSTAYM ELSSLRSEDTAVYYCAR**TSPYYYSSYD** **VMDA**WGQGTTVTVSS
	hBDI-1E1.4	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTDYVMH**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
	hBDI-1E1.4	CDR-H2	Residues 50-66 of SEQ ID NO.:	**TIIPLIDTTSYNQKFKG**
	hBDI-1E1.4	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TSPYYYSSYDVMDA**
	hBDI-1E1.4 VL			EIVLTQSPATLSLSPGERATLSC**KGSQ** **NINNYLA**WYQQKPGQAPRLLIY**KTNNL** **QT**GIPARFSGSGSGTDYTLTISSLEPE DFATYYC**YQYDNGYT**FGQGTKLEIK
	hBDI-1E1.4	CDR-L1	Residues 24-34 of SEQ ID NO.:	**KGSQNINNYLA**
	hBDI-1E1.4	CDR-L2	Residues 50-56 of SEQ ID NO.:	**KTNNLQT**
	hBDI-1E1.4	CDR-L3	Residues 89-96 of SEQ ID NO.:	**YQYDNGYT**
	hBDI-1E1.5 VH			EVQLVQSGAEVKKPGSSVKVSCKAS**GY** **TFTDYVMH**WVRQAPGQGLEWIG**TIIPL** **IDTTSYNQKFKG**RATLTADKSTNTAYM ELSSLRSEDTAVYYCAR**TSPYYYSSYD** **VMDA**WGQGTTVTVSS
	hBDI-1E1.5	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTDYVMH**
	hBDI-1E1.5	CDR-H2	Residues 50-66 of SEQ ID NO.:	**TIIPLIDTTSYNQKFKG**
	hBDI-1E1.5	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TSPYYYSSYDVMDA**
	hBDI-1E1.5 VL			AIQLTQSPSSLSASVGDRVTITC**KGSQ** **NINNYLA**WYQQKPGKAPKLLIY**KTNNL** **QT**GVPSRFSGSGSGTDFTLTISSLQPE DFATYYC**YQYDNGYT**FGQGTKLEIK
	hBDI-1E1.5	CDR-L1	Residues 24-34 of SEQ ID NO.:	**KGSQNINNYLA**
	hBDI-1E1.5	CDR-L2	Residues 50-56 of SEQ ID NO.:	**KTNNLQT**
	hBDI-1E1.5	CDR-L3	Residues 89-96 of SEQ ID NO.:	**YQYDNGYT**
	hBDI-1E1.6 VH			EVQLVQSGAEVKKPGSSVKVSCKAS**GY** **TFTDYVMH**WVRQAPGQGLEWIG**TIIPL** **IDTTSYNQKFKG**RATLTADKSTNTAYM ELSSLRSEDTAVYYCAR**TSPYYYSSYD** **VMDA**WGQGTTVTVSS
	hBDI-1E1.6	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTDYVMH**
	hBDI-1E1.6	CDR-H2	Residues 50-66 of SEQ ID NO.:	**TIIPLIDTTSYNQKFKG**
	hBDI-1E1.6	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TSPYYYSSYDVMDA**
	hBDI-1E1.6 VL			AIQLTQSPSSLSASVGDRVTITC**KGSQ** **NINNYLA**WYQQKPGKAPKLLIY**KTNNL** **QT**GIPSRFSGSGSGTDYTLTISSLQPE DFATYYC**YQYDNGYT**FGQGTKLEIK

SEQ ID NO:	Clone	Protein Region	Residues	V Region
	hBDI-1E1.6	CDR-L1	Residues 24-34 of SEQ ID NO.:	**KGSQNINNYLA**
	hBDI-1E1.6	CDR-L2	Residues 50-56 of SEQ ID NO.:	**KTNNLQT**
	hBDI-1E1.6	CDR-L3	Residues 89-96 of SEQ ID NO.:	**YQYDNGYT**
	hBDI-1E1.7 VH			EVQLVQSGAEVKKPGSSVKVSCKAS**GY** **TFTDYVMH**WVRQAPGQGLEWIG**TIIPL** **IDTTSYNQKFKG**RATLTADKSTNTAYM ELSSLRSEDTAVYYCAR**TSPYYYSSYD** **VMDA**WGQGTTVTVSS
	hBDI-1E1.7	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTDYVMH**
	hBDI-1E1.7	CDR-H2	Residues 50-66 of SEQ ID NO.:	**TIIPLIDTTSYNQKFKG**
	hBDI-1E1.7	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TSPYYYSSYDVMDA**
	hBDI-1E1.7 VL			EIVLTQSPATLSLSPGERATLSC**KGSQ** **NINNYLA**WYQQKPGQAPRLLIY**KTNNL** **QT**GIPARFSGSGSGTDFTLTISSLEPE DFAVYYC**YQYDNGYT**FGQGTKLEIK
	hBDI-1E1.7	CDR-L1	Residues 24-34 of SEQ ID NO.:	**KGSQNINNYLA**
	hBDI-1E1.7	CDR-L2	Residues 50-56 of SEQ ID NO.:	**KTNNLQT**
	hBDI-1E1.7	CDR-L3	Residues 89-96 of SEQ ID NO.:	**YQYDNGYT**
	hBDI-1E1.8 VH			EVQLVQSGAEVKKPGSSVKVSCKAS**GY** **TFTDYVMH**WVRQAPGQGLEWIG**TIIPL** **IDTTSYNQKFKG**RATLTADKSTNTAYM ELSSLRSEDTAVYYCAR**TSPYYYSSYD** **VMDA**WGQGTTVTVSS
	hBDI-1E1.8	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTDYVMH**
	hBDI-1E1.8	CDR-H2	Residues 50-66 of SEQ ID NO.:	**TIIPLIDTTSYNQKFKG**
	hBDI-1E1.8	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TSPYYYSSYDVMDA**
	hBDI-1E1.8 VL			EIVLTQSPATLSLSPGERATLSC**KGSQ** **NINNYLA**WYQQKPGQAPRLLIY**KTNNL** **QT**GIPARFSGSGSGTDYTLTISSLEPE DFATYYC**YQYDNGYT**FGQGTKLEIK
	hBDI-1E1.8	CDR-L1	Residues 24-34 of SEQ ID NO.:	**KGSQNINNYLA**
	hBDI-1E1.8	CDR-L2	Residues 50-56 of SEQ ID NO.:	**KTNNLQT**
	hBDI-1E1.8	CDR-L3	Residues 89-96 of SEQ ID NO.:	**YQYDNGYT**
	hBDI-1E1.9 VH			EVQLVQSGAEVKKPGSSVKVSCKAS**GY** **TFTDYVMH**WVRQAPGQGLEWIG**TIIPL** **IDTTSYNQKFKG**RVTITADKSTSTAYM

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				ELSSLRSEDTAVYYCAR**TSPYYYSSYD VMDA**WGQGTTVTVSS
	hBDI-1E1.9	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTDYVMH**
	hBDI-1E1.9	CDR-H2	Residues 50-66 of SEQ ID NO.:	**TIIPLIDTTSYNQKFKG**
	hBDI-1E1.9	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TSPYYYSSYDVMDA**
	hBDI-1E1.9 VL			AIQLTQSPSSLSASVGDRVTITC**KGSQ NINNYLA**WYQQKPGKAPKLLIY**KTNNL QT**GVPSRFSGSGSGTDFTLTISSLQPE DFATYYC**YQYDNGYT**FGQGTKLEIK
	hBDI-1E1.9	CDR-L1	Residues 24-34 of SEQ ID NO.:	**KGSQNINNYLA**
	hBDI-1E1.9	CDR-L2	Residues 50-56 of SEQ ID NO.:	**KTNNLQT**
	hBDI-1E1.9	CDR-L3	Residues 89-96 of SEQ ID NO.:	**YQYDNGYT**
	hBDI-5H1.1 VH			EVTLRESGPALVKPTQTLTLTCTFS**GF SLSTFGMGVG**WIRQPPGKALEWLA**NIW WDDDKYYNPSLKN**RLTISKDTSKNQVV LTMTNMDPVDTATYYCAR**ISTGISSYY VMDA**WGQGTTVTVSS
	hBDI-5H1.1	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTFGMGVG**
	hBDI-5H1.1	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	hBDI-5H1.1	CDR-H3	Residues 100-112 of SEQ ID NO.:	**ISTGISSYYVMDA**
	hBDI-5H1.1 VL			NFMLTQPHSVSESPGKTVTISC**ERSSG DIGDTYVS**WYQQRPGSSPTTVIY**GNDQ RPS**GVPDRFSGSIDSSSNSASLTISGL KTEDEADYYC**QSYDSDIDIV**FGGGTKL TVL
	hBDI-5H1.1	CDR-L1	Residues 23-35 of SEQ ID NO.:	**ERSSGDIGDTYVS**
	hBDI-5H1.1	CDR-L2	Residues 51-57 of SEQ ID NO.:	**GNDQRPS**
	hBDI-5H1.1	CDR-L3	Residues 92-101 of SEQ ID NO.:	**QSYDSDIDIV**
	hBDI-5H1.10 VH			EVTLRESGPALVKPTQTLTLTCTFS**GF SLSTFGMGVG**WIRQPPGKALEWLA**NIW WDDDKYYNPSLKN**RLTISKDTSKNQAV LTITNMDPVDTATYYCAR**ISTGISSYY VMDA**WGQGTTVTVSS
	hBDI-5H1.10	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTFGMGVG**
	hBDI-5H1.10	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	hBDI-5H1.10	CDR-H3	Residues 100-	**ISTGISSYYVMDA**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
			112 of SEQ ID NO.:	
	hBDI-5H1.10 VL			DFQLTQSPSSLSASVGDRVTITC**ERSS** **GDIGDTYVS**WYQQKPGKAPKNVIY**GND** **QRPS**GVPSRFSGSGSGNSATLTISSLQ PEDFATYFC**QSYDSDIDIV**FGQGTKVE IK
	hBDI-5H1.10	CDR-L1	Residues 24-36 of SEQ ID NO.:	**ERSSGDIGDTYVS**
	hBDI-5H1.10	CDR-L2	Residues 52-58 of SEQ ID NO.:	**GNDQRPS**
	hBDI-5H1.10	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYDSDIDIV**
	hBDI-5H1.11 VH			EVQLVESGGGLVQPGGSLRLSCAFS**GF** **SLSTFGMGVG**WIRQAPGKGLEWLA**NIW** **WDDDKYYNPSLKN**RLTISKDTSKNQAY LQINSLRAEDTAVYYCAR**ISTGISSYY** **VMDA**WGQGTLVTVSS
	hBDI-5H1.11	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTFGMGVG**
	hBDI-5H1.11	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	hBDI-5H1.11	CDR-H3	Residues 100-112 of SEQ ID NO.:	**ISTGISSYYVMDA**
	hBDI-5H1.11 VL			DFVLTQSPDSLAVSLGERATINC**ERSS** **GDIGDTYVS**WYQQKPGQPPKNVIY**GND** **QRPS**GVPDRFSGSGSGNSATLTISSLQ AEDVAVYFC**QSYDSDIDIV**FGGGTKVE IK
	hBDI-5H1.11	CDR-L1	Residues 24-36 of SEQ ID NO.:	**ERSSGDIGDTYVS**
	hBDI-5H1.11	CDR-L2	Residues 52-58 of SEQ ID NO.:	**GNDQRPS**
	hBDI-5H1.11	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYDSDIDIV**
	hBDI-5H1.12 VH			EVQLVESGGGLVQPGGSLRLSCAFS**GF** **SLSTFGMGVG**WIRQAPGKGLEWLA**NIW** **WDDDKYYNPSLKN**RLTISKDTSKNQAY LQINSLRAEDTAVYYCAR**ISTGISSYY** **VMDA**WGQGTLVTVSS
	hBDI-5H1.12	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTFGMGVG**
	hBDI-5H1.12	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	hBDI-5H1.12	CDR-H3	Residues 100-112 of SEQ ID NO.:	**ISTGISSYYVMDA**
	hBDI-5H1.12 VL			DFQLTQSPSSLSASVGDRVTITC**ERSS** **GDIGDTYVS**WYQQKPGKAPKNVIY**GND** **QRPS**GVPSRFSGSGSGNSATLTISSLQ PEDFATYFC**QSYDSDIDIV**FGQGTKVE

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				IK
	hBDI-5H1.12	CDR-L1	Residues 24-36 of SEQ ID NO.:	**ERSSGDIGDTYVS**
	hBDI-5H1.12	CDR-L2	Residues 52-58 of SEQ ID NO.:	**GNDQRPS**
	hBDI-5H1.12	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYDSDIDIV**
	hBDI-5H1.13 VH			EVTLKESGPALVKPTQTLTLTCTFS**GF** **SLSTFGMGVG**WIRQPPGKALEWLA**NIW** **WDDDKYYNPSLKN**RLTISKDTSKNQAV LTITNMDPVDTATYYCAR**ISTGISSYY** **VMDA**WGQGTTVTVSS
	hBDI-5H1.13	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTFGMGVG**
	hBDI-5H1.13	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	hBDI-5H1.13	CDR-H3	Residues 100-112 of SEQ ID NO.:	**ISTGISSYYVMDA**
	hBDI-5H1.13 VL			DFQLTQSPSSLSASVGDRVTITC**ERSS** **GDIGDTYVS**WYQQKPGKAPKNVIY**GND** **QRPS**GVPSRFSGSGSGNSATLTISSLQ PEDFATYFC**QSYDSDIDIV**FGQGTKVE IK
	hBDI-5H1.13	CDR-L1	Residues 24-36 of SEQ ID NO.:	**ERSSGDIGDTYVS**
	hBDI-5H1.13	CDR-L2	Residues 52-58 of SEQ ID NO.:	**GNDQRPS**
	hBDI-5H1.13	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYDSDIDIV**
	hBDI-5H1.16 VH			EVTLKESGPALVKPTQTLTLTCTFS**GF** **SLSTFGMGVG**WIRQPPGKGLEWLA**NIW** **WDDDKYYNPSLKN**RLTISKDTSNSQAV LTITNMDPVDTATYYCAR**ISTGISSYY** **VMDA**WGQGTTVTVSS
	hBDI-5H1.16	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTFGMGVG**
	hBDI-5H1.16	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	hBDI-5H1.16	CDR-H3	Residues 100-112 of SEQ ID NO.:	**ISTGISSYYVMDA**
	hBDI-5H1.16 VL			EFVLTQSPGTLSLSPGERATLSC**ERSS** **GDIGDTYVS**WYQQKPGQPPRNVIY**GND** **QRPS**GVPDRFSGSGSGTDFTLTISRLE PEDFAVYFC**QSYDSDIDIV**FGGGTKVE IK
	hBDI-5H1.16	CDR-L1	Residues 24-36 of SEQ ID NO.:	**ERSSGDIGDTYVS**
	hBDI-5H1.16	CDR-L2	Residues 52-58 of SEQ ID NO.:	**GNDQRPS**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
	hBDI-5H1.16	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYDSDIDIV**
	hBDI-5H1.17 VH			EVTLKESGPALVKPTQTLTLTCTFS**GF** **SLSTFGMGVG**WIRQPPGKGLEWLA**NIW** **WDDDKYYNPSLKN**RLTISKDTSNSQAV LTITNMDPVDTATYYCAR**ISTGISSYY** **VMDA**WGQGTTVTVSS
	hBDI-5H1.17	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTFGMGVG**
	hBDI-5H1.17	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	hBDI-5H1.17	CDR-H3	Residues 100-112 of SEQ ID NO.:	**ISTGISSYYVMDA**
	hBDI-5H1.17 VL			EFVLTQSPGTLSLSPGERATLSC**ERSS** **GDIGDSYVS**WYQQKPGQAPRLVIY**ADD** **QRPS**GIPDRFSGSGSGTDFTLTISRLE PEDFAVYYC**QSYDINIDIV**FGGGTKVE IK
	hBDI-5H1.17	CDR-L1	Residues 24-36 of SEQ ID NO.:	**ERSSGDIGDSYVS**
	hBDI-5H1.17	CDR-L2	Residues 52-58 of SEQ ID NO.:	**ADDQRPS**
	hBDI-5H1.17	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYDINIDIV**
	hBDI-5H1.2 VH			EVTLRESGPALVKPTQTLTLTCTFS**GF** **SLSTFGMGVG**WIRQPPGKALEWLA**NIW** **WDDDKYYNPSLKN**RLTISKDTSKNQVV LTMTNMDPVDTATYYCAR**ISTGISSYY** **VMDA**WGQGTTVTVSS
	hBDI-5H1.2	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTFGMGVG**
	hBDI-5H1.2	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	hBDI-5H1.2	CDR-H3	Residues 100-112 of SEQ ID NO.:	**ISTGISSYYVMDA**
	hBDI-5H1.2 VL			NFMLTQPHSVSESPGKTVTISC**ERSSG** **DIGDTYVS**WYQQRPGSPPTNVIY**GNDQ** **RPS**GVPDRFSGSIDSSSNSASLTISGL KTEDEADYFC**QSYDSDIDIV**FGGGTKL TVL
	hBDI-5H1.2	CDR-L1	Residues 23-35 of SEQ ID NO.:	**ERSSGDIGDTYVS**
	hBDI-5H1.2	CDR-L2	Residues 51-57 of SEQ ID NO.:	**GNDQRPS**
	hBDI-5H1.2	CDR-L3	Residues 92-101 of SEQ ID NO.:	**QSYDSDIDIV**
	hBDI-5H1.3 VH			EVTLRESGPALVKPTQTLTLTCTFS**GF** **SLSTFGMGVG**WIRQPPGKALEWLA**NIW** **WDDDKYYNPSLKN**RLTISKDTSKNQVV

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				LTMTNMDPVDTATYYCAR**ISTGISSYY** **VMDA**WGQGTTVTVSS
	hBDI-5H1.3	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTFGMGVG**
	hBDI-5H1.3	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	hBDI-5H1.3	CDR-H3	Residues 100-112 of SEQ ID NO.:	**ISTGISSYYVMDA**
	hBDI-5H1.3 VL			EIVLTQSPGTLSLSPGERATLSC**ERSS** **GDIGDTYVS**WYQQKPGQAPRLLIY**GND** **QRPS**GIPDRFSGSGSGTDFTLTISRLE PEDFAVYYC**QSYDSDIDIV**FGGGTKVE IK
	hBDI-5H1.3	CDR-L1	Residues 24-36 of SEQ ID NO.:	**ERSSGDIGDTYVS**
	hBDI-5H1.3	CDR-L2	Residues 52-58 of SEQ ID NO.:	**GNDQRPS**
	hBDI-5H1.3	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYDSDIDIV**
	hBDI-5H1.4 VH			EVTLRESGPALVKPTQTLTLTCTFS**GF** **SLSTFGMGVG**WIRQPPGKALEWLA**NIW** **WDDDKYYNPSLKN**RLTISKDTSKNQVV LTMTNMDPVDTATYYCAR**ISTGISSYY** **VMDA**WGQGTTVTVSS
	hBDI-5H1.4	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTFGMGVG**
	hBDI-5H1.4	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	hBDI-5H1.4	CDR-H3	Residues 100-112 of SEQ ID NO.:	**ISTGISSYYVMDA**
	hBDI-5H1.4 VL			EFVLTQSPGTLSLSPGERATLSC**ERSS** **GDIGDTYVS**WYQQKPGQAPRLVIY**GND** **QRPS**GIPDRFSGSGSGTDFTLTISRLE PEDFAVYYC**QSYDSDIDIV**FGGGTKVE IK
	hBDI-5H1.4	CDR-L1	Residues 24-36 of SEQ ID NO.:	**ERSSGDIGDTYVS**
	hBDI-5H1.4	CDR-L2	Residues 52-58 of SEQ ID NO.:	**GNDQRPS**
	hBDI-5H1.4	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYDSDIDIV**
	hBDI-5H1.5 VH			EVTLKESGPALVKPTQTLTLTCTFS**GF** **SLSTFGMGVG**WIRQPPGKALEWLA**NIW** **WDDDKYYNPSLKN**RLTISKDTSKNQAV LTITNMDPVDTATYYCAR**ISTGISSYY** **VMDA**WGQGTTVTVSS
	hBDI-5H1.5	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTFGMGVG**
	hBDI-5H1.5	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
	hBDI-5H1.5	CDR-H3	Residues 100-112 of SEQ ID NO.:	**ISTGISSYYVMDA**
	hBDI-5H1.5 VL			NFMLTQPHSVSESPGKTVTISC**ERSSG** **DIGDTYVS**WYQQRPGSSPTTVIY**GNDQ** **RPS**GVPDRFSGSIDSSSNSASLTISGL KTEDEADYYC**QSYDSDIDIV**FGGGTKL TVL
	hBDI-5H1.5	CDR-L1	Residues 23-35 of SEQ ID NO.:	**ERSSGDIGDTYVS**
	hBDI-5H1.5	CDR-L2	Residues 51-57 of SEQ ID NO.:	**GNDQRPS**
	hBDI-5H1.5	CDR-L3	Residues 92-101 of SEQ ID NO.:	**QSYDSDIDIV**
	hBDI-5H1.6 VH			EVTLKESGPALVKPTQTLTLTCTFS**GF** **SLSTFGMGVG**WIRQPPGKALEWLA**NIW** **WDDDKYYNPSLKN**RLTISKDTSKNQAV LTITNMDPVDTATYYCAR**ISTGISSYY** **VMDA**WGQGTTVTVSS
	hBDI-5H1.6	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTFGMGVG**
	hBDI-5H1.6	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	hBDI-5H1.6	CDR-H3	Residues 100-112 of SEQ ID NO.:	**ISTGISSYYVMDA**
	hBDI-5H1.6 VL			NFMLTQPHSVSESPGKTVTISC**ERSSG** **DIGDTYVS**WYQQRPGSPPTNVIY**GNDQ** **RPS**GVPDRFSGSIDSSSNSASLTISGL KTEDEADYFC**QSYDSDIDIV**FGGGTKL TVL
	hBDI-5H1.6	CDR-L1	Residues 23-35 of SEQ ID NO.:	**ERSSGDIGDTYVS**
	hBDI-5H1.6	CDR-L2	Residues 51-57 of SEQ ID NO.:	**GNDQRPS**
	hBDI-5H1.6	CDR-L3	Residues 92-101 of SEQ ID NO.:	**QSYDSDIDIV**
	hBDI-5H1.7 VH			EVTLKESGPALVKPTQTLTLTCTFS**GF** **SLSTFGMGVG**WIRQPPGKALEWLA**NIW** **WDDDKYYNPSLKN**RLTISKDTSKNQAV LTITNMDPVDTATYYCAR**ISTGISSYY** **VMDA**WGQGTTVTVSS
	hBDI-5H1.7	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTFGMGVG**
	hBDI-5H1.7	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	hBDI-5H1.7	CDR-H3	Residues 100-112 of SEQ ID NO.:	**ISTGISSYYVMDA**
	hBDI-5H1.7 VL			EIVLTQSPGTLSLSPGERATLSC**ERSS** **GDIGDTYVS**WYQQKPGQAPRLLIY**GND** **QRPS**GIPDRFSGSGSGTDFTLTISRLE

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				PEDFAVYYC**QSYDSDIDIV**FGGGTKVE IK
	hBDI-5H1.7	CDR-L1	Residues 24-36 of SEQ ID NO.:	**ERSSGDIGDTYVS**
	hBDI-5H1.7	CDR-L2	Residues 52-58 of SEQ ID NO.:	**GNDQRPS**
	hBDI-5H1.7	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYDSDIDIV**
	hBDI-5H1.8 VH			EVTLKESGPALVKPTQTLTLTCTFS**GF SLSTFGMGVG**WIRQPPGKALEWLA**NIW WDDDKYYNPSLKN**RLTISKDTSKNQAV LTITNMDPVDTATYYCAR**ISTGISSYY VMDA**WGQGTTVTVSS
	hBDI-5H1.8	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTFGMGVG**
	hBDI-5H1.8	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	hBDI-5H1.8	CDR-H3	Residues 100-112 of SEQ ID NO.:	**ISTGISSYYVMDA**
	hBDI-5H1.8 VL			EFVLTQSPGTLSLSPGERATLSC**ERSS GDIGDTYVS**WYQQKPGQAPRLVIY**GND QRPS**GIPDRFSGSGSGTDFTLTISRLE PEDFAVYYC**QSYDSDIDIV**FGGGTKVE IK
	hBDI-5H1.8	CDR-L1	Residues 24-36 of SEQ ID NO.:	**ERSSGDIGDTYVS**
	hBDI-5H1.8	CDR-L2	Residues 52-58 of SEQ ID NO.:	**GNDQRPS**
	hBDI-5H1.8	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYDSDIDIV**
	hBDI-5H1.9 VH			EVTLRESGPALVKPTQTLTLTCTFS**GF SLSTFGMGVG**WIRQPPGKALEWLA**NIW WDDDKYYNPSLKN**RLTISKDTSKNQAV LTITNMDPVDTATYYCAR**ISTGISSYY VMDA**WGQGTTVTVSS
	hBDI-5H1.9	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTFGMGVG**
	hBDI-5H1.9	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	hBDI-5H1.9	CDR-H3	Residues 100-112 of SEQ ID NO.:	**ISTGISSYYVMDA**
	hBDI-5H1.9 VL			DFVLTQSPDSLAVSLGERATINC**ERSS GDIGDTYVS**WYQQKPGQPPKNVIY**GND QRPS**GVPDRFSGSGSGNSATLTISSLQ AEDVAVYFC**QSYDSDIDIV**FGGGTKVE IK
	hBDI-5H1.9	CDR-L1	Residues 24-36 of SEQ ID NO.:	**ERSSGDIGDTYVS**
	hBDI-5H1.9	CDR-L2	Residues 52-58 of SEQ ID NO.:	**GNDQRPS**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
	hBDI-5H1.9	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYDSDIDIV**
	hBDI-9E8.1 VH			EVTLRESGPALVKPTQTLTLTCTFS**GF** **SLSTYGMGVG**WIRQPPGKALEWLA**NIW** **WDDDKYYNPSLKN**RLTISKDTSKNQVV LTMTNMDPVDTATYYCAR**IESIGTTYS** **FDY**WGQGTMVTVSS
	hBDI-9E8.1	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTYGMGVG**
	hBDI-9E8.1	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	hBDI-9E8.1	CDR-H3	Residues 100-111 of SEQ ID NO.:	**IESIGTTYSFDY**
	hBDI-9E8.1 VL			NFMLTQPHSVSESPGKTVTISC**ERSSG** **DIGDSYVS**WYQQRPGSSPTTVIY**ADDQ** **RPS**GVPDRFSGSIDSSSNSASLTISGL KTEDEADYYC**QSYDINIDIV**FGGGTKL TVL
	hBDI-9E8.1	CDR-L1	Residues 23-35 of SEQ ID NO.:	**ERSSGDIGDSYVS**
	hBDI-9E8.1	CDR-L2	Residues 51-57 of SEQ ID NO.:	**ADDQRPS**
	hBDI-9E8.1	CDR-L3	Residues 92-101 of SEQ ID NO.:	**QSYDINIDIV**
	hBDI-9E8.10 VH			EVTLRESGPALVKPTQTLTLTCTFS**GF** **SLSTYGMGVG**WIRQPPGKALEWLA**NIW** **WDDDKYYNPSLKN**RLTISKDTSKNQAV LTITNMDPVDTATYYCAR**IESIGTTYS** **FDY**WGQGTTVTVSS
	hBDI-9E8.10	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTYGMGVG**
	hBDI-9E8.10	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	hBDI-9E8.10	CDR-H3	Residues 100-111 of SEQ ID NO.:	**IESIGTTYSFDY**
	hBDI-9E8.10 VL			DFQLTQSPSSLSASVGDRVTITC**ERSS** **GDIGDSYVS**WYQQKPGKAPKNVIY**ADD** **QRPS**GVPSRFSGSGSGNSASLTISSLQ PEDFATYYC**QSYDINIDIV**FGQGTKVE IK
	hBDI-9E8.10	CDR-L1	Residues 24-36 of SEQ ID NO.:	**ERSSGDIGDSYVS**
	hBDI-9E8.10	CDR-L2	Residues 52-58 of SEQ ID NO.:	**ADDQRPS**
	hBDI-9E8.10	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYDINIDIV**
	hBDI-9E8.11 VH			EVQLVESGGGLVQPGGSLRLSCAFS**GF** **SLSTYGMGVG**WIRQAPGKGLEWLA**NIW** **WDDDKYYNPSLKN**RLTISKDTSKNQAY

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				LQINSLRAEDTAVYYCAR**IESIGTTYS FDY**WGQGTLVTVSS
	hBDI-9E8.11	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTYGMGVG**
	hBDI-9E8.11	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	hBDI-9E8.11	CDR-H3	Residues 100-111 of SEQ ID NO.:	**IESIGTTYSFDY**
	hBDI-9E8.11 VL			DFVLTQSPDSLAVSLGERATINC**ERSS GDIGDSYVS**WYQQKPGQPPKNVIY**ADD QRPS**GVPDRFSGSGSGNSASLTISSLQ AEDVAVYFC**QSYDINIDIV**FGGGTKVE IK
	hBDI-9E8.11	CDR-L1	Residues 24-36 of SEQ ID NO.:	**ERSSGDIGDSYVS**
	hBDI-9E8.11	CDR-L2	Residues 52-58 of SEQ ID NO.:	**ADDQRPS**
	hBDI-9E8.11	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYDINIDIV**
	hBDI-9E8.12 VH			EVQLVESGGGLVQPGGSLRLSCAFS**GF SLSTYGMGVG**WIRQAPGKGLEWLA**NIW WDDDKYYNPSLKN**RLTISKDTSKNQAY LQINSLRAEDTAVYYCAR**IESIGTTYS FDY**WGQGTLVTVSS
	hBDI-9E8.12	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTYGMGVG**
	hBDI-9E8.12	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	hBDI-9E8.12	CDR-H3	Residues 100-111 of SEQ ID NO.:	**IESIGTTYSFDY**
	hBDI-9E8.12 VL			DFQLTQSPSSLSASVGDRVTITC**ERSS GDIGDSYVS**WYQQKPGKAPKNVIY**ADD QRPS**GVPSRFSGSGSGNSASLTISSLQ PEDFATYYC**QSYDINIDIV**FGQGTKVE IK
	hBDI-9E8.12	CDR-L1	Residues 24-36 of SEQ ID NO.:	**ERSSGDIGDSYVS**
	hBDI-9E8.12	CDR-L2	Residues 52-58 of SEQ ID NO.:	**ADDQRPS**
	hBDI-9E8.12	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYDINIDIV**
	hBDI-9E8.13 VH			EVTLRESGPALVKPTQTLTLTCTFS**GF SLSTYGMGVG**WIRQPPGKGLEWLA**NIW WDDDKYYNPSLKN**RLTISKDTSKNQAV LTITNMDPVDTATYYCAR**IESIGTTYS FDY**WGQGTMVTVSS
	hBDI-9E8.13	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTYGMGVG**
	hBDI-9E8.13	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
	hBDI-9E8.13	CDR-H3	Residues 100-111 of SEQ ID NO.:	**IESIGTTYSFDY**
	hBDI-9E8.13 VL			DFQLTQSPSSLSASVGDRVTITC**ERSS** **GDIGDSYVS**WYQQKPGKAPKNVIY**ADD** **QRPS**GVPSRFSGSGSGNSASLTISSLQ PEDFATYYC**QSYDINIDIV**FGQGTKVE IK
	hBDI-9E8.13	CDR-L1	Residues 24-36 of SEQ ID NO.:	**ERSSGDIGDSYVS**
	hBDI-9E8.13	CDR-L2	Residues 52-58 of SEQ ID NO.:	**ADDQRPS**
	hBDI-9E8.13	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYDINIDIV**
	hBDI-9E8.2 VH			EVTLRESGPALVKPTQTLTLTCTFS**GF** **SLSTYGMGVG**WIRQPPGKALEWLA**NIW** **WDDDKYYNPSLKN**RLTISKDTSKNQVV LTMTNMDPVDTATYYCAR**IESIGTTYS** **FDY**WGQGTMVTVSS
	hBDI-9E8.2	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTYGMGVG**
	hBDI-9E8.2	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	hBDI-9E8.2	CDR-H3	Residues 100-111 of SEQ ID NO.:	**IESIGTTYSFDY**
	hBDI-9E8.2 VL			NFMLTQPHSVSESPGKTVTISC**ERSSG** **DIGDSYVS**WYQQRPGSPPTNVIY**ADDQ** **RPS**GVPDRFSGSIDSSSNSASLTISGL KTEDEADYFC**QSYDINIDIV**FGGGTKL TVL
	hBDI-9E8.2	CDR-L1	Residues 23-35 of SEQ ID NO.:	**ERSSGDIGDSYVS**
	hBDI-9E8.2	CDR-L2	Residues 51-57 of SEQ ID NO.:	**ADDQRPS**
	hBDI-9E8.2	CDR-L3	Residues 92-101 of SEQ ID NO.:	**QSYDINIDIV**
	hBDI-9E8.3 VH			EVTLRESGPALVKPTQTLTLTCTFS**GF** **SLSTYGMGVG**WIRQPPGKALEWLA**NIW** **WDDDKYYNPSLKN**RLTISKDTSKNQVV LTMTNMDPVDTATYYCAR**IESIGTTYS** **FDY**WGQGTMVTVSS
	hBDI-9E8.3	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTYGMGVG**
	hBDI-9E8.3	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	hBDI-9E8.3	CDR-H3	Residues 100-111 of SEQ ID NO.:	**IESIGTTYSFDY**
	hBDI-9E8.3 VL			EIVLTQSPGTLSLSPGERATLSC**ERSS** **GDIGDSYVS**WYQQKPGQAPRLLIY**ADD** **QRPS**GIPDRFSGSGSGTDFTLTISRLE

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				PEDFAVYYC**QSYDINIDIV**FGGGTKVE IK
	hBDI-9E8.3	CDR-L1	Residues 24-36 of SEQ ID NO.:	**ERSSGDIGDSYVS**
	hBDI-9E8.3	CDR-L2	Residues 52-58 of SEQ ID NO.:	**ADDQRPS**
	hBDI-9E8.3	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYDINIDIV**
	hBDI-9E8.4 VH			EVTLRESGPALVKPTQTLTLTCTFS**GF SLSTYGMGVG**WIRQPPGKALEWLA**NIW WDDDKYYNPSLKN**RLTISKDTSKNQVV LTMTNMDPVDTATYYCAR**IESIGTTYS FDY**WGQGTMVTVSS
	hBDI-9E8.4	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTYGMGVG**
	hBDI-9E8.4	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	hBDI-9E8.4	CDR-H3	Residues 100-111 of SEQ ID NO.:	**IESIGTTYSFDY**
	hBDI-9E8.4 VL			EFVLTQSPGTLSLSPGERATLSC**ERSS GDIGDSYVS**WYQQKPGQAPRLVIY**ADD QRPS**GIPDRFSGSGSGTDFTLTISRLE PEDFAVYYC**QSYDINIDIV**FGGGTKVE IK
	hBDI-9E8.4	CDR-L1	Residues 24-36 of SEQ ID NO.:	**ERSSGDIGDSYVS**
	hBDI-9E8.4	CDR-L2	Residues 52-58 of SEQ ID NO.:	**ADDQRPS**
	hBDI-9E8.4	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYDINIDIV**
	hBDI-9E8.5 VH			EVTLRESGPALVKPTQTLTLTCTFS**GF SLSTYGMGVG**WIRQPPGKGLEWLA**NIW WDDDKYYNPSLKN**RLTISKDTSKNQAV LTITNMDPVDTATYYCAR**IESIGTTYS FDY**WGQGTMVTVSS
	hBDI-9E8.5	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTYGMGVG**
	hBDI-9E8.5	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	hBDI-9E8.5	CDR-H3	Residues 100-111 of SEQ ID NO.:	**IESIGTTYSFDY**
	hBDI-9E8.5 VL			NFMLTQPHSVSESPGKTVTISC**ERSSG DIGDSYVS**WYQQRPGSSPTTVIY**ADDQ RPS**GVPDRFSGSIDSSSNSASLTISGL KTEDEADYYC**QSYDINIDIV**FGGGTKL TVL
	hBDI-9E8.5	CDR-L1	Residues 23-35 of SEQ ID NO.:	**ERSSGDIGDSYVS**
	hBDI-9E8.5	CDR-L2	Residues 51-57 of SEQ ID NO.:	**ADDQRPS**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
	hBDI-9E8.5	CDR-L3	Residues 92-101 of SEQ ID NO.:	**QSYDINIDIV**
	hBDI-9E8.6 VH			EVTLRESGPALVKPTQTLTLTCTFS**GF** **SLSTYGMGVG**WIRQPPGKGLEWLA**NIW** **WDDDKYYNPSLKN**RLTISKDTSKNQAV LTITNMDPVDTATYYCAR**IESIGTTYS** **FDY**WGQGTMVTVSS
	hBDI-9E8.6	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTYGMGVG**
	hBDI-9E8.6	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	hBDI-9E8.6	CDR-H3	Residues 100-111 of SEQ ID NO.:	**IESIGTTYSFDY**
	hBDI-9E8.6 VL			NFMLTQPHSVSESPGKTVTISC**ERSSG** **DIGDSYVS**WYQQRPGSPPTNVIY**ADDQ** **RPS**GVPDRFSGSIDSSSNSASLTISGL KTEDEADYFC**QSYDINIDIV**FGGGTKL TVL
	hBDI-9E8.6	CDR-L1	Residues 23-35 of SEQ ID NO.:	**ERSSGDIGDSYVS**
	hBDI-9E8.6	CDR-L2	Residues 51-57 of SEQ ID NO.:	**ADDQRPS**
	hBDI-9E8.6	CDR-L3	Residues 92-101 of SEQ ID NO.:	**QSYDINIDIV**
	hBDI-9E8.7 VH			EVTLRESGPALVKPTQTLTLTCTFS**GF** **SLSTYGMGVG**WIRQPPGKGLEWLA**NIW** **WDDDKYYNPSLKN**RLTISKDTSKNQAV LTITNMDPVDTATYYCAR**IESIGTTYS** **FDY**WGQGTMVTVSS
	hBDI-9E8.7	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTYGMGVG**
	hBDI-9E8.7	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	hBDI-9E8.7	CDR-H3	Residues 100-111 of SEQ ID NO.:	**IESIGTTYSFDY**
	hBDI-9E8.7 VL			EIVLTQSPGTLSLSPGERATLSC**ERSS** **GDIGDSYVS**WYQQKPGQAPRLLIY**ADD** **QRPS**GIPDRFSGSGSGTDFTLTISRLE PEDFAVYYC**QSYDINIDIV**FGGGTKVE IK
	hBDI-9E8.7	CDR-L1	Residues 24-36 of SEQ ID NO.:	**ERSSGDIGDSYVS**
	hBDI-9E8.7	CDR-L2	Residues 52-58 of SEQ ID NO.:	**ADDQRPS**
	hBDI-9E8.7	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYDINIDIV**
	hBDI-9E8.8 VH			EVTLRESGPALVKPTQTLTLTCTFS**GF** **SLSTYGMGVG**WIRQPPGKGLEWLA**NIW** **WDDDKYYNPSLKN**RLTISKDTSKNQAV

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				LTITNMDPVDTATYYCAR**IESIGTTYS FDY**WGQGTMVTVSS
	hBDI-9E8.8	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTYGMGVG**
	hBDI-9E8.8	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	hBDI-9E8.8	CDR-H3	Residues 100-111 of SEQ ID NO.:	**IESIGTTYSFDY**
	hBDI-9E8.8 VL			EFVLTQSPGTLSLSPGERATLSC**ERSS GDIGDSYVS**WYQQKPGQAPRLVIY**ADD QRPS**GIPDRFSGSGSGTDFTLTISRLE PEDFAVYYC**QSYDINIDIV**FGGGTKVE IK
	hBDI-9E8.8	CDR-L1	Residues 24-36 of SEQ ID NO.:	**ERSSGDIGDSYVS**
	hBDI-9E8.8	CDR-L2	Residues 52-58 of SEQ ID NO.:	**ADDQRPS**
	hBDI-9E8.8	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYDINIDIV**
	hBDI-9E8.9 VH			EVTLRESGPALVKPTQTLTLTCTFS**GF SLSTYGMGVG**WIRQPPGKALEWLA**NIW WDDDKYYNPSLKN**RLTISKDTSKNQAV LTITNMDPVDTATYYCAR**IESIGTTYS FDY**WGQGTTVTVSS
	hBDI-9E8.9	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTYGMGVG**
	hBDI-9E8.9	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	hBDI-9E8.9	CDR-H3	Residues 100-111 of SEQ ID NO.:	**IESIGTTYSFDY**
	hBDI-9E8.9 VL			DFVLTQSPDSLAVSLGERATINC**ERSS GDIGDSYVS**WYQQKPGQPPKNVIY**ADD QRPS**GVPDRFSGSGSGNSASLTISSLQ AEDVAVYFC**QSYDINIDIV**FGGGTKVE IK
	hBDI-9E8.9	CDR-L1	Residues 24-36 of SEQ ID NO.:	**ERSSGDIGDSYVS**
	hBDI-9E8.9	CDR-L2	Residues 52-58 of SEQ ID NO.:	**ADDQRPS**
	hBDI-9E8.9	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYDINIDIV**
	hBDI-9E8.4E VH			EVTLRESGPALVKPTQTLTLTCTFS**GF SLSTYGMGVG**WIRQPPGKALEWLA**NIW WDDDKYYNPSLKN**RLTISKDTSKNQVV LTMTNMDPVDTATYYCAR**IESIGTTYS FDY**WGQGTMVTVSS
	hBDI-9E8.4E	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTYGMGVG**
	hBDI-9E8.4E	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
	hBDI-9E8.4E	CDR-H3	Residues 100-111 of SEQ ID NO.:	**IESIGTTYSFDY**
	hBDI-9E8.4E VL			EFVLTQSPGTLSLSPGERATLSC**ERSS** **GDIGESYVS**WYQQKPGQAPRLVIY**ADD** **QRPS**GIPDRFSGSGSGTDFTLTISRLE PEDFAVYYC**QSYDINIDIV**FGGGTKVE IK
	hBDI-9E8.4E	CDR-L1	Residues 24-36 of SEQ ID NO.:	**ERSSGDIGESYVS**
	hBDI-9E8.4E	CDR-L2	Residues 52-58 of SEQ ID NO.:	**ADDQRPS**
	hBDI-9E8.4E	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYDINIDIV**
	hBFU-3E2.1 VH			EVQLVQSGAEVKKPGSSVKVSCKAS**GY** **TFTESYMY**WVKQAPGQGLELIG**RIDPE** **DGSTDYVEKFKN**KATLTADKSTSTAYM ELSSLRSEDTAVYFCAR**FGARSYFYPM** **DA**WGQGTTVTVSS
	hBFU-3E2.1	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTESYMY**
	hBFU-3E2.1	CDR-H2	Residues 50-66 of SEQ ID NO.:	**RIDPEDGSTDYVEKFKN**
	hBFU-3E2.1	CDR-H3	Residues 99-110 of SEQ ID NO.:	**FGARSYFYPMDA**
	hBFU-3E2.1 VL			ETVLTQSPATLSLSPGERATLSC**RASE** **SVSTLMH**WYQQKPGQQPRLLIY**GASNL** **ES**GVPARFSGSGSGTDFTLTISSLEPE DFAVYFC**QQSWNDPWT**FGGGTKVEIK
	hBFU-3E2.1	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASESVSTLMH**
	hBFU-3E2.1	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	hBFU-3E2.1	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQSWNDPWT**
	hBFU-3E2.2 VH			EVQLVQSGAEVKKPGSSVKVSCKAS**GY** **TFTESYMY**WVRQAPGQGLELIG**RIDPE** **DGSTDYVEKFKN**RVTLTADKSTSTAYM ELSSLRSEDTAVYYCAR**FGARSYFYPM** **DA**WGQGTTVTVSS
	hBFU-3E2.2	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTESYMY**
	hBFU-3E2.2	CDR-H2	Residues 50-66 of SEQ ID NO.:	**RIDPEDGSTDYVEKFKN**
	hBFU-3E2.2	CDR-H3	Residues 99-110 of SEQ ID NO.:	**FGARSYFYPMDA**
	hBFU-3E2.2 VL			ETVLTQSPATLSLSPGERATLSC**RASE** **SVSTLMH**WYQQKPGQQPRLLIY**GASNL** **ES**GVPARFSGSGSGTDFTLTISSLEPE DFAVYFC**QQSWNDPWT**FGGGTKVEIK

SEQ ID NO:	Clone	Protein Region	Residues	V Region
	hBFU-3E2.2	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASESVSTLMH**
	hBFU-3E2.2	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	hBFU-3E2.2	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQSWNDPWT**
	hBFU-3E2.3 VH			EVQLVQSGAEVKKPGSSVKVSCKAS**GY** **TFTESYMY**WVKQAPGQGLELIG**RIDPE** **DGSTDYVEKFKN**KATLTADKSTSTAYM ELSSLRSEDTAVYFCAR**FGARSYFYPM** **DA**WGQGTTVTVSS
	hBFU-3E2.3	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTESYMY**
	hBFU-3E2.3	CDR-H2	Residues 50-66 of SEQ ID NO.:	**RIDPEDGSTDYVEKFKN**
	hBFU-3E2.3	CDR-H3	Residues 99-110 of SEQ ID NO.:	**FGARSYFYPMDA**
	hBFU-3E2.3 VL			ATQLTQSPSSLSASVGDRVTISC**RASE** **SVSTLMH**WYQQKPGKQPRLLIY**GASNL** **ES**GVPSRFSGSGSGTDFTLTISSLQPE DFATYFC**QQSWNDPWT**FGGGTKVEIK
	hBFU-3E2.3	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASESVSTLMH**
	hBFU-3E2.3	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	hBFU-3E2.3	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQSWNDPWT**
	hBFU-3E2.4 VH			EVQLVQSGAEVKKPGSSVKVSCKAS**GY** **TFTESYMY**WVRQAPGQGLELIG**RIDPE** **DGSTDYVEKFKN**RVTLTADKSTSTAYM ELSSLRSEDTAVYYCAR**FGARSYFYPM** **DA**WGQGTTVTVSS
	hBFU-3E2.4	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTESYMY**
	hBFU-3E2.4	CDR-H2	Residues 50-66 of SEQ ID NO.:	**RIDPEDGSTDYVEKFKN**
	hBFU-3E2.4	CDR-H3	Residues 99-110 of SEQ ID NO.:	**FGARSYFYPMDA**
	hBFU-3E2.4 VL			ATQLTQSPSSLSASVGDRVTISC**RASE** **SVSTLMH**WYQQKPGKQPRLLIY**GASNL** **ES**GVPSRFSGSGSGTDFTLTISSLQPE DFATYFC**QQSWNDPWT**FGGGTKVEIK
	hBFU-3E2.4	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASESVSTLMH**
	hBFU-3E2.4	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	hBFU-3E2.4	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQSWNDPWT**

Table 29. VH and VL Amino Acid Sequences of Humanized Versions of Rat Anti-Human VEGFR II Monoclonal Antibodies (CDRs in bold)

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				12345678901234567890123456
	hBCU-6B1.1 VH			EVQLVQSGSELKKPGASVKVSCKAS**G** **YTFTNYGMY**WVKQAPGQGLEFMG**WIN** **TETGQPTYADDFKG**RFVFSLDTSVST AYLQISSLKAEDTAVYFCAR**LGNNYG** **IWFAY**WGQGTLVTVSS
	hBCU-6B1.1	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBCU-6B1.1	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGQPTYADDFKG**
	hBCU-6B1.1	CDR-H3	Residues 99-109 of SEQ ID NO.:	**LGNNYGIWFAY**
	hBCU-6B1.1 VL			DIQMTQSPSSLSASVGDRVTIEC**RAS** **DDLYSTLA**WYQQKPGKSPKLLIF**DAN** **RLAA**GVPSRFSGSGSGTDYSLTISSL QPEDVATYFC**QQYNKFPWT**FGGGTKV EIK
	hBCU-6B1.1	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASDDLYSTLA**
	hBCU-6B1.1	CDR-L2	Residues 50-56 of SEQ ID NO.:	**DANRLAA**
	hBCU-6B1.1	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQYNKFPWT**
	hBCU-6B1.2 VH			EVQLVQSGAEVKKPGASVKVSCKAS**G** **YTFTNYGMY**WVKQAPGQGLEFMG**WIN** **TETGQPTYADDFKG**RFTFTLDTSTST AYMELRSLRSDDTAVYFCAR**LGNNYG** **IWFAY**WGQGTLVTVSS
	hBCU-6B1.2	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBCU-6B1.2	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGQPTYADDFKG**
	hBCU-6B1.2	CDR-H3	Residues 99-109 of SEQ ID NO.:	**LGNNYGIWFAY**
	hBCU-6B1.2 VL			DIQMTQSPSSLSASVGDRVTIEC**RAS** **DDLYSTLA**WYQQKPGKSPKLLIF**DAN** **RLAA**GVPSRFSGSGSGTDYSLTISSL QPEDVATYFC**QQYNKFPWT**FGGGTKV EIK
	hBCU-6B1.2	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASDDLYSTLA**
	hBCU-6B1.2	CDR-L2	Residues 50-56 of SEQ ID NO.:	**DANRLAA**
	hBCU-6B1.2	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQYNKFPWT**
	hBCU-6B1.3 VH			EVQLVQSGAEVKKPGASVKVSCKAS**G**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				YTFTNYGMYWVRQAPGQGLEFMG**WIN TETGQPTYADDFKG**RFTFTLDTSTST AYMELRSLRSDDTAVYYCAR**LGNNYG IWFAY**WGQGTLVTVSS
	hBCU-6B1.3	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBCU-6B1.3	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGQPTYADDFKG**
	hBCU-6B1.3	CDR-H3	Residues 99-109 of SEQ ID NO.:	**LGNNYGIWFAY**
	hBCU-6B1.3 VL			DIQMTQSPSSLSASVGDRVTIEC**RAS DDLYSTLA**WYQQKPGKSPKLLIF**DAN RLAA**GVPSRFSGSGSGTDYSLTISSL QPEDVATYFC**QQYNKFPWT**FGGGTKV EIK
	hBCU-6B1.3	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASDDLYSTLA**
	hBCU-6B1.3	CDR-L2	Residues 50-56 of SEQ ID NO.:	**DANRLAA**
	hBCU-6B1.3	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQYNKFPWT**
	hBCU-6B1.4 VH			EVQLVQSGAEVKKPGASVKVSCKAS**G YTFTNYGMY**WVRQAPGQGLEFMG**WIN TETGQPTYADDFKG**RFTFTLDTSTST AYMELRSLRSDDTAVYYCAR**LGNNYG IWFAY**WGQGTLVTVSS
	hBCU-6B1.4	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	hBCU-6B1.4	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WINTETGQPTYADDFKG**
	hBCU-6B1.4	CDR-H3	Residues 99-109 of SEQ ID NO.:	**LGNNYGIWFAY**
	hBCU-6B1.4 VL			DIQMTQSPSSLSASVGDRVTITC**RAS DDLYSTLA**WYQQKPGKSPKLLIF**DAN RLAA**GVPSRFSGSGSGTDYTLTISSL QPEDVATYFC**QQYNKFPWT**FGGGTKV EIK
	hBCU-6B1.4	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASDDLYSTLA**
	hBCU-6B1.4	CDR-L2	Residues 50-56 of SEQ ID NO.:	**DANRLAA**
	hBCU-6B1.4	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQYNKFPWT**

Table 30. VH and VL Amino Acid Sequences of Humanized Versions of Rat Anti-Human PDGFR b Monoclonal Antibodies (CDRs in bold)

SEQ ID NO:	Clone	Protein Region	Residues	V Region

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				12345678901234567890123456789O
	hBDE-3C9.1 VH			EVQLVESGGGLVQPGGSLRLSCAAS**G FTFSNYGMA**WVRQAPGKGLEWVA**SIT NSGGNTYYRDSVKG**RFTISRDNAKNT QYLQMNSLRAEDTAVYFCAR**HTPGAN YFDY**WGQGTMVTVSS
	hBDE-3C9.1	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GFTFSNYGMA**
	hBDE-3C9.1	CDR-H2	Residues 50-66 of SEQ ID NO.:	**SITNSGGNTYYRDSVKG**
	hBDE-3C9.1	CDR-H3	Residues 99-108 of SEQ ID NO.:	**HTPGANYFDY**
	hBDE-3C9.1 VL			DIQMTQSPSSLSASVGDRVTITC**QAS QSIKNYIA**WYQLKPGKAPRLLMR**YTS TLES**GTPSRFSGSGSGRDYTFTISSL QPEDIATYYC**VQYANLYT**FGGGTKVE IK
	hBDE-3C9.1	CDR-L1	Residues 24-34 of SEQ ID NO.:	**QASQSIKNYIA**
	hBDE-3C9.1	CDR-L2	Residues 50-56 of SEQ ID NO.:	**YTSTLES**
	hBDE-3C9.1	CDR-L3	Residues 89-96 of SEQ ID NO.:	**VQYANLYT**
	hBDE-3C9.2 VH			EVQLVESGGGLVQPGGSLRLSCAAS**G FTFSNYGMA**WVRQAPGKGLEWVA**SIT NSGGNTYYRDSVKG**RFTISRDNAKNS LYLQMNSLRAEDTAVYYCAR**HTPGAN YFDY**WGQGTMVTVSS
	hBDE-3C9.2	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GFTFSNYGMA**
	hBDE-3C9.2	CDR-H2	Residues 50-66 of SEQ ID NO.:	**SITNSGGNTYYRDSVKG**
	hBDE-3C9.2	CDR-H3	Residues 99-108 of SEQ ID NO.:	**HTPGANYFDY**
	hBDE-3C9.2 VL			DIQMTQSPSSLSASVGDRVTITC**QAS QSIKNYIA**WYQQKPGKAPRLLIR**YTS TLES**GVPSRFSGSGSGRDYTFTISSL QPEDIATYYC**VQYANLYT**FGGGTKVE IK
	hBDE-3C9.2	CDR-L1	Residues 24-34 of SEQ ID NO.:	**QASQSIKNYIA**
	hBDE-3C9.2	CDR-L2	Residues 50-56 of SEQ ID NO.:	**YTSTLES**
	hBDE-3C9.2	CDR-L3	Residues 89-96 of SEQ ID NO.:	**VQYANLYT**

Generation Of Humanized Antibodies

[0376] All variants were cloned into pHybE vectors and were transiently transfected into 50 mls of HEK 293 6e suspension cell cultures in a ratio of 60% to 40% light to heavy chain construct. 1 mg/ml PEI was used to transfect the cells. Cell supernatants were harvested after six days in shaking flasks, spun down to pellet cells, and filtered through 0.22 μm filters to separate IgG from culture contaminates. All were batch purified by adding 1 supernatant volume of protein A IgG binding buffer (Thermo Scientific 21001) and 1 ml of rProteinA sepharose fast flow beads (GE Healthcare, 17-1279-04). Supernatants, with beads and buffer added, were rocked overnight at 4°C, and the day after beads were collected by gravity over poly prep chromatography columns (Bio Rad, 731-1550). Once supernatants had passed through the columns the beads were washed with 10 column volumes of binding buffer, and IgG was eluted with Immunopure IgG elution buffer (Pierce, 185 1520) and collected in 1 ml aliquots. Fractions containing IgG were pooled and dialyzed in 15mM Histidine pH 6 overnight at 4°C.

[0377] Purified variants were further characterized for their affinities for recombinant human target proteins by binding ELISA, by Biacore, and by cell-based potency assays.

Table 31. Summary of Protein Expression and Purification for Humanized Anti-Human VEGF-A And Humanized Anti-Human PDGF-BB Monoclonal Antibodies

Name	Octet Titer (mg/L)[1]	~Yield (mg/L)[2]	SEC (% monomer)[3]
hBDB-4G8.1	19.9	19.7	100.0
hBDB-4G8.2	105.3	95.8	100.0
hBDB-4G8.3	34.8	31.9	100.0
hBDB-4G8.4	45.8	34.2	100.0
hBDB-4G8.5	24.7	27.4	100.0
hBDB-4G8.6	28.6	34.2	100.0
hBDB-4G8.7	75.8	63.4	100.0
hBDB-4G8.8	145.9	101.4	100.0
hBDB-4G8.9	38.8	39.0	100.0
hBDB-4G8.10	40.7	32.9	89.1
hBDB-4G8.11	47.9	38.0	87.2
hBDB-4G8.12	37.5	38.3	100.0
hBDB-4G8.13	44.8	35.1	100.0
hBDB-4G8.14	73.0	47.0	100.0
hBDB-4G8.15	161.2	94.9	100.0
hBDI-5H1.1	49.8	38.7	100.0
hBDI-5H1.2	63.4	62.0	100.0
hBDI-5H1.3	94.2	86.5	99.1
hBDI-5H1.4	109.0	123.1	99.2
hBDI-5H1.5	23.0	27.7	100.0
hBDI-5H1.6	41.2	46.0	100.0

Name	Octet Titer (mg/L)[1]	~Yield (mg/L)[2]	SEC (% monomer)[3]
hBDI-5H1.7	9.6	9.6	88.1
hBDI-5H1.8	36.0	41.5	100.0
hBDI-5H1.9	56.0	60.2	85.6
hBDI-5H1.10	34.2	31.1	85.2
hBDI-5H1.11	41.0	34.4	96.3
hBDI-5H1.12	37.7	30.2	100.0
hBDI-9E8.1	90.0	72.4	100.0
hBDI-9E8.2	89.9	89.1	99.3
hBDI-9E8.3	28.8	24.4	97.1
hBDI-9E8.4	52.8	54.8	98.2
hBDI-9E8.5	78.0	57.7	100.0
hBDI-9E8.6	60.6	61.4	100.0
hBDI-9E8.7	30.4	27.9	88.1
hBDI-9E8.8	37.1	38.0	98.4
hBDI-9E8.9	50.3	44.9	94.6
hBDI-9E8.10	93.0	56.2	94.7
hBDI-9E8.11	78.4	52.7	99.1
hBDI-9E8.12	92.3	68.5	100.0
hBDI-5H1.13	13.6	10.5	88.1
hBDI-9E8.13	53.5	66.9	100.0
hBDI-1E1.1	133.5	ND	ND
hBDI-1E1.2	115.6	ND	ND
hBDI-1E1.3	83.4	ND	ND
hBDI-1E1.4	137.6	ND	ND
hBDI-1E1.5	97.4	ND	ND
hBDI-1E1.6	70.6	ND	ND
hBDI-1E1.7	91.9	ND	ND
hBDI-1E1.8	71.2	ND	ND
hBDI-1E1.9	94.3	ND	ND
hBDI-1E1.10	72.7	ND	ND
hBDI-1E1.11	57.4	ND	ND
hBDI-1E1.12	151.6	ND	ND
hBEW-9A8.1	0.2	ND	ND
hBEW-9A8.2	0.2	ND	ND
hBEW-9A8.3	0.2	ND	ND
hBEW-9A8.4	0.2	ND	ND
hBEW-9A8.5	0.5	ND	ND
hBEW-9A8.6	0.2	ND	ND
hBEW-9A8.7	0.3	ND	ND
hBEW-9A8.8	3.5	ND	ND
hBEW-9A8.9	15.3	18.6	ND
hBEW-9A8.10	5.2	ND	ND
hBEW-9A8.11	30.6	18.9	ND

Name	Octet Titer (mg/L)[1]	~Yield (mg/L)[2]	SEC (% monomer)[3]
hBEW-9A8.12	38.3	28.4	ND
hBEW-9A8.13	0.4	ND	ND
hBEW-9A8.14	0.3	ND	ND
hBEW-9A8.15	0.3	ND	ND
hBEW-9A8.16	3.2	ND	ND
hBEW-6C2.1	5.4	ND	ND
hBEW-6C2.2	1.5	ND	ND
hBEW-6C2.3	14.8	7.8	ND
hBEW-6C2.4	79.6	29.5	ND
hBEW-6C2.5	4.7	ND	ND
hBEW-6C2.6	3.9	ND	ND
hBEW-6C2.7	140.8	39.7	ND
hBEW-6C2.8	75.3	24.8	ND
hBDI-5H1.16	ND	23.9	93.4
hBDI-5H1.17	ND	21.0	92.1
hBFU-3E2.1	ND	40.2	88.1
hBFU-3E2.2	ND	34.6	93.6
hBFU-3E2.3	ND	33.6	84.2
hBFU-3E2.4	ND	38.4	94.7
hBEW-9A8.17	ND	20.0	98.7
hBEW-9A8.20	ND	17.6	86.6
hBEW-9A8.21	ND	13.3	97.5
hBEW-5C3.1	ND	20.8	85.0
hBEW-5C3.2	ND	17.7	74.6
hBEW-5C3.3	ND	6.9	93.7
hBEW-5C3.4	ND	32.0	88.7
hBEW-5C3.5	ND	30.6	85.1
hBEW-5C3.6	ND	19.4	75.4
hBEW-9E10.1	ND	42.7	98.0
hBEW-9E10.2	ND	46.1	98.0
hBEW-9E10.3	ND	45.9	97.6
hBEW-9E10.4	ND	47.1	98.0
hBEW-9E10.5	ND	56.2	97.9
hBEW-9E10.6	ND	52.9	97.6
hBEW-1B10.1	ND	34.1	97.8
hBEW-1B10.2	ND	45.3	98.1
hBEW-1E3.1	ND	29.6	95.5
hBEW-1E3.2	ND	20.9	98.3
hBEW-1E3.3	ND	22.0	98.5
hBEW-1E3.4	ND	48.0	98.1
hBEW-1E3.5	ND	23.8	98.5
hBEW-1E3.6	ND	17.0	98.7

ND = Not Determined

[1]Octet titer is the amout of IgG in the unpurified supernatant as determined by protein A binding compared to a standard curve using an Octet instrument.

[2]Yield is determined by the total amount of purified protein in mg divided by the total cell culture volume in liters.

[3]SEC % monomer is determined using HPLC size exclusion chromatography.

[0378] Humanized anti-VEGF antibodies were tested for their binding to human VEGF-A according to the method described in Example 1.1. The on-rate, off-rate and binding kinetics are summarized in Table 32 below.

Table 32. Biacore Binding of Humanized Anti-VEGF Antibodies

Antibody	k_{on} (M-1 s-1)	k_{off} (M-1)	K_D (M)
hBDB-4G8.1	1.8 E+07	1.0 E-04	5.8 E-12
hBDB-4G8.2	1.7 E+07	6.2 E-05	3.6 E-12
hBDB-4G8.3	1.0 E+07	4.8 E-05	4.8 E-12
hBDB-4G8.4	2.7 E+07	1.5 E-04	5.5 E-12
hBDB-4G8.5	2.5 E+07	4.0 E-05	1.6 E-12
hBDB-4G8.6	2.6 E+07	3.7 E-05	1.4 E-12
hBDB-4G8.7	3.7 E+07	1.3 E-03	3.4 E-11
hBDB-4G8.8	1.8 E+07	8.6 E-04	4.7 E-11
hBDB-4G8.9	1.4 E+07	8.8 E-04	6.2 E-11
hBDB-4G8.10	2.7 E+07	2.2 E-04	8.1 E-12
hBDB-4G8.11	2.6 E+07	3.4 E-05	1.3 E-12
hBDB-4G8.12	2.6 E+07	3.2 E-05	1.2 E-12
hBDB-4G8.13	2.2 E+07	1.7 E-04	7.6 E-12
hBDB-4G8.14	1.5 E+07	5.6 E-05	3.7 E-12
hBDB-4G8.15	2.0 E+07	8.7 E-05	4.4 E-12
hBEW-9A8.9	1.0 E+07	8.2 E-03	8.2 E-10
hBEW-9A8.11	1.5 E+07	1.1 E-03	7.4 E-11
hBEW-9A8.12	9.6 E+06	1.4 E-04	1.5 E-11
hBEW-9A8.17	7.9 E+06	1.4 E-05	1.7 E-12
hBEW-9A8.20	7.6 E+06	1.2 E-05	1.6 E-12
hBEW-9A8.21	5.8 E+06	3.9 E-05	6.7 E-12
hBEW-5C3.1	1.1 E+07	6.9 E-05	6.0 E-12
hBEW-5C3.4	9.9 E+06	8.5 E-05	8.6 E-12
hBEW-5C3.5	1.2 E+07	9.7 E-05	8.5 E-12
hBEW-9E10.1	1.2 E+07	2.5 E-05	2.1 E-12
hBEW-9E10.2	1.6 E+07	1.9 E-04	1.2 E-11
hBEW-9E10.3	1.3 E+07	4.2 E-05	3.2 E-12
hBEW-9E10.4	1.2 E+07	2.5 E-05	2.1 E-12
hBEW-9E10.5	1.6 E+07	2.3 E-04	1.5 E-11
hBEW-9E10.6	1.5 E+07	4.0 E-05	2.6 E-12
hBEW-1B10.1	7.6 E+06	1.4 E-04	1.8 E-11
hBEW-1B10.2	7.5 E+06	1.5 E-04	2.0 E-11
hBEW-1E3.1	1.1 E+07	8.5 E-05	7.7 E-12
hBEW-1E3.2	1.1 E+07	1.0 E-04	9.2 E-12
hBEW-1E3.4	9.8 E+06	9.6 E-05	9.7 E-12

hBEW-1E3.5	1.0 E+07	1.0 E-04	1.0 E-11

[0379] Humanized anti-VEGF-A antibodies were tested for potency against $hVEGF_{165}$-induced cell proliferation in one of two cellular assay formats. The HMVEC-d bioassay utilizes cells which natively express VEGFR2 (Example 1.10). The VEGFR2-3T3 cells are stably transfected with VEGFR2 (Example 1.7). The data is summarized in Table 33 below.

Table 33. Summary of Characterization of Humanized Anti-Human VEGF-A Monoclonal Antibodies.

Humanized Molecules	$hVEGF_{165}$ IC50 (nM)	
	HMVEC-d	VEGFR2-3T3
hBDB-4G8.1	NT	0.847
hBDB-4G8.2	NT	0.603
hBDB-4G8.3	NT	0.665
hBDB-4G8.3 half-body	NT	>10
hBDB-4G8.4	NT	0.918
hBDB-4G8.5	NT	0.620
hBDB-4G8.6	NT	0.488
hBDB-4G8.7	NT	>10
hBDB-4G8.8	NT	>10
hBDB-4G8.9	NT	>10
hBDB-4G8.10	NT	>10
hBDB-4G8.11	NT	0.385
hBDB-4G8.12	NT	0.563
hBDB-4G8.13	NT	0.791
hBDB-4G8.14	NT	0.499
hBDB-4G8.15	NT	0.963
hBEW-1B10.1	0.168	NT
hBEW-1B10.2	0.222	NT
hBEW-1E3.1	0.138	NT
hBEW-1E3.4	0.212	NT
hBEW-1E3.2	0.161	NT
hBEW-1E3.3	0.205	NT
hBEW-1E3.5	0.184	NT
hBEW-1E3.6	0.26	NT
hBEW-5C3.1	0.071	NT
hBEW-5C3.2	0.162	NT
hBEW-5C3.3	>2	NT
hBEW-5C3.4	0.098	NT
hBEW-5C3.5	0.123	NT
hBEW-5C3.6	> 2	NT

hBEW-9A8.9	NT	>10
hBEW-9A8.11	NT	>10
hBEW-9A8.12	NT	0.598
hBEW-9A8.17	0.059	NT
hBEW-9A8.20	0.064	NT
hBEW-9A8.21	0.09	NT
hBEW-9E10.1	0.064	NT
hBEW-9E10.2	0.181	NT
hBEW-9E10.3	0.062	NT
hBEW-9E10.4	0.071	NT
hBEW-9E10.5	0.229	NT
hBEW-9E10.6	0.068	NT

NT = Not tested

[0380] Humanized anti-PDGF-BB antibodies were tested for their binding to human PDGF-BB according to the method described in Example 1.1. The on-rate, off-rate and binding kinetics are summarized in Table 34 below.

Table 34. Biacore Binding of Humanized Anti-PDGF Antibodies

Antibody	k_{on} (M-1 s-1)	k_{off} (M-1)	K_D (M)
hBDI-9E8.1	≥1.0E+07	5.6E-03	≤5.6E-10
hBDI-9E8.2	≥1.0E+07	5.1E-03	≤5.1E-10
hBDI-9E8.3	≥1.0E+07	6.5E-04	≤6.5E-11
hBDI-9E8.4	≥1.0E+07	2.1E-04	≤2.1E-11
hBDI-9E8.5	≥1.0E+07	2.1E-03	≤2.1E-10
hBDI-9E8.6	≥1.0E+07	2.1E-03	≤2.1E-10
hBDI-9E8.7	≥1.0E+07	4.5E-04	≤4.5E-11
hBDI-9E8.8	≥1.0E+07	1.7E-04	≤1.7E-11*
hBDI-9E8.9	≥1.0E+07	1.5E-03	≤1.5E-10
hBDI-9E8.10	≥1.0E+07	1.8E-03	≤1.8E-10
hBDI-9E8.11	≥1.0E+07	7.4E-04	≤7.4E-11
hBDI-9E8.12	≥1.0E+07	2.1E-03	≤2.1E-10
hBDI-9E8.13	≥ 1.0 E+07	1.0 E-03 *	≤1.0 E-10 *
hBDI-5H1.1	≥ 1.0 E+07	4.1 E-03	≤ 4.1 E-10
hBDI-5H1.2	≥ 1.0 E+07	1.9 E-03	≤ 1.9 E-10
hBDI-5H1.3	≥ 1.0 E+07	4.5 E-03	≤ 4.5 E-10
hBDI-5H1.4	≥ 1.0 E+07	1.4 E-02	≤ 1.4 E-09
hBDI-5H1.5	≥ 1.0 E+07	1.7 E-03	≤1.7 E-10
hBDI-5H1.6	≥ 1.0 E+07	8.2 E-04	≤8.2 E-11
hBDI-5H1.7	≥ 1.0 E+07	2.9 E-02 *	≤2.9 E-09 *
hBDI-5H1.8	≥ 1.0 E+07	7.2 E-01 *	≤7.2 E-08 *
hBDI-5H1.9	≥ 1.0 E+07	3.1 E-03	≤ 3.1 E-10
hBDI-5H1.10	≥ 1.0 E+07	2.3 E-03	≤ 2.3 E-10
hBDI-5H1.11	≥ 1.0 E+07	3.7 E-03	≤ 3.7 E-10
hBDI-5H1.12	≥ 1.0 E+07	2.3 E-03	≤ 2.3 E-10
hBDI-5H1.13	≥ 1.0 E+07	4.9 E-03 *	≤ 4.9 E-10 *

*Heterogeneous off-rate

[0381] Humanized anti-PDGF-BB antibodies were tested for potency against hPDGF-BB in functional assays. The ability to neutralize hPDGF-BB -induced cell proliferation was assessed (Example 1.15) as well as the ability to block binding of hPDGF-BB to hPDGF-Rβ in a competition ELISA format (Example 1.13). The data is summarized in Table 35 below.

Table 35. Summary of Characterization of Humanized Anti-Human PDGF-BB Monoclonal Antibodies

Humanized Molecules	hPDGF-BB IC50 (nM)	hPDGF-BB/hPDGFRβ Competition IC50 (nM)
hBDI-9E8.1	>5	+
hBDI-9E8.2	>5	+
hBDI-9E8.3	1.583	+
hBDI-9E8.4	0.061	4.301
hBDI-9E8.4 half body	>5	NT
hBDI-9E8.5	>5	+
hBDI-9E8.6	>5	+
hBDI-9E8.7	0.350	+
hBDI-9E8.8	0.105	+
hBDI-9E8.9	0.574	+
hBDI-9E8.10	0.562	+
hBDI-9E8.11	0.309	1.730
hBDI-9E8.12	0.525	+
hBDI-5H1.1	<10	+
hBDI-5H1.2	<10	+
hBDI-5H1.3	<10	-
hBDI-5H1.4	<10	-
hBDI-5H1.9	<10	+
hBDI-5H1.10	<10	-
hBDI-5H1.11	<10	-
hBDI-5H1.12	<10	-
hBDI-5H1.5	<10	+
hBDI-5H1.6	<10	+
hBDI-5H1.7	<10	-
hBDI-5H1.8	<10	-
hBDI-5H1.13	<10	+
hBDI-5H1.16	<10	NT
hBDI-5H1.17	<10	NT
hBFU-3E2.1	0.183	NT
hBFU-3E2.2	0.659	NT
hBFU-3E2.3	0.335	NT
hBFU-3E2.4	0.571	NT

NT – Not tested

[0382] Humanized anti-VEGFR2 antibodies were tested for potency against hVEGFR2 in functional assay formats. The antibodies were characterized for the ability to block VEGFR2 binding to $hVEGF_{165}$ in a competition ELISA format (Example 1.22). The antibodies were also tested for the ability to bind exogeneous hVEGFR2 and allow signaling in response to $hVEGF_{165}$ (Example 1.23). The data is summarized in Table 36 below.

Table 36. Summary of Characterization of Humanized Anti-Human VEGFR II Monoclonal Antibodies.

Humanized Molecules	Potency (nM)	
	$hVEGF_{165}$ / hVEGFR2-Fc Competition	$hVEGF_{165}$ / Tyr1054 phospho-assay
hBCU-6B1.1	0.474	NT
hBCU-6B1.2	0.340	NT
hBCU-6B1.3	0.319	NT
hBCU-6B1.4	0.335	NT

NT – Not tested

[0383] Humanized anti-PDGF-Rβ antibodies were characterized for activity in functional assays. Antibodies were assessed for the ability to bind hPDGF-Rβ (Example 1.26) and block binding of hPDGF-Rβ to hPDGF-BB in a competition ELISA format (Example 1.27). They were also tested for the ability to bind exogenoeous hPDGF-Rβ and allow signaling in response to hPDGF-BB (Example 1.28). The data is summarized in Table 37 below.

Table 37. Summary of Characterization of Humanized Anti-Human PDGFR-B Monoclonal Antibodies

Humanized Molecules	Potency (nM)		
	hPDGFRβ-Fc Binding	hPDGF-BB/ hPDGFRβ-Fc Competition	hPDGF-BB Tyr751 phospho-assay
hBDE-3C9.1	NT	0.217	1.053
hBDE-3C9.2	NT	0.260	0.882

NT – Not tested

Example 7: Affinity Maturation of Anti-Human VEGF-A Antibody 4G8

Library Designs And Strategy

[0384] Two different hBDB-4G8.3 parental sequences were made: One with "DT" and another with "EI" at the beginning of VL. Both parentals were tested as scFv, and the "EI" was chosen as the template for the libraries. Two libraries were made by dope primers: HC and LC.

After library selection and diversity reduction, libraries were combined into one recombined library (rHC+LC). Final selected clones from each of 3 libraries were converted to IgG.

HC Library

- Doping (X) 11 residues at 76080808: 30, 31, 33, 53, 56, 58, 95, 96, 100, 100a and 100c

- Co-evolve (1): D61Q/D62G/K64T. Library will contain **DDFKG** or **QGFTG**

[0385] A 10^9 library will be able to sample mutants carrying up to 4 doped residues at least 4 times. On average, library members will have 5 doped residues.

LC Library

- Doping (X) 10 residues at 76080808: 30, 31, 32, 50, 53, 91-94 and 96

- Germline toggle (Z): E27Q, V58I and F87Y

- Co-evolve (1): M33L/H34A. Library will contain H**MH**W or Y**LA**W

[0386] A 10^9 library will be able to sample mutants carrying up to 4 doped residues at least 4 times. On average, library members will have 5 doped residues.

Recombined Library

H1+H2 library is recombined with H3 library into a HC library. HC library is combined with LC library for a total recombined library rHC+LC.

Codons Specified For Residues To Be Doped

For instance, if a proline is to be doped, the doping oligo will have $C_{(5\text{-}85\text{-}5\text{-}5)}C_{(5\text{-}85\text{-}5\text{-}5)}S$ codon regardless of the original codon in the antibody sequence. These codons are selected based on the following criteria: Increase non-synonymous mutation; increase coverage of more amino acids when mutated; and uses high frequency codons and avoid SSS and WWW codons

[0387] Doping order is A-C-G-T

$A_{(70\text{-}10\text{-}10\text{-}10)}$ $C_{(10\text{-}70\text{-}10\text{-}10)}$ $G_{(10\text{-}10\text{-}70\text{-}10)}$ $T_{(10\text{-}10\text{-}10\text{-}70)}$

Alanine (A):
GCN $G_{(10\text{-}10\text{-}70\text{-}10)}C_{(10\text{-}70\text{-}10\text{-}10)}S$
Threonine (T):
ACN $A_{(70\text{-}10\text{-}10\text{-}10)}C_{(10\text{-}70\text{-}10\text{-}10)}S$
Proline (P):
CCN $C_{(10\text{-}70\text{-}10\text{-}10)}C_{(10\text{-}70\text{-}10\text{-}10)}S$
Serine (S):
TCN $T_{(10\text{-}10\text{-}10\text{-}70)}C_{(10\text{-}70\text{-}10\text{-}10)}S$
AGY $A_{(70\text{-}10\text{-}10\text{-}10)}G_{(10\text{-}10\text{-}70\text{-}10)}C_{(10\text{-}70\text{-}10\text{-}10)}$
Valine (V):
GTN $G_{(10\text{-}10\text{-}70\text{-}10)}T_{(10\text{-}10\text{-}10\text{-}70)}S$
Glycine (G):
GGN $G_{(10\text{-}10\text{-}70\text{-}10)}G_{(10\text{-}10\text{-}70\text{-}10)}S$

Leucine (L):
CTN $C_{(10-70-10-10)}T_{(10-10-10-70)}S$
TTR $T_{(10-10-10-70)}T_{(10-10-10-70)}G_{(10-10-70-10)}$
Arginine (R):
CGN $C_{(10-70-10-10)}G_{(10-10-70-10)}S$
AGR $A_{(70-10-10-10)}G_{(10-10-70-10)}G_{(10-10-70-10)}$
Methionine (M):
ATG $A_{(70-10-10-10)}T_{(10-10-10-70)}G_{(10-10-70-10)}$
Tryptophan (W):
TGG $T_{(10-10-10-70)}G_{(10-10-70-10)}G_{(10-10-70-10)}$
Pheylalanine (F):
TTY $T_{(10-10-10-70)}T_{(10-10-10-70)}C_{(10-70-10-10)}$
Isoleucine (I):
50% ATY $A_{(70-10-10-10)}T_{(10-10-10-70)}C_{(10-70-10-10)}$
50% ATA $A_{(70-10-10-10)}T_{(10-10-10-70)}A_{(70-10-10-10)}$
Tyrosine (Y):
TAY $T_{(10-10-10-70)}A_{(70-10-10-10)}C$
Histidine (H):
CAY $C_{(10-70-10-10)}A_{(70-10-10-10)}C_{(10-70-10-10)}$
Glutamine (Q):
CAR $C_{(10-70-10-10)}A_{(70-10-10-10)}G_{(10-10-70-10)}$
Asparagine (N):
AAY $A_{(70-10-10-10)}A_{(70-10-10-10)}C_{(10-70-10-10)}$
Lysine (K):
AAR $A_{(70-10-10-10)}A_{(70-10-10-10)}G_{(10-10-70-10)}$
Aspartic Acid (D):
GAY $G_{(10-10-70-10)}A_{(70-10-10-10)}C_{(10-70-10-10)}$
Glutamic acid (E):
GAR $G_{(10-10-70-10)}A_{(70-10-10-10)}G_{(10-10-70-10)}$
Cysteine (C):
TGY NNS

List of Amino Acid Sequences of Affinity Matured H4g8.3 VH Variants.

Table 38 provides a list of amino acid sequences of unique, functional VH regions of affinity matured humanized anti-VEGF antibodies derived from hBDB-4G8.3. Amino acid residues of individual CDRs of each VH sequence are indicated in bold.

Table 38. List of Amino Acid Sequences of Affinity Matured H4g8.3 VH Variants

Clone	SEQ ID NO:	VH
CL-27663		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYRMY**WVRQAPGQ GLEWMG**WINTETGXPAYADDFKR**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TKYYYSSYIFYFDY**WGQGTMVTVSS
CL-27664		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYSMY**WVRQAPGQ GLEWMG**WINTETGKPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TKYYYRFYLFYFDY**WGQGTMVTVSS
CL-27665		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTYYGMY**WVRQAPGQ GLEWMG**WINTKTGKPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYGSYIFYFDY**WGQGTMVTVSS

Clone	SEQ ID NO:	VH
CL-27666		EVQLVQSGSELKKPGASVKVSCKAS**GYTFINYRMY**WVRQAPGQ GLEWMG**WINTETGKPVYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYSSYKFYFDY**WGQGTMVTVSS
CL-27667		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYAMY**WVRQAPGQ GLEWMG**WINTETGKPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TIYYYXKYIFYFDY**WGQGTMVTVSS
CL-27668		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**PTYYYWIYIFYFDY**WGQGTMVTVSS
CL-27669		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYCMY**WVRQAPGQ GLEWMG**WINTETGKPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**RNYYYXCYIFYFDY**WGQGTMVTVSS
CL-27670		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTTYDMY**WVRQAPGQ GLEWMG**WINTVTGSPAYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TTYYYCSYTFYFDY**WGQGTMVTVSS
CL-27671		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTGTGXPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**XNYYYXSYXFYFDY**WGQGTMVTVSS
CL-27672		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSKYGMY**WVRQAPGQ GLEWMG**WINTYTGKPLYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYMGYRFYFDY**WGQGTMVTVSS
CL-27673		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTPYGMY**WVRQAPGQ GLEWMG**WINTETGVPSYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**SNYYYRSYRFYFDY**WGQGTMVTVSS
CL-27674		EVQLVQSGSELKKPGASVKVSCKAS**GYTFINYVMY**WVRQAPGQ GLEWMG**WINTATGXPSYAQGFTG**RFVFSFDTSVSTTYLQISSL KAEDTAVYYCAR**TTYYYRRYIFYFDY**WGQGTMVTVSS
CL-27675		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTKYDMY**WVRQAPGQ GLEWMG**WINTATGKPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TLYYYRRYIFYFDY**WGQGTMVTVSS
CL-27676		EVQLVQSGSELKKPGASVKVSCKAS**GYTFIKYGMY**WVRQAPGQ GLEWMG**WINTETGRPAYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**IRYYYGSYIFYFDY**WGQGTMVTVSS
CL-27677		EVQLVQSGSELKKPGASVKVSCKAS**GYTFKNYEMY**WVRQAPGQ GLEWMG**WINTETGKPRYADDFKG**RFVFSLDTSVNTAYLQISSL KAEDTAVYYCAR**TNYYYRSYVFYFDY**WGQGTMVTVSS
CL-27678		EVQLVQSGSELKKPGASVKVSCKAS**GYTFPLYSMY**WVRQAPGQ GLEWMG**WINTHTGNPSYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYTFYFDY**WGQGTMVTVSS
CL-27679		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTATGKPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**MNYYYRSYIFYFDY**WGQGTMVTVSS
CL-27680		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYCMY**WVRQAPGQ GLEWMG**WINTETGKPLYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**RNYYYGGYIFYFDY**WGQGTMVTVSS
CL-27681		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTXYGMY**WVRQAPGQ GLEWMG**WINTQTGPPPYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TYYYYRWYIFYFDY**WGQGTMVTVSS

Clone	SEQ ID NO:	VH
CL-27682		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTIYEMY**WVRQAPGQ GLEWMG**WINTETGTPPYAXDFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**XXYYYXSYIFYFDY**WGQGTMVTVSS
CL-27683		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYVMY**WVRQAPGQ GLEWMG**WINTDTGNPAYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TTYYYRVYMFYFDY**WGQGTMVTVSS
CL-27685		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYCMY**WVRQAPGQ GLEWMG**WINTATGNPSYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYASYIFYFDY**WGQGTMVTVSS
CL-27686		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYAMY**WVRQAPGQ GLEWMG**WINTPTGMPNYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TSYYYSSYLFYFDY**WGQGTMVTVSS
CL-27687		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTDTGTPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TEYYYRSYIFYFDY**WGQGTMVTVSS
CL-27688		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYEMY**WVRQAPGQ GLEWMG**WINTATGKPSYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TIYYYVRYIFYFDY**WGQGTMVTVSS
CL-27689		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTETGTPSYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TVYYYRSYLFYFDY**WGQGTMVTVSS
CL-27690		EVQLVQSGSELKKPGASVKVSCKAS**GYTFATYGMY**WVGQAPGQ GLEWMG**WINTETGMPAYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**IRYYYGRYLFYFDY**WGQGTMVTVSS
CL-27691		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSIYYMY**WVRQAPGQ GLEWMG**WINTGTGTPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TSYYYRSYLFYFDY**WGQGTMVTVSS
CL-27692		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYAMY**WVRQAPGQ GLEWMG**WINTQTGKPRYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**PQYYYTSYIFYFDY**WGQGTMVTVSS
CL-27694		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTXTGXPTYAXDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**XXYYYRSYXFYFDY**WGQGTMVTVSS
CL-27695		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTYYNMY**WVRQAPGQ GLEWMG**WINTATGSPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**STYYYRSYIFYFDY**WGQGTMVTVSS
CL-27696		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTKYGMY**WVRQAPGQ GLEWMG**WINTQTGKPRYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYWSYIFYFDY**WGQGTMVTVSS
CL-27697		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYPMY**WVRQAPGQ GLEWMG**WINTETGXPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**XXYYYXRYIFYFDY**WGQGTMVTVSS
CL-27699		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYDMY**WVRQAPGQ GLEWMG**WINTATGKPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**ANYYYRSYLFYFDY**WGQGTMVTVSS
CL-27700		EVQLVQSGSELKKPGASVKVSCKAS**GYTFAHYGMY**WVRQAPGQ GLEWMG**WINTETGNPDYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRCYIFYFDY**WGQGTMVTVSS

Clone	SEQ ID NO:	VH
CL-27701		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTIYGMY**WVRQAPGQ GLEWMG**WINTETGKPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRCYMFYFDY**WGQGTMVTVSS
CL-27702		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTVTGAPIYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYWGYRFYFDY**WGQGTMVTVSS
CL-27703		EVQLVQSGSELKKPGASVKVSCKAS**GYTFRSYVMY**WVRQAPGQ GLEWMG**WINTDTGTPSYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**PYYYYRRYIFYFDY**WGQGTMVTVSS
CL-27704		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYCMY**WVRQAPGQ GLEWMG**WINTKTGNPAYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**XIYYYRRYVLYFDY**WGQGTMVTVSS
CL-27705		EVQLVQSGSELKKPGASVKVSCKAS**GYTFANYSMY**WVRQAPGQ GLEWMG**WINTETGKPKYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRRYSFYFDY**WGQGTMVTVSS
CL-27706		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYCMY**WVRQAPGQ GLEWMG**WINTTTGKPNYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**SNYYYRRYLFYFDY**WGQGTMVTVSS
CL-27708		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTMTGKPNYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TDYYYRSYDFYFDY**WGQGTMVTVSS
CL-27709		EVQLVQSGSELKKPGASVKVSCKAS**GYTFPKYAMY**WVRQAPGQ GLEWMG**WINTETGXPRYAHDFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRGYIFYFDY**WGQGTMVTVSS
CL-27710		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSNYVMY**WVRQAPGQ GLEWMG**WINTETGTPMYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**RDYYYRRYVFYFDY**WGQGTMVTVSS
CL-27711		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTKYDMY**WVRQVPGQ GLEWMG**WVNTDTGKPPYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**SKYYYWTYVFYFDY**WGQGTMVTVSS
CL-27712		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTYYDMY**WVRQAPGQ GLEWMG**WINTXTGKPIYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TIYYYGRYSFYFDY**WGQGTMVTVSS
CL-27713		EVQLVQSGSELKKPGASVKVSCKAS**GYTFPFYVMY**WVRQAPGQ GLEWMG**WINTETGKPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRRYIFYFDY**WGQGTMVTVSS
CL-27714		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTTYSMY**WVRQAPGQ GLEWMG**WINTKTGKPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TIYYYMCYVFYFDY**WGQGTMVTVSS
CL-27715		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTETGNPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**KHYYYGSYLFYFDY**WGQGTMVTVSS
CL-27716		EVQLVQSGSELKKPGASVKVSCKAS**GYTFPDYDMY**WVRQAPGQ GLEWMG**WINTETGMPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRGYIFYFDY**WGQGTMVTVSS
CL-27717		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTDTGKPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TYYYYKKYIFYFDY**WGQGTMVTVSS

Clone	SEQ ID NO:	VH
CL-27718		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTGTGRPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TQYYYRRYIFYFDY**WGQGTMVTVSS
CL-27719		EVQLVQSGSELKKPGASVKVSCKAS**GYTFPNYGMY**WVRQAPGQ GLEWMG**WINTKTGKPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**KNYYYKSYVFYFDY**WGQGTMVTVSS
CL-27721		EVQLVQSVSELKKPGASVKVSCKAS**GYTFTKYTMY**WVRQAPGQ GLEWMG**WINTETGNPMYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRIYIFYFDY**WGQGTMVTVSS
CL-27722		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTATGKPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**SSYYYRNYIFYFDY**WGQGTMVTVSS
CL-27723		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTVTGKPDYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**QKYYYRSYFFYFDY**WGQGTMVTVSS
CL-27725		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYDMY**WVRQAPGQ GLEWMG**WINTDTGKPAYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**PSYYYVXYIFYFDY**WGQGTMVTVSS
CL-27726		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTLYXMY**WVRQAPGQ GLEWMG**WINTATGKPTYAHDFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TXYYYRSYIFYFDY**WGQGTMVTVSS
CL-27727		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTKYGMY**WVRQAPGQ GLEWMG**WINTHTGNPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRCYIFYFDY**WGQGTMVTVSS
CL-27728		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTETGKPEYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**PNYYYRSYFFYFDY**WGQGTMVTVSS
CL-27729		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WINTETGRPGYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**LWYYYWMYIFYFDY**WGQGTMVTVSS
CL-27730		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTYYGMY**WVRQAPGQ GLEWMG**WINTETGTPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**VYYYYGSYSFYFDY**WGQGTMVTVSS
CL-27731		EVQLVQSGSELKKPGASVKVSCKAS**GYTFVNYAMY**WVRQAPGQ GLEWMG**WINTXTGKPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**KTYYYRGYIFYFDY**WGQGTMVTVSS
CL-27733		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTHYYMY**WVRQAPGQ GLEWMG**WINTETGKPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**SKYYYRSYTFYFDY**WGQGTMVTVSS
CL-27734		EVQLVQSGSELKKPGASVKVSCKAS**GYTFLHYGMY**WVRQAPGQ GLEWMG**WINTETGWPRYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TSYYYVSYIFYFDY**WGQGTMVTVSS
CL-27735		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTIYGMY**WVRQAPGQ GLEWMG**WINTATGKPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TXYYYRSYVFYFDY**WGQGTMVTVSS
CL-27736		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTETGNPIYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**AHYYYRTYXFYFDY**WGQGTMVTVSS

Clone	SEQ ID NO:	VH
CL-27737		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTETGNPIYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**AHYYYRTYNFYFDY**WGQGTMVTVSS
CL-27738		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSNYWMY**WVRQAPGQ GLEWMG**WINTETGRPRYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**VYYYYRCYSFYFDY**WGQGTMVTVSS
CL-27739		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTHYWMY**WVRQAPGQ GLEWMG**WINTETGTPSYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TTYYYRSYIFYFDY**WGQGTMVTVSS
CL-27741		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTKYGMY**WVRQAPGQ GLEWMG**WINTNTGKPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**AYYYYWSYIFYFDY**WGQGTMVTVSS
CL-27742		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTSYVMY**WVRQAPGQ GLEWMG**WINTKTGMPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TTYYYMSYIFYFDY**WGQGTMVTVSS
CL-27744		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTQYGMY**WVRQAPGQ GLEWMG**WINTETGKPKYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYWSYKFYFDY**WGQGTMVTVSS
CL-27747		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSTYMMY**WVRQAPGQ GLEWMG**WINTETGXPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**SNYYYRSYIFYFDY**WGQGTMVTVSS
CL-27750		EVQLVQSGSELKKPGASVKVSCKAS**GYTFMNYVMY**WVRQAPGQ GLEWMG**WINTKTGMPRYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYMRYIFYFDY**WGQGTMVTVSS
CL-27751		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTTYGMY**WVRQAPGQ GLEWMG**WINTQTGEPPYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TGYYYWNYLFYFDY**WGQGTMVTVSS
CL-27752		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYRMY**WVRQAPGQ GLEWMG**WINTETGKPPYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYMSYIFYFDY**WGQGTMVTVSS
CL-27753		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTETGSPRYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYVSYIFYFDY**WGQGTMVTVSS
CL-27755		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTETGXPTYAHDFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**XNYYYXXYIFYFDY**WGQGTMVTVSS
CL-27756		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTIYGMY**WVRQAPGQ GLEWMG**WINTDTGRPIYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**IIYYYCSYIFYFDY**WGQGTMVTVSS
CL-27757		EVQLVQSGSELKKPGASVKVSCKAS**GYTFNNYGMY**WVRQAPGQ GLEWMG**WINTETGKPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYIFYFDY**WGQGTMVTVSS
CL-27758		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSLYAMY**WVRQAPGQ GLEWMG**WINTETGKPTYADDFKG**QFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYNFYFDY**WGQGTMVTVSS
CL-27760		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTETGKPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYIFYFDY**WGQGTMVTVSS

Clone	SEQ ID NO:	VH
CL-27824		EVQLVQSGSELNXPGASLKVSCKAS**GYTFXNYGXY**WVRQAPGQ GLEWMG**WINTETGKPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYIFYFDY**WGQGTMVTVSS
CL-27833		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGIY**WVRQAPGQ GLEWMG**WINTETGKPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYIFYFDY**WGQGTMVTVSS
CL-29884		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRLYMFYFDY**WGQGTMVTVSS
CL-29885		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYQSYMFYFDY**WGQGTMVTVSS
CL-29887		EVQLVQSGSELKKPGASVKVSCKAS**GYTFPNYGMY**WVRQAPGQ GLEWMG**WINTETGEPSYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPSYMFYFDY**WGQGTMVTVSS
CL-29888		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**ANYYYRTYMFYFDY**WGQGTMVTVSS
CL-29889		EVQLVQSGSELKKPGASVKVSCKAS**GYTFADYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**SNYYYRTYMFYFDY**WGQGTMVTVSS
CL-29890		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTTYGMY**WVRQAPGQ GLEWMG**WINTETGXPTYAXDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**RXYYYXSYXFYFDY**WGQGTMVTVSS
CL-29891		EVQLVQSGSELKKPGASVKVSCKAS**GYTFPNYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPSYMFYFDY**WGQGTMVTVSS
CL-29892		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSNYGMY**WVRQAPGQ GLEWMG**WINTETGQPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPSYMFYFDY**WGQGTMVTVSS
CL-29893		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**VNYYYRNYMFYFDY**WGQGTMVTVSS
CL-29895		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSDYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**VNYYYMSYMFYFDY**WGQGTMVTVSS
CL-29896		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRMYMFYFDY**WGQGTMVTVSS
CL-29897		EVQLVQSGSELKKPGASVKVSCKAS**GYTFLNYGMY**WVRQAPGQ GLEWMG**WINTETGKPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TKYYYWRYIFYFDY**WGQGTMVTVSS
CL-29898		EVQLVQSGSELKKPGASVKVSCKAS**GYTFNDYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-29899		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**INYYYRSYMFYFDY**WGQGTMVTVSS

Clone	SEQ ID NO:	VH
CL-29901		EVQLVQSGSELKKPGASVKVSCKAS**GYTFMNYGMY**WVRQAPGQ GLEWMG**WIDTETGXXXYAHDFTG**RFVFSLDTSVSTAYLEISSL KAEDTAVYYCAR**XNYYYXXYMFYFDY**WGQGTMVTVSS
CL-29902		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTSYGMY**WVRQAPGQ GLEWMG**WINTETGQPMYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**RIYYYRCYLFYFDY**WGQGTMVTVSS
CL-29904		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WIDTDTGMPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**ANYYYRSYMFYFDY**WGQGTMVTVSS
CL-29906		EVQLVQSGSELKKPGASVKVSCKAS**GYTFNNYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRNYMFYFDY**WGQGTMVTVSS
CL-29907		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WINTETGEPSYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**SNYYYRSYMFYFDY**WGQGTMVTVSS
CL-29908		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSNYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYKSYMFYFDY**WGQGTMVTVSS
CL-29909		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**ANYYYRSYMFYFDY**WGQGTMVTVSS
CL-29910		EVQLVQSGSELKKPGASVKVSCKAS**GYTFNYYGMY**WVRQAPGQ RLEWMG**WINTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYESYMFYFDY**WGQGTMVTVSS
CL-29912		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WINTDTGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-29913		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTKYRMY**WVRQAPGQ GLEWMG**WINTVTGKPKYADDFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**FKYYYGSYFFYFDY**WGQGTMVTVSS
CL-29914		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTETGQPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPSYMFYFDY**WGQGTMVTVSS
CL-29915		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRNYMFYFDY**WGQGTMVTVSS
CL-29916		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WINTETGDPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-29917		EVQLVQSGSELKKPGASVKVSCKAS**GYTFNNYGMY**WVRQAPGQ GLEWMG**WIDTETGQPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPRYMFYFDY**WGQGTMVTVSS
CL-29918		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSNYGMY**WVRQAPGQ GLEWMG**WINTDTGEPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYASYMFYFDY**WGQGTMVTVSS
CL-29919		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYQSYMFYFDY**WGQGTMVTVSS

Clone	SEQ ID NO:	VH
CL-29921		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSHYGMY**WVRQAPGQ GLEWMG**WINTETGSPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPSYMFYFDY**WGQGTMVTVSS
CL-29922		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTDTGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPSYMFYFDY**WGQGTMVTVSS
CL-29924		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WINTETGNPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-29925		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSNYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYAXGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-29926		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSNYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**SNYYYTSYMFYFDY**WGQGTMVTVSS
CL-29927		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WINTETGQPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRMYMFYFDY**WGQGTMVTVSS
CL-29928		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTETGEPYYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPKYMFYFDY**WGQGTMVTVSS
CL-29929		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTHYWMY**WVRQAPGQ GLEWMG**WINTETGKPAYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYIYYLFYFDY**WGQGTMVTVSS
CL-29931		EVQLVQSGSELKKPGASVKVSCKAS**GYTFPNYGMY**WVRQAPGQ GLEWMG**WINTGTGKPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRNYMFYFDY**WGQGTMVTVSS
CL-29932		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTPYGMY**WVRQAPGQ GLEWMG**WINTDTGXPPYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYTCYIFYFDY**WGQGTMVTVSS
CL-29934		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTHYGMY**WVRQAPGQ GLEWMG**WINTETGXPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPRYMFYFDY**WGQGTMVTVSS
CL-29935		EVQLVQSGSELKKPGASVKVSCKAS**GYTFPDYGMY**WVRQAPGQ GLEWMG**WIDTETGMPXYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRNYMFYFDY**WGQGTMVTVSS
CL-29936		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-29937		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTETGDPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**XNYYYRXYMFYFDY**WGQGTMVTVSS
CL-29938		EVQLVQSGSELKKPGASVKVSCKAS**GYTFNKYDMY**WVRQAPGQ GLEWMG**WINTKTGKPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TAYYYRNYKSTLIT**GGQGTMVTVSS
CL-29939		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYKGYMFYFDY**WGQGTMVTVSS

Clone	SEQ ID NO:	VH
CL-29940		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTETGTPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TYYYYRTYIFYFDY**WGQGTMVTVSS
CL-29941		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSNYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRGYMFYFDY**WGQGTMVTVSS
CL-29942		EVQLVQSGSELKKPGASVKVSCKAS**GYNFTKYEMY**WVRQAPGQ GLEWMG**WINTETGNPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TKYYYRSYVFYFDY**WGQGTMVTVSS
CL-29943		EVQLVQSGSELKKPGASVKVSCKAS**GYTFPNYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYLSYMFYFDY**WGQGTMVTVSS
CL-29946		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTHYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPSYMFYFDY**WGQGTMVTVSS
CL-29947		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WINTDTGDPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**ANYYYRTYMFYFDY**WGQGTMVTVSS
CL-29948		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WIDTETGTPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPSYMFYFDY**WGQGTMVTVSS
CL-29949		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WIDTETGDPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**VNYYYRSYMFYFDY**WGQGTMVTVSS
CL-29950		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WIDTQTGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**SNYYYRLYMFYFDY**WGQGTMVTVSS
CL-29951		EVQLVQSGSELKKPGASVKVSCKAS**GYTFPDYGMY**WVRQAPGQ GLEWMG**WIDTETGQPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**ADYYYPTYMFYFDY**WGQGTMVTVSS
CL-29952		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTHYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPTYMFYFDY**WGQGTMVTVSS
CL-29955		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSNYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**SNYYYRSYMFYFDY**WGQGTMVTVSS
CL-29957		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTVTGQPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**THYYYRTYLFYFDY**WGQGTMVTVSS
CL-29958		EVQLVQSGSELKKPGASVKVSCKAS**GYTFPNYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-29959		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRGYMFYFDY**WGQGTMVTVSS
CL-29960		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYSMY**WVRQAPGQ GLEWMG**WINTXTGKPIYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TKYYYRTYRFYFDY**WGQGTMVTVSS

Clone	SEQ ID NO:	VH
CL-29961		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSNYGMY**WVRQAPGQ GLEWMG**WIDTETGTPVYADDFKG**RFVFSLDTSVNTAYLQISSL KAEDTAVYYCAR**TNYYYKSYMFYFDY**WGQGTMVTVSS
CL-29962		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSNYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**SNYYYSSYMFYFDY**WGQGTMVTVSS
CL-29963		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSEYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-29966		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WIDTETGKPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**VNYYYRWYMFYFDY**WGQGTMVTVSS
CL-29967		EVQLVQSGSELKKPGASVKVSCKAS**GYTFPNYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPSYMFYFDY**WGQGTMVTVSS
CL-29968		EVQLVQSGSELKKPGASVKVSCKAY**GYTFTDYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYEKYMFYFDY**WGQGTMVTVSS
CL-29969		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**SNYYYRGYMFYFDY**WGQGTMVTVSS
CL-29970		EVQLVQSGSELKKPGASVKVSCKAS**GYTFMTYVMY**WVRQAPGQ GLEWMG**WINTETGKPSYAHDFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**MXYYYXIYMFYFDY**WGQGTMVTVSS
CL-29971		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSNYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-29972		EVQLVQSGSELKKPGASVKVSCNAS**GXTFTNYGMY**WVRQAPGQ GLEWMG**WINTETGKPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**INYYYRSYIFYFDY**WGQGTMVTVSS
CL-29973		EVQLVQSGSELKKPGASVKVSCKAS**GYTFNDYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYAXXFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYEGYMFYFDY**WGQGTMVTVSS
CL-29974		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSDYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-29975		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYKSYMFYFDY**WGQGTMVTVSS
CL-29976		EVQLVQSGSELRKPGASVKVSCKAS**GYTFNNYGMY**WVRQAPGQ GLEWMG**WIDTETGRPWYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYQGYMFYFDY**WGQGTMVTVSS
CL-29980		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMH**WVRQAPGQ GLEWMG**WINTETGKPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYIFYFDY**WGQGTMVTVSS
CL-30036		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTETGKPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSHIFYFDY**WGQGTMVTVSS

Clone	SEQ ID NO:	VH
CL-30060		EVQLVQSGSELKKPGASVRVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTETGKPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYIFYFDY**WGQGTMVTVSS
CL-30075		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTXTGKPTYAXGFTG**RFVFSLDTSVSTAYLQIXXL XAXDTAVYYCAR**XKYYYXSYIFYFDY**WGQGTMVTVSS
CL-30076		EVQLVQSGSELKKPGASVKVSCKAS**GYTFYNYCMY**WVRQAPGQ GLEWMG**WINTETGIPKYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**INYYYKRYIFYFDY**WGQGTMVTVSS
CL-30077		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYYMY**WVRQAPGQ GLEWMG**WINTETGKPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TXYYYXRYXFYFDY**WGQGTMVTVSS
CL-30078		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTETGKPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYIFYFDY**WGQGTMVTVFS
CL-30079		EVQLVQSGSELKKPGASVKVSCKAS**GYTFIHYGMY**WVRQAPGQ GLEWMG**WINTETGRPTYADDFKG**RFVFSLDTSVSTAYLQISSL KXEDTAVYYCAR**TVYYYPRYTFYFDY**WGQGTMVTVSS
CL-30082		EVQLVQSGSELKKPGASVKVSCKAS**GYTFMNYGMY**WVRQAPGQ GLEWMG**WINTETGKPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPGYIFYFDY**WGQGTMVTVSS
CL-30083		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTLYGMY**WVRQAPGQ GLEWMG**WINTDTGKPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYXSYIFYFDY**WGQGTMVTVSS
CL-30084		EVQLVQSGSELKKPGASVKVSCKAS**GYTFNKYGMY**WVRQAPGQ GLEWMG**WINTETGKPSYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**AKYYYRSYIFYFDY**WGQGTMVTVSS
CL-30086		EVQLVQSGSELKKPGASVKVSCKAS**GYTFLNYGMY**WVRQAPGQ GLEWMG**WINTETGRPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRIYRFYFDY**WGQGTMVTVSS
CL-30087		EVQLVQSGSELKKPGASVKVSCKAS**GYTFYNYGMY**WVRQAPGQ GLEWMG**WINTATGKPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**XKYYYXSXXFYFDY**WGQGTMVTVSS
CL-30091		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSNYDMY**WVRQAPGQ GLEWMG**WINTVTGLPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TIYYYKSYIFYFDY**WGQGTMVTVSS
CL-30092		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSNYGMY**WVRQAPGQ GLEWMG**WINTGTGIPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TSYYYRNYLFYFDY**WGQGTMVTVSS
CL-30093		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTKYGMY**WVRQAPGQ GLEWMG**WINTETGKPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TTYYYRRYIFYFDY**WGQGTMVTVSS
CL-30096		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTTYAMY**WVRQAPGQ GLEWMG**WINTETGKPRYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**ANYYYRSYIFYFDY**WGQGTMVTVSS
CL-30097		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSNYGMY**WVRQAPGQ GLEWMG**WINTETGKPTYADDFKG**RFVFSLDTSVSTAYLQIXXL KTEDTAVYYCAR**SNYYYRGYIFYFDY**WGQGTMVTVSS

Clone	SEQ ID NO:	VH
CL-30103		EVQLVQSGSELKKPGASVKVSCKAS**GYTFAIYRMY**WVRQAPGQ GLEWMG**WINTDTGKPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**SKYYYGFYMFYFDY**WGQGTMVTVSS
CL-30107		EVQLVQSGSELKKPGASVKVSCKAS**GYTFMNYGMY**WVRQAPGQ GLEWMG**WINTETGRPVYAQGFTG**RFVFSLDTSVSTAYLQISSL KAXDTAVYYCAR**TNYYYLRYVFYFDY**WGQGTMVTVSS
CL-30108		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTGTGMPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**NKYYYRSYMFYFDY**WGQGTMVTVSS
CL-30110		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYDMY**WVRQAPGQ GLEWMG**WINTETGKPPYADGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYIFYFDY**WGQGTMVTVSS
CL-30113		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTSYGMY**WVRQAPGQ GLEWMG**WINTETGIPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**WDYYYTSYKFYFDY**WGQGTMVTVSS
CL-30114		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTIYGMY**WVRQAPGQ GLEWMG**WINTVTGNPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TEYYYMNYIFYFDY**WGQGTMVTVSS
CL-30116		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYDMY**WVRQAPGQ GLEWMG**WINTGTGKPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**ANYYYSRYDFYFDY**WGQGTMVTVSS
CL-30119		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTKYGMY**WVRQAPGQ GLEWMG**WINTQTGKPAYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**AIYYYRIYIFYFDY**WGQGTMVTVSS
CL-30124		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYAMY**WVRQAPGQ GLEWMG**WINTQTGEPSYAQGFTG**XFVFSLDTSASTEYLXISIL XDXDTAVYYCAR**XTYYYXNYIFYFDY**WGXGTMVTVSS
CL-30127		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTTYGMY**WVRQAPGQ GLEWMG**WINTETGRPTYADDFNG**WFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRIYIFYFDY**WGQGTMVTVSS
CL-30128		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WIDTETGKPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYIFYFDY**WGQGTMVTVSS
CL-30129		EVQLVQSGSELKKPGASVKVSCKAS**GYTFNNYGMY**WVRQAPGQ GLEWMG**WINTGTGKPTYAQGFTG**RFVFSLDTSVSTAYLQIXSL KAEDTAVYYCAR**PIYYYIRYIFYFDY**WGQGTMVTVSS
CL-30130		EVQLVQSGSELKKPGASVKVSCKAS**GYTFADYPMY**WVRQAPGQ GLEWMG**WINTXTGQPLYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TSYYYRSYIFYFDY**WGQGTMVTVSS
CL-30135		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTETGKPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAXDTAVYYCAR**TNYYYRSYIFYFDY**WGQGTMVTVSS
CL-30136		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYSMY**WVRQAPGQ GLEWMG**WINTETGKPRYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TSYYYRSYIFYFDY**WGQGTMVTVSS
CL-30138		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTTYWMY**WVRQAPGQ GLEWMG**WINTETGEPRYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TEYYYKSYNFYFDY**WGQGTMVTVSS

Clone	SEQ ID NO:	VH
CL-30140		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTAYGMY**WVRQAPGQ GLEWMG**WINTETGMPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TKYYYRSYMFYFDY**WGQGTMVTVSS
CL-30141		EVQLVQSGSELKKPGASVKVSCKAS**GYTFHNYGMY**WVRQAPGQ GLEWMG**WINTETGKPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TSYYYRSYFFYFDY**WGQGTMVTVSS
CL-30142		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYVMY**WVRQAPGQ GLEWMG**WINTETGNPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**LIYYYXTYIFYFDY**WGQGTMVTVSS
CL-30145		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSNYAMY**WVRQAPGQ GLEWMG**WINTETGKPPYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TLYYYRTYIFYFDY**WGQGTMVTVSS
CL-30147		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTHYCMY**WVRQAPGQ GLEWMG**WINTETGKPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRRYIFYFDY**WGQGTMVTVXS
CL-30148		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSNYGMY**WVRQAPGQ GLEWMG**WINTETGQPSYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRCYIFYFDY**WGQGTMVTVSS
CL-30151		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTETGKPNYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**PNYYYRSYIFYFDY**WGQGTMVTVSS
CL-30154		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYAMY**WVRQAPGQ GLEWMG**WINTETGNPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYGIYLFYFDY**WGQGTMVTVSS
CL-30156		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYDMY**WVRQAPGQ GLEWMG**WINTVTGRPAYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**ITYYYRMYRFYFDY**WGQGTMVTVSS
CL-30159		EVQLVQSGSELKKPGASVKVSCKAS**GYTFIDYLMY**WVRQAPGQ GLEWMG**WINTVTGKPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**THYYYRSYAFYFDY**WGQGTMVTVSS
CL-30161		EVQLVQSGSELKKPGASVKVSCKAS**GYTFAKYEMY**WVRQAPGQ GLEWMG**WINTETGNPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRDYTFYFDY**WGQGTMVTVSS
CL-30162		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTTYRMY**WVRQAPGQ GLEWMG**WINTVTGRPSYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**NIYYYRSYIFYFDY**WGQGTMVTVSS
CL-30164		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYIFYFDY**WGQGTMVTVSS
CL-30165		EVQLVQSGSELKKPGASVKVSCKAS**GYTFRNYVMY**WVRQAPGQ GLEWMG**WINTQTGEPSYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYGIYIFYFDY**WGQGTMVTVSS
CL-30166		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTETGKPTYADDFKG**RFVFSLDTSVSTAYLQISSL QAEDTAVYYCAR**TNYYYRSYIFYFDY**WGQGTMVTVSS
CL-30168		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WINTETGMPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**SNYYYRGYIFYFDY**WGQGTMVTVSS

Clone	SEQ ID NO:	VH
CL-30169		EVQLVQSGSELKKPGASVKVSCKAS**GYTFLGYSMY**WVRQAPGQ GLEWMG**WINTETGKPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**KFYYYESYIFYFDY**WGQGTMVTVSS
CL-30170		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTYYCMY**WVRQAPGQ GLEWMG**WINTHTGKPMYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**KKYYYRSYIFYFDY**WGQGTMVTVSS
CL-30593		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSDYGMY**WVRQAPGQ GLEWMG**WIDTETGDPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYMSYMFYFDY**WGQGTMVTVSS
CL-30594		EVQLVQSGSELKKPGASVKVSCKAS**GYTFMNYGMY**WVRQAPGQ GLEWMG**WINTETGKPMYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TIYYYPRYIFYFDY**WGQGTMVTVSS
CL-30595		EVQLVQSGSELKKPGASVKVSCKAS**GYTFAMYKMY**WVRQAPGQ GLEWMG**WINTQTGGPSYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TKYYYWRYVFYFDY**WGQGTMVTVSS
CL-30597		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSNYGMY**WVRQAPGQ GLEWMG**WINTETGQPMYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPSYMFYFDY**WGQGTMVTVSS
CL-30599		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WIDTETGNPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**SNYYYSSYMFYFDY**WGQGTMVTVSS
CL-30600		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTATGQPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**ANYYYMYYLFYFDY**WGQGTMVTVSS
CL-30602		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**ANYYYRLYMFYFDY**WGQGTMVTVSS
CL-30604		EVQLVQSGSELKKPGASVKVSCKAS**GYTFPNYGMY**WVRQAPGQ GLEWMG**WINTWTGKPTYAXDFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPSYMFYFDY**WGQGTMVTVSS
CL-30605		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**ANYYYRTYMFYFDY**WGQGTMVTVSS
CL-30606		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYRMY**WVRQAPGQ GLEWMG**WINTETGKPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYSSYMFYFDY**WGQGTMVTVSS
CL-30608		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTTYDMY**WVRQAPGQ GLEWMG**WINTVTGXPTYAXXFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**SXYYYRSYIFYFDY**WGQGTMVTVSS
CL-30609		EVQLVQSGSELKKPGASVKVSCKAS**GYTFNNYGMY**WVRQAPGQ GLEWMG**WINTETGKPRYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TDYYYRRYTFYFDY**WGQGTMVTVSS
CL-30611		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSNYGMY**WVRQAPGQ GLEWMG**WINTYTGIPSYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**VNYYYSTYIFYFDY**WGQGTMVTVSS
CL-30613		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGIY**WVRQAPGQ GLEWMG**WINTETGKPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**SNYYYRGYMFYFDY**WGQGTMVTVSS

Clone	SEQ ID NO:	VH
CL-30614		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**SNYYYRSYMFYFDY**WGQGTMVTVSS
CL-30615		EVQLVQSGSELKKPGASVKVSCKAS**GYTFNNYGMY**WVRQAPGQ GLEWMG**WINTDTGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**VNYYYRSYMFYFDY**WGQGTMVTVSS
CL-30616		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTTYGMY**WVRQAPGQ GLEWMG**WINTLTGAPMYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYSSYIFYFDY**WGQGTMVTVSS
CL-30617		EVQLVQSGSELKKPGASVKVSCKAS**GYTFKNYSMY**WVRQAPGQ GLEWMG**WINTDTGMPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRFYIFYFDY**WGQGTMVTVSS
CL-30618		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSNYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**VNYYYRSYMFYFDY**WGQGTMVTVSS
CL-30619		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSNYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYADDFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**ANYYYRSYMFYFDY**WGQGTMVTVSS
CL-30620		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRGYMFYFDY**WGQGTMVTVSS
CL-30623		EVQLVQSGSELKKPGASVKVSCKAS**GYTFANYGMY**WVRQAPGQ GLEWMG**WINTETGQPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYQSYMFYFDY**WGQGTMVTVSS
CL-30624		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTDTGTPAYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYTRYNFYFDY**WGQGTMVTVSS
CL-30626		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-30628		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSNYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**ANYYYRSYMFYFDY**WGQGTMVTVSS
CL-30629		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYDMY**WVRQAPGQ GLEWMG**WINTETGNPTYAXXFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**XNYYYSSYIFYFDY**WGQGTMVTVSS
CL-30630		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**SNYYYRTYMFYFDY**WGQGTMVTVSS
CL-30631		EVQLVQSGSELKKPGASVKVSCKAS**GYTFNNYGMY**WVRQAPGQ GLEWMG**WINTETGKPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPSYMFYFDY**WGQGTMVTVSS
CL-30632		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPSYMFYFDY**WGQGTMVTVSS
CL-30634		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTYYGMY**WVRQAPGQ GLEWMG**WINTETGKPSYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TIYYYTTYIFYFDY**WGQGTMVTVSS

Clone	SEQ ID NO:	VH
CL-30635		EVQLVQSGSELKKPGASVKVSCKAS**GYTFPNYGMY**WVRQAPGQ GLEWMG**WIDTETGEPIYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**INYYYPNYMFYFDY**WGQGTMVTVSS
CL-30636		EVQLVQSGSELKKPGASVKVSCKTS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRGYMFYFDY**WGQGTMVTVSS
CL-30637		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPSYMFYFDY**WGQGTMVTVSS
CL-30638		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSNYGMY**WVRQAPGQ GLEWMG**WIDTETGNPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**ANYYYRSYMFYFDY**WGQGTMVTVSS
CL-30639		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WIDTETGTPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-30640		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSSYGMY**WVRQAPGQ GLEWMG**WIDTETGEPKYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPSYMFYFDY**WGQGTMVTVSS
CL-30642		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSNYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**YNYYYRIYLFYFDY**WGQGTMVTVSS
CL-30643		EVQLVQSGSELKKPGASVKVSCKAS**GYTFPYYSMY**WVRQAPGQ GLEWMG**WINTDTGTPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TTYYYWSYIFYFDY**WGQGTMVTVSS
CL-30644		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTETGDPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPSYMFYFDY**WGQGTMVTVSS
CL-30645		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTXTGKPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TSYYYRCYIFYFDY**WGQGTMVTVSS
CL-30647		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WINTETGQPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-30649		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSNYGMY**WVRQAPGQ GLEWMG**WIDTDTGKPTYAXDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYTGYMFYFDY**WGQGTMVTVSS
CL-30651		EVQLVQSGSELEKPGASVKVSCKAS**GYTFPNYGMY**WVRQAPGQ GLEWMG**WIDTDTGKPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**ANYYYRSYMFYFDY**WGQGTMVTVSS
CL-30653		EVQLVQSGSELKKPGASVKVSCKAS**GYTFNNYGMY**WVRQAPGQ GLEWMG**WIDTETGDPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**ANYYYLSYMFYFDY**WGQGTMVTVSS
CL-30654		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSNYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYIFYFDY**WGQGTMVTVSS
CL-30655		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTETGEPSYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPSYMFYFDY**WGQGTMVTVSS

Clone	SEQ ID NO:	VH
CL-30657		EVQLVQSGSELKKPGASVKVSCKAS**GYTFANYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYKSYMFYFDY**WGQGTMVTVSS
CL-30658		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSNYGMY**WVRQAPGQ GLEWMG**WINTDTGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-30659		EVQLVQSGSELKKPGASVKVSCKAS**GYTFPYYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYADDFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**ANYYYRMYMFYFDY**WGQGTMVTVSS
CL-30660		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WIDTETGDPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRGYMFYFDY**WGQGTMVTVSS
CL-30662		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTETGSPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**IIYYYLSYLFYFDY**WGQGTMVTVSS
CL-30663		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSNYGMY**WVRQAPGQ GLEWMG**WINTETGDPTYAQGFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPSYMFYFDY**WGQGTMVTVSS
CL-30664		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**ANYYYSGYMFYFDY**WGQGTMVTVSS
CL-30665		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRYYMFYFDY**WGQGTMVTVSS
CL-30666		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPSYMFYFDY**WGQGTMVTVSS
CL-30669		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTKYAMY**WVRQAPGQ GLEWMG**WINTYTGVPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**GHYYYMMYIFYFDY**WGQGTMVTVSS
CL-30670		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSNYGMY**WVRQAPGQ GLEWMG**WIDTETGKPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**YKYYYRSYKFYFDY**WGQGTMVTVSS
CL-30671		EVQLVQSGSELKKPGASVKVSCKAS**GYTFPDYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRGYMFYFDY**WGQGTMVTVSS
CL-30674		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSHYGMY**WVRQAPGQ GLEWMG**WINTETGDPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPSYMFYFDY**WGQGTMVTVSS
CL-30675		EVQLVQSGSELKKPGASVKVSCKAS**GYTFPNYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-30676		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WIDTETGYPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**ANYYYRTYMFYFDY**WGQGTMVTVSS
CL-30677		EVQLVQSGSELKKPGASVKVSCKAS**GYTFNNYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRTYMFYFDY**WGQGTMVTVSS

Clone	SEQ ID NO:	VH
CL-30678		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSHYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**ANYYYRSYMFYFDY**WGQGTMVTVSS
CL-30679		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTSYRMY**WVRQAPGQ GLEWMR**WINTETGWPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TSYYYRNYMFYFDY**WGQGTMVTVSS
CL-30682		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WINTETGNPMYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPSYMFYFDY**WGQGTMVTVSS
CL-30684		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRNYMFYFDY**WGQGTMVTVSS
CL-30685		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCVR**TNYYYRTYMFYFDY**WGQGTMVTVSS
CL-32447		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WXRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-32466		EVQLVQSGSELKKPGASVKVSCKAS**GYTFHDYGMY**WVRQAPGQ GLEWMG**WIDTETGTPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYSSYMFYFDY**WGQGTMVTVSS
CL-32470		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WIDTETGXPTYAXXFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-32507		EVQLVQSGSELKKPGASVKVSCKAS**GYTFNDYGMY**WVRQAPGQ GLEWMG**WIDTETGKPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYSSYMFYFDY**WGQGTMVTVSS
CL-34445		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYADDFXG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-34457		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYAHDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**XNYYYRSYMFYFDY**WGQGTMVTVSS
CL-34458		EVQLVQSGSELKKPGAPVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-34465		EVQLVQSGSELKKPGASVKVSCKAS**GYTFPDYGMY**WVRQAPGQ GLEWMG**WIDTETGQPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRTYMFYFDY**WGQGTMVTVSS
CL-34466		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WIDTETGEPIYAQGFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYNSYMFYFDY**WGQGTMVTVSS
CL-34468		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WIDTETGEPRYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPSYMFYFDY**WGQGTMVTVSS
CL-34478		EVQLVQSGSELKKPGASVKVSCKAS**GYTFPHYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYSSYMFYFDY**WGQGTMVTVSS

Clone	SEQ ID NO:	VH
CL-34480		EVQLVQSGSELKKPGASVKVSCKAS**GYTFEDYGMY**WVRQAPGQ GLEWMG**WINTETGEPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRNYMFYFDY**WGQGTMVTVSS
CL-34482		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRTYMFYFDY**WGQGTMVTVSS
CL-34488		EVQLVQSGSELKKPGASVKVSCKAS**GYTFDDYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-34490		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WIDTETGTPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-34493		EVQLVQSGSELKKPGASVKVSCKAS**GYTFGDYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**VNYYYRNYMFYFDY**WGQGTMVTVSS
CL-34495		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WIDTETGQPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYKSYMFYFDY**WGQGTMVTVSS
CL-34496		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRGYMFYFDY**WGQGTMVTVSS
CL-34499		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSDYGMY**WVRQAPGQ GLEWMG**WIDTETGDPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-34502		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSNYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-34503		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSDYGMY**WVRQAPGQ GLEWMG**WIDTETGTPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYKSYMFYFDY**WGQGTMVTVSS
CL-34505		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WIDTETGQPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPSYMFYFDY**WGQGTMVTVSS
CL-34510		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSHYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYMSYMFYFDY**WGQGTMVTVSS
CL-34512		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WIDTDTGTPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPKYMFYFDY**WGQGTMVTVSS
CL-34527		EVQLVQSGSELKKPGASVKVSCKAS**GYTFANYGMY**WVRQAPGQ GLEWMG**WIDTETGTPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-34528		EVHLVQSGSELKKPGASVKVSCKAS**GYTFSNYGMY**WVRQAPGQ GLEWMG**WIDTETGKPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-34529		EVQLVQSGSELNKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WIDTETGEPSYADDFKG**RFVFSLDTXVSTAYXQISSL KAEDXAVYXCAR**TNYYYSSYMFYFDY**WGQGTXVTVSS

Clone	SEQ ID NO:	VH
CL-34534		EVQLVQSGSELKKPGASVKVSCKAS**GYTFNDYGMY**WVRQAPGQ GLEWMG**WIDTETGNPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**ANYYYRSYMFYFDY**WGQGTMVTVSS
CL-34539		EVQLVPSGSHFNNPGASXKVSCSAS**GYTFSDYGMY**WVRQAPGQ GLEWMG**WIDTETGDPTYADDFKG**XFVFSLDTSVXXAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-34548		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WIDTETGDPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPSYMFYFDY**WGQGTMVTVSS
CL-34562		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WIDTETGKPTYADDFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRTYMFYFDY**WGQGTMVTVSS
CL-34568		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WIDTETGQPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-34577		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WIDTETGTPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYESYMFYFDY**WGQGTMVTVSS
CL-34582		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSNYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPSYMFYFDY**WGQGTMVTVSS
CL-34586		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYAXXFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-34590		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WIDTETGKPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-34592		EVQLVQSGSELKKPGASVKVSCKAS**GYTFNDYGMY**WVRQAPGQ GLEWMG**WIDTETGTPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYSSYMFYFDY**WGQGTMVTVSS
CL-34595		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRTYMFYFDY**WGQGTMVTVSS
CL-34596		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRNYMFYFDY**WGQGTMVTVSS
CL-34597		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-34599		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSDYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPSYMFYFDY**WGQGTMVTVSS
CL-34600		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISNL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-34617		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPRYMFYFDY**WGQGTMVTVSS

Clone	SEQ ID NO:	VH
CL-40631		EVQLVQSGSELKKPGASVKVSCXAS**GYTFSDYGMY**WVRQAPGQ GLEWMG**WIDTETGDPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**ANYYYRSYMFYFDY**WGQGTMVTVSS
CL-40642		RVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-40646		EVQLVQSGSELKKPGASVKVSCEAS**GYTFSDYGMY**WVRQAPGQ GLEWMG**WIDTETGDPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**ANYYYRSYMFYFDY**WGQGTMVTVSS
CL-40665		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPSYMFYFDY**WGQGTMVTSLQ
CL-40668		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KVEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-40671		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WIDTETGTPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYSSYMFYFDY**WGQGTMVTVSS
CL-40687		ASAAVQSGSELKKPGASVKVSCKAS**GYTFENYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYSSYMFYFDY**WGQGTMVTVSS
CL-40688		EVQLVQSGSELKKPGASVKVSCKAS**GYTFENYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYSSYMFYFDY**WGQGTMVTVSS
CL-40694		EVQLVQSGSELKKPGASVKVSCKAS**GYTFENYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLGTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYSSYMFYFDY**WGQGTMVTVSS
CL-40708		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYSSYMFYFDY**WGQGTMVTVSS
CL-40716		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSDYGMY**WVRQAPGQ GLEWMG**WIDTETGDPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**ANYYYRSYMFYFDY**WGQGTMVTVSS
CL-40717		EVQLVQSGSELKKPGASVKVSCKAS**GYTFDDYGMY**WVRQAPGQ GLEWMG**WIDTETGTPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYSSYMFYFDY**WGQGTMVTVSS
CL-40721		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPSYMFYFDY**WGQGTMVTVSS
CL-40722		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-40723		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-40736		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTHYGMY**XVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS

Clone	SEQ ID NO:	VH
CL-40740		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSDYGMY**WVRQAPGQ GLEWMG**WIDTETGDPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPSYMFYFDY**WGQGTMVTVSS
CL-40741		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GPEWMG**WIDTETGNPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPSYMFYFDY**WGQGTMVTVSS
CL-40742		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTHYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAENTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-40745		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-40746		EVQLVQSGSXLKXPGXSXKVSCXVS**GYTFQNYGMY**CVRPAPGQ WLXWMG**WIDXXTGEPTYAYDFKG**WFLFSLHTSVSMSSLQNXSL KXDDTAVYYCAK**TNYYYNSYMFYFDY**WGQGTXXTVSS
CL-40747		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WIDTETGQPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRNYMFYFDY**WGQGTMVTVSS
CL-40753		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WIDTETGDPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRNYMFYFDY**WGQGTMVTVSS
CL-40758		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYAQGFTG**RFVFSLDTSVSTAYLQISSL KAEDTAVHYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-40760		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSNYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYSSYMFYFDY**WGQGTMVTVSS
CL-40763		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTHYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-40764		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WIDTETGNPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPSYMFYFDY**WGQGTMVTVSS
CL-40765		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WIDTETGQPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-40766		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSNYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEGTAVYYCAR**TNYYYSSYMFCFDY**WGQGTMVTVSS
CL-40768		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSNYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYSSYMFYFDY**WGQGAMVTVSS
CL-40770		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTHYGMY**WVRRAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-40774		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSDYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KVEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS

Clone	SEQ ID NO:	VH
CL-40779		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPSYMFYFDY**WGQGTMVTVSS
CL-40780		EVQLVQSGSELEKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRGYMFYFDY**WGQGTMVTSLQ
CL-40788		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WIDAETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRGYMFYFDY**WGQGTMVTVSS
CL-40790		EGHLGQSGSELKNPGASVKVSCXAS**GYTFXNYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYAXDFKG**RFVFSLGTSVSTAYLQIXSL RAEDTAVYYCEX**TNYYYSRYMFYFXY**WGQGTMVTVSS
CL-40791		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**XIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYKSYMFYFDY**WGQGTMVTVSS
CL-40793		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSDYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVFS
CL-40795		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRGYMLYFDY**WGQGTMVTVSS
CL-40796		EVQLVQSGSELKKPGASVKVSCKAS**GYTFPNYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYKSYMFYFDY**WGQGTMVTVSS
CL-40800		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRRAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRGYMFYFDY**WGQGTMVTVSS
CL-40801		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RLVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYKSYMFYFDY**WGQGTMVTVSS
CL-40805		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYSSYMFYFDY**WGQGTMVTVSS
CL-40806		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRGYMFYFDY**WGQGTMVTVSS
CL-40811		EVQLVQSGSELKKPGASVKVSCKAS**GYTFPNYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS
CL-40812		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYXSYMFYFDY**WGQGTMVTVSS
CL-40815		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYKSYMFYFDY**WGQGTMVTVSS
CL-40816		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**QFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPSYMFYFDY**WGQGTMVTVSS

Clone	SEQ ID NO:	VH
CL-40817		EVQLVQSGSELKKPGASVKVSCKAS**GYTFTDYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYPSHMFYFDY**WGQGTMVTVSS
CL-40819		EVQLVQSGSELKKPGASVKVSCKAS**GYTFSDYGMY**WVRQAPGQ GLEWMG**WIDTETGEPTYADDFKG**RFVFSLDTSVSTAYLQISSL KAEDTAVYYCAR**TNYYYRSYMFYFDY**WGQGTMVTVSS

List of amino acid sequences of affinity matured h4G8.3 VL variants

Table 39 provides a list of amino acid sequences of unique, functional VL regions of affinity matured humanized VEGF antibodies derived from hBDB-4G8.3. Amino acid residues of individual CDRs of each VL sequence are indicated in bold.

Table 39. List of Amino Acid Sequences of Affinity Matured H4g8.3 VL Variants

Clone	SEQ ID NO:	VL
CL-27686		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG XAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWNDPFT**FGQGTKLEIK
CL-27698		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSRSGTDFTLTISSLEPED FAVYFC**QQSWNDPFT**FGQGTKLEIK
CL-27717		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWNDPFT**FGQGAKLEIK
CL-27741		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWNDPFT**FGLGTKLEIK
CL-27758		EIVLTQFPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWNDPFT**FGQGTKLEIK
CL-27762		EIVLTQSPATLSLSPGERATLSC**RASQSVTPHMH**WYQQKPG QAPRLLIY**GASTLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSCNDPFT**FGQGTKLEIK
CL-27763		EIVLTQSPATLSLSPGERATLSG**RASESVDKYMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSRNDPLT**FGQGTKLEIK
CL-27764		EIVLTQSPATLSLSPGERATLSC**RASQSVKTDMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSRNEPFT**FGQGTKLEIK
CL-27765		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHLA**WYQQKPG QAPRLLIY**RASKLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQNWNDPLT**FGQGTKLEIK
CL-27766		EIVLTQSPATLSLSPGERATLSC**RASQSVRTHMH**WYQQKPG QAPRLLIY**GASALES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQGCNXPFT**FGQGTKLEIK
CL-27767		EIVLTQSPATLSLSPGERATLSC**RASQSVRTHMH**WYQQKPG QAPRLLIY**EASNLES**GIPARFSGSGSGTDFTLTISSLEPED

Clone	SEQ ID NO:	VL
		FAVYFC**QQSCNDPFT**FGQGTKLEIK
CL-27768		EIVLTQSPATLSLSPGERATLSC**RASQSVSTDMH**WYQQKPG QAPRLLIY**GASKLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWNDPFT**FGQGTKLEIK
CL-27770		EIVLTQSPATLSLSPGERATLSC**RASQSVSPHMH**WYQQKPG QAPRLLIY**GASKLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTSNEPFT**FGQGTKLEIK
CL-27771		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASDLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSXIDPVT**FGQGTKLEIK
CL-27772		EIVLTQSPATPSLSPGERATLSC**RASESVNAHMH**WYQQKPG QAPRLLIY**DASKLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWSDPFT**FGQGTKLEIK
CL-27773		EIVLTQSPATLSLSPGERATLSC**RASESVRTQLA**WYQQKPG QAPRLLIY**SASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSRTEPFT**FGQGTKLEIK
CL-27774		EIVLTQSPATLSLSPGERATLSC**RASQSVSTPMH**WYQQKPG QAPRLLIY**SASNLES**GIPARFSDSGSGTDFTLTISSLEPED FAVYYC**QQFWDDPYT**FGQGTKLEIK
CL-27775		EIVLTQSPATLSLSPGERATLSC**RASESVITHLA**WYQQKPG QAPRLLIY**SASILES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQCCIDPFT**FGQGTKLEIK
CL-27776		EIVLTQSPATLSLSPGERATLSC**RASQSVRSQLA**WYQQKPG QAPRLLIY**VASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSXNDPFT**FGQGTKLEIK
CL-27779		EIVLTQSPATLSLSPGERATLSC**RASESVRTHMH**WYQQKPG QAPRLLIY**GASKLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWIDPFT**FGQGTKLEIK
CL-27780		EIVLTQSPATLSLSPGERATLSC**RASESVSIHLA**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNDPFT**FGQGTKLEIK
CL-27781		EIVLTQSPATLSLSPGERATLSC**RASQSVSTPMH**WYQQKPG QAPRLLIY**GASYLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNEPYT**FGQGTKLEIK
CL-27782		EIVLTQSPATLSLSPGERATLSC**RASESVSAHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWIYPFT**FGQGTKLEIK
CL-27783		EIVLTQSPATLSLSPGERATLSC**RASQSVRTHMH**WYQQKPG QAPRLLIY**GASHLES**GIPARFSGSGSGIDFTLTISSLEPED FAVYYC**QQSXRYPFT**FGQGTKLEIK
CL-27784		EIVLTQSPATLSLSPGERATLSC**RASQSVRTHMH**WYQQKPG QAPRLLIY**RASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQRSNEPFT**FGQGTKLEIK
CL-27785		EIVLTQSPATLSLSPGERATLSC**RASQSVRSHMH**WYQQKPG QAPRLLIY**GASGLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQRWNEPST**FGQGTKLEIK
CL-27786		EIVLTQSPATLSLSPGERATLSC**RASQSVRFHMH**WYQQKPG QAPRLLIY**GASPLES**GIPARFSGSGSGTDFTLTISSLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QQSRRHPFT**FGQGTKLEIK
CL-27787		EIVLTQSPATLSLSPGERATLSC**RASQSVSIQMH**WYQQKPG QAPRLLIY**GASKLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQQWNVPFT**FGQGTKLEIK
CL-27788		EIVLTQSPATLSLSPGERATLSC**RASQSVSTPMH**WYQQKPG QAPRLLIY**RASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQGGNDPYT**FGQGTKLEIK
CL-27790		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**WASDLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQCWNGPLT**FGQGTKLEIK
CL-27791		EIVLTQSPATLSLSPGERATFSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGCGTDFTLTISSLEPED FAVYXC**QQSGNDPFT**FGQGTKLEIK
CL-27792		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**RASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQGGNVPCT**FGQGTKLEIK
CL-27794		EIVLTQSPATLSLSPGERATLSC**RASESVSWHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQIRADPFT**FGQGTKLEIK
CL-27795		EIVLTQSPATLSLSPGERATLSC**RASESVCAHMH**WYQQKPG QAPRLLIY**WASKLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSGLDPVT**FGQGTKLEIK
CL-27796		EIVLTQSPATLSLSPGERATLSC**RASESVSTQMH**WYQQKPG QAPRLLIY**GASILES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSGNNPFT**FGQGTKLEIK
CL-27797		EIVLTQSPATLSLSPGERATLSC**RASQSVSTLMH**WYQQKPG QAPRLLIY**RASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQGWNKPFT**FGQGTKLEIK
CL-27798		EIVLTQSPATLSLSPGERATLSC**RASQSVTTHLA**WYQQKPG QAPRLLIY**WASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSSKNPFT**FGQGTKLEIK
CL-27799		EIVLTQSPATLSLSPGERATLSC**RASESVSXHMH**WYQQKPG QAPRLLIY**WASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWNDPPT**FGQGTKLEIK
CL-27800		EIVLTQSPATLSLSPGERATLSC**RASQSVSSHLA**WYQQKPG QAPRLLIY**GASKLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSSRDPFT**FGQGTKLEIK
CL-27801		EIVLTQSPATLSLSPGERATLSC**RASQSVTTNMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQRWNDPFT**FGQGTKLEIK
CL-27802		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHLA**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQKSNXPFT**FGQGTKLEIK
CL-27803		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**RASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWKDPYT**FGQGTKLEIK
CL-27805		EIVLTQSPATLSLSPGERATLSC**RASQSVSAHLA**WYQQKPG QAPRLLIY**EASNLES**GVPARFSGSGSGTDFTLTISSLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QQSWNVPFT**FGQGTKLEIK
CL-27806		EIVLTQSPATLSLSPGERATLSC**RASESVLILMH**WYQQKPG QAPRLLIY**EASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSSNDPFT**FGQGTKLEIK
CL-27807		EIVLTQSPATLSLSPGERATLSC**RASQSVSSLMH**WYQQKPG QAPRLLIY**GASCLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQYXNDPYT**FGQGTKLEIK
CL-27809		EIVLTQSPATLSLSPGERATLSC**RASQSVITHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQRWKFPFT**FGQGTKLEIK
CL-27810		EIVLTQSPATLSLSPGERATLSC**RASESVSTQLA**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQNWNNPLT**FGQGTKLEIK
CL-27811		EIVLTQSPATLSLSPGERATLSC**RASQSVSRDMH**WYQQKPG QAPRLLIY**GASYLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQRWKEPFT**FGQGTKLEIK
CL-27812		EIVLTQSPATLSLSPGERATLSC**RASQSVTTLMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQGCNDPLT**FGQGTKLEIK
CL-27813		EIVLTQSPATLSLSPGERATLSC**RASESVVTHMH**WYQQKPG QAPRLLIY**RASGLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWQHPFT**FGQGTKLEIK
CL-27814		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSGNDPCT**FGQGTKLEIK
CL-27815		EIVLTQSPATLSLSPGERATLSC**RASQSVNSYLA**WYQQKPG QAPRLLIY**WASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQAWNDPST**FGQGTKLEIK
CL-27816		EIVLTQSPATLSLSPGERATLSC**RASQSVSNPMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWNDPFT**FGQGTKLEIK
CL-27818		EIVLTQSPATLSLSPGERATLSC**RASQSVSTLMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQGLTDPFT**FGQGTKLEIK
CL-27819		EIVLTQSPATLSLSPGERATLSC**RASESVSPPLA**WYQQKPG QAPRLLIY**GASHLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSENDPLT**FGQGTKLEIK
CL-27820		EIVLTQSPATLSLSPGERATLSC**RASESVNTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQTWNHPFT**FGQGTKLEIK
CL-27821		EIVLTQSPATLSLSPGERATLSC**RASESVSYPMH**WYQQKPG QAPRLLIY**GASRLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQRWSDPFT**FGQGTKLEIK
CL-27822		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**IASFLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSXFEPST**FGQGTKLEIK
CL-27823		EIVLTQSPATLSLSPGERATLSC**RASESVSTQMH**WYQQKPG QAPRLLIY**GASYLES**GIPARFSGSGSGTDFTLTISSLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QQSWKDPFT**FGQGTKLEIK
CL-27824		EIVLTQSPATLSLSPGERATLSC**RASQSVSTKMH**WYQQKPG QAPRLLIY**RASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWIDPFT**FGQGTKLEIK
CL-27826		EIVLTQSPATLSLSPGERATLSC**RASQSVGTHMH**WYQQKPG QAPRLLIY**RASYLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWKDPFT**FGQGTKLEIK
CL-27827		EIVLTQSPATLSLSPGERATLSC**RASQSVMTHLA**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNEPFT**FGQGTKLEIK
CL-27828		EIVLTQSPATLSLSPGERATLSC**RASQSVXTHLA**WYQQKPG QAPRLLIY**GASKLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWQDPIT**FGQGTKLEIK
CL-27833		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**AASKLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYXX**QQSWNDPFT**FGQGTKLEIK
CL-27838		EIVLTQSPATLSLSPGERATLSC**RASQSVSSLMH**WYQQKPG QAPRLLIY**VASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNYPFT**FGQGTKLEIK
CL-27840		EIVLTQSPATLSLSPGERATLSC**RASQSVITPLA**WYQQKPG QAPRLLIY**GASRLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQIWNDPFT**FGQGTKLEIK
CL-27841		EIVLTQSPATLSLSPGERATLSC**RASQSVSPLLA**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQRWNEPFT**FGQGTKLEIK
CL-27842		EIVLTQSPATLSLSPGERATLSC**RASQSVNPHLA**WYQQKPG QAPRLLIY**WASSLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQNWNDPFT**FGQGTKLEIK
CL-27843		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASRLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQGWNYPFT**FGQGTKLEIK
CL-27844		EIVLTQSPATLSLSPGERATLSC**RASQSVSTRMH**WYQQKPG QAPRLLIY**GASYLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTRYDPFT**FGQGTKLEIK
CL-27845		EIVLTQSPATLSLSPGERATLSC**RASESVSSHMH**WYQQKPG QAPRLLIY**GASRLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNDPFT**FGQGTKLEIK
CL-27846		EIVLTQSPATLSLSPGERATLSC**RASQSVTTHMH**WYQQKPG QAPRLLIY**AASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWNHPFT**FGQGTKLEIK
CL-27847		EIVLTQSPATLSLSPGERATLSC**RASQSVKTQLA**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQRCNGPFT**FGQGTKLEIK
CL-27848		EIVLTQSPATLSLSPGERATLSC**RASQSVSTQLA**WYQQKPG QAPRLLIY**GASHLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTGNDPFT**FGQGTKLEIK
CL-27849		EIVLTQSPATLSLSPGERATLSC**RASESVSPLMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED

Clone	SEQ ID NO:	VL
		FAVYFC**QQSWKDPFT**FGQGTKLEIK
CL-27850		EIVLTQSPATLSLSPGERATLSC**RASESVSAHMH**WYQQKPG QAPRLLIY**GASKLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQWWNNPFT**FGQGTKLEIK
CL-27851		EIVLTQSPATLSLSPGERATLSC**RASQSVNTHMH**WYQQKPG QAPRLLIY**RASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNEPLT**FGQGTKLEIK
CL-29979		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWQDPLT**FGQGTKLEIK
CL-29980		EIVLTQSPATLSLSPGERATLSC**RASQSVNTNMH**WYQQKPG QAPRLLIY**GASILES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWNVPFT**FGQGTKLEIK
CL-29981		EIVLTQSPATLSLSPGERATLSC**RASESVSTAMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQTWNVPIT**FGQGTKLEIK
CL-29982		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASMLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNDPLT**FGQGTKLEIK
CL-29983		EIVLTQSPATLSLSPGERATLSC**RASESVNDHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNNPIT**FGQGTKLEIK
CL-29984		EIVLTQSPATLSLSPGERATLSC**RASQSVGTHMH**WYQQKPG QAPRLLIY**GASYLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWNDPLT**FGQGTKLEIK
CL-29985		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQTWDDPIT**FGQGTKLEIK
CL-29986		EIVLTQSPATLSLSPGERATLSC**RASQSVGTHMH**WYQQKPG QAPRLLIY**GASKLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSFLDPIT**FGQGTKLEIK
CL-29987		EIVLTQSPATLSLSPGERATLSC**RASESVSTNMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQGWSDPLT**FGQGTKLEIK
CL-29988		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWIDPLT**FGQGTKLEIK
CL-29989		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASHLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWIDPIT**FGQGTKLEIK
CL-29990		EIVLTQSPATLSLSPGERATLSC**RASQSVGTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGCGTDFTLTISSLEPED FAVYFC**QQSWHDPLT**FGQGTKLEIK
CL-29991		EIVLTQSPATLSLSPGERATLSC**RASQSVSNHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQTWDDPIT**FGQGTKLEIK
CL-29992		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASELES**GVPARFSGSGSGTDFTLTISSLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QQTWNDPIT**FGQGTKLEIK
CL-29993		EIVLTQSPATLSLSPGERATLSC**RASESVNTLMH**WYQQKPG QAPRLLIY**GASHLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWNEPIT**FGQGTKLEIK
CL-29994		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWSDPLT**FGQGTKLEIK
CL-29995		EIVLTQSPATLSLSPGERATLSC**RASQSVSKHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNNPIT**FGQGTKLEIK
CL-29996		EIVLTQSPATLSLSPGERATLSC**RASQSVDTHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWHDPIT**FGQGTKLEIK
CL-29997		EIVLTQSPATLSLSPGERATLSC**RASESVSNHMH**WYQQKPG QAPRLLIY**GASKLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWTDPLT**FGQGTKLEIK
CL-29998		EIVLTQSPATLSLSPGERATLSC**RASQSVSSHMH**WYQQKPG QAPRLLIY**GASHLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWNDPLT**FGQGTKLEIK
CL-29999		EIVLTQSPATLSLSPGERATLSC**RASESVSTNMH**WYQQKPG QAPRLLIY**AASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWNEPFT**FGQGTKLEIK
CL-30000		EIVLTQSPATLSLSPGERATLSC**RASQSVDTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWGDPLT**FGQGTKLEIK
CL-30001		EIVLTQSPATLSLSPGERATLSC**RASESVSNNLA**WYQQKPG QAPRLLIY**GASHLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWNDPIT**FGQGTKLEIK
CL-30002		EIVLTQSPATLSLSPGERATLSC**RASQSVSNHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNDPIT**FGQGTKLEIK
CL-30003		EIVLTQSPATLSLSPGERATLSC**RASQSVGTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWNEPWT**FGQGTKLEIK
CL-30004		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASKLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWIDPLT**FGQGTKLEIK
CL-30005		EIVLTQSPATLSLSPGERATLSC**RASQSVGNNMH**WYQQKPG QAPRLLIY**GASHLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNDPLT**FGQGTKLEIK
CL-30006		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFGGSGSGTDFTLTISSLEPED FAVYYC**QQSWTDPLT**FGQGTKLEIK
CL-30007		EIVLTQSPATLSLSPGERATLSC**RASESVYTXLA**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQILNDPFT**FGQGTKLEIK
CL-30009		EIVLTQSPATLSLSPGERATLSC**RASQSVSNHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QQSWNDPLT**FGQGTKLEIK
CL-30010		EIVLTQSPATLSLSPGERATLSC**RASQSVGTNMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWNDPIT**FGQGTKLEIK
CL-30011		EIVLTQSPATLSLSPGERATLSC**RASESVATHMH**WYQQKPG QAPRLLIY**GASYLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNDPLT**FGQGTKLEIK
CL-30012		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASHLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNDPLT**FGQGTKLEIK
CL-30013		EIVLTQSPATLSLSPGERATLSC**RASESVMNHLA**WYQQKPG QAPRLLIY**GASYLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWSDPLT**FGQGTKLEIK
CL-30014		EIVLTQSPATLSLSPGERATLSC**RASQSVGTSMH**WYQQKPG QAPRLLIY**AASELES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNDPFT**FGQGTKLEIK
CL-30015		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWNDPLT**FGQGTKLEIK
CL-30017		EIVLTQSPATLSLSPGERATLSC**RASESVSNNMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWSDPFT**FGQGTKLEIK
CL-30018		EIVLTQSPATLSLSPGERATLSC**RASQSVSSHMH**WYQQKPG QAPRLLIY**GASKLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSFSDPIT**FGQGTKLEIK
CL-30019		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASHLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWSDPLT**FGQGTKLEIK
CL-30020		EIVLTQSPATLSLSPGERATLSC**RASQSVSNHMH**WYQQKPG QAPRLLIY**GASHLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNDPLT**FGQGTKLEIK
CL-30021		EIVLTQSPATLSLSPGERATLSC**RASQSVSNHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNPPIT**FGQGTKLEIK
CL-30022		EIVLTQSPATLSLSPGERATLSC**RASESVSNHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNEPFT**FGQGTKLEIK
CL-30023		EIVLTQSPATLSLSPGERATLSC**RASQSVGTNMH**WYQQKPG QAPRLLIY**GASILES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWNEPIT**FGQGTKLEIK
CL-30024		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWYDPVT**FGQGTKLEIK
CL-30025		EIVLTQSPATLSLSPGERATLSC**RASESVGTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQTWNDPLT**FGQGTKLEIK
CL-30026		EIVLTQSPATLSLSPGERATLSC**RASQSVSSHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-30027		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-30028		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQTWSDPLT**FGQGTKLEIK
CL-30029		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMN**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNVPYT**FGQGTKLEIK
CL-30030		EIVLTQSPATLSLSPGERATLSC**RASESVTSNMH**WYQQKPG QAPRLLIY**AASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWQNPIT**FGQGTKLEIK
CL-30031		EIVLTQSPATLSLSPGERATLSC**RASESVSDHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWTDPLT**FGQGTKLEIK
CL-30032		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNDPLT**FGQGTKLEIK
CL-30033		EIVLTQSPATLSLSPGERATLSC**RASESVSNYMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWTDPLT**FGQGTKLEIK
CL-30034		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASILES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWNDPIT**FGQGTKLEIK
CL-30035		EIVLTQSPATLSLSPGERATLSC**RASQSVGTAMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWDAPFT**FGQGTKLEIK
CL-30036		EIVLTQSPATLSLSPGERATLSC**RASQSVRSHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWTPPIT**FGQGTKLEIK
CL-30037		EIVLTQSPATLSLSPGERATLSC**RASESVSTSMN**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWKDPIT**FGQGTKLEIK
CL-30038		EIVLTQSPATLSLSPGERATLSC**RASQSVSNHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNVPWT**FGQGTKLEIK
CL-30039		EIVLTQSPATLSLSPGERATLSC**RASESVSNSMH**WYQQKPG QAPRLLIY**GASTLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQTWTDPLT**FGQGTKLEIK
CL-30040		EIVLTQSPATLSLSPGERATLSC**RASESVGTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQTWNDPST**FGQGTKLEIK
CL-30041		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNDPLT**FGQGTKLEIK
CL-30042		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASTLES**GVPARFSGSGSGTDFTLTISSLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QQTWSDPLT**FGQGTKLEIK
CL-30043		EIVLTQSPATLSLSPGERATLSC**RASESVDSNMH**WYQQKPG QAPRLLIY**RASILES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWGDPIT**FGQGTKLEIK
CL-30044		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASYLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNDPLT**FGQGTKLEIK
CL-30045		EIVLTQSPATLSLSPGERATLSC**RASESVSNHMH**WYQQKPG QAPRLLIY**GASYLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNDPLT**FGQGTKLEIK
CL-30046		EIVLTQSPATLSLSPGERATLSC**RASESVSDHMH**WYQQKPG QAPRLLIY**GASKLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWTDPLT**FGQGTKLEIK
CL-30047		EIVLTQSPATLSLSPGERATLSC**RASESVGTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNDPLT**FGQGTKLEIK
CL-30048		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWSDPLT**FGQGTKLEIK
CL-30049		EIVLTQSPATLSLSPGERATLSC**RASESVNTHLA**WYQQKPG QAPRLLIY**GASMLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWSLPYT**FGQGTKLEIK
CL-30050		EIVLTQSPATLSLSPGERATLSC**RASQSVSSHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNDPLT**FGQGTKLEIK
CL-30053		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMN**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWNDPFT**FGQGTKLEIK
CL-30054		EIVLTQSPATLSLSPGERATLSC**RASESVGTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWNEPYT**FGQGTKLEIK
CL-30055		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASKLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWGDPIT**FGQGTKLEIK
CL-30056		EIVLTQSPATLSLSPGERATLSC**RASQSVSTNMH**WYQQKPG QAPRLLIY**AASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWNEPIT**FGQGTKLEIK
CL-30057		EIVLTQSPATLSLSPGERATLSC**RASESVGKHMH**WYQQKPG QAPRLLIY**GASKLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWNDPIT**FGQGTKLEIK
CL-30058		EIVLTQSPATLSLSPGERATLSC**RASESVSNHMH**WYQQKPG QAPRLLIY**GASFLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWTNPIT**FGQGTKLEIK
CL-30059		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWDDPLT**FGQGTKLEIK
CL-30060		EIVLTQSPATLSLSPGERATLSC**RASESVGTHMH**WYQQKPG QAPRLLIY**GASYLES**GIPARFSGSGSGTDFTLTISSLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QQSWTDPIT**FGQGTKLEIK
CL-30061		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASHLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWIDPIT**FGQGTKLEIK
CL-30062		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASKLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNDPIT**FGQGTKLEIK
CL-30063		EIVLTQSPATLSLSPGERATLSC**RASESVCTRMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNDPYT**FGQGTKLEIK
CL-30064		EIVLTQSPATLSLSPGERATLSC**RASQSVSNHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTFDDPLT**FGQGTKLEIK
CL-30066		EIVLTQSPATLSLSPGERATLSC**RASQSVGDSLA**WYQQKPG QAPRLLIY**AASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQTWNVPIT**FGQGTKLEIK
CL-30067		EIVLTQSPATLSLSPGERATLSC**RASESVANHLA**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPIT**FGQGTKLEIK
CL-30068		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMN**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQGWYDPLT**FGQGTKLEIK
CL-30069		EIVLTQSPATLSLSPGERATLSC**RASESVSSHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNDPIT**FGQGTKLEIK
CL-30070		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWNVPFT**FGQGTKLEIK
CL-30071		EIVLTQSPATLSLSPGERATLSC**RASESVNKHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQTWIDPFT**FGQGTKLEIK
CL-30072		EIVLTQSPATLSLSPGERATLSC**RASQSVGNHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNMPIT**FGQGTKLEIK
CL-30073		EIVLTQSPATLSLSPGERATLSC**RASESVGEHMH**WYQQKPG QAPRLLIY**AASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWYDPLT**FGQGTKLEIK
CL-30074		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWDVPLT**FGQGTKLEIK
CL-30078		ENVLTQSPATLSLSPGERATLSC**RASESVITHMN**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNDPFT**FGQGTKLEIK
CL-30090		EIVLTQSPATLSLSPGERATLSC**RASQSVSNHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-30095		EIVLTQSPATLSLSPGERATLSC**RASESVSNHMH**WYQQKPG QAPRLLIY**GASELES**GIPARFSGSGSGTDFTLTISSLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QQSWSDPLT**FGQGTKLEIK
CL-30098		EIVLTQSPATLSLSPGERATLSC**RASQSVDTHMH**WYQQKPG QAPRLLIY**GASHLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWIDPIT**FGQGTKLEIK
CL-30099		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWIDPLT**FGQGTKLEIK
CL-30103		EIVLTQSPATPSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWNDPFT**FGQGTKLEIK
CL-30104		EIVLTQSPATLSLSPGERATLSC**RASESVSSHMH**WYQQKPG QAPRLLIY**GASILES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWNDPIT**FGQGTKLEIK
CL-30106		EIVLTQSPATLSLSPGERATLSC**RASQSVSNHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNDPLT**FGQGTKLEIK
CL-30109		EIVLTQSPATLSLSPGERATLSC**RASQSVITHMN**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWNDPIT**FGQGTKLEIK
CL-30115		EIVLTQSPATLSLSPGERATLSC**RASESVQTHMN**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNDPFT**FGQGTKLEIK
CL-30120		EIVLTQSPATLSLSPGERATLSC**RASQSVGTHMH**WYQQKPG QAPRLLIY**AASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWYDPLT**FGQGTKLEIK
CL-30121		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWNDPLT**FGQGTKLEIK
CL-30123		EIVLTQSPATLSLSPGERATLSC**RASESVITHMN**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWDNPIT**FGQGTKLEIK
CL-30126		EIVLTQSPATLSLSPGERATLSC**RASQSVHKHMN**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQGWDDPLT**FGQGTKLEIK
CL-30128		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASHLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNDPLT**FGQGTKLEIK
CL-30131		EIVLTQSPATLSLSPGERATLSC**RASESVLTHMN**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQTWYEPWT**FGQGTKLEIK
CL-30132		EIVLTQSPATLSLSPGERATLSC**RASESVDTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWYDPIT**FGQGTKLEIK
CL-30133		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWSDPIT**FGQGTKLEIK
CL-30134		EIVLTQSPATLSLSPGERATLSC**RASQSVGTHMN**WYQQKPG QAPRLLIY**GASFLES**GIPARFSGSGSGTDFTLTISSLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QQSWSDPIT**FGQGTKLEIK
CL-30135		EIVLTQSPATLSLSPGERATLSC**RASQSVGTPMH**WYQQKPG QAPRLLIY**GASTLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWYDPLT**FGQGTKLEIK
CL-30137		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASYLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWYDPIT**FGQGTKLEIK
CL-30143		EIVLTQSPATLSLSPGERATLSC**RASESVDTHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWYDPIT**FGQGTKLEIK
CL-30144		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASMLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQTWTDPIT**FGQGTKLEIK
CL-30147		EIVLTQSPATLSLXPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASNLEY**GVPARFSGSGCGTDFTLTISSIEHED FAVYFC**QQSWNDPFT**FGQGTKLEIK
CL-30150		EIVLTQSPATLSLSPGERATLSC**RASQSVANHLA**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWTDPIT**FGQGTKLEIK
CL-30152		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASMLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNNPIT**FGQGTKLEIK
CL-30155		EIVLTQSPATLSLSPGERATLSC**RASQSVSNHMH**WYQQKPG QAPRLLIY**AASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWDDPLT**FGQGTKLEIK
CL-30158		EIVLTQSPATLSLSPGERVTLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASHLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNDPIT**FGQGTKLEIK
CL-30160		EIVLTQSPATLSLSPGERATLSC**RASQSVSNHMH**WYQQKPG QAPRLLIY**AASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNDPLT**FGQGTKLEIK
CL-30163		EIVLTQSPATLSLSPGERATLSC**RASQSVSSHMH**WYQQKPG QAPRLLIY**AASKLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWYDPLT**FGQGTKLEIK
CL-30164		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWMDPIT**FGQGTKLEIK
CL-30166		EIVLTQSPATLSLSPGERATLSC**RASESVSTNMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWSEPWT**FGQGTKLEIK
CL-30167		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWSDPLT**FGQGTKLEIK
CL-30593		EIVLTQSPATLSLSPGERATLSC**RASQSVDTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-30594		EIVLTQSPATLSLSPGERATLSC**RASQSVSNHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QQSWNEPFT**FGQGTKLEIK
CL-30595		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASHLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNDPIT**FGQGTKLEIK
CL-30597		EIVLTQSPATLSLSPGERATLSC**RASESVSNHMH**WYQQKPG QAPRLLIY**GASTLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNDPLT**FGQGTKLEIK
CL-30598		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASVLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWDDPLT**FGQGTKLEIK
CL-30600		EIVLTQSPATLSLSPGERATLSC**RASQSVSNHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWLDPIT**FGQGTKLEIK
CL-30601		EIVLTQSPATLSLSPGERATLSC**RASQSVNTHLA**WYQQKPG QAPRLLIY**AASHLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQTWTDPLT**FGQGTKLEIK
CL-30602		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWSDPLT**FGQGTKLEIK
CL-30604		EIVLTQSPATLSLSPGERATLSC**RASQSVSNPMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNXPFT**FGQGTKLEIK
CL-30606		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASKLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWDDPFT**FGQGTKLEIK
CL-30608		EIVLTQSPATLSLSPGERATLSC**RASQSVGTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQTWSDPLT**FGQGTKLEIK
CL-30609		EIVLTQSPATLSLSPGERATLSC**RASESVNSNMH**WYQQKPG QAPRLLIY**GASHLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWYDPLT**FGQGTKLEIK
CL-30610		EIVLTQSPATLSLSPGERATLSC**RASQSVRNHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWDDPLT**FGQGTKLEIK
CL-30611		EIVLTQSPATLSLSPGERATLSC**RASESVSNHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWDDPLT**FGQGTKLEIK
CL-30613		EIVLTQSPATLSLSPGERATLSC**RASQSVNTAMH**WYQQKPG QAPRLLIY**GASSLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNDPLT**FGQGTKLEIK
CL-30614		EIVLTQSPATLSLSPGERATLSC**RASESVGSHMH**WYQQKPG QAPRLLIY**GASHLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNLPLT**FGQGTKLEIK
CL-30615		EIVLTQSPATLSLSPGERATLSC**RASESVSNHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWYDPIT**FGQGTKLEIK
CL-30616		EIVLTQSPATLSLSPGERATLSC**RASQSVITHMN**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QQSWGDPWT**FGQGTKLEIK
CL-30617		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWIDPLT**FGQGTKLEIK
CL-30618		EIVLTQSPATLSLSPGERATLSC**RASQSVGTHMH**WYQQKPG QAPRLLIY**GASMLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWDDPLT**FGQGTKLEIK
CL-30619		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**AASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPIT**FGQGTKLEIK
CL-30620		EIVLTQSPATLSLSPGERATLSC**RASQSVSNHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNDPIT**FGQGTKLEIK
CL-30624		EIVLTQSPATPSLSPGERATLSC**RASESVGSCMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQTWYDPLT**FGQGTKLEIK
CL-30626		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWNDPLT**FGQGTKLEIK
CL-30627		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNDPLT**FGQGTKLEIK
CL-30628		EIVLTQSPATLSLSPGERATLSC**RASESVSRHMH**WYQQKPG QAPRLLIY**GASHLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNNPLT**FGQGTKLEIK
CL-30629		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNDPAT**FGQGTKLEIK
CL-30630		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNDPLT**FGQGTKLEIK
CL-30631		EIVLTQSPATLSLSPGERATLSC**RASQSVGRHMH**WYQQKPG QAPRLLIY**GASKLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWTDPLT**FGQGTKLEIK
CL-30632		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWSDPIT**FGQGTKLEIK
CL-30634		EIVLTQSPATLSLSPGERATLSC**RASQSVSNHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNDPLT**FGQGTKLEIK
CL-30635		EIVLTQSPATLSLSPGERATLSC**RASESVSSNMN**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSFYDPIT**FGQGTKLEIK
CL-30636		EIVLTQSPATLSLSPGERATLSC**RASESVSSHMH**WYQQKPG QAPRLLIY**GASKLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWSDPLT**FGQGTKLEIK
CL-30637		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASHLES**GVPARFSGSGSGTDFTLTISSLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QQSWHDPLT**FGQGTKLEIK
CL-30638		EIVLTQSPATLSLSPGERATLSC**RASESVSNHMH**WYQQKPG QAPRLLIY**AASKLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWIDPIT**FGQGTKLEIK
CL-30639		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASKLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWTDPLT**FGQGTKLEIK
CL-30640		EIVLTQSPATLSLSPGERATLSC**RASESVRSHLA**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSIEPED FAVYFC**QQSWNAPFT**FGQGTKLEIK
CL-30641		EIVLTQSPATLSLSPGERATLSC**RASQSVSNHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWSDPLT**FGQGTKLEIK
CL-30642		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASILES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWDDPIT**FGQGTKLEIK
CL-30643		EIVLTQSPATLSLSPGERATLSC**RASESVSNHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNEPLT**FGQGTKLEIK
CL-30644		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMP**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNDPLT**FGQGTKLEIK
CL-30645		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWSDPLT**FGQGTKLEIK
CL-30647		EIVLTQSPATLSLSPGERATLSC**RASQSVSTAMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWFDPLT**FGQGTKLEIK
CL-30648		EIVLTQSPATLSLSPGERATLSC**RASESVSNHMH**WYQQKPG QAPRLLIY**GASILES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQTWSDPIT**FGQGTKLEIK
CL-30649		EIVLTQSPATLSLSPGERATLSC**RASESVNSDMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-30650		EIVLTQSPATLSLSPGERATLSC**RASESVSNHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNVPIT**FGQGTKLEIK
CL-30651		EIVLTQSPATLSLSPGERATLSC**RASESVSTNLA**WYQQKPG QAPRLLIY**GASKLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQTWNDPIT**FGQGTKLEIK
CL-30653		EIVLTQSPATLSLSPGERATLSC**RASESVSNHMH**WYQQKPG QAPRLLIY**AASHLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWTDPIT**FGQGTKLEIK
CL-30654		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMN**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWTDPIT**FGQGTKLEIK
CL-30655		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED

Clone	SEQ ID NO:	VL
		FAVYFC**QQTWDVPFT**FGQGTKLEIK
CL-30657		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWSDPIT**FGQGTKLEIK
CL-30658		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASHLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQCRNDPFT**FGQGTKLEIK
CL-30659		EIVLTQSPATLSLSPGERATLSC**RASESVSKHMN**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWTDPLT**FGQGTKLEIK
CL-30660		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASRLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNDPLT**FGQGTKLEIK
CL-30662		EIVLTQSPATLSLSPGERATLSC**RASESVGTHMH**WYQQKPG QAPRLLIY**GASHLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWDDPLT**FGQGTKLEIK
CL-30663		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWNEPYT**FGQGTKLEIK
CL-30664		EIVLTQSPATLSLSPGERATLSC**RASESVGMHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNDPLT**FGQGTKLEIK
CL-30665		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMN**WYQQKPG QAPRLLIY**AASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSFNNPLT**FGQGTKLEIK
CL-30666		EIVLTQSPATLSLSPGERATLSC**RASQSVNTHLH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWFDPLT**FGQGTKLEIK
CL-30667		EIVLTQSPATLSLSPGERATLSC**RASQSVGTHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWNDPLT**FGQGTKLEIK
CL-30669		EIVLTQSPATLSLSPGERATLSC**RASESVSNHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWYDPLT**FGQGTKLEIK
CL-30670		EIVLTQSPATLSLSPGERATLSC**RASQSVSNHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWLDPLT**FGQGTKLEIK
CL-30671		EIVLTQSPATLSLSPGERATLSC**RASESVSNHMH**WYQQKPG QAPRLLIY**GASILES**GVLARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNDPLT**FGQGTKLEIK
CL-30672		EIVLTQSPATLSLSPGERATLSC**RASESVSSHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWNYPIT**FGQGTKLEIK
CL-30673		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWYDPIT**FGQGTKLEIK
CL-30674		EIVLTQSPATLSLSPGERATLSC**RASESVGNHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QQSWIDPLT**FGQGTKLEIK
CL-30675		EIVLTQSPATLSLSPGERATLSC**RASESVSNHMH**WYQQKPG QAPRLLIY**AASKLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWVEPFT**FGQGTKLEIK
CL-30676		EIVLTQSPATLSLSPGERATLSC**RASQSVETHMH**WYQQKPG QAPRLLIY**GASHLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWRDPLT**FGQGTKLEIK
CL-30677		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMN**WYQQKPG QAPRLLIY**GASHLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWDDPLT**FGQGTKLEIK
CL-30678		EIVLTQSPATLSLSPGERATLSC**RASQSVGSSMH**WYQQKPG QAPRLLIY**GASKLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWNDPLT**FGQGTKLEIK
CL-30679		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNDPLT**FGQGTKLEIK
CL-30681		EIVLTQSPATLSLSPGERATLSC**RASQSVTNHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWHDPLT**FGQGTKLEIK
CL-30682		EIVLTQSPATLSLSPGERATLSC**RASESVSSHLA**WYQQKPG QAPRLLIY**GASTLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWGDPFT**FGQGTKLEIK
CL-30683		EIVLTQSPATLSLSPGERATLSC**RASQSVSNHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWSDPLT**FGQGTKLEIK
CL-30684		EIVLTQSPATLSLSPGERATLSC**RASESVHDHMH**WYQQKPG QAPRLLIY**AASHLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNDPLT**FGQGTKLEIK
CL-30685		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWADPLT**FGQGTKLEIK
CL-34444		EIVLTQSPATLSLSPGERATLSC**RASQSVGTHMH**WYQQKPG QAPRLLIY**GASILES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-34445		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASHLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNDPFT**FGQGTKLEIK
CL-34446		EIVLTQSPATLSLSPGERATLSC**RASESVSNHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSFYDPLT**FGQGTKLEIK
CL-34447		EIVLTQSPATLSLSPGERATLSC**RASESVGTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-34448		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASMLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWMDPIT**FGQGTKLEIK
CL-34450		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QQSWMDPLT**FGQGTKLEIK
CL-34451		EIVLTQSPATLSLSPGERATLSC**RASESVSNHMH**WYQQKPG QAPRLLIY**GASILES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-34452		EIVLTQSPATLSLSPGERATLSC**RASESVGTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWHDPLT**FGQGTKLEIK
CL-34453		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSFTNPLT**FGQGTKLEIK
CL-34454		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-34457		EIVLTQSPATLSLSPGERATLSC**RASXSVNTHMH**WYQQKPG QAPRLLIY**GASXLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQXWYDPIT**FGQGTKLEIK
CL-34458		EIVLTQSPATLSLSPGERATLSC**RASESVRTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-34459		EIVLTQSPATLSLSPGERATLSC**RASQSVGTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWYDPLT**FGQGTKLEIK
CL-34460		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASHLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-34461		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASHLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-34462		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASVLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-34464		EIVLTQSPATLSLSPGERATLSC**RASQSVSRHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPIT**FGQGTKLEIK
CL-34465		EIVLTQSPATLSLSPGERATLSC**RASQSVSSHMH**WYQQKPG QAPRLLIY**GASILES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWDDPIT**FGQGTKLEIK
CL-34467		EIVLTQSPATLSLSPGERATLSC**RASESVSTSMH**WYQQKPG QAPRLLIY**GASQLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNVPFT**FGQGTKLEIK
CL-34468		EIVLTQSPATLSLSPGERATLSC**RASESVGTHMH**WYQQKPG QAPRLLIY**GASRLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWTVPLT**FGQGTKLEIK
CL-34472		EIVLTQSPATLSLSPGERATLSC**RASQSVGTHMH**WYQQKPG QAPRLLIY**GASHLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWYDPLT**FGQGTKLEIK
CL-34473		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASVLES**GVPARFSGSGSGTDFTLTISSLEPED

Clone	SEQ ID NO:	VL
		FAVYFC**QQSWYDPLT**FGQGTKLEIK
CL-34474		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASTLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWYDPLT**FGQGTKLEIK
CL-34478		EIVLTQSPATLSLSPGERATLSC**RASQSVGTHMH**WYQQKPG QAPRLLIY**GASYLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQTWYDPLT**FGQGTKLEIK
CL-34479		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASTLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWYDPLT**FGQGTKLEIK
CL-34480		EIVLTQSPATLSLSPGERATLSC**RASQSVGTHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-34481		EIVLTQSPATLSLSPGERATLSC**RASQSVNNHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-34482		EIVLTQSPATLSLSPGERATLSC**RASQSVGEHMH**WYQQKPG QAPRLLIY**GASHLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPIT**FGQGTKLEIK
CL-34485		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASHLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWYDPLT**FGQGTKLEIK
CL-34487		EIVLTQSPATLSLSPGERATLSC**RASQSVSTNMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQTWYDPIT**FGQGTKLEIK
CL-34488		EIVLTQSPATLSLSPGERATLSC**RASESVGTHMH**WYQQKPG QAPRLLIY**GASTLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-34490		EIVLTQSPATLSLSPGERATLSC**RASQSVSNHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWYDPLT**FGQGTKLEIK
CL-34494		EIVLTQSPATLSLSPGERATLSC**RASQSVGSHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWYDPIT**FGQGTKLEIK
CL-34496		EIVLTQSPATLSLSPGERATLSC**RASQSVGNHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWYDPLT**FGQGTKLEIK
CL-34498		EIVLTQSPATLSLSPGERATLSC**RASESVGTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWYDPLT**FGQGTKLEIK
CL-34499		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWYDPIT**FGQGTKLEIK
CL-34500		EIVLTQSPATLSLSPGERATLSC**RASESVGTHMH**WYQQKPG QAPRLLIY**GASHLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPIT**FGQGTKLEIK
CL-34502		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASKLES**GVPARFSGSGSGTDFTLTISSLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-34504		EIVLTQSPATLSLSPGERATLSC**RASESVSRHMN**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQTWYDPIT**FGQGTNLEIK
CL-34505		EIVLTQSPATLSLSPGERATLSC**RASQSVGTHMH**WYQQKPG QAPRLLIY**GASYLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWYDPIT**FGQGTKLEIK
CL-34506		EIVLTQSPATLSLSPGERATLSC**RASQSVGTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWYDPIT**FGQGTKLEIK
CL-34508		EIVLTQSPATLSLSPGERATLSC**RASESVDTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-34509		EIVLTQSPATLSLSPGERATLSC**RASQSVSNHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPIT**FGQGTKLEIK
CL-34511		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-34512		EIVLTQSPATLSLSPGERATLSC**RASQSVGTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-34514		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASILES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-34515		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQTWYDPIT**FGQGTKLEIK
CL-34517		EIVLTQSPATLSLSPGERATLSC**RASESVGTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-34520		EIVLTQSPATLSLSPGERATLSC**RASESVGTHMH**WYQQKPG QAPRLLIY**GASILES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWYDPLT**FGQGTKLEIK
CL-34521		EIVLTQSPATLSLSPGERATLSC**RASESVDRHMH**WYQQKPG QAPRLLIY**GASHLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWYDPLT**FGQGTKLEIK
CL-34523		EIVLTQSPATLSLSPGERATLSC**RASQSVTNHMH**WYQQKPG QAPRLLIY**GASVLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-34524		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPIT**FGQGTKLEIK
CL-34525		EIVLTQSPATLSLSPGERATLSC**RASESVSNHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWYDPIT**FGQGTKLEIK
CL-34526		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QQTWYDPLT**FGQGTKLEIK
CL-34529		EIVLTQSPATLYLXPGERATLSC**RASQSVSTHMH**WYQQKPG QAARLVMY**GASNLEF**GVPARFSGSGSGTEFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-34533		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPIT**FGQGTKLEIK
CL-34534		EIVLTQSPATLSLSPGERATLSC**RASQSVGTHMH**WYQQKPG QAPRLLIY**GASHLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-34536		EIVLTQSPATLSLSPGERATLSC**RASQSVGAHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWYDPLT**FGQGTKLEIK
CL-34539		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWSDPLT**FGQGTKLEIK
CL-34541		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASILES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPIT**FGQGTKLEIK
CL-34548		EIVLTQSPATLSLSPGERATLSC**RASQSVSNHMH**WYQQKPG QAPRLLIY**GASHLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-34556		EIVLTQSPATLSLSPGERATLSC**RASESVSXHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-34558		EIVLTQSPATLSLSPGERATLSC**RASESVSTAMH**WYQQKPG QAPRLLIY**AASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-34561		EIVLTQSPATLSLSPGERATLSC**RASESVGTHMH**WYQQKPG QAPRLLIY**GASYLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWYDPIT**FGQGTKLEIK
CL-34562		EIVLTQSPATLSLSPGERATLSC**RASQSVGSHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWYDPLT**FGQGTKLEIK
CL-34563		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWYDPLT**FGQGTKLEIK
CL-34566		EIVLTQSPATLSLSPGERATLSC**RASQSVGTNMH**WYQQKPG QAPRLLIY**GASVLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQTWYDPIT**FGQGTKLEIK
CL-34568		EIVLTQSPATLSLSPGERATLSC**RASESVGKHMH**WYQQKPG QAPRLLIY**GASHLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWMDPLT**FGQGTKLEIK
CL-34573		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASFLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-34574		EIVLTQSPATLSLSPGERATLSC**RASESVGTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QQSWGDPLT**FGQGTKLEIK
CL-34577		EIVLTQSPATLSLSPGERATLSC**RASESVSKHMH**WYQQKPG QAPRLLIY**GASHLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-34580		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASMLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWDDPLT**FGQGTKLEIK
CL-34582		EIVLTQSPATLSLSPGERATLSC**RASQSVGTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-34585		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWYDPLT**FGQGTKLEIK
CL-34586		EIVLTQSPATLSLSPGERATLSC**RASQSVXXHMH**WYQQKPG QAPRLLIY**GASTLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWTDPXT**FGQGTKLEIK
CL-34587		EIVLTQSPATLSLSPGERATLSC**RASESVSTHLH**WYQQKPG QAPRLLIY**GASILES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-34590		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-34591		EIVLTQSPATLSLSPGERATLSC**RASQSVGTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWYDPIT**FGQGTKLEIK
CL-34592		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPIT**FGQGTKLEIK
CL-34593		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASMLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-34594		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWYDPIT**FGQGTKLEIK
CL-34598		EIVLTQSPATLSLSPGERATLSC**RASQSVSNHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWIEPYT**FGQGTKLEIK
CL-34599		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWYDPIT**FGQGTKLEIK
CL-34600		EIVLTQSPATLSLSPGERATLSC**RASESVNTHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWNDPFT**FGQGTKLEIK
CL-34601		EIVLTQSPATLSLSPGERATLSC**RASQSVGTHMH**WYQQKPG QAPRLLIY**GASILES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWYDPLT**FGQGTKLEIK
CL-34602		EIVLTQSPATLSLSPGERATLSC**RASQSVGTHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED

Clone	SEQ ID NO:	VL
		FAVYFC**QQSWYDPGT**FGQGTKLEIK
CL-34604		EIVLTQSPATLSLSPGERATLSC**RASQSVNNHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-34610		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWYDPLT**FGQGTKLEIK
CL-34612		EIVLTQSPATLSLSPGERATLSC**RASQSVGTHMQ**WYQQKPG QAPRLLIY**GASILES**GIPARFSGSGSGTDFTLTISSLEHED FAVYXC**QQSWYDPLT**FGQGTKLEIK
CL-34613		EIVLTQSPATLSLSPGERATLSC**RASESVGRHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQTWYDPIT**FGQGTKLEIK
CL-34614		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASYLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWYDPLT**FGQGTKLEIK
CL-34617		EIVLTQSPATLSLSPGERATLSC**RASESVDSSMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWYDPLT**FGQGTKLEIK
CL-34618		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWYDPIT**FGQGTKLEIK
CL-40245		EIVLTQSPATLSLSPGERAALSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-40250		EIVLTQSPATLSLSPGERATLSY**RASQSVGTHMH**WYQQKPG QAPRLLIY**GASHLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWYDPLT**FGQGTKLEIK
CL-40251		EIVLTQSPGTLSLSPGERATLSC**RASQSVGTHMH**WYQQKPG QAPRLLIY**GASKLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-40253		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGADFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-40255		EIVLTQSPGTLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-40258		EIVLTQSPATLSLSPGERATLSC**RASQSVGTHMH**WYQQKPG QAPRLLIY**GASHPES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWYDPLT**FGQGTKLEIK
CL-40266		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWYDPMT**FGQGTKLEIK
CL-40271		EIVLTQSPATLSLSPGERATLSC**RASQSVGTHMH**WYQQKPG QAPRLLIY**GASHLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWYDPLT**FGQGTKLGSN
CL-40272		EIVLTQSPATLSLSPGERATLSC**RASQSVGTHMH**WYQQKPG QAPRLLIY**GASKLES**GVPARFSGSGSGTDFTLTISSLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QQSWYDPLT**FGQGTKLRSN
CL-40283		EIVLTQSPGTLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWYDPMT**FGQGTKLEIK
CL-40284		EIVLTQSPATLSLSPGERAILSC**RASQSVGTHMH**WYQQKPG QAPRLLIY**GASKLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLA**FGQGTKLEIK
CL-40286		EIVLPQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASNLEP**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWNDPFT**FGQGTKLEIK
CL-40287		EIVLTQSPGTLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWNDPFT**FGQGTKLEIK
CL-40288		EIVLTQSPGTLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-40299		RNCVTQSPATLSLSPGERATLSC**RASQSVGTHMH**WYQQKPG QAPRLLIY**GASHLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWYDPLT**FGQGTKLEIK
CL-40302		EIVLTQSPATLSLSPGERATLSC**RASQSVGTHMH**WYQQKPG QAPRLLIY**GASKLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWCDPLT**FGQGTKLEIK
CL-40303		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLPIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-40317		EIVLTQSPATLSLSPGERATLSC**RASQSVGTHMH**WYQQKPG QAPRLLIY**GASKLES**GVPARFSGSGSGTDFTLTISSLGPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-40324		EIVLTQSPATLSLSPGERATLSC**RASQSVGTHMH**WYQQKPG QAPRLLIY**GASHLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWYDPLT**FGQGTKLEIK
CL-40327		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWYDPMT**FGQGTKLEIK
CL-40328		EIVLTQSPGTLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASKLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-40331		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQRTKLEIK
CL-40332		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWYDPMA**FGQGTKLEIK
CL-40335		RNCVDKSPATLSLSPGERATLSC**RASQSVGTHMH**WYQQKPG QAPRLLIY**GASHLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWYDPLT**FGQGTKLEIK
CL-40336		EIVLTQSPATLSLSPGERATLSC**RASQSVGTHMH**WYQQKPG QAPRLLIY**GASKLES**GVPARFSGSGSGTDFTLTISSLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-40337		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QRSWYDPLT**FGQGTKLEIK
CL-40338		EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWNDPFT**FGQGTKLEIK
CL-40339		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-40341		EIVLTQSPATLSLSPGERATLFC**RASQSVSNHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FVVYYC**QQSWYDPIT**FGQGTKLEIK
CL-40342		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQTCYDPLT**FGQGTKLEIK
CL-40350		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGADFTLTISSLEPED FAVYFC**QQSWYDPLT**FGQGTKLEIK
CL-40356		EIVLTQSPATLSLSPGERATLSC**RASESVGKHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQTWYDPIT**FGQGTKLEIK
CL-40357		EIVLTQSPATLSLSPGERATLFC**RASQSVSNHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWYDPLT**FGQGTKLEIK
CL-40364		EIVLTQSPGTLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSFYDPLT**FGQGTKLEIK
CL-40367		EIVLTQSPGTLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQTWYDPLT**FGQGTKLEIK
CL-40370		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFILTISSLEPED FAVYYC**QQSFYDPLT**FGQGTKLEIK
CL-40373		EIVLTQSPGTLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWYDPLT**FGQGTKLEIK
CL-40381		EIVLTQSPGTLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAIYFC**QQTWYDPLT**FGQGTKLEIK
CL-40382		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGIDFTLTISSLEPED FAVYFC**QQTWYDPLT**FGQGTKLEIK
CL-40390		EIVLTQSPATLSLSPGERATLSC**RASGSVGKHMH**WYQQKPG QAPRLLIY**AASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-40394		EIVLTQSPGTLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPEE

Clone	SEQ ID NO:	VL
		FAVYFC**QQTWYDPLT**FGQGTKLEIK
CL-40399		EIVLTQSPATLSLSPGERATLSC**RASQSVSKHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDSTLTISSLEPED FAVYFC**QQTWYDPIT**FGQGTKLEIK
CL-40408		EIVLTQSPATLSLPPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSFYDPLT**FGQGTKLEIK
CL-40414		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFGGSGSGTDFTLTISSLEPED FAVYYC**QQSFYDPLT**FGQGTKLEIK
CL-40426		EIVSTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTIGSLEPED FAVYFC**QQSWYDPLT**FGQGTKLEIK
CL-40440		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTNLEIK
CL-40441		EIVLTQSPATLSLSPGERATFSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASKLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-40443		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAAYFC**QQTWYDPLT**FGQGTKLEIK
CL-40445		EIVLTQSPSTLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQTWYDPLT**FGQGTKLEIK
CL-40447		EIVLTQSPATLSLSPGERATLSC**RASQSVNNHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWYDPLT**FGQGTKLEIX
CL-40453		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WCQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQTWYDPLT**FGQGTKLEIK
CL-40463		EIVLTQSPGTLSLSPGERATLSC**RASQSVNNHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWYDPLT**FGQGTKLEIK
CL-40466		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWYDPLT**FGQGTKLEIK
CL-40470		EIVLTQSPGTLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWYDPLT**FGQGTKLEIK
CL-40472		EIVLTQSPATLSLSPGERATLSC**RASQSVNNHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-40476		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASKLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLRSN
CL-40479		EIVLTQSPATLSLSPGERATLSC**RASQSVATHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QQSWYDPLT**FGQGTKLRSN
CL-40480		EIVLTQSPGTLSLSPGERATLSC**RASQSVSTHMH**WYQQEPG QAPRLLIY**GASKLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-40484		EIVLTQSPGTLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-40485		RNLLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQTWYDPLT**FGQGTKLEIK
CL-40489		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQTWYDPLT**FGQGTKLVIK
CL-40494		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGADFTLTISSLEPED FAVYFC**QQTWYDPLT**FGQGTKLEIK
CL-40498		EIVLTQSPATLSLSPGERATLSC**RASQSVNNHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSRYDPLT**FGQGTKLEIK
CL-40503		EIVLTQSPGTLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQTWYDPLT**FGQGTKLEIK
CL-40505		EIVLTQSPGTLSLSPGERATLSC**RASQSVATHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-40511		AIVLTQSPATLSLSPGERATLSC**RASQSVATHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-40526		EIVLTQSPAALSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQTWYDPLT**FGQGTKLEIK
CL-40531		EIVLTQSPATLSLSPGERATLSC**RASQSVNNHMH**WYQQKPG QAPRLLIY**GASIPES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWYDPLT**FGQGTKLEIK
CL-41836		AIVLTQSPGTLSLSPGERATLSC**RASQSVATHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-41845		EIVLTQSPATLSLSPGERATLSC**RASQSVNNHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWYDPLT**FGQGTKLEIK
CL-41849		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASKLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-41850		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWYDPLT**FGQGTKLEIK
CL-41852		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-41854		EIVLTQSPATLSLSPGERATLSC**RASQSVATHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-41855		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQTWYDPLT**FGQGTKLEIK
CL-41885		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTITSLEPED FAVYFC**XQTWYDPLT**FGQGTKLEIK
CL-41886		EIVLTQSPATLSLSPGERATLFC**RASQSVSNHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPIT**FGQGTKLRSN
CL-41888		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWYDPLT**FGQGTKLEIK
CL-41920		EIVLTQSPGTLSLSPGERASLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSFYDPLT**FGRGTKLEIK
CL-41923		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQSWYDPLT**FGQGTKLEIN
CL-41928		EIVLTQSPATLSLSPGERATLSC**RTSESVGKHMH**WYQQKPG QAPRLLIY**AASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-41938		EIVLTQSPATLSLSPGERATLSC**RASESVGKHMH**WYQQKPG QAPRLLIY**AASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPLT**FGQGTKLEIK
CL-41940		EIVLTQSPATLSLSPGERATLFC**RASQSVSNHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSWYDPIT**FGQGTKLEIK
CL-41941		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASILES**GVPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQTWYDPLT**FGQGTKLEIK
CL-41947		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSFYDPLT**FGQGTKLEIQ
CL-41949		EIVLTQSPATLSLSPGERATLSC**RASQSVSKHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYFC**QQTWYDPIT**FGQGTKLEIK
CL-41950		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQTWYDPLT**FGQGTKLEIK
CL-41951		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED FAVYYC**QQSFYDPLT**FGQGTKLEIK
CL-41952		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPG QAPRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPED

Clone	SEQ ID NO:	VL
		FAVYFC**QQSWYDPLT**FGQGTKLEIK

Table 40. Amino Acid Residues Found In Each Position of the Heavy Chain Variable Region During The Affinity Maturation Of Humanized Anti-Human VEGF Antibody Hbdb-4G8.3

hBDB-4G8| Heavy Chain Variable Region	
SEQ ID NO:	Sequence
XX	1 2 3 4 5 6 1234567890123456789012345**6789012345**6789012345678901234567890 EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPGQGLEWMG**WINTETGKPTY** R S **S S** **Y N I** N **QK D** **L D M** **DY K** **V T K** **ET C** **W P A** **NM V** **A W N** **AG E** **Q Y P** **GA L** **H V L** **HI W** **G S V** **KL P** **K M W** **ME Y** **N A D** **LP M** **M I Y** **RQ N** **T G G** **IF T** **P R E** **Y** **L** **V**
	7 8 9 **10** **11** 12 **123456**7890123456789012345678901234567**8901234567890123**4567890 **ADDFKG**RFVFSLDTSVSTAYLQISSLKAEDTAVYYCAR**TNYYYRSYIFYFDY**WGQGTMVT **Y N** T D **H N L** **H** T **YI ST N**

hBDB-4G8| Heavy Chain Variable Region

SEQ ID NO:	Sequence
	GT NK T ID EM V S MY A KF LC R NL TI F PE WF D LV QL WY GD S MA IW FG AX RW CV QQ V R
	123 VSS SFQ L

hBDB-4G8| Heavy Chain Variable Region	
SEQ ID NO:	Sequence

Table 41. Amino Acid Residues Found In Each Position of the Light Chain Variable Region During The Affinity Maturation Of Humanized Anti-Human VEGF Antibody Hbdb-4G8.3

hBDB-4G8| Light Chain Variable Region	
SEQ ID NO:	Sequence
XX	1 2 3 4 5 6 12345678901234567890123**4567890123**4567890123456789**01234567**890 EIVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPGQAPRLLIY**GASNLES**GVPA A **NSA A** **W H Y** **DRD P** **V Y** **C** **I M** **TAP** **E T** **RER** **S F** **HDY** **D V** **EM** **R** **IPL** **Q** **LYQ** **A** **QIK** **S** **CW** **E** **MF** **G** **Y** **C** **K** **D** **V** **P**
	7 8 9 10 12345678901234567890123456789**01234567**8901234567 RFSGSGSGTDFTLTISSLEPEDFAVYFC**QQSWNDPFT**FGQGTKLEIK **CCIN M** G **GLTY G** **IGDA Y** **W GL** **REM A** **NSSM W** **A HP S** **Y AG V** **K RH C** **Q VF P** **F LK** **F** **K** **Q**

Table 42. Variable Region Sequences of hBDB-4G8.3 Affinity Matured Clones Converted To IgG

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				12345678901234567890123456789O
	CL-32416 VH			EVQLVQSGSELKKPGASVKVSCKAS**GYT** **FTDYGMY**WVRQAPGQGLEWMG**WIDTETG** **EPTYADDFKG**RFVFSLDTSVSTAYLQIS SLKAEDTAVYYCAR**TNYYYRSYMFYFDY** WGQGTMVTVSS
	CL-32416	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTDYGMY**
	CL-32416	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WIDTETGEPTYADDFKG**
	CL-32416	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TNYYYRSYMFYFDY**
	CL-32416 VL			EIVLTQSPATLSLSPGERATLSC**RASES** **VSTHMH**WYQQKPGQAPRLLIY**GASNLES** GVPARFSGSGSGTDFTLTISSLEPEDFA VYFC**QQSWNDPFT**FGQGTKLEIK
	CL-32416	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASESVSTHMH**
	CL-32416	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	CL-32416	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQSWNDPFT**
	CL-34449 VH			EVQLVQSGSELKKPGASVKVSCKAS**GYT** **FTDYGMY**WVRQAPGQGLEWMG**WIDTETG** **EPTYADDFKG**RFVFSLDTSVSTAYLQIS SLKAEDTAVYYCAR**TNYYYRSYMFYFDY** WGQGTMVTVSS
	CL-34449	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTDYGMY**
	CL-34449	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WIDTETGEPTYADDFKG**
	CL-34449	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TNYYYRSYMFYFDY**
	CL-34449 VL			EIVLTQSPATLSLSPGERATLSC**RASQS** **VGTHMH**WYQQKPGQAPRLLIY**GASHLES** GIPARFSGSGSGTDFTLTISSLEPEDFA VYYC**QQTWYDPLT**FGQGTKLEIK
	CL-34449	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASQSVGTHMH**
	CL-34449	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASHLES**
	CL-34449	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQTWYDPLT**
	CL-34455 VH			EVQLVQSGSELKKPGASVKVSCKAS**GYT** **FTNYGMY**WVRQAPGQGLEWMG**WIDTETG** **EPTYAQGFTG**RFVFSLDTSVSTAYLQIS SLKAEDTAVYYCAR**TNYYYPSYMFYFDY**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				WGQGTMVTVSS
	CL-34455	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	CL-34455	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WIDTETGEPTYAQGFTG**
	CL-34455	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TNYYYPSYMFYFDY**
	CL-34455 VL			EIVLTQSPATLSLSPGERATLSC**RASQS** **VGTHMH**WYQQKPGQAPRLLIY**GASKLES** GVPARFSGSGSGTDFTLTISSLEPEDFA VYYC**QQSWYDPLT**FGQGTKLEIK
	CL-34455	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASQSVGTHMH**
	CL-34455	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASKLES**
	CL-34455	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQSWYDPLT**
	CL-34463 VH			EVQLVQSGSELKKPGASVKVSCKAS**GYT** **FTDYGMY**WVRQAPGQGLEWMG**WIDTETG** **NPTYADDFKG**RFVFSLDTSVSTAYLQIS SLKAEDTAVYYCAR**TNYYYPSYMFYFDY** WGQGTMVTVSS
	CL-34463	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTDYGMY**
	CL-34463	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WIDTETGNPTYADDFKG**
	CL-34463	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TNYYYPSYMFYFDY**
	CL-34463 VL			EIVLTQSPATLSLSPGERATLSC**RASQS** **VSKHMH**WYQQKPGQAPRLLIY**GASNLES** GIPARFSGSGSGTDFTLTISSLEPEDFA VYFC**QQTWYDPIT**FGQGTKLEIK
	CL-34463	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASQSVSKHMH**
	CL-34463	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	CL-34463	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQTWYDPIT**
	CL-34469 VH			EVQLVQSGSELKKPGASVKVSCKAS**GYT** **FTNYGMY**WVRQAPGQGLEWMG**WIDTETG** **EPTYADDFKG**RFVFSLDTSVSTAYLQIS SLKAEDTAVYYCAR**TNYYYRSYMFYFDY** WGQGTMVTVSS
	CL-34469	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	CL-34469	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WIDTETGEPTYADDFKG**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
	CL-34469	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TNYYYRSYMFYFDY**
	CL-34469 VL			EIVLTQSPATLSLSPGERATLSC**RASQS** **VSTHMH**WYQQKPGQAPRLLIY**GASNLES** GVPARFSGSGSGTDFTLTISSLEPEDFA VYYC**QQSWYDPLT**FGQGTKLEIK
	CL-34469	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASQSVSTHMH**
	CL-34469	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	CL-34469	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQSWYDPLT**
	CL-34475 VH			EVQLVQSGSELKKPGASVKVSCKAS**GYT** **FTDYGMY**WVRQAPGQGLEWMG**WIDTETG** **EPTYADDFKG**RFVFSLDTSVSTAYLQIS SLKAEDTAVYYCAR**TNYYYSSYMFYFDY** WGQGTMVTVSS
	CL-34475	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTDYGMY**
	CL-34475	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WIDTETGEPTYADDFKG**
	CL-34475	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TNYYYSSYMFYFDY**
	CL-34475 VL			EIVLTQSPATLSLSPGERATLSC**RASQS** **VSTHMH**WYQQKPGQAPRLLIY**GASNLES** GIPARFSGSGSGTDFTLTISSLEPEDFA VYYC**QQSWYDPLT**FGQGTKLEIK
	CL-34475	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASQSVSTHMH**
	CL-34475	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	CL-34475	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQSWYDPLT**
	CL-34483 VH			EVQLVQSGSELKKPGASVKVSCKAS**GYT** **FPNYGMY**WVRQAPGQGLEWMG**WIDTETG** **EPTYADDFKG**RFVFSLDTSVSTAYLQIS SLKAEDTAVYYCAR**TNYYYRSYMFYFDY** WGQGTMVTVSS
	CL-34483	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFPNYGMY**
	CL-34483	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WIDTETGEPTYADDFKG**
	CL-34483	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TNYYYRSYMFYFDY**
	CL-34483 VL			EIVLTQSPATLSLSPGERATLSC**RASQS** **VATHMH**WYQQKPGQAPRLLIY**GASNLES** GVPARFSGSGSGTDFTLTISSLEPEDFA

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				VYYC**QQSWYDPLT**FGQGTKLEIK
	CL-34483	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASQSVATHMH**
	CL-34483	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	CL-34483	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQSWYDPLT**
	CL-34489 VH			EVQLVQSGSELKKPGASVKVSCKAS**GYT FSNYGMY**WVRQAPGQGLEWMG**WIDTETG EPTYADDFKG**RFVFSLDTSVSTAYLQIS SLKAEDTAVYYCAR**TNYYYSSYMFYFDY** WGQGTMVTVSS
	CL-34489	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFSNYGMY**
	CL-34489	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WIDTETGEPTYADDFKG**
	CL-34489	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TNYYYSSYMFYFDY**
	CL-34489 VL			EIVLTQSPATLSLSPGERATLSC**RASQS VSTHMH**WYQQKPGQAPRLLIY**GASNLES** GIPARFSGSGSGTDFTLTISSLEPEDFA VYFC**QQSWYDPLT**FGQGTKLEIK
	CL-34489	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASQSVSTHMH**
	CL-34489	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	CL-34489	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQSWYDPLT**
	CL-34501 VH			EVQLVQSGSELKKPGASVKVSCKAS**GYT FSDYGMY**WVRQAPGQGLEWMG**WIDTETG DPTYADDFKG**RFVFSLDTSVSTAYLQIS SLKAEDTAVYYCAR**TNYYYPSYMFYFDY** WGQGTMVTVSS
	CL-34501	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFSDYGMY**
	CL-34501	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WIDTETGDPTYADDFKG**
	CL-34501	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TNYYYPSYMFYFDY**
	CL-34501 VL			EIVLTQSPATLSLSPGERATLSC**RASQS VSTHMH**WYQQKPGQAPRLLIY**GASILES** GVPARFSGSGSGTDFTLTISSLEPEDFA VYFC**QQTWYDPLT**FGQGTKLEIK
	CL-34501	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASQSVSTHMH**
	CL-34501	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASILES**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
	CL-34501	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQTWYDPLT**
	CL-34513 VH			EVQLVQSGSELKKPGASVKVSCKAS**GYT** **FTDYGMY**WVRQAPGQGLEWMG**WIDTETG** **EPTYADDFKG**RFVFSLDTSVSTAYLQIS SLKAEDTAVYYCAR**TNYYYRGYMFYFDY** WGQGTMVTVSS
	CL-34513	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTDYGMY**
	CL-34513	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WIDTETGEPTYADDFKG**
	CL-34513	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TNYYYRGYMFYFDY**
	CL-34513 VL			EIVLTQSPATLSLSPGERATLSC**RASQS** **VNNHMH**WYQQKPGQAPRLLIY**GASILES** GVPARFSGSGSGTDFTLTISSLEPEDFA VYFC**QQSWYDPLT**FGQGTKLEIK
	CL-34513	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASQSVNNHMH**
	CL-34513	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASILES**
	CL-34513	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQSWYDPLT**
	CL-34518 VH			EVQLVQSGSELKKPGASVKVSCKAS**GYT** **FTNYGMY**WVRQAPGQGLEWMG**WIDTETG** **EPTYADDFKG**RFVFSLDTSVSTAYLQIS SLKAEDTAVYYCAR**TNYYYKSYMFYFDY** WGQGTMVTVSS
	CL-34518	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTNYGMY**
	CL-34518	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WIDTETGEPTYADDFKG**
	CL-34518	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TNYYYKSYMFYFDY**
	CL-34518 VL			EIVLTQSPATLSLSPGERATLSC**RASQS** **VSTHMH**WYQQKPGQAPRLLIY**GASKLES** GVPARFSGSGSGTDFTLTISSLEPEDFA VYYC**QQSWYDPLT**FGQGTKLEIK
	CL-34518	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASQSVSTHMH**
	CL-34518	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASKLES**
	CL-34518	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQSWYDPLT**
	CL-34522 VH			EVQLVQSGSELKKPGASVKVSCKAS**GYT** **FENYGMY**WVRQAPGQGLEWMG**WIDTETG** **EPTYADDFKG**RFVFSLDTSVSTAYLQIS SLKAEDTAVYYCAR**TNYYYSSYMFYFDY**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				WGQGTMVTVSS
	CL-34522	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFENYGMY**
	CL-34522	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WIDTETGEPTYADDFKG**
	CL-34522	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TNYYYSSYMFYFDY**
	CL-34522 VL			EIVLTQSPATLSLSPGERATLSC**RASQS** **VGTHMH**WYQQKPGQAPRLLIY**GASKLES** GVPARFSGSGSGTDFTLTISSLEPEDFA VYYC**QQSWYDPLT**FGQGTKLEIK
	CL-34522	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASQSVGTHMH**
	CL-34522	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASKLES**
	CL-34522	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQSWYDPLT**
	CL-34537 VH			EVQLVQSGSELKKPGASVKVSCKAS**GYT** **FSDYGMY**WVRQAPGQGLEWMG**WIDTETG** **DPTYADDFKG**RFVFSLDTSVSTAYLQIS SLKAEDTAVYYCAR**ANYYYRSYMFYFDY** WGQGTMVTVSS
	CL-34537	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFSDYGMY**
	CL-34537	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WIDTETGDPTYADDFKG**
	CL-34537	CDR-H3	Residues 99-112 of SEQ ID NO.:	**ANYYYRSYMFYFDY**
	CL-34537 VL			EIVLTQSPATLSLSPGERATLSC**RASQS** **VSTHMH**WYQQKPGQAPRLLIY**GASNLES** GIPARFSGSGSGTDFTLTISSLEPEDFA VYFC**QQSWYDPMT**FGQGTKLEIK
	CL-34537	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASQSVSTHMH**
	CL-34537	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	CL-34537	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQSWYDPMT**
	CL-34538 VH			EVQLVQSGSELKKPGASVKVSCKAS**GYT** **FTDYGMY**WVRQAPGQGLEWMG**WIDTETG** **EPTYADDFKG**RFVFSLDTSVSTAYLQIS SLKAEDTAVYYCAR**TNYYYPSYMFYFDY** WGQGTMVTVSS
	CL-34538	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTDYGMY**
	CL-34538	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WIDTETGEPTYADDFKG**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
	CL-34538	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TNYYYPSYMFYFDY**
	CL-34538 VL			EIVLTQSPATLSLSPGERATLSC**RASQS** **VSTHMH**WYQQKPGQAPRLLIY**GASNLES** GVPARFSGSGSGTDFTLTISSLEPEDFA VYFC**QQTWYDPLT**FGQGTKLEIK
	CL-34538	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASQSVSTHMH**
	CL-34538	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	CL-34538	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQTWYDPLT**
	CL-34540 VH			EVQLVQSGSELKKPGASVKVSCKAS**GYT** **FTDYGMY**WVRQAPGQGLEWMG**WIDTETG** **QPTYADDFKG**RFVFSLDTSVSTAYLQIS SLKAEDTAVYYCAR**TNYYYRSYMFYFDY** WGQGTMVTVSS
	CL-34540	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTDYGMY**
	CL-34540	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WIDTETGQPTYADDFKG**
	CL-34540	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TNYYYRSYMFYFDY**
	CL-34540 VL			EIVLTQSPATLSLSPGERATLSC**RASES** **VGKHMH**WYQQKPGQAPRLLIY**AASNLES** GVPARFSGSGSGTDFTLTISSLEPEDFA VYYC**QQSWYDPLT**FGQGTKLEIK
	CL-34540	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASESVGKHMH**
	CL-34540	CDR-L2	Residues 50-56 of SEQ ID NO.:	**AASNLES**
	CL-34540	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQSWYDPLT**
	CL-34565 VH			EVQLVQSGSELKKPGASVKVSCKAS**GYT** **FTDYGMY**WVRQAPGQGLEWMG**WIDTETG** **DPTYADDFKG**RFVFSLDTSVSTAYLQIS SLKAEDTAVYYCAR**TNYYYRNYMFYFDY** WGQGTMVTVSS
	CL-34565	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTDYGMY**
	CL-34565	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WIDTETGDPTYADDFKG**
	CL-34565	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TNYYYRNYMFYFDY**
	CL-34565 VL			EIVLTQSPATLSLSPGERATLFC**RASQS** **VSNHMH**WYQQKPGQAPRLLIY**GASILES** GVPARFSGSGSGTDFTLTISSLEPEDFA

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				VYYC**QQSWYDPIT**FGQGTKLEIK
	CL-34565	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASQSVSNHMH**
	CL-34565	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASILES**
	CL-34565	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQSWYDPIT**
	CL-34570 VH			EVQLVQSGSELKKPGASVKVSCKAS**GYT FDDYGMY**WVRQAPGQGLEWMG**WIDTETG TPTYADDFKG**RFVFSLDTSVSTAYLQIS SLKAEDTAVYYCAR**TNYYYSSYMFYFDY** WGQGTMVTVSS
	CL-34570	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFDDYGMY**
	CL-34570	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WIDTETGTPTYADDFKG**
	CL-34570	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TNYYYSSYMFYFDY**
	CL-34570 VL			EIVLTQSPATLSLSPGERATLSC**RASQS VSTHMH**WYQQKPGQAPRLLIY**GASNLES** GIPARFSGSGSGTDFTLTISSLEPEDFA VYYC**QQSWYDPLT**FGQGTKLEIK
	CL-34570	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASQSVSTHMH**
	CL-34570	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	CL-34570	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQSWYDPLT**
	CL-34603 VH			EVQLVQSGSELKKPGASVKVSCKAS**GYT FTDYGMY**WVRQAPGQGLEWMG**WIDTETG EPTYAQGFTG**RFVFSLDTSVSTAYLQIS SLKAEDTAVYYCAR**TNYYYRSYMFYFDY** WGQGTMVTVSS
	CL-34603	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTDYGMY**
	CL-34603	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WIDTETGEPTYAQGFTG**
	CL-34603	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TNYYYRSYMFYFDY**
	CL-34603 VL			EIVLTQSPATLSLSPGERATLSC**RASQS VSTHMH**WYQQKPGQAPRLLIY**GASNLES** GVPARFSGSGSGTDFTLTISSLEPEDFA VYYC**QQTWYDPLT**FGQGTKLEIK
	CL-34603	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASQSVSTHMH**
	CL-34603	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
	CL-34603	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQTWYDPLT**
	CL-34605 VH			EVQLVQSGSELKKPGASVKVSCKAS**GYT** **FTHYGMY**WVRQAPGQGLEWMG**WIDTETG** **EPTYADDFKG**RFVFSLDTSVSTAYLQIS SLKAEDTAVYYCAR**TNYYYRSYMFYFDY** WGQGTMVTVSS
	CL-34605	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFTHYGMY**
	CL-34605	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WIDTETGEPTYADDFKG**
	CL-34605	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TNYYYRSYMFYFDY**
	CL-34605 VL			EIVLTQSPATLSLSPGERATLSC**RASQS** **VSTHMH**WYQQKPGQAPRLLIY**GASNLES** GIPARFSGSGSGTDFTLTISSLEPEDFA VYYC**QQSFYDPLT**FGQGTKLEIK
	CL-34605	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASQSVSTHMH**
	CL-34605	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	CL-34605	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQSFYDPLT**
	CL-34633 VH			EVQLVQSGSELKKPGASVKVSCKAS**GYT** **FSDYGMY**WVRQAPGQGLEWMG**WIDTETG** **EPTYADDFKG**RFVFSLDTSVSTAYLQIS SLKAEDTAVYYCAR**TNYYYRSYMFYFDY** WGQGTMVTVSS
	CL-34633	CDR-H1	Residues 26-35 of SEQ ID NO.:	**GYTFSDYGMY**
	CL-34633	CDR-H2	Residues 50-66 of SEQ ID NO.:	**WIDTETGEPTYADDFKG**
	CL-34633	CDR-H3	Residues 99-112 of SEQ ID NO.:	**TNYYYRSYMFYFDY**
	CL-34633 VL			EIVLTQSPATLSLSPGERATLSC**RASQS** **VSTHMH**WYQQKPGQAPRLLIY**GASNLES** GVPARFSGSGSGTDFTLTISSLEPEDFA VYFC**QQSWYDPLT**FGQGTKLEIK
	CL-34633	CDR-L1	Residues 24-34 of SEQ ID NO.:	**RASQSVSTHMH**
	CL-34633	CDR-L2	Residues 50-56 of SEQ ID NO.:	**GASNLES**
	CL-34633	CDR-L3	Residues 89-97 of SEQ ID NO.:	**QQSWYDPLT**

Table 43. Summary of Protein Expression and Purification Affinity Matured Humanized Anti-Human VEGF-A Antibodies

Name	Yield (mg/L)[1]	SEC (% monomer)[2]
CL-32416-IgG	28.5	100.0
CL-34449-IgG	16.1	100.0
CL-34455-IgG	34.1	100.0
CL-34469-IgG	21.3	100.0
CL-34475-IgG	33.6	100.0
CL-34522-IgG	18.4	100.0
CL-34538-IgG	40.8	100.0
CL-34540-IgG	80.0	100.0
CL-34565-IgG	133.6	100.0
CL-34570-IgG	28.3	100.0
CL-34633-IgG	49.9	100.0

[1]Yield is determined by the total amount of purified protein in mg divided by the total cell culture volume in liters.

[2]SEC % monomer is determined using HPLC size exclusion chromatography.

Table 44. Biacore Binding of Affinity Matured Humanized Anti-VEGF Antibodies

Antibody	k_{on} (M-1 s-1)	k_{off} (M-1)	K_D (M)
CL-28815-IgG (EI version of parent mAb)	9.2 E+06	1.1 E-04	1.2 E-11
CL-32416-IgG	2.0 E+07	1.1 E-05	5.4 E-13
CL-34449-IgG	1.1 E+07	9.1 E-06	8.5 E-13
CL-34455-IgG	2.2 E+07	1.0 E-05	4.6 E-13
CL-34469-IgG	1.5 E+07	9.5 E-06	6.2 E-13
CL-34475-IgG	2.7 E+07	1.4 E-05	5.2 E-13
CL-34522-IgG	2.0 E+07	1.0 E-05	5.3 E-13
CL-34538-IgG	3.3 E+07	8.1 E-06	2.4 E-13
CL-34540-IgG	8.4 E+06	7.1 E-06	8.5 E-13
CL-34565-IgG	2.0 E+07	7.8 E-06	4.0 E-13
CL-34570-IgG	1.9 E+07	5.5 E-06	2.9 E-13
CL-34633-IgG	1.7 E+07	4.1 E-06	2.4 E-13

[0388] Affinity matured humanized anti-VEGF antibodies were characterized for $hVEGF_{165}$ binding and potency. Binding affinity of these molecules to $hVEGF_{165}$ was determined by Biacore analysis (Example 1.1). Potency was evaluated in both cell-based and ELISA formats. The ability to block binding of $hVEGF_{165}$ to hVEGFR2 was evaluated in a competition ELISA (Example 1.4). Inhibition of $hVEGF_{165}$-induced cell proliferation was assessed using HMVEC-d cells (Example 1.10). The data is summarized in Table 45 below.

Table 45. Summary of Characterization of Affinity Matured Humanized Anti-Human VEGF-A Antibodies

Affinity Matured Humanized IgG	$hVEGF_{165}$ IC50 (nM)		
	VEGFR2 Competition	Potency HMVEC-d	Potency VEGFR2-3T3
CL-32416-IgG	<0.1	0.117	NT
CL-34449-IgG	<0.1	0.077	NT
CL-34455-IgG	<0.1	0.105	NT
CL-34469-IgG	<0.1	0.094	NT
CL-34475-IgG	<0.1	0.106	NT
CL-34522-IgG	<0.1	0.116	NT
CL-34540-IgG	<0.1	0.139	NT
CL-34633-IgG	<0.1	0.138	NT
CL-34538-IgG	<0.1	0.127	NT
CL-34570-IgG	<0.1	0.11	NT
CL-34565-IgG	<0.1	0.126	NT

Example 8: Affinity Maturation of Anti-Human PDGF-BB Antibody hBDI-9E8

[0389] The PDGF-β antibody hBDI-9E8.4 was obtained from rat hybridomas generated at Aldevron and was humanized at AbbVie Bioresearch Center (100 Research Drive, Worcester, MA 01605). The human germlines for this clone are VH2-70 and IGKV3-20. To improve the affinity of hBDI-9E8.4, hypermutated CDR residues were identified from other human antibody sequences in the IgBLAST database that also shared high identity to germlines VHVH2-70 and IGKV3-20. The corresponding h9E8.4 CDR residues were then subjected to limited mutagenesis by PCR with primers having low degeneracy at these positions to create three antibody libraries in the scFv format suitable for surface display. To improve the affinity of hBDI-9E8.4 to PDGFβ we generated three antibody libraries in scFv format suitable for surface display. In the first library, residues 30, 32, 34, 35, and 35b in the VH CDR1 and residues 50, 52, 54, 56, 57, 58, 60, 61 and 65 (Kabat numbering) in the VH CDR2 were subjected to limited mutagenesis by primers. In the second library residues 95-100a, 100c and 102 (Kabat numbering) in the VH CDR3 were subjected to limited mutagenesis by primers. In the third library residues 24, 25, 27b, and 29-32 in the VL CDR1, residues 47, 50, 51, 53, 55, and 56 in the VL CDR2 and residues 90, 93-95a, 96 and 97 (Kabat numbering) in the VL CDR3 were subjected to limited mutagenesis by primers.

[0390] These hBDI-9E8.4 libraries were displayed to be selected against a low concentration of biotinylated PDGFβ by magnetic then fluorescence activated cell sorting. Selections for improved on-rate, off-rate, or both were carried out and antibody protein sequences of affinity-modulated hBDI-9E8.4 clones.

[0391] Table 46 provides a list of amino acid sequences of VH regions of affinity matured humanized PDGF antibodies derived from hBDI-9E8.4. Amino acid residues of individual CDRs of each VH sequence are indicated in bold.

Table 46. List of amino Acid Sequences Of Affinity Matured hBDI-9E8.4 VH Variants

Clone	SEQ ID NO:	VH
CL-22556		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGVGVG**WIRQPP GKALEWLA**NIWWVDEIFYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22557		EVTLRESGPALVKPTQTLTLTCTFS**GFSLWTSGMGVV**WIRQPP GKALEWLA**LIDWADVKSYNPSLKN**RLTISEDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22558		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGVSVG**WIRQPP GKALEWLA**LIDWYDDMYYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22559		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTSGVRVV**WIRQPP GKALEWLA**NIWWDDYLDYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22560		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMSVG**WIRQPP GKALEWLA**LIDWADDTYYNPSLNN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22561		EVTLRESGPALVKPTQTLTLTCTFS**GFSLATYGMSVA**WIRQPP GKALEWLA**LIDWYDDEYYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22562		EVTLRESGPALVKPTQTLTLTCTFS**GFSLXTYGVGVG**WIRQPP GKALEWLA**NIWWVDDKYYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22563		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTSGVGVG**WIRQPP GKALEWLA**LIDWADDKYYNPSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22564		EVTLRESGPALVKPTQTLTLTCTFS**GFSLCTSGVRVR**WIRQPP GKALEWLA**LIDWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22565		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTSGVGVG**WIRQPP GKALEWLA**NIWWDDNXYYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22567		EVTLRESGPALVKPTQTLTLTCTFS**GFSLATSGVSVG**WIRQPP GKALEWLA**LIDWEDDKGYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22569		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMRVG**WIRQPP GKALEWLA**LIDWDDHKYYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22570		EVTLRESGPALVKPTQTLTLTCTFS**GFSLCTSGVGVG**WIRQPP GKALEWLA**LIDWDDDNYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22571		EVTLRESGPALVKPTQTLTLTCTFS**GFSLFTYGMGVG**WIRQPP GKALEWLA**LIDWVDDKFYSTSLKT**RLTISKDTSKNQVVLTMTN

Clone	SEQ ID NO:	VH
		MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22572		EVTLRESGPALVKPTQTLTLTCTFS**GFSLCTSGVGVG**WIRQPP GKALEWLA**NIWWDDDRYYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22573		EVTLRESGPALVKPTQTLTLTCTFS**GFSLCTSGMSVG**WIRQPP GKALEWLA**LICWDDDRYYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22575		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTSGMRVG**WIRQPP GKALEWLA**LIDWGDDMSYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22576		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTSGMGVG**WIRQPP GKALEWLA**LIDWEDDKYYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22578		EVTLRESGPALVKPTQTLTLTCTFS**GFSLLTYGVGVC**WIRQPP GKALEGWLN**IWWADGKCYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22581		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTSGVRVS**WIRQPP GKALEWLA**LIDWDDEECYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22582		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTSGMSVS**WIRQPP GKALEWLA**LIDWVDDMGYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22583		EVTLRESGPALVKPTQTLTLTCTFS**GFSLXTYGMGVG**WIRQPP GKALEWLA**LIDWADYRSYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22584		EVTLRESGPALVKPTQTLTLTCTFS**GFSLATYGVGVG**WIRQPP GKALEWLA**LIDWEDAVNYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22585		EVTLRESGPALVKPTQTLTLTCTFS**GFSLCTYGMGVC**WIRQPP GKALEWLA**LIGWDDENYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22586		EVTLRESGPALVKPTQTLTLTCTFS**GFSLTTYGVRVG**WIRQPP GKALEWLA**LIDWDDDKYYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22587		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMSVC**WIRQPP GKALEWLA**NIWWDDGCCYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22588		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTSGMRVG**WIRQPP GKALEWLA**LIDWCDDKYYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22589		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTSGMGVS**WIRQPP GKALEWLA**LIDWDDHXHYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22591		EVTLRESGPALVKPTQTLTLTCTFS**GFSLWTSGVGVG**WIRQPP GKALEWLA**LIDWEDNKDYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22593		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTSGVRVG**WIRQPP GKALEWLA**LIDWVDDMYYSTSLKT**RLTISKDTSKNQVVLTMTN

Clone	SEQ ID NO:	VH
		MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22595		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVE**WIRQPP GKALEWLA**LIDWDDDKDYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22596		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTSGMGVG**WIRQPP GKALEWLA**LIDWCDNRYYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22597		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTSGMRVG**WIRQPP GKALEWLA**LIDWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22598		EVTLRESGPALVKPTQTLTLTCTFS**GFSLRTYGVSVG**WIRQPP GKALEWLA**LIDWYDGKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22599		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVD**WIRQPP GKALEWLA**LIDWEDDKSYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22600		EVTLRESGPALVKPTQTLTLTCTFS**GFSLWTYGVSVR**WIRQPP GKALEWLA**LIDWDDVKYYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22601		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTSGVGVG**WIRQPP GKALEWLA**LIDWDDDKFYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22602		EVTLRESGPALVKPTQTLTLTCTFS**GFSLPTYGVRVG**WIRQPP GKALEWLA**NIWWVDNKYYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22603		EVTLRESGPALVKPTQTLTLTCTFS**GFSLXTSGVRVG**WIRQPP GKALEWLA**LIDWDDYQYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22604		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGVSVG**WIRQPP GKALEWLA**NIWWYDLKYYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22605		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGVGVG**WIRQPP GKALEWLA**LIDWDDDKCYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22606		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTSGVSVG**WIRQPP GKALEWLA**NIWWDDEKAYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22607		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTSGVGVS**WIRQPP GKALEWLA**LIDWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22608		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**LIDWDDDKYYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22609		EVTLRESGPALVKPTQTLTLTCTFS**GFSLPTSGVSVG**WIRQPP GKALEWLA**NIWWADSKFYSTSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22610		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGVSVD**WIRQPP GKALEWLA**LIDWGDQTNYNPSLKN**RLTISKDTSKNQVVXTMTN

Clone	SEQ ID NO:	VH
		MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22611		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGVGVE**WIRQPP GKALEWLA**LIDWYDDKYYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22612		EVTLRESGPALVKPTQTLTLTCTFS**GFSLPTSGVGVG**WIRQPP GKALEWLA**LIDWEDHMDYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22614		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMRVG**WIRQPP GKALEWLA**LIDWXDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22615		EVTLRESGPALVKPTQTLTLTCTFS**GFSLTTSGVGVG**WIRQPP GKALEWLA**LIDWYDERFYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22617		EVTLRESGPALVKPTQTLTLTXTFS**GFSLSTYGMRVG**WIRQPP GKALEWLA**NIWWADNXSYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22618		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMSVG**WIRQPP GKALEWLA**LIDWADDNYYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22619		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTSGVSVG**WIRQPP GKALEWLA**LIDWEDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22620		EVTLRESGPALVKPTQTLTLTCTFS**GFSLWTSGMGVG**WIRQPP GKALEWLA**LIDWDDEKAYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22621		EVTLRESGPALVKPTQTLTLTCTFS**GFSLWTSGMRVG**WIRQPP GKALEWLA**NIWWDDDKYYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22622		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGVSVG**WIRQPP GKALEWLA**LIDWHDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22624		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMSVG**WIRQPP GKALEWLA**LIDWNDNKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22625		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTSGVGVG**WIRQPP GKALEWLA**LIDWDDDKYYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22626		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTSGVRVC**WIRQPP GKALEWLA**LIDWDDDKSYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22627		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGVSVT**WIRQPP GKALEWLA**LIDWNDDNHYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22628		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTSGVSVV**WIRQPP GKALEWLA**NIWWDDEKCYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22629		EVTLRESGPALVKPTQTLTLTCTFT**GFSLYTSGMGVG**WIRQPP GKALEWLA**LIDWDDDKNYSTSLKT**RLTISKDTSKNQVVLTMTN

Clone	SEQ ID NO:	VH
		MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22630		EVTLRESGPALVKPTQTLTLTCTFS**GFSLFTYGVGVD**WIRQPP GKALEWLA**NIWWPDDNYYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22631		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTSGVGVG**WIRQPP GKALEWLA**LIDWDDDXCYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22633		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGVSVG**WIRQPP GKALEWLA**LIDWDDEKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22634		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTSGVGVG**WIRQPP GKALEWLA**LIDWIDDEDYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22635		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTSGVSVR**WIRQPP GKALEWLA**NIWWDDNKYYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22636		EVTLRESGPALVKPTQTLTLTCTFS**GFSLCTSGMGVG**WIRQPP GKALEWLA**NIWWDDDNYYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22637		EVTLRESGPALVKPTQTLTLTCTFS**GFSLLTYGMGVG**WIRQPP GKALEWLA**NIWWHDDKYYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22638		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTSGVSVA**WIRQPP GKALEWLA**NIWWDDDKYYSTSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22639		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTSGVRVG**WIRQPP GKALEWLA**LIDWEDYLCYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22640		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTSGVGVG**WIRQPP GKALEWLA**LIDWDDDYYYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22641		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22642		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTSGMGVG**WIRQPP GKALEWLA**NIWWVDDNYYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22643		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVY**WIRQPP GKALEWLA**LIDWDDDNYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22644		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTSGVSVG**WIRQPP GKALEWLA**LIDWDDGKYYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22645		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTSGVRVV**WIRQPP GKALEWLA**LIDWNDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22646		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTSGVSVV**WIRQPP GKALEWLA**NIWWHDDKYYSTSLKT**RLTISKDTSKNQVVLTMTN

Clone	SEQ ID NO:	VH
		MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22648		EVTLRESGPALVKPTQTLTLTCTFS**GFSLMTSGMSVC**WIRQPP GKALEWLA**NIWWYDHKYYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22649		EVTLRESGPALVKPTQTLTLTCTFS**GFSLRTYGVSVG**WIRQPP GKALEWLA**NIWWDDAKYYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22650		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGVRVA**WIRQPP GKALEWLA**NIWWDDVKYYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22651		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIAASYSFDY**WGQGTMVTVSS
CL-22652		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**FEYLGAMYXFDY**WGQGTMVTVSS
CL-22653		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**XDSFRKPYSFDY**WGQGTMVTVSS
CL-22654		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IXSIGSTYWFDY**WGQGTMVTVSS
CL-22655		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**LVSIVTKYSFDY**WGQGTMVTVSS
CL-22656		XVTLXESGPALXKPTXTLTLTCTFS**GFXLSTXGMGVG**WIRQPP RKALXWLA**NXWWDDDKYYNPSLXN**RLXISKDTSKNQVVLTMTN MDPVDTAXYYCAR**XXXXXMXYSFDY**WGQGTMVTXSX
CL-22658		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**LEPIPMTYSFDY**WGQGTMVTVSS
CL-22659		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IEWSAITYSFDY**WGQGTMVTVSS
CL-22660		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IECTXNRYXFDY**WGQGTMVTVSS
CL-22661		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IECNSTTYSFDY**WGQGTMVTVSS
CL-22664		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**LASLCATYYFDY**WGQGTMVTVSS
CL-22665		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IGWRLRMYSFDY**WGQGTMVTVSS
CL-22666		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN

Clone	SEQ ID NO:	VH
		MDPVDTATYYCAR**IVSIGGTYSFDY**WGQGTMVTVSS
CL-22668		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**VESIGTTYYFDY**WGQGTMVTVSS
CL-22669		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**YAPIGTTYWFDY**WGQGTMVTVSS
CL-22670		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESTRTTYLFDY**WGQGTMVTVSS
CL-22671		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESTGTAYSFDY**WGQGTMVTVSS
CL-22672		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IASVGTSYSFDY**WGQGTMVTVSS
CL-22673		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**EESTCPTYYFDY**WGQGTMVTVSS
CL-22675		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**TESIDRAYSFDY**WGQGTMVTVSS
CL-22677		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IGSTGISYSFDY**WGQGTMVTVSS
CL-22678		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**RESIGTTYSFDY**WGQGTMVTVSS
CL-22679		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**KVTIETAYYFDY**WGQGTMVTVSS
CL-22680		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATXYCAR**FASIGTTYSFDY**WGQGTMVTVSS
CL-22681		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**MKSIATTYSFDY**WGQGTMVTVSS
CL-22682		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESRRATYSFDY**WGQGTMVTVSS
CL-22683		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IGXIGSAYTFDY**WGQGTMVTVSS
CL-22685		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**TGSGVTTYSFDY**WGQGTMVTVSS
CL-22688		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN

Clone	SEQ ID NO:	VH
		MDPVDTATYYCAR**IGSIESAYSFDY**WGQGTMVTVSS
CL-22689		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**VYSKGTTYSFDY**WGQGTMVTVSS
CL-22691		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**FEALGLSYSFDY**WGQGTMVTVSS
CL-22692		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATXYCAR**RGTIRTTYSFDY**WGQGTMVTVSS
CL-22694		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IYWIGPTYCFDY**WGQGTMVTVSS
CL-22695		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESMRTTYSFDY**WGQGTMVTVSS
CL-22696		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IRSIVTTYSFDY**WGQGTMVTVSS
CL-22698		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**TQSSAMTYSFDY**WGQGTMVTVSS
CL-22702		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**NESMGTSYSFDY**WGQGTMVTVSS
CL-22703		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IEFVRAIYSFDY**WGQGTMVTVSS
CL-22704		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**FESLGETYSFDY**WGQGTMVTVSS
CL-22705		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IEAIGNQYSFDY**WGQGTMVTVSS
CL-22706		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**KDSMVTTYLFDY**WGQGTMVTVSS
CL-22707		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**VEWQGSTYSFDY**WGQGTMVTVSS
CL-22708		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYMFDY**WGQGTMVTVSS
CL-22709		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**CASVSTTYCFDY**WGQGTMVTVSS
CL-22710		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN

Clone	SEQ ID NO:	VH
		MDPVDTATYYCAR**ILSIGNTYSFDY**WGQGTMVTVSS
CL-22711		EVTLRESGPALVKPTQTLTLTCTFF**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWCDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESNGNTYSFDY**WGQGTMVTVSS
CL-22712		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**RDSTGTPYSFDY**WGQGTMVTVSS
CL-22713		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**VESIVTTYYFDY**WGQGTMVTVSS
CL-22714		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**LEKFGRTYPFDY**WGQGTMVTVSS
CL-22715		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**FKSNRPSYSFDY**WGQGTMVTVSS
CL-22716		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSXKN**RLXISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESLDTTYXFDX**XGQGXMXTVSS
CL-22717		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IXATGMLYSFDY**WGQGTMVTVSS
CL-22718		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIETTYXFDY**WGQGTMVTVSS
CL-22719		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IEXMAPMYSFDY**WGQGTMVTVSS
CL-22720		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**VRPLVTIYSFDY**WGQGTMVTVSS
CL-22721		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IDSVWTTYSFDY**WGQGTMVTVSS
CL-22722		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**VEEIGNTYNFDY**WGQGTMVTVSS
CL-22723		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**RGLFRIRYSFDY**WGQGTMVTVSS
CL-22724		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RXTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22725		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IEVIGTAYSFDY**WGQGTMVTVSS
CL-22726		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN

Clone	SEQ ID NO:	VH
		MDPVDTATYYCAR**LDVIGMLYAFDY**WGQGTMVTVSS
CL-22728		EVTLRESGPALVKPTKTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IMSIGSSYXFDY**WGQGTMVTVSS
CL-22729		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IDWIGTTYSFDY**WGQGTMVTVSS
CL-22730		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**NSSIGSTYSFDY**WGQGTMVTVSS
CL-22731		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESPGTWYSFDY**WGQGTMVTVSS
CL-22732		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IEWIGITYCFDY**WGQGTMVTVSS
CL-22733		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IEXLGTTYSFDY**WGQGTMVTVSS
CL-22734		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**KELTCSTYSFDY**WGQGTMVTVSS
CL-22736		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IEXIRMRYSFDY**WGQGTMVTVSS
CL-22737		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**KAAIATLYLFDY**WGQGTMVTVSS
CL-22738		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**RRPIVTTYSFDY**WGQGTMVTVSS
CL-22740		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTVYSFDY**WGQGTMVTVSS
CL-22741		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IASIGSMYSFDY**WGQGTMVTVSS
CL-22742		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESRATTYSFDY**WGQGTMVTVSS
CL-22743		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**NVWLGTTYSFDY**WGQGTMVTVSS
CL-22744		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IMSIGTAYSFDY**WGQGTMVTVSS
CL-22745		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN

Clone	SEQ ID NO:	VH
		MDPVDTATYYCAR**IKWIWTTYSFDY**WGQGTMVTVSS
CL-22746		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IEXRGSTYIFDY**WGQGTMVTVSS
CL-22759		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCXR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22763		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN XDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-22806		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYXFXY**WGQGTMVTVSS
CL-22812		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATXYCAR**IESIGTTYSFDY**XGQGTMVTVSS
CL-22819		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAX**IESIGTTYSFDY**WGQGTMVTVSS
CL-22833		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYXCAR**IESIGTTYSXDY**WGQGTXVTVSS
CL-25629		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRKPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-25633		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN VDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-25645		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKELEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-25649		EVTLRESGPALVKPTQTLTLTCTFS**GFSLATSGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-25656		EVTLRESGPALVKPTQTLTLTCTFS**GFRLSTYGMGVG**WIRKPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-25657		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTANYYCAR**IASIPTMYAFDY**WGQGTMVTVSS
CL-25676		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWMA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-25679		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDHDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-25684		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTSGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKT**RLTISKDTSKNQVVLTMTN

Clone	SEQ ID NO:	VH
		MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-25696		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGVGVG**WIRQPP GKALEWLA**NIWWDDDKYYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-25697		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRKPP GKALEWLA**NIWWDDDKYYNPSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-25699		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTSGMGVG**WIRQPP GKALEWLA**NIWWDDDRYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-25700		EVTLRESGPALVKPTQTLTLTCTFS**GFSLMTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-25702		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNTSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-25710		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLE**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-25738		EVTLKKSGPALVKPXQTLTLTCTFS**GFSLSTYGMGVG**WIRXPP GKGLEWLA**NIWWDDDKYYNPSLKN**RLTIXKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-25739		EVTLKESGPALVKPTXTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-25745		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSX
CL-25749		EVTLRESGPALVKPTXTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-25755		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**MKSIGSTYSFDY**WGQGTMVTVSS
CL-25763		EVTLKESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-25765		EVTLRESGPALVKPTXTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGXMVTVSS
CL-25769		EVTLKESGPALVKPTXTLTLTCTFS**GFSLSTYGMGVG**WIRHPP GKALEWLA**NIWWNNDNYYNPSLKN**RLTINKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-25773		EVTLKESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEGLA**NIWWDDDKYYNPSLKN**RLTINKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-25789		EVTLRESGPALVKPTHTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN

Clone	SEQ ID NO:	VH
		MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-25791		EVTLKESGPALVKPTQTLTLTCTFS**GFRLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-25797		EVTLXESGPALVKPTXTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-25815		EVTLKESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTINKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-28144		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESGWTTYSFDY**WGQGTMVTVSS
CL-28145		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIWTSYSFDY**WGQGTMVTVSS
CL-28146		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IVSSWTIYSFDY**WGQGTMVTVSS
CL-28147		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IYSSGTVYSFDY**WGQGTMVTVSS
CL-28148		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESLGISYSFDY**WGQGTMVTVSS
CL-28149		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESTGTSYSFDY**WGQGTMVTVSS
CL-28151		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESLGPSYSFDY**WGQGTMVTVSS
CL-28152		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGSSYSFDY**WGQGTMVTVSS
CL-28155		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IVSIGWSYSFDY**WGQGTMVTVSS
CL-28156		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IYSDWTIYSFDY**WGQGTMVTVSS
CL-28157		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSWITYSFDY**WGQGTMVTVSS
CL-28160		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESEWTTYNFDY**WGQGTMVTVSS
CL-28161		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN

Clone	SEQ ID NO:	VH
		MDPVDTATYYCAR**IESSPTTYSFDY**WGQGTMVTVSS
CL-28162		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGISYSFDY**WGQGTMVTVSS
CL-28163		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSATIYSFDY**WGQGTMVTVSS
CL-28164		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESTGTTYSFDY**WGQGTMVTVSS
CL-28167		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTSYSFDY**WGQGTMVTVSS
CL-28169		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IVSTWTTYSFDY**WGQGTMVTVSS
CL-28170		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESLGTSYNFDY**WGQGTMVTVSS
CL-28173		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESTWWTYSFDY**WGQGTMVTVSS
CL-28175		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSGWSYAFDY**WGQGTMVTVSS
CL-28177		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGYSYSFDY**WGQGTMVTVSS
CL-28180		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWMA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IETLGISYSFDY**WGQGTMVTVSS
CL-28181		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESMWSSYSFDY**WGQGTMVTVSS
CL-28182		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IETIGTSYSFDY**WGQGTMVTVSS
CL-28186		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IVSDVTTYSFDY**WGQGTMVTVSS
CL-28187		EVTLRESGPALVKPTKTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESFGTSYSFDY**WGQGTMVTVSS
CL-28189		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IKSIGWTYSFDY**WGQGTMVTVSS
CL-28190		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN

Clone	SEQ ID NO:	VH
		MDPVDTATYYCAR**IESNFWSYSFDY**WGQGTMVTVSS
CL-28195		EVTLRESGPALVKPTHTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IMSLETRYDFYY**WGQGTMVTVSS
CL-28196		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESVETSYNFDY**WGQGTMVTVSS
CL-28198		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESFWTTYSFDY**WGQGTMVTVSS
CL-28204		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESMGTSYSFDY**WGQGTMVTVSS
CL-28205		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIWSSYSFDY**WGQGTMVTVSS
CL-28208		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGFSYSFDY**WGQGTMVTVSS
CL-28212		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESVGPSYSFDY**WGQGTMVTVSS
CL-28213		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESLGWTYSFDY**WGQGTMVTVSS
CL-28215		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESDWTTYSFDY**WGQGTMVTVSS
CL-28219		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGPSYSFDY**WGQGTMVTVSS
CL-28233		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESLVTSYDFDY**WGQGTMVTVSS
CL-28235		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESVGTSYNFDY**WGQGTMVTVSS
CL-29595		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESTEASYSFDY**WGQGTMVTVSS
CL-29596		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESNGASYSFDY**WGQGTMVTVSS
CL-29597		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSVTTYSFDY**WGQGTMVTVSS
CL-29598		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDNYYNPSLKN**RLTISKDTSKNQVVLTMTN

Clone	SEQ ID NO:	VH
		MDPVDTATYYCAR**XESXWTSYSFDY**WGQGTMVTVSS
CL-29600		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGASYSFDY**WGQGTMVTVSS
CL-29601		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESTGRSYGFDY**WGQGTMVTVSS
CL-29607		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IETLGTSYSFDY**WGQGTMVTVSS
CL-29608		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESLGTTYSFDY**WGQGTMVTVSS
CL-29611		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIPTAYSFDY**WGQGTMVTVSS
CL-29612		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESLGTTYSFDY**WGQGTMVTVSS
CL-29613		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**LESIATTYSFDY**WGQGTMVTVSS
CL-29614		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGPSYSFDY**WGHGTMVTVSS
CL-29617		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSYTSYSFDY**WGQGTMVTVSS
CL-29618		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESTWTSYSFDY**WGQGTMVTVSS
CL-29620		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSVTNYQFDY**WGQGTMVTVSS
CL-29621		EVTLRESGPALVKPTQTLTLICTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTSYSFDY**WGQGTMVTVSS
CL-29625		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESLGPAYSFDY**WGQGTMVTVSS
CL-29627		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSNNQVVLTMTN MDPVDTATYYCAR**IESFGSSYSFDY**WGQGTMVTVSS
CL-29629		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSETTYTFDY**WGQGTMVTVSS
CL-29630		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN

Clone	SEQ ID NO:	VH
		MDPVDTATYYCAR**IESIWTTYSFDY**WGQGTMVTVSS
CL-29631		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**LLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESFGTSYSFDY**WGQGTMVTVSS
CL-29632		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IASXGTSYSFDY**WGQGTMVTVSS
CL-29634		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDEKYYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTSYSFDY**WGQGTMVTVSS
CL-29635		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSPTSYSFDY**WGQGTMVTVSS
CL-29636		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTSGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGWSYAFDY**WGQGTMVTVSS
CL-29637		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGWTYSFDY**WGQGTMVTVSS
CL-29638		EVTLRESGPALVKPTQTLTLTCTFS**GFSLATSGVSVL**WIRQPP GKALEWLA**NIWWDDGXYYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESFGTSYSFDY**WGQGTMVTVSS
CL-29639		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESLWTTYSFDY**WGQGTMVTVSS
CL-29643		EVTLRESGPALVKPTQTLTLTCTFS**GFSLDTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSGYTYSFDY**WGQGTMVTVSS
CL-29644		EVTLRESGPALVKPTQTLTLTCTFS**GFSLTTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSGSSYSFDY**WGQGTMVTVSS
CL-29645		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**VASSWVEYSFDY**WGQGTMVTVSS
CL-29647		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESFGTSYSFDY**WGQGTMVTVSS
CL-29648		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSGTTYSFDY**WGQGTMVTVSS
CL-29649		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRKPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESMGISYSFDY**WGQGTMVTVSS
CL-29651		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGIAYSFDY**WGQGTMVTVSS
CL-29654		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIXWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN

Clone	SEQ ID NO:	VH
		MDPVDTATYYCAR**IESIVTTYSFDY**WGQGTMVTVSS
CL-29658		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESGWTIYSFDY**WGQGTMVTVSS
CL-29662		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESLGPTYSFDY**WGQGTMVTVSS
CL-29663		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESVGTSYSFDY**WGQGTMVTVSS
CL-29665		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTSGMGVG**WIRQPP GKALEWLA**NIWWDDDQYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSWTTYSFDY**WGQGTMVTVSS
CL-29667		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESFGPSYSFDY**WGQGTMVTVSS
CL-29668		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSGTSYSFDY**WGQGTMVTVSS
CL-29673		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**XXSIVTTYSFDY**WGQGTMVTVSS
CL-29674		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYSTSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTSYSFDY**WGQGTMVTVSS
CL-29676		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**LIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESVGTSYSFDY**WGQGTMVTVSS
CL-29678		EVTLKESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IGSSGTTYSFDY**WGQGTMVTVSS
CL-29679		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNTSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IDSFGAIYSFDY**WGQGTMVTVSS
CL-29680		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKELEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVETATYYCAR**IESIGTAYNFDY**WGQGTMVTVSS
CL-29683		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESLGTSYSFDY**WGQGTMFTVSS
CL-29688		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTSGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESLGTSYSFDY**WGQGTMVTVSS
CL-29689		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IEAKGTTYSFDY**WGQGTMVTVSS
CL-29699		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN

Clone	SEQ ID NO:	VH
		MDPVDTATYYCAR**IESRGTSYSFDY**WGQGTMVTVSS
CL-29706		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESMGPTYSFDY**WGQGTMVTVSS
CL-29707		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIETSYSFDY**WGQGTMVTVSS
CL-29709		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYRAR**IESLGTTYSFDY**WGQGTMVTVSS
CL-29711		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRHPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESMGTSYSFDY**WGQGTMVTVSS
CL-29713		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESMGTTYSFDY**WGQGTMVTVSS
CL-29714		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAL**IESSGTTYSFDY**WGQGTMVTVSS
CL-29720		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESKGVSYSFDY**WGQGTMVTVSS
CL-29721		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIPTTYSFDY**WGQGTMVTVSS
CL-29727		EVTLRESXPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKELEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESLGTTYSFDY**WGQGTMVTVSS
CL-29728		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESLGITYSFDY**WGQGTMVTVSS
CL-29730		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESMGRSYSFDY**WGQGTMVTVSS
CL-29731		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIATSYSFDY**WGQGTMVTVSS
CL-29732		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYNFDY**WGQGTMVTVSS
CL-29735		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESMGPMYSFDY**WGQGTMVTVSS
CL-29736		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTAYSFDY**WGQGTMVTVSS
CL-29738		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN

Clone	SEQ ID NO:	VH
		MDPVDTATYYCAR**MESSWTTYSFDY**WGQGTMVTVSS
CL-29739		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESTGATYSFDY**WGQGTMVTVSS
CL-29740		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESMGPKYSFDY**WGQGTMVTVSS
CL-29742		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESMGMSYSFDY**WGQGTMVTVSS
CL-29744		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGLSYSFDY**WGQGTMVTVSS
CL-29745		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYRAR**IESLGMSYSFDY**WGQGTMVTVSS
CL-29746		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**LXSTGTNYSFDY**WGQGTMVTVSS
CL-29748		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSDTIYSFDY**WGQGTMVTVSS
CL-29749		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTSGMGVD**WIRQPP GKALEWLA**LIDWDDDIHYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-29751		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESVGTTYSFDY**WGQGTMVTVSS
CL-29753		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWYDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESTGTTYSFDY**WGQGTMVTVSS
CL-29756		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**NESFGRMYXFDY**WGQGTMVTVSS
CL-29757		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**XESIGTTYSFDY**WGQGTMVTVSS
CL-29758		EVTLRESGPSLVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESFGTTYSFDY**WGQGTMVTVSS
CL-29759		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IETLGTAYSFDY**WGQGTMVTVSS
CL-29761		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESFGSSYSFDY**WGQGTMVTVSS
CL-29763		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN

Clone	SEQ ID NO:	VH
		MDPVDTATYYCAR**IESGPTTYSFDY**WGQGTMVTVSS
CL-29765		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTMYSFDY**WGQGTMVTVSS
CL-29771		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESTXTTYSXDY**WGQGTMVTVSS
CL-29772		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGITYSFDY**WGQGTMVTVSS
CL-29773		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESMETTYSFDY**WGQGTMVTVSS
CL-29776		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESNAITYSFDY**WGQGTMVTVSS
CL-29777		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSETTYMFDY**WGQGTMVTVSS
CL-29780		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLT**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESMGTSYSFDY**WGQGTMVTVSS
CL-29786		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IYSIGTSYSFDY**WGQGTMVTVSS
CL-33292		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSPWTYSFDY**WGQGTMVTVSS
CL-33332		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESRPDTYSFDY**WGQGTMVTVSS
CL-33361		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IQSSASNYEFDY**WGQGTMVTVSS
CL-33368		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IQSGWTNXEFDY**WGQGTMVTVSS
CL-33583		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IQSIWTRYDFDY**WGQGTMVTVSS
CL-33588		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IQSFATNYEFDY**WGQGTMVTVSS
CL-33591		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESVPWSYSFDY**WGQGTMVTVSS
CL-33592		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN

Clone	SEQ ID NO:	VH
		MDPVDTATYYCAR**IESTPFSYSFDY**WGQGTMVTVSS
CL-33599		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSWTSYDFDY**WGQGTMVTVSS
CL-33601		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IQSSSTNYEFDY**WGQGTMVTVSS
CL-33612		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IQSSWRRYEFDY**WGQGTMVTVSS
CL-33616		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IKTSATNYDFDY**WGQGTMVTVSS
CL-33618		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSAFSYNFDY**WGQGTMVTVSS
CL-33626		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVFLTMTN MDPVDTATYYCAR**IVSSLTEYNFDY**WGQGTMVTVSS
CL-33627		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESRVDSYSFDY**WGQGTMVTVSS
CL-33628		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESTWTSYDFDY**WGQGTMVTVSS
CL-33654		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESVAWRYDFDY**WGQGTMVTVSS
CL-33657		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESLPTSYNFDY**WGQGTMVTVSS
CL-33663		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSPFTYSFDY**WGQGTMVTVSS
CL-33665		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESDYTKYDFDY**WGQGTMVTVSS
CL-33667		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESLPTRYDFDY**WGQGTMVTVSS
CL-33674		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWMA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIPTSYSFDY**WGQGTMVTVSS
CL-33679		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESKPTSYSFDY**WGQGTMVTVSS
CL-33680		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTSGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN

Clone	SEQ ID NO:	VH
		MDPVDTATYYCAR**IESSWTTYSFDY**WGQGTMVTVSS
CL-33687		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTSYSFDY**WGQGTMVTVSS
CL-33688		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTFKNQVVLTMTN MDPVDTATYYCAR**IESIPTSYSFDY**WGQGTMVTVSS
CL-33690		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDETYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESDFTSYMFDY**WGQGTMVTVSS
CL-33693		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESNWWSYSFDY**WGQGTMVTVSS
CL-33696		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSFTTYSFDY**WGQGTMVTVSS
CL-33698		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESXGXSYSFDY**WGQGTMVTVSS
CL-33705		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESRLDTYSFDY**WGQGTMVTVSS
CL-33707		EVTLRESGPALVKPTQTLTLTCTFS**GFSLDTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTSYSFDY**WGQGTMVTVSS
CL-33709		EVTLRESGPALVKPTQTLTLTCTFS**GFSLATSGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIPWSYSFDY**WGQGTMVTVSS
CL-33711		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESTGYSYSFDY**WGQGTMVTVSS
CL-33712		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRKPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSWTSYSFDY**WGQGTMVTVSS
CL-33722		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSFFSYSFDY**WGQGTMVTVSS
CL-33725		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDEYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESLGTSYSFDY**WGQGTMVTVSS
CL-33734		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESLPGSYDFDY**WGQGTMVTVSS
CL-33735		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKELEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESNPLTYSFDY**WGQGTMVTVSS
CL-33741		EVTLRESGPALVKPTKTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN

Clone	SEQ ID NO:	VH
		MDPVDTATYYCAR**IESIGISYSFDY**WGQGTMVTVSS
CL-33743		EVTLRESGPALVKPTQTLTLTCTFS**GFSLATYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESLPTSYSFDY**WGQGTMVTVSS
CL-33745		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSPFAYSFDY**WGQGTMVTVSS
CL-33746		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSWFTYAFDY**WGQGTMVTVSS
CL-33747		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IETIXPKYSFDY**WGQGTMVTVSS
CL-33754		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSWTTYAFDY**WGQGTMVTVSS
CL-33755		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSEWTYSFDY**WGQGTMVTVSS
CL-33756		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IQSSWTTYEFDY**WGQGTMVTVSS
CL-33760		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IETLGSSYSFDY**WGQGTMVTVSS
CL-33766		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRKPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSFTSYSFDY**WGQGTMVTVSS
CL-33770		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESGGISYSFDY**WGQGTMVTVSS
CL-33773		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESLPTTYSFDY**WGQGTMVTVSS
CL-33777		EVTLRESGPALVKPTQTLTLTCTFS**GFSLYTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESVGTSYSFDY**WGQGTMVTVSS
CL-33781		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSWYSYNFDY**WGQGTMVTVSS
CL-33782		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSWRSYCFDY**WGQGTMVTVSS
CL-33784		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSPMSYSFDY**WGQGTMVTVSS
CL-33789		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN

Clone	SEQ ID NO:	VH
		MDPVDTATYYCAR**IESLPTSYCFDY**WGQGTMVTVSS
CL-33791		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSWWTYSFDY**WGQGTMVTVSS
CL-33794		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESRPTSYCFDY**WGQGTMVTVSS
CL-33795		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESVPTSYSFDY**WGQGTMVTVSS
CL-33798		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTSGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IQSDGPMYSFDY**WGQGTMVTVSS
CL-33802		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESTGASYSFDY**WGQGTMVTVSS
CL-33813		EVTLRESGPALVKPTQTLTLTCTFS**GFSLYTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESLPTSYSFDY**WGQGTMVTVSS
CL-33814		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDTVDTATYYCAR**IESTPWSYSFDY**WGQGTMVTVSS
CL-33816		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSWTSYAFDY**WGQGTMVTVSS
CL-33823		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKELEWLA**NIWWDDDKYYNPSLNN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSGPKYSFDY**WGQGTMVTVSS
CL-33833		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGWSYSFDY**WGQGTMVTVSS
CL-33840		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSAWTYSFDY**WGQGTMVTVSS
CL-33842		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESYGPKYSFDY**WGQGTMVTVSS
CL-33844		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKT**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IETSWWKYSFDY**WGQGTMVTVSS
CL-33847		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNLSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSPTSYSFDY**WGQGTMVTVSS
CL-33849		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IVSSYFTYSFDY**WGQGTMVTVSS
CL-33858		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDEEYYNPSLKN**RLTISKDTSKNQVVLTMTN

Clone	SEQ ID NO:	VH
		MDPVDTATYYCAR**IESIGISYSFDY**WGQGTMVTVSS
CL-33861		EVTLRESGPALVKPTQTLTLTCTFS**GFSLYTSGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSWTTYSFDY**WGQGTMVTVSS
CL-33862		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIPTRYDFDY**WGQGTMVTVSS
CL-41180		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNRVVLTMTN MDPVDTATYYCAR**IVSDWTTYSFDY**WGQGTMVTVSS
CL-41185		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTD MDPVDTATYYCAR**IESSWTTYSFDY**WGQGTMVTVSS
CL-41193		RXHWRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IETFGPKYSFDY**WGQGTMVTVSS
CL-41204		RGNTEESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTTTYYCAR**IESLPTSYSFDY**WGQGTMVTVSS
CL-41213		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESLXTNYSFDY**WGQGTMVTVSS
CL-41224		EVTLREGGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESHWWSYAFDY**WGQGTMVTVSS
CL-41229		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSFTSYSFDY**WGQGTMVTEXC
CL-41232		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESHWWSYAFDY**WGQGTMVTVSS
CL-41233		RXHXGESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSWTTYSFDY**WGQGTMVTVSS
CL-41246		EVTLRESGPALAKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESHWWSYAFDY**WGQGTMVTVSS
CL-41252		EVTLRESGPALVKPTQTLTLTCAFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSWTTYSFDY**WGQGTMVTVSS
CL-41255		EVTLRESGPALVEPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESNPWKYSFDY**WGQGTMVTVSS
CL-41257		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESNWRTYSFDY**WGQGTMVTVSS
CL-41260		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN

Clone	SEQ ID NO:	VH
		MDPVDTATYYCAR**IESSFTSYSFDY**WGQGTMVTVSS
CL-41261		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESHWWSYAFDY**WGQGTMVTVSI
CL-41262		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IVSDWTTYSFDY**WGQGTMVTVSS
CL-41268		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESLGWSYSFDY**WGQGTMVTVSS
CL-41269		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESLPTSYSFDY**WGQGTMVTVSS
CL-41270		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSWTTYSFDY**WGQGTMVTVSS
CL-41272		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESNPWKYSFDY**WGQGTMVTVSS
CL-41273		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IETFGPKYSFDY**WGQGTMVTVSS
CL-41276		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGIG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESMGPKYAFDY**WGQGTMVTVSS
CL-41283		EVTLRESGPALVKPTQTLTLTRTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIPTSYSFDY**WGQGTMVTVSS
CL-41325		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRKPP GKALEWLA**NIWWDGDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSGPKYSFDY**WGQGTMVTVSS
CL-41342		EVTLRESGPALVKPTQTLTLACTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESVWTKYYFDX**GGQGTMVTVSS
CL-41348		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYEMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTPKNQVVLTMTN MDPVDTATYYCAR**IESVWTRYDFDY**WGQGTMVKXVV
CL-41353		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESLGTSYSFDY**WGQGTMVTVSS
CL-41358		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGPKYSFDY**WGQGTMVTVSS
CL-41361		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESVWTRYDFDY**WGQGTMVTVSS
CL-41362		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN

Clone	SEQ ID NO:	VH
		MDPVDTATYYCAR**IETMGPKYSFDY**WGQGTMVTVSS
CL-41365		RGNTRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALKWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGPKYSFDY**WGQGTMVTVSS
CL-41366		EVTLRESGPAQVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIPTSYSFDY**WGQGTMVTVSS
CL-41367		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRKPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSGPKYSFDY**WGQGTMVTVSS
CL-41368		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGPKYSFDX**GGQGTMVTVSS
CL-41369		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIPTSYSFDY**WGQGTMVTVSS
CL-41376		EVKLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IQTIGTNYSFDY**WGQGTMVTVSS
CL-41377		EGQLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSWTSYSFDY**WGQGTMVTVSS
CL-41381		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSWTSYSFDY**WGQSTMVTVSS
CL-41385		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSWTSYSFDY**WGQGTIVTVSS
CL-41399		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKS**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSWTSYSFDY**WGQGTMVTVSS
CL-41405		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTAAYYCAR**IETIGPKYSFDY**WGQGTMVTVSS
CL-41411		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IQSGWTNYEFDY**WGQGTMVTVVV
CL-41420		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IQSMWTRYDFDY**WGQGTMVTVSS
CL-41425		RXHXRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSGPKYSFDY**WGQGTMVTVSS
CL-41427		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDAATYYCAR**IQSGWTNYEFDY**WGQGTMVTVSS
CL-41436		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN

Clone	SEQ ID NO:	VH
		MDPVDTATYYCAR**IESSWTSYSFDY**WSQGTMVTVSS
CL-41439		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IETIGPKYSFDY**WGQGTMVTVSS
CL-41443		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSGPKYSFDY**WGQGTMVTVSS
CL-41446		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSWTSYSFDY**WGQGTMVTVSS
CL-41447		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQAVLTMTN MDPVDTATYYCAR**IQSGWTNYEFDY**WGQGTMVTVSS
CL-41448		RGNTEKSGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESSWTSYSFDY**WGQGTMVTVSS
CL-41449		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IQSGWTNYEFDY**WGQGTMVTVSS
CL-41452		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMEXVVR
CL-41459		EVTLRESGPALVKPTQTLTLTCTFS**GFILSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-41463		EVTLRESGPALVKSTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
CL-41465		EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPP GKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTN MDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS

Table 47 provides a list of amino acid sequences of VL regions of affinity matured humanized PDGF antibodies derived from hBDI-9E8.4. Amino acid residues of individual CDRs of each VL sequence are indicated in bold.

Table 47. List of Amino Acid Sequences Of Affinity Matured hBDI-9E8.4 VL Variants

Clone	SEQ ID NO:	VL
CL-22656		EIVLTQSXGTLSLSPGXRXTLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDIV**FGGGTKVEIK
CL-22715		EIVLXQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDIV**FGGGTKVEIK
CL-22747		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIWYSYVS**WYQQKP GQAPRLVIY**ADDQRPT**GIPDRFSGSGSGTDFTLTISRLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QSYDINKDLT**FGGGTKVEIK
CL-22748		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIGYSYVS**WYQQKP GQAPRLVIY**AADQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYGIIIDIT**FGGGTKVEIK
CL-22749		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIEHAYVS**WYQQKP GQAPRLLIY**GADHRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDFNNTIT**FGGGTKVEIK
CL-22750		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGHCYVS**WYQQKP GQAPRLVIY**AADHRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYGKNIDGT**FGGGTKVEIK
CL-22752		EIVLTQSPGTLSLSPGERATLSC**RASSGDIGDFCVS**WYQQKP GQAPRLLIY**VDDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGRRLDIT**FGGGTKVEIK
CL-22753		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIVLPYVS**WYQQKP GQAPRLVIY**AADWRPT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYDITIDTV**FGGGTKVEIK
CL-22754		EIVLTQSPGTLSLSPGERATLSC**RASSGSIGYECVS**WYQQKP GQAPRLVIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIDRQIV**FGGGTKVEIK
CL-22755		EIVLTQSPGTLSLSPGERATLSC**RASSGSIVGSYVS**WYQQKP GQAPRLVIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYGVHIDIT**FGGGTKVEIK
CL-22756		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGHSDVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIGQV**FGGGTKVEIK
CL-22758		EIVLTQSPGTLSLSPGERATLSC**RASSGSIGHPYVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGCHIYNV**FGGGTKVEIK
CL-22759		EIVLTQSPGTLSLSPGERATLSC**ERSSGSICDTYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIYIHIV**FGGGTKVEIK
CL-22760		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGYSCVS**WYQQKP GQAPRLVIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYGIDIVIV**FGGGTKVEIK
CL-22761		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIGYSDVS**WYQQKP GQAPRLLIY**ADDKRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIDKYIV**FGGGTKVEIK
CL-22763		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWHFYVS**WYQQKP GQAPRLVIY**AADHRPT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYGTNIEIV**FGGGTKVEIK
CL-22764		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGXADVS**WYQQKP GQAPRLVIY**VDDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGEYIDRT**FGGGTKVEIK
CL-22765		EIVLTQSPGTLSLSPGERATLSC**RASSGSIGGSYVS**WYQQKP GQAPRLLIY**ADDHRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYGINIGTV**FGGGTKVEIK
CL-22766		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIECDFVS**WYQQKP GQAPRLVIY**ADDHRAS**GIPDRFSGSGSGTDFTLTISRLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QQYGINNDIT**FGGGTKVEIK
CL-22767		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGCSYVS**WYQQKP GQAPRLVIY**GDDQRPT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGINKEIT**FGGGTKVEIK
CL-22768		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIGHSRVS**WYQQKP GQAPRLVIY**VDDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDNNIATV**FGGGTKVEIK
CL-22769		EIVLTQSPGTLSLSPGERATLSC**ERSSGSINHCHVS**WYQQKP GQAPRLVIY**AADXRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIILDIT**FGGGTKVEIK
CL-22770		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLVIY**ADDHRPT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYDFDIDIT**FGGGTKVEIK
CL-22771		EIVLTQSPGTLSLSPGERATLSC**RASSGSIRYTYVS**WYQQKP GQAPRLVIY**AADEPPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINRNIV**FGGGTKVEIK
CL-22772		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGCTYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGISTVLV**FGGGTKVEIK
CL-22773		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIRYCYVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDVDIV**FGGGTKVEIK
CL-22774		EIVLTQSPGTLSLSPGERATLSC**RASSGSISQSYVS**WYQQKP GQAPRLVIY**ADDLRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYGINIDIT**FGGGTKVEIK
CL-22775		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIFYGCVS**WYQQKP GQAPRLLIY**ADDQRPT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYDINIVIT**FGGGTKVEIK
CL-22776		EIVLTQSPGTLSLSPGERATLSC**RASSGSIWYSYVS**WYQQKP GQAPRLVIY**AADQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINKYAV**FGGGTKVEIK
CL-22777		EIVLTQSPGTLSLSPGERATLSC**RASSGDISYSYVS**WYQQKP GQAPRLVIY**VDDERAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYDIYKDLT**FGGGTKVEIK
CL-22778		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLVIY**ADDXRPT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYDSNIDIV**FGGGTKVEIK
CL-22779		EIVLTQSPGTLSLSPGERATLSC**ERSSGSICYXYVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYDVNLEHT**FGGGTKVEIK
CL-22780		EIVLTQSPGTLSLSPGERATLSC**RASSGDIRHCYVS**WYQQKP GQAPRLLIY**PDDLRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDIV**FGGGTKVEIK
CL-22781		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLVIY**VDDHRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYGTSLDNT**FGGGTKVEIK
CL-22782		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGHSYVS**WYQQKP GQAPRLVIY**AADHRPT**GIPDRFSGSGSGTDFTLTISRLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QQYGVNIYIT**FGGGTKVEIK
CL-22783		EIVLTQSPGTLSLSPGERATLSC**RASSGSIRYSYVS**WYQQKP GQAPRLVIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYDINKVIV**FGGGTKVEIK
CL-22784		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGKPTSP**WYQQKP GQAPRLVIY**SADERPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYGVNRDIV**FGGGTKVEIK
CL-22785		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIGPCYVS**WYQQKP GQAPRLVIY**ADDHRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYDINLVIT**FGGGTKVEIK
CL-22786		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIHYSYVS**WYQQKP GQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGISIDIT**FGGGTKVEIK
CL-22787		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDPYVS**WYQQKP GQAPRLVIY**AADPRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYDISIYIV**FGGGTKVEIK
CL-22788		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIKHCCVS**WYQQKP GQAPRLVIY**LDDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYDISIDIT**FGGGTKVEIK
CL-22789		EIVLTQSPGTLSLSPGERATLSC**RASSGSIVQSYVS**WYQQKP GQAPRLLIY**SDDPRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGLYRDIT**FGGGTKVEIK
CL-22790		EIVLTQSPGTLSLSPGERATLSC**RASSGSISYSYVS**WYQQKP GQAPRLLIY**ADDXRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QHYDIHINIT**FGGGTKVEIK
CL-22791		EIVLTQSPGTLSLSPGERATLSC**RASSGDIGYAHVS**WYQQKP GQAPRLLIY**GDDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGKNSEIT**FGGGTKVEIK
CL-22792		EIVLTQSPGTLSLSPGERATLSC**RASSGSIGHSYVS**WYQQKP GQAPRLLIY**DDDPRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYGINVDIV**FGGGTKVEIK
CL-22794		EIVLTQSPGTLSLSPGERATLSC**RASSGSIGHSCVS**WYQQKP GQAPRLVIY**SADERAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYDLNTLFV**FGGGTKVEIK
CL-22795		EIVLTQSPGTLSLSPGERATLSC**RASSGDIGHXYVS**WYQQKP GQAPRLVIY**AADHRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYGISIAVV**FGGGTKVEIK
CL-22796		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIGLSYVS**WYQQKP GQAPRLVIY**AADQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYDRHLDAT**FGGGTKVEIK
CL-22797		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGCSYVS**WYQQKP GQAPRLLIY**GADHRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYGIDIDIT**FGGGTKVEIK
CL-22798		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDASVS**WYQQKP GQAPRLLIY**AADQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDITIGVV**FGGGTKVEIK
CL-22799		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGYCFVS**WYQQKP GQAPRLVIY**AADLRAS**GIPDRFSGSGSGTDFTLTISRLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QSYGIKIGIT**FGGGTKVEIK
CL-22800		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGYWDVS**WYQQKP GQAPRLLIY**ADDERAS**GIPDRFSGSGSGTDFTLTISRLEPED FSVYYC**QSYGINKDFV**FGGGTKVEIK
CL-22801		EIVLTQSPGTLSLSPGERATLSC**RASSGDIGHTYVS**WYQQKP GQAPRLVIY**TDDLRAS**GIPDRFSGSGSGTDFTLTISRLDPED FAVYYC**QQYDLNIDIV**FGGGTKVEIK
CL-22802		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIGXSHVS**WYQQKP GQAPRLLIY**VDDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIKKGXT**FGGGTKVEIK
CL-22803		EIVLTQSPGTLSLSPGERATLSC**RASSGDIGHSFVS**WYQQKP GQAPRLVIY**ADDHRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGVNIDIT**FGGGTKVEIK
CL-22804		EIVLTQSPGTLSLSPGERATLSC**RASSGSIFQSDVS**WYQQKP GQAPRLVIY**ADDHRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYGKNIYIV**FGGGTKVEIK
CL-22805		EIVLTQSPGTLSLSPGERATLSC**RASSGDIGYSAVS**WYQQKP GQAPRLVXY**VDDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIKLDFV**FGGGTKVEIK
CL-22806		EIVLTQSPGTLSLSPGERATLSC**RASSGSIVYSSVS**WYQQKP GQAPRLVIY**VXDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYDIHIDIT**FGGGTKVEIK
CL-22807		EIVLTQSPGTLSLSPGERATLSC**RASSGSIRDFYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYGINLDNT**FGGGTKVEIK
CL-22808		EIVLTQSPGTLSLSPGERATLSC**ERSSGDISDSHVS**WYQQKP GQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDIT**FGGGTKVEIK
CL-22811		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIALSYVS**WYQQKP GQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGINLDIV**FGGGTKVEIK
CL-22812		EIVLTQSPGTLSLSPGERATLSC**ERSSGDMRYSDVS**WYQQKP GQAPRMVIY**AVDQRAS**GIPDRLSGSGSGTDFTLTISRLEPED FAVYYC**QQYDVGMVLT**FGGGTKVEIK
CL-22813		EIVLTQSPGTLSLSPGERATLSC**RASSGDIGHFYVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGISIDLT**FGGGTKVEIK
CL-22815		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIDHSYVS**WYQQKP GQAPRLVIY**ADDPRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGLNIDLT**FGGGTKVEIK
CL-22816		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIRHSCVS**WYQQKP GQAPRLVIY**ADDHRAS**GIPDRFSDSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDIV**FGGGTKVEIK
CL-22818		EIVLTQSPGTLSLSPGERATLSC**RASSGDIWHSYVS**WYQQKP GQAPRLVIY**TDDHRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYGCDKDIT**FGGGTKVEIK
CL-22819		EIVLTQSPGTLSLSPGERATLSC**RASSGSIGDFYVS**WYQQKP GQAPRLVIY**ADDQRPT**GIPDRLSGSGSGTDFTLTISRLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QQYGIHIEIV**FGGGTKVEIK
CL-22820		EIVLTQSPGTLSLSPGERATLSC**RASSGDIGHSAVS**WYQQKP GQAPRLLIY**ADDPRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYGKNKELV**FGGGTKVEIK
CL-22821		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGYSYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYGINSYLV**FGGGTKVEIK
CL-22822		EIVLTQSPGTLSLSPGERATLSC**RASSGDIGPSYVS**WYQQKP GQAPRLLIY**PDDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYDINKELV**FGGGTKVEIK
CL-22823		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWYSYVS**WYQQKP GQAPRLVIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYGKNVDIV**FGGGTKVEIK
CL-22824		EIVLTQSPGTLSLSPGERATLSC**RASSGSILDTYVS**WYQQKP GQAPRLVIY**ADDSRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYDVNVDIV**FGGGTKVEIK
CL-22825		EIVLTQSPGTLSLSPGERATLSC**RASSGSISQSYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDXTIGIV**FGGGTKVEIK
CL-22826		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIGFSYVS**WYQQKP GQAPRLVIY**EDDPRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYGANIEIV**FGGGTKVEIK
CL-22827		EIVLTQSPGTLSLSPGERATLSC**RASSGYISHEYVS**WYQQKP GQAPRLVIY**AADQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYGIHIHVT**FGGGTKVEIK
CL-22828		EIVLTQSPGTLSLSPGERATLSC**RASSGDIGHSYVS**WYQQKP GQAPRLVIY**EDDQRPT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGGNIGIV**FGGGTKVEIK
CL-22829		EIVLTQSPGTLSLSPGERATLSC**RASSGSIDASYVS**WYQQKP GQAPRLLIY**TDDRRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYGIILDIV**FGGGTKVEIK
CL-22830		EIVLTQSPGTLSLSPGERATLSC**RASSGSIGYSYVS**WYQQKP GQAPRLLIY**ADDHRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYGVIIYIT**FGGGTKVEIK
CL-22832		EIVLTQSPGTLSLSPGERATLSC**RASSGDIFYSYVS**WYQQKP GQAPRLVIY**ADDXRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDIV**FGGGTKVEIK
CL-22833		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGYLYVS**WYQQKP GQAPXLVIY**PDDXRAS**GIPDRFSGSGSGXDFTLTISRLEPED XAVYYC**QQYDKTIDIV**FGGGTKVEIK
CL-22834		EIVLTQSPGTLSLSPGERATLSC**RASSGDICESCVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGINKDIV**FGGGTKVEIK
CL-22835		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGYSNVS**WYQQKP GQAPRLLIY**EDDKRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYGXLVPIV**FGGGTKVEIK
CL-22836		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGHSYVS**WYQQKP GQAPRLVIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QQYGIKVDST**FGGGTKVEIK
CL-22837		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIQSLHVS**WYQQKP GQAPRLLIY**ADDXRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGRHIGLV**FGGGTKVEIK
CL-22838		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIGYCYVS**WYQQKP GQAPRLVIY**ADDHRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYDLCIYIT**FGGGTKVEIK
CL-22839		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSHVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIAIT**FGGGTKVEIK
CL-22840		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGYTYVS**WYQQKP GQAPRLLIY**PDDKRPT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIIRPTT**FGGGTKVEIK
CL-22841		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIAHSYVS**WYQQKP GQAPRLVIY**AADYRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYDSHNNIV**FGGGTKVEIK
CL-22842		EIVLTQSPGTLSLSPGERATLSC**RASSGSIRGLRVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGLNFDIV**FGGGTKVEIK
CL-25631		EIVLTQSPGTLSLSPGERATLSC**RASSGSITYYYVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINTDIV**FGGGTKVEIK
CL-25634		EFVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDIV**FGGGTKVEIK
CL-25648		EIVLTQSPGTLSLSPGEXATLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLVIY**VDDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDIV**FGGGTKVEIK
CL-25655		EIVLTQSPGTLSLSPGERXTLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDIV**FGGGTKVEIK
CL-25666		EIVLTQXPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDIV**FGGGTKVEIK
CL-25690		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLVIY**SDDQRPG**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDIV**FGGGTKVEIK
CL-25721		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLVIY**ADDQRPS**GIPDRFSGYGSGTDFTLTISRLEPED FAVYYC**QSYDINIDIV**FGGGTKVEIK
CL-25724		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLLIY**VDDWRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIDIDVV**FGGGTKVEIK
CL-25725		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIDYSYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDIDIV**FGGGTKVEIK
CL-25726		EIVLTQSPGTLSLSPGERATLSC**RASSGSIGYSYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QSYDINTDVV**FGGGTKVEIK
CL-25727		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWYSYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIYIDVT**FGGGTKVEIK
CL-25728		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIGYSYVS**WYQQKP GQAPRLVIY**SDDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDIDIV**FGGGTKVEIK
CL-25729		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIAGYYVS**WYQQKP GQAPRLVIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIIIDIT**FGGGTKVEIK
CL-25730		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGESYVS**WYQQKP GQAPRLVIY**ADDLRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIVIDIX**FGGGTKVEIK
CL-25731		EIVLTQSPGTLSLSPGERATLSC**RASSGSIVYSYVS**WYQQKP GQAPRLVIY**SDDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIYIDIT**FGGGTKVEIK
CL-25732		EIVLTQSPGTLSLSPGERATLSC**RASSGDIVYSYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIDIDVT**FGGGTKVEIK
CL-25733		EIVLTQSPGTLSLSPGERATLSC**RASSGDIWDAYVS**WYQQKP GQAPRLLIY**ADDHRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIIIDIT**FGGGTKVEIK
CL-25734		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGYAYVS**WYQQKP GQAPRLVIY**ADDYRPT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDVDIV**FGGGTKVEIK
CL-25735		EIVLTQSPGTLSLSPGERATLSC**RASSGDILDSYVS**WYQQKP GQAPRLVIY**SDDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDTIIDIT**FGGGTKVEIK
CL-25736		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIDDYYVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIYIDVT**FGGGTKVEIK
CL-25737		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWDFYVS**WYQQKP GQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDVTIDVT**FGGGTKVEIK
CL-25738		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGLSYVS**WYQQKP GQAPRLVIY**SDDLRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDVDIDVT**FGGGTKVEIK
CL-25739		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIFYTYVS**WYQQKP GQAPRLVIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLDIDIT**FGGGTKVEIK
CL-25740		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLLIY**ADDQRAI**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIYVDVV**FGGGTKVEIK
CL-25741		EIVLTQSPGTLSLSPGERATLSC**RASSGDIEGSYVS**WYQQKP GQAPRLVIY**SDDLRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIIIDIV**FGGGTKVEIK
CL-25742		EIVLTQSPGTLSLSPGERATLSC**RASSGDISCSYVS**WYQQKP GQAPRLVIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QSYDINTDIV**FGGGTKVEIK
CL-25743		EIVLTQSPGTLSLSPGERATLSC**RASSGSIGSYYVS**WYQQKP GQAPRLVIY**SDDQRPT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIYIDVV**FGGGTKVEIK
CL-25745		EIVLTQSPGTLSLSPGERATLSC**RASSGDIWYSYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIEIDVT**FGGGTKVEIK
CL-25747		EIVLTQSPGTLSLSPGERATLSC**RASSGDIGYSYVS**WYQQKP GQAPRLLIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIISDIT**FGGGTKVEIK
CL-25748		EIVLTQSPGTLSLSPGERATLSC**RASSGSIDYAYVS**WYQQKP GQAPRLVIY**ADDQRPT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGITIDVV**FGGGTKVEIK
CL-25749		EIVLTQSPGTLSLSPGERATLSC**RASSGSIYFAYVS**WYQQKP GQAPRLVIY**SDDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGITIDVV**FGGGTKVEIK
CL-25751		EIVLTQSPGTLSLSPGERATLSC**RASSGSIWYSYVS**WYQQKP GQAPRLVIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGINVDIV**FGGGTKVEIK
CL-25752		EIVLTQSPGTLSLSPGERATLSC**RASSGDIAHSYVS**WYQQKP GQAPRLVIY**TDDARAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIIVDIV**FGGGTKVEIK
CL-25754		EIVLTQSPGTLSLSPGERATLSC**ERSSGDICQYYVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLNIDVT**FGGGTKVEIK
CL-25756		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIGDSYVS**WYQQKP GQAPRLLIY**NDDDRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLTIDVT**FGGGTKVEIK
CL-25758		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGYSYVS**WYQQKP GQAPRLVIY**ADDQRPT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIIIDIV**FGGGTKVEIK
CL-25759		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGHSYVS**WYQQKP GQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDVDIV**FGGGTKVEIK
CL-25760		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIWDMYVS**WYQQKP GQAPRLVIY**ADDQRPT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIEIDIT**FGGGTKVEIK
CL-25761		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLVIY**GDDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIIIDIT**FGGGTKVEIK
CL-25763		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWESYVS**WYQQKP GQAPRLVIY**ADDERAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGINIDIV**FGGGTKVEIK
CL-25765		EIVLTQSPGTLSLSPGERATLSC**RASSGDIAYSYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDIV**FGGGTKVEIK
CL-25767		EIVLTQSPGTLSLSPGERATLSC**RASSGSIFGAYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QSYGIITDIV**FGGGTKVEIK
CL-25769		EIVLTQSPGTLSLSPGERATLSC**RASSGSIADSLVS**WYQQKP GQAPRLVIY**TDDWRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGINIDVV**FGGGTKVEIK
CL-25770		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIGDSYVS**WYQQKP GQAPRLLIY**TDDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDITIDIV**FGGGTKVEIK
CL-25771		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDYYVS**WYQQKP GQAPRLVIY**SDDQRPT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLDIDIT**FGGGTKVEIK
CL-25772		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIVHSYVS**WYQQKP GQAPRLVXY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIXVDIV**FGGGTKVEIK
CL-25773		EIVLTQSPGTLSLSPGERATLSC**RASSGDIWYSYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGITVDIV**FGGGTKVEIK
CL-25775		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIFYSYVS**WYQQKP GQAPRLVIY**ADDERAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIEIDIV**FGGGTKVEIK
CL-25776		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLVIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDVDIV**FGGGTKVEIK
CL-25778		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGLSYVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLIIDIV**FGGGTKVEIK
CL-25779		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGYSYVS**WYQQKP GQAPRLVIY**SDDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDIDIV**FGGGTKVEIK
CL-25780		EIVLTQSPGTLSLSPGERATLSC**RASSGDIGYSYVS**WYQQKP GQAPRLVIY**ADDERAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIEIDIT**FGGGTKVEIK
CL-25782		EIVLTQSPGTLSLSPGERATLSC**RASSGDIGYSYVS**WYQQKP GQAPRLLIY**FDDYRPT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIEIDIV**FGGGTKVEIK
CL-25783		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGYYYVS**WYQQKP GQAPRLVIY**ADDERAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIYIDVV**FGGGTKVEIK
CL-25784		EIVLTQSPGTLSLSPGERATLSC**RASSGDISDSYVS**WYQQKP GQAPRLVIY**TDDHRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGINIDIV**FGGGTKVEIK
CL-25785		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIGDSYVS**WYQQKP GQAPRLVIY**VDDWRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIDVDIV**FGGGTKVEIK
CL-25786		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGHSYVS**WYQQKP GQAPRLVIY**SDDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIIIDIV**FGGGTKVEIK
CL-25787		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWYSYVS**WYQQKP GQAPRLVIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QQYDIIDDIV**FGGGTKVEIK
CL-25788		EIVLTQSPGTLSLSPGERATLSC**RASSGDIGYSYVS**WYQQKP GQAPRLLIY**ADDFRPT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIITDIT**FGGGTKVEIK
CL-25789		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIYYSYVS**WYQQKP GQAPRLVIY**SDDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDVT**FGGGTKVEIK
CL-25790		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGYSYVS**WYQQKP GLAPRLLIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGTYVDIV**FGGGTKVEIK
CL-25791		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDTYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRXSGSGSGTDFTLTISRLEPED FAVYYC**QSYGINIDXV**FGGGTKVEIK
CL-25792		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIWQYYVS**WYQQKP GQAPRLVIY**SDDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDIV**FGGGTKVEIK
CL-25793		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLVIY**ADDWRPT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIYIDIV**FGGGTKVEIK
CL-25794		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGHSYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDTIIDIV**FGGGTKVEIK
CL-25795		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDYYVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDIDVV**FGGGTKVEIK
CL-25796		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDTIIDIV**FGGGTKVEIK
CL-25797		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWQYYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLNIDIT**FGGGTKVEIK
CL-25798		EIVLTQSPGTLSLSPGERATLSC**RASSGDIGESYVS**WYQQKP GQAPRLVIY**SDDSRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIIIDIV**FGGGTKVEIK
CL-25799		EIVLTQSPGTLSLSPGERATLSC**RASSGDIGYSYVS**WYQQKP GQAPRLVIY**ADDLRPT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIIIDIV**FGGGTKVEIK
CL-25800		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDYYVS**WYQQKP GQAPRLVIY**WDDYRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDVILDIT**FGGGTKVEIK
CL-25801		EIVLTQSPGTLSLSPGERATLSC**ERSSGDISYTYVS**WYQQKP GQAPRLVIY**SDDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIITDIV**FGGGTKVEIK
CL-25802		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGESYVS**WYQQKP GQAPRLVIY**TDDWRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGSNIDVV**FGGGTKVEIK
CL-25803		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWDYYVS**WYQQKP GQAPRLVIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QSYGILTDIT**FGGGTKVEIK
CL-25804		EIVLTQSPGTLSLSPGERATLSC**RASSGSIAHSYVS**WYQQKP GQAPRLVIY**SDDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIIVDIV**FGGGTKVEIK
CL-25805		EIVLTQSPGTLSLSPGERATLSC**RASSGSIVYSYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIITDIV**FGGGTKVEIK
CL-25806		EIVLTQSPGTLSLSPGERATLSC**ERSSGDISYSYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDIDIT**FGGGTKVEIK
CL-25807		EIVLTQSPGTLSLSPGERATLSC**RASSGSIGDTYVS**WYQQKP GQAPRLLIY**ADDWRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIEIDIV**FGGGTKVEIK
CL-25808		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWDTYVS**WYQQKP GQAPRLVIY**SDDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGINIDIV**FGGGTKVEIK
CL-25809		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIGETYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGTIIDIV**FGGGTKVEIK
CL-25810		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWDTYVS**WYQQKP GQAPRLVIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIIIDIV**FGGGTKVEIK
CL-25812		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWYSYVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIIIDIV**FGGGTKVEIK
CL-25813		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLLIY**ADDYRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIIVDIT**FGGGTKVEIK
CL-25814		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGQSYVS**WYQQKP GQAPRLVIY**SDDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIIIDIV**FGGGTKVEIK
CL-25815		EIVLTQSPGTLSLSPGERATLSC**RESSGDILYTYVS**WYQQKP GQAPRLVIY**SDDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIEIDIT**FGGGTKVEIK
CL-25816		EIVLTQSPGTLSLSPGERATLSC**RASSGDIGHSYVS**WYQQKP GQAPRLVIY**ADDQRPT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIIIDVT**FGGGTKVEIK
CL-25818		EIVLTQSPGTLSLSPGERATLSC**RASSGDISDSYVS**WYQQKP GQAPRLLIY**SDDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIIIDIV**FGGGTKVEIK
CL-25819		EIVLTQSPGTLSLSPGERATLSC**RASSGSIGHSYVS**WYQQKP GQAPRLVIY**GDDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDVDIDVV**FGGGTKVEIK
CL-28175		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLVIY**VDDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDIV**FGGGTKVEIK
CL-28178		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QSYDINIDIV**CGGGTKVEIK
CL-28195		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLVIY**ADDQRPS**GIPGRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDIV**FGGGTKVEIK
CL-28212		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDFYVS**WYQQKP GQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDIV**FGGGTKVEIK
CL-28215		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDYYVS**WYQQKP GQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTINRMEPED FAVYYC**QSYDINMDIV**FGGGTKVEIK
CL-28233		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLVIY**GDDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDIV**FGGGTKVEIK
CL-29595		EIVLTQSPGTLSLSPGERATLSC**RASSGSISYSYVS**WYQQKP GQAPRLVIY**ADDLRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGINIDVV**FGGGTKVEIK
CL-29596		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWYSYVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPYRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINVDTV**FGGGTKVEIK
CL-29597		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIGDAYVS**WYQQKP GQAPRLVIY**SDDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIIVDVV**FGGGTKVEIK
CL-29598		EIVLTQSPGTLSLSPGERATLSC**RASSGSIGDSYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIAIDIV**FGGGTKVEIK
CL-29599		EIVLTQSPGTLSLSPGERATLSC**RASSGSIEYSYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIIVDIV**FGGGTKVEIK
CL-29600		EIVLTQSPGTLSLSPGERATLSC**RASSGSIEGAYVS**WYQQKP GQAPRLVIY**SDDERAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIITDIV**FGGGTKVEIK
CL-29601		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIGGTYVS**WYQQKP GQAPRLVIY**ADDLRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIEIDIT**FGGGTKVEIK
CL-29602		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGSCYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDIDVV**FGGGTKVEIK
CL-29603		EIVLTQSPGTLSLSPGERATLSC**RASSGDIGYTYVS**WYQQKP GQAPRLVIY**ADDVRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIDVDIV**FGGGTKVEIK
CL-29604		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIWGYYVS**WYQQKP GQAPRLVIY**ADDHRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIIIDIT**FGGGTKVEIK
CL-29605		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGEAYVS**WYQQKP GQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIIIDIT**FGGGTKVEIK
CL-29606		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGYSYVS**WYQQKP GQAPRLLIY**SDDNRAS**GIPDRFSGSGSGTDFTLTISRLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QSYGTIIDIT**FGGGTKVEIK
CL-29607		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGYSYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDITIDIV**FGGGTKVEIK
CL-29608		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWYSYVS**WYQQKP GQAPRLLIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLIIDVV**FGGGTKVEIK
CL-29609		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWHSYVS**WYQQKP GQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIIIDIT**FGGGTKVEIK
CL-29610		EIVLTQSPGTLSLSPGERATLSC**RASSGDIGDSYVS**WYQQKP GQAPRLVIY**ADDDRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIDVDVT**FGGGTKVEIK
CL-29611		EIVLTQSPGTLSLSPGERATLSC**RASSGDIAHSYVS**WYQQKP GQAPRLLIY**VDDLRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDITIDIV**FGGGTKVEIK
CL-29612		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIYSYYVS**WYQQKP GQAPRLLIY**SDDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLNIDVV**FGGGTKVEIK
CL-29613		EIVLTQSPGTLSLSPGERATLSC**RASSGDISESYVS**WYQQKP GQAPRLLIY**TDDLRPT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDTDIV**FGGGTKVEIK
CL-29614		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSLVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGVIVDIV**FGGGTKVEIK
CL-29615		EIVLTQSPGTLSLSPGERATLSC**RASSGDIYESYVS**WYQQKP GQAPRLVIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDVTIDIV**FGGGTKVEIK
CL-29617		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGFAYVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIDIDIV**FGGGTKVEIK
CL-29618		EIVLTQSPGTLSLSPGERAPLSC**ERSSGSIWDSYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDVDIDIV**FGGGTKVEIK
CL-29620		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWDSYVS**WYQQKP GQAPRLVIY**SDDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIIIDIT**FGGGTKVEIK
CL-29621		EIVLTQSPGTLSLSPGERATLSC**RASSGSIGYSYVS**WYQQKP GQAPRLVIY**ADDRRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIIRDIV**FGGGTKVEIK
CL-29622		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGYSYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIIVDIV**FGGGTKVEIK
CL-29623		EIVLTQSPGTLSLSPGERATLSC**RASSGSIWYSYVS**WYQQKP GQAPRLVIY**SDDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGINIDVT**FGGGTKVEIK
CL-29624		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWDSYVS**WYQQKP GQAPRLVIY**SDDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QSYGIIIDIV**FGGGTKVEIK
CL-29625		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGYFYVS**WYQQKP GQAPRLVIY**VDDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGINIDVV**FGGGTKVEIK
CL-29626		EIVLTQSPGTLSLSPGERATLSC**RASSGSIGDTYVS**WYQQKP GQAPRLLIY**SDDHRPT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDIV**FGGGTKVEIK
CL-29627		EIVLTQSPGTLSLSPGERATLSC**RASSGDIWYSFVS**WYQQKP GQAPRLLIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIISDIV**FGGGTKVEIK
CL-29628		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIGETYVS**WYQQKP GQAPRLVIY**ADDLRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIIVDIV**FGGGTKVEIK
CL-29629		EIVLTQSPGTLSLSPGERATLSC**RASSGDIGDCFVS**WYQQKP GQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGINIDVV**FGGGTKVEIK
CL-29630		EIVLTQSPGTLSLSPGERATLSC**RASSGDIRHSFVS**WYQQKP GQAPRLVIY**WDDYRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDIDVT**FGGGTKVEIK
CL-29631		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIDECYVS**WYQQKP GQAPRLVIY**ADDDRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDIDVV**FGGGTKVEIK
CL-29632		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGESYVS**WYQQKP GQAPRLVIY**TDDRRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGSNIDVV**FGGGTKVEIK
CL-29634		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGYSYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QQYDIDTDIV**FGGGTKVEIK
CL-29635		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGHSYVS**WYQQKP GQAPRLVIY**SDDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIIIDIT**FGGGTKVEIK
CL-29636		EIVLTQSPGTLSLSPGERATLSC**RASSGDICHSYVS**WYQQKP GQAPRLVIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIIVDIV**FGGGTKVEIK
CL-29637		EIVLTQSPGTLSLSPGERATLSC**ERSSGSINESYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIDIDIV**FGGGTKVEIK
CL-29638		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIWYSYVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDIDVT**FGGGTKVEIK
CL-29639		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWDTYVS**WYQQKP GQAPRLLIY**ADDERAS**RIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIDIDVV**FGGGTKVEIK
CL-29640		EIVLTQSPGTLSLSPGERATLSC**RASSGDIWYSYVS**WYQQKP GQAPRLVIY**ADDQRPT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDIDIT**FGGGTKVEIK
CL-29641		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWQSYVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QSYDIVIDIT**FGGGTKVEIK
CL-29642		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWYSYVS**WYQQKP GQAPRLLIY**SDDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIIIDIV**FGGGTKVEIK
CL-29643		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDYYVS**WYQQKP GQAPRLVIY**SDDQRPT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLIIDIT**FGGGTKVEIK
CL-29644		EIVLTQSPGTLSLSPGERATLSC**RASSGDIGYTYVS**WYQQKP GQAPRLVIY**SDDHRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIIVDIV**FGGGTKVEIK
CL-29645		EIVLTQSPGTLSLSPGERATLSC**ERSSGDISGAYVS**WYQQKP GQAPRLVIY**GDDERAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIIIDVT**FGGGTKVEIK
CL-29646		EIVLTQSPGTLSLSPGERATLSC**RASSGDIGRSYVS**WYQQKP GQAPRLVIY**ADDLRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDVNTDIV**FGGGTKVEIK
CL-29647		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIWHTYVS**WYQQKP GQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIIIDIT**FGGGTKVEIK
CL-29648		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGYAYVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIILDVT**FGGGTKVEIK
CL-29649		EIVLTQSPGTLSLSPGERATLSC**RASSGDIEHSYVS**WYQQKP GQAPRLLIY**VDDQRPT**GIPDRFSGSGSGTDFTLTISRLXPED FAVYYC**QSYGIREDIV**FGGGTKVEIK
CL-29650		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIGFSYVS**WYQQKP GQAPRLVIY**ADDLRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGTYVDVV**FGGGTKVEIK
CL-29651		EIVLTQSPGTLSLSPGERATLSC**RASSGDIWYSYVS**WYQQKP GQAPRLVIY**SDDERPT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGVDVDVV**FGGGTKVEIK
CL-29652		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGYSYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIIIDIV**FGGGTKVEIK
CL-29653		EIVLTQSPGTLSLSPGERATLSC**RASSGDIEHSYVS**WYQQKP GQAPRLLIY**ADDYRPT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIDPDIT**FGGGTKVEIK
CL-29654		EIVLTQSPGTLSLSPGERATLSC**RASSGDISHSYVS**WYQQKP GQAPRLVIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDIDIT**FGGGTKVEIK
CL-29655		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDAYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIFIDIV**FGGGTKVEIK
CL-29656		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGEYYVS**WYQQKP GQAPRLVIY**ADDRRPT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDIDVT**FGGGTKVEIK
CL-29657		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIDYAYVS**WYQQKP GQAPRLVIY**SDDYRAT**GIPDRFSGSGSGTDFTLTISRLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QSYDIDIDIT**FGGGTKVEIK
CL-29658		EIVLTQSPGTLSLSPGERATLSC**RASSGDIWYSYVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIVIDIV**FGGGTKVEIK
CL-29659		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIGYSYVS**WYQQKP GQAPRLVMY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDVIIDVV**FGGGTKVEIK
CL-29660		EIVLTQSPGTLSLSPGERATLSC**RASSGDIGYSYVS**WYQQKP GQAPRLVIY**SDDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIIIDVT**FGGGTKVEIK
CL-29661		EIVLTQSPGTLSLSPGERATLSC**RASSGSIWHSYVS**WYQQKP GQAPRLVIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**KSYGINIDVT**FGGGTKVEIK
CL-29662		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGYSYVS**WYQQKP GQAPRLVIY**SDDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDVV**FGGGTKVEIK
CL-29663		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDTYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIDIDIT**FGGGTKVEIK
CL-29664		EIVLTQSPGTLSLSPGERATLSC**RASSGDIRHSYVS**WYQQKP GQAPRLVIY**ADDDRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGINTDIV**FGGGTKVEIK
CL-29665		EIVLTQSPGTLSLSPGERATLSC**RASSGDIGGSYVS**WYQQKP GQAPRLVIY**TDDWRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGINIDVV**FGGGTKVEIK
CL-29666		EIVLTQSPGTLSLSPGERATLSC**RASSGDISYSYVS**WYQQKP GQAPRLLIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIIIDVV**FGGGTKVEIK
CL-29667		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDMYVS**WYQQKP GQAPRLVIY**SDDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIIIDIV**FGGGTKVEIK
CL-29668		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIDYTYVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLTLDIT**FGGGTKVEIK
CL-29669		EIVLTQSPGTLSLSPGERATLSC**ERSSSSIWHSYVS**WYQQKP GQAPRLVIY**ADDYRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDIDVV**FGGGTKVEIK
CL-29670		EIVLTQSPGTLSLSPGERATLSC**RASSGSIDYSYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIYIDVV**FGGGTKVEIK
CL-29671		EIVLTQSPGTLSLSPGERATLSC**RASSGSIWYSFVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGQYIDVV**FGGGTKVEIK
CL-29672		EIVLTQSPGTLSLSPGERATLSC**RASSGDIDESYVS**WYQQKP GQAPRLVIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIIIDIV**FGGGTKVEIK
CL-29673		EIVLTQSPGTLSLSPGERATLSC**RASSGDIXYSYVS**WYQQKP GQAPRLVIY**SDDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QSYDSIIDVT**FGGGTKVEIK
CL-29674		EIVLTQSPGTLSLSPGERATLSC**RASSGDIWYSYVS**WYQQKP GQAPRLLIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGINVDIV**FGGGTKVEIK
CL-29675		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIMYAYVS**WYQQKP GQAPRLVIY**ADDQRPT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLIIDVT**FGGGTKVEIK
CL-29676		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDTYVS**WYQQKP GQAPRLVIY**ADDARAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLDIDIT**FGGGTKVEIK
CL-29677		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWHSYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDISIDVT**FGGGTKVEIK
CL-29678		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIGETYVS**WYQQKP GQAPRLLIY**SDDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIDIDIV**FGGGTKVEIK
CL-29679		EIVLTQSPGTLSLSPGERATLSC**RASSGSIGDSYVS**WYQQKP GQAPRLLIY**SDDDRPT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGISIDVT**FGGGTKVEIK
CL-29681		EIVLTQSPGTLSLSPGERATLSC**RASSGDIGHSYVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIIIDIT**FGGGTKVEIK
CL-29682		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDTYVS**WYQQKP GQAPRLVIY**SDDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIIIDIV**FGGGTKVEIK
CL-29683		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIYSYYVS**WYQQKP GQAPRLLIY**SDDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGINIDVT**FGGGTKVEIK
CL-29684		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIWHSYVS**WYQQKP GQAPRLVIY**SDDQQAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIIIDIV**FGGGTKVEIK
CL-29685		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGYSYVS**WYQQKP GQAPRLVIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIVIDIV**FGGGTKVEIK
CL-29686		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDTYVS**WYQQKP GQAPRLVIY**ADDQRPT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLTIDIV**FGGGTKVEIK
CL-29687		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLVIY**SDDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDICIDVT**FGGGTKVEIK
CL-29688		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLLIY**SDDHRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIIIDIV**FGGGTKVEIK
CL-29689		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIGGYYVS**WYQQKP GQAPRLLIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIIIDIV**FGGGTKVEIK
CL-29690		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGYSYVS**WYQQKP GQAPRLVIY**GADLRAS**GIPDRFSGSGSGTDFTLTISRLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QSYGIDIDIV**FGGGTKVEIK
CL-29722		EIVLTQSPGTLSLSPGERATLSC**ERSXGDIGDSYVS**WYQQKP GQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDIV**FGGGTKVEIK
CL-29732		EIVLTQSPGTLSLSPGERATLSC**ERSSVDIGDSYVS**WYQQKP GQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDIV**FGGGTKVEIK
CL-29741		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLVIH**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDIV**FGGGTKVEIK
CL-29746		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP VQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDIV**FGGGTKVEIK
CL-29756		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP GQATRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDIV**FGGGTKVEIK
CL-29759		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLVIY**AYDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDIV**FGGGTKVEIK
CL-29765		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLVIY**SDDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDIV**FGGGTKVEIK
CL-29771		EXXLTQSPGTLSLSPGERATXSC**ERSSGDXGDSYVS**WYQQKP GQAPRLVIY**XDDQRPS**GIPDRFSGSGSGTDFTLTISGLEPED FAVYYC**QSXDINMDIV**FGGGTKVEIK
CL-29780		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDIV**FGVGTKVEIK
CL-29781		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FVVYYC**QSYDINIDIV**FGGGTKVEIK
CL-33580		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLVIY**XDDQRPS**GIPDRFSGSGSGGDFTLTISRLEPED FAVYYC**QSYDINIDIV**FGGGTKVEIK
CL-33673		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWEYYVS**WYQQKP GQAPRLVIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLEVDIV**FGGGTKVEIK
CL-33674		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIWDTYVS**WYQQKP GQAPRLVIY**SDDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGINVDIV**FGGGTKVEIK
CL-33676		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWGYYVS**WYQQKP GQAPRLLIY**ADDLRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDVV**FGGGTKVEIK
CL-33677		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIYYTYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDVDVV**FGGGTKVEIK
CL-33678		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWGYYVS**WYQQKP GQAPRLLIY**ADDLRAS**GIPDRFSGSGSGTDFTLTISRLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QSYGIDIDIT**FGGGTKVEIK
CL-33679		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWDTYVS**WYQQKP GQAPRLVIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGLNVDVV**FGGGTKVEIK
CL-33680		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIYETYVS**WYQQKP GQAPRLVIY**SDDHRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDIDVV**FGGGTKVEIK
CL-33681		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIWYSYVS**WYQQKP GQAPRLLIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIITDVT**FGGGTKVEIK
CL-33684		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWGYYVS**WYQQKP GQAPRLLIY**ADDLRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDVV**FGGGTEVEIK
CL-33685		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIYYTYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGINIDVV**FGGGTKVEIK
CL-33687		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWDYYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLDIDVV**FGGGTKVEIK
CL-33688		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIWQSYVS**WYQQKP GQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIIIDIV**FGGGTKVEIK
CL-33690		EIVLTQSPGTLSLSPGERATLSC**KRSSGSIYDTYVS**WYQQKP GQAPRLVIY**SDDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDVDSDIV**FGGGTKVEIK
CL-33691		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWDYYVS**WYQQKP GQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIDIDVT**FGGGTKVEIK
CL-33692		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWDYYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLDIDVT**FGGGTKVEIK
CL-33693		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIYESYVS**WYQQKP GQAPRLLIY**SDDQRPT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIDIDVV**FGGGTKVEIK
CL-33694		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIYHTYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLDIDVT**FGGGTKVEIK
CL-33695		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIYDTYVS**WYQQKP GQAPRLVIY**SDDQRPT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLDIDIV**FGGGTKVEIK
CL-33697		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWQTYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDVDIV**FGGGTKVEIK
CL-33698		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWXYYVS**WYQQKP GQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLFIDVT**FGGGTKVEIK
CL-33700		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWHYYVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QSYDLEIDVT**FGGGTKVEIK
CL-33704		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWSYYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLTVDVV**FGGGTKVEIK
CL-33707		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWSYYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLDIDVT**FGGGTKVEIK
CL-33708		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWDYYVS**WYQQKP GQAPRLVIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDIDVT**FGGGTKVEIK
CL-33709		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWQTYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDIDVT**FGGGTKVEIK
CL-33710		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWEYYVS**WYQQKP GQAPRLVIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLDIDVV**FGGGTKVEIK
CL-33712		EIVLTQSPGTLSLSPGERATLSC**RASSGSIYYSYVS**WYQQKP GQAPRLVIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDIDVV**FGGGTKVEIK
CL-33713		EIVLTQSPGTLSLSPGERATLSC**ERYSGDIWYTYVS**WYQQKP GQAPRLVIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDVDVV**FGGGTKVEIK
CL-33716		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWEYYVS**WYQQKP GQAPRLVIY**ADDLRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLDIDVT**FGGGTKVEIK
CL-33718		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWEYYVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLNIDVV**FGGGTKVEIK
CL-33719		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWEYYVS**WYQQKP GQAPRLVIY**ADDLRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLDIDVT**FGGGTKVEIK
CL-33720		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWEYYVS**WYQQKP GQAPRLVIY**TDDLRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIETDIV**FGGGTKVEIK
CL-33721		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWYSYVS**WYQQKP GQAPRLVIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDVDVT**FGGGTKVEIK
CL-33722		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWYSYVS**WYQQKP GQAPRLVIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIYIDVV**FGGGTKVEIK
CL-33723		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWEYYVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDVCIDVV**FGGGTKVEIK
CL-33725		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWEYYVS**WYQQKP GQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLDIDVV**FGGGTKVEIK
CL-33726		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIWYSYVS**WYQQKP GQAPRLVIY**SDDLRAS**GIPDRFSGSGSGTDFTLTISRLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QSYDINIDVV**FGGGTKVEIK
CL-33727		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLVIY**WDDYRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIDVDIV**FGGGTKVEIK
CL-33729		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWSYYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLDIDIT**FGGGTKVEIK
CL-33730		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWSYYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLNIDTV**FGGGTKVEIK
CL-33732		EIVLTQSPGTLSLSPGERATLSC**ERSSCDIWQYYVS**WYQQKP GQAPRLLIY**ADDQRAT**GIPDRFSGSGSGTDFTLIISRLEPED FAVYYC**QSYDLDIDVV**FGGGTKVEIK
CL-33733		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWEYYVS**WYQQKP GQAPRLVIY**SDDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIITDVV**FGGGTKVEIK
CL-33734		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWHTYVS**WYQQKP GQAPRLVIY**ADDQRPT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDVNIDVV**FGGGTKVEIK
CL-33740		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIWSTYVS**WYQQKP GQAPRLLIY**SDDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDVVIDIV**FGGGTKVEIK
CL-33741		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWEYYVS**WYQQKP GQAPRLLIY**SDDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLIIDIV**FGGGTKVEIK
CL-33742		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWHYYVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLDIDVT**FGGGTKVEIK
CL-33743		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIWGYYVS**WYQQKP GQAPRLVIY**ADDHRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDETIDIV**FGGGTKVEIK
CL-33745		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIYYTYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDIDIT**FGGGTKVEIK
CL-33746		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWQSYVS**WYQQKP GQAPRLVIY**SDDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDVDIV**FGGGTKVEIK
CL-33747		EIVLTQSPGTLSLSPGERATLSC**RASSGSIWYSFVS**WYQQKP GQAPRLVIY**SDDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGINIDVV**FGGGTKVEIK
CL-33755		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLVIY**SDDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGTNIDVV**FGGGTKVEIK
CL-33756		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWESYVS**WYQQKP GQAPRLVIY**ADDQRPT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIIDDIV**FGGGTKVEIK
CL-33757		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWETYVS**WYQQKP GQAPRLVIY**SDDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QSYDIDIDVT**FGGGTKVEIK
CL-33758		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWQTYVS**WYQQKP GQAPRLVIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDIDVV**FGGGTKVEIK
CL-33760		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGLNIDVV**FGGGTKVEIK
CL-33761		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWSYYVS**WYQQKP GQAPRLLIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDICIDVT**FGGGTKVEIK
CL-33763		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWEYYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDIDIV**FGGGTKVEIK
CL-33766		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIYDAYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDVDVV**FGGGTKVEIK
CL-33768		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIWDTYVS**WYQQKP GQAPRLVIY**SDDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDIDVV**FGGGTKVEIK
CL-33771		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIWQYYVS**WYQQKP GQAPRLLIY**ADDKRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDEDIDIT**FGGGTKVEIK
CL-33773		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWSYYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLNIDVT**FGGGTKVEIK
CL-33774		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWSYYVS**WYQQKP GQAPRLLIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLYIDIV**FGGGTKVEIK
CL-33775		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWQTYVS**WYQQKP GQAPRLVIY**ADDMRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLNIDVT**FGGGTKVEIK
CL-33776		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGYSYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIIIDIV**FGGGTKVEIK
CL-33777		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIYETYVS**WYQQKP GQAPRLLIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDIDVV**FGGGTKVEIK
CL-33778		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWEYYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGLITDVT**FGGGTKVEIK
CL-33779		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIWETYVS**WYQQKP GQAPRLVIY**ADDRRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIDIDVV**FGGGTKVEIK
CL-33781		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWEYYVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIDTDIV**FGGGTKVEIK
CL-33782		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWDTYVS**WYQQKP GQAPRLVIY**SDDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QSYGINIDVV**FGGGTKVEIK
CL-33785		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIWQTYVS**WYQQKP GQAPRLVIY**SDDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIVIDVV**FGGGTKVEIK
CL-33787		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWQYYVS**WYQQKP GQAPRLVIY**ADDHRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLDIDVT**FGGGTKVEIK
CL-33790		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWHTYVS**WYQQKP GQAPRLVIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDVDIDIT**FGGGTKVEIK
CL-33791		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWQAYVS**WYQQKP GQAPRLVIY**SDDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIIEDIT**FGGGTKVEIK
CL-33792		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIYETYVS**WYQQKP GQAPRLVIY**SDDHRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIITDIV**FGGGTKVEIK
CL-33794		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIWDYYVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLITDIV**FGGGTKVEIK
CL-33795		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWQTYVS**WYQQKP GQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGINIDVV**FGGGTKVEIK
CL-33796		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWEYYVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLIRDIV**FGGGTKVEIK
CL-33799		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIYETYVS**WYQQKP GQAPRLLIY**ADDWRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDITVDVV**FGGGTKVEIK
CL-33801		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWESYVS**WYQQKP GQAPRLVIY**SDDQRPT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIIDDIV**FGGGTKVEIK
CL-33802		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWEYYVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLDIDIT**FGGGTKVEIK
CL-33813		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWQTYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIDIDVV**FGGGTKVEIK
CL-33814		EIVLTQSPGTLSLSPGERATLSC**RASSGSIWYSYVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGINIDVV**FGGGTKVEIK
CL-33815		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIYETYVS**WYQQKP GQAPRLVIY**SDDHRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIDVDVV**FGGGTKVEIK
CL-33816		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIYETYVS**WYQQKP GQAPRLVIY**SDDHRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGINVDVV**FGGGTKVEIK
CL-33817		EIVLTQSPGTLSLSPGERATLSC**RASSGDISDKYVS**WYQQKP GQAPRLVIY**ADDYRAS**GIPDRFSGSGSGTDFTLTISRLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QSYDLCIDVT**FGGGTKVEIK
CL-33819		EIVLTQSPGTLSLSPGERATLSC**RASSGDISDKYVS**WYQQKP GQAPRLLIY**ADDWRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIDVDVV**FGGGTKVEIK
CL-33825		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIWQYYVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLDIDVT**FGGGTKVEIK
CL-33826		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWDYYVS**WYQQKP GQAPRLVIY**SDDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLEIDVV**FGGGTKVEIK
CL-33828		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWDTYVS**WYQQKP GQAPRLLIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDITVDVV**FGGGTKVEIK
CL-33829		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIWYSYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDIDVT**FGGGTKVEIK
CL-33832		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWDYYVS**WYQQKP GQAPRLVIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLIIDVT**FGGGTKVEIK
CL-33833		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWETYVS**WYQQKP GQAPRLVIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDVDIV**FGGGTKVEIK
CL-33834		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIWYSYVS**WYQQKP GQAPRLVIY**SDDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDSDIV**FGGGTKVEIK
CL-33836		EIVLTQSPGTLSLSPGERATLSC**RASSGSIWYSFVS**WYQQKP GQAPRLVIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGINVDIV**FGGGTKVEIK
CL-33837		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIYQTYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIDIDVV**FGGGTKVEIK
CL-33839		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIWETYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGVDIDVV**FGGGTKVEIK
CL-33840		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIYETYVS**WYQQKP GQAPRLVIY**SDDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDIDVV**FGGGTKVEIK
CL-33841		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIWQYYVS**WYQQKP GQAPRLVIY**SDDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLFIDVT**FGGGTKVEIK
CL-33844		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWDTYVS**WYQQKP GQAPRLLIY**SDDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIYVDIV**FGGGTKVEIK
CL-33847		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIYYTYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIEIDIT**FGGGTKVEIK
CL-33848		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIYETYVS**WYQQKP GQAPRLVIY**SDDHRPS**GIPDRFSGSGSGTDFTLTISRLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QSYDIDTDIV**FGGGTKVEIK
CL-33849		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWYSYVS**WYQQKP GQAPRLVIY**SDDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGINIDVV**FGGGTKVEIK
CL-33854		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWHTYVS**WYQQKP GQAPRLLIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGINVDVV**FGGGTKVEIK
CL-33857		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWESYVS**WYQQKP GQAPRLLIY**SDDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGINIDVV**FGGGTKVEIK
CL-33858		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGHTYVS**WYQQKP GQAPRLVIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIISDVV**FGGGTKVEIK
CL-33862		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIWGTYVS**WYQQKP GQAPRLVIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDIDVT**FGGGTKVEIK
CL-41468		EIVLTQSPGTLSLPPGERATLSC**KRSSGSIYDTYVS**WYQQKP GQAPRLVIY**SDDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLTIDIT**FGGGTKVEIK
CL-41469		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIWHSYVS**WYQQKP GQAPRLLIY**SDDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIYIDVV**FGGGTRSKLS
CL-41472		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWDTYVS**WYQQKP GQAPRLLIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLTIDIT**FGGGTKVEIK
CL-41477		EIVLTQSPGTLSLSPGERATPSC**RASSGSIWYSFVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGINIDVV**FGGGTKVEIK
CL-41479		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWDYYVS**WYQQKP GQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QPYDLFIDVT**FGGGTKVEIK
CL-41480		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWQSYVS**WYQQKP GQAPRLVIY**SDDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAGYYC**QSYGINIDVV**FGGGTKVEIK
CL-41486		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDYYVS**WYQQKP GQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLFIDVT**FGGGTKVEIK
CL-41505		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIWHSYVS**WYQQKP GQAPRLLIY**SDDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIETDIV**FGGGTKVEIK
CL-41509		EIVLTQSPGTWSLSPGERATLSC**ERSSGSNYDTYVS**WYQQKP GQAPRLLIY**ADDLRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIETDIV**FGGGTKVEIK
CL-41528		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIWHSYVS**WYQQKP GQAPRLLIY**SDDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIYIDVV**FGGDTKVEIK
CL-41529		EIVLTQSPGTLSLSSGERATLSC**ERSSGSNYDTYVS**WYQQKP GQAPRLLIY**ADDLRAS**GIPDRFSGSGSGTDFTLTISRLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QSYGIETDIV**FGGGTKVEIK
CL-41532		EIVLTQSPGTLSLSPGERATLSC**RASSGSTWYSFVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGINIDVV**FGGGTKVEIK
CL-41535		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWDYYVS**WYQQKP GQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLTIDIT**FGGGTKVEIK
CL-41536		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWDYYVS**WYQQKP GQAPRLVIY**SDDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLFIDXT**FGGGTKVEIK
CL-41539		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWDTYVS**WYQQKP GQAPRLLIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPEG FAVYYC**QSYDIIIDIV**FGGGTKVEIK
CL-41543		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWDTYVS**WYQQKP GQASRLLIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIIIDIV**FGGGTKVEIK
CL-41547		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIWHSYVS**WYQQKP GQAPRLLIY**SDDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIYIDVV**FGGGTNVEIK
CL-41550		EIVLTQSPGTLSLSPGERATLSC**KRSSGSIYDTYVS**WYQQKP GQAPRLVIY**SDDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLTIDIT**FGGGTKVEIK
CL-41554		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWQSYVS**WYQQKP GQAPRLVIY**SDDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGINIDVV**FGGGTKVEIK
CL-41556		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIWHSYVS**WYQQKP GQAPRLLIY**SDDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIYIDVV**FGGGTKVEIK
CL-41557		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWDTYVS**WYQQKP GQAPRLLIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIIIDIV**FGGGTKVEIK
CL-41560		EIFLTQSPGTLSLSPGKKATLSG**KRSSGSIYNTYFS**GYQQKP GQAPKRVIY**SDDRRPS**GIPDRFSGSGXGTDFTLTISXLEPKD FAVYYC**QSYDLTINLX**FGGGTKVXIX
CL-41561		EIVLTQSPGTLSLSPGERATLSC**ERSSGSNYDTYVS**WYQQKP GQAPRLLIY**ADDLRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIETDIV**FGGGTKVEIK
CL-41562		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP GQSPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDIV**FGGGTKVEIK
CL-41569		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLVIY**ADDQRPR**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDIV**FGGGTKVEIK
CL-41577		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIWQSYVS**WYQQKP GQAPRLVIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDIDVV**FGGGTKVEIS
CL-41581		EIVLTQSPGTLSLSPGERATLSC**RASSGSIWYSFVS**RYQQKP GQAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QSYGINIDVV**FGGGTKVEIK
CL-41591		EIVLTQSPGTLSLSPGERATLSC**RASSGSIWYSFVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGIDIDVV**FGGGTKVEIK
CL-41599		KSSLTQSPGTLSLSPGERATLSC**RASSGSIWYSFVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGINIDVV**FGGGTKVEIK
CL-41600		EIVLTQSLGTLSLSPGERATLSC**RASSGSIWYSFVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGINIDVV**FGGGTKVEIK
CL-41615		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWQMYVS**WYQQKP GQAPRLVIY**GDDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDIDIT**FGGGTKVEIK
CL-41616		EIVLTQSPGTLSLPPGERATLSC**ERSSGDIWQTYVS**WYQQKP GQAPRLVIY**GDDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDIDIT**FGGGHKGRNX
CL-41639		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWDYYVS**WYQQKP GQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED SAVYYC**QSYDLFIDVT**FGGGTKVEIK
CL-41642		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWDYYVS**WYQRKP GQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGINIDVV**FGGGTKVEIK
CL-41645		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWQTYVS**WYQQKP GQAPRLVIY**GDDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDIDIT**FGGGTKVEIK
CL-41646		EIVLTQSPGTLSLSPGERATLSC**ERSSGSIWQSYVS**WYQQKP GQAPRLVIY**ADDQRAT**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDIDIDVV**FGGGTKVEIK
CL-41649		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWDYYVS**WYQQKP GQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDLFIDVT**FGGGTKVEIK
CL-41654		EIVLTQSPGTLSLSPGERATLSC**RASSGSIWYSFVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVHYC**QSYGINIDVV**FGGGTKVEIK
CL-41655		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIWQTYVS**WYQQKP GQAPRLVIY**GDDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGINIDVV**FGGGTKVEIK
CL-41668		EIVLTQSPGTLSLSPGERATLSC**RASSGSIWYSFVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVCYC**QSYGINIDVV**FGGGTKVEIK
CL-41673		EIVLTQSPGTLSLSPGERAPLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDIV**FGGGTKVEIX
CL-41685		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTINRLEPED FAVYYC**QSYDINIDIV**FGGGTKVEIK
CL-41705		EIVLTQSPGTLSLSPGERATLSC**RASSGSIWYSFVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPDRLSGSGSGTDFTLTISRLEPED

Clone	SEQ ID NO:	VL
		FAVYYC**QSYGINIDVV**FGGGTKVEIK
CL-41707		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLVIY**ADGQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDIV**FGGGTKVEIK
CL-41710		EIVLTQSPSTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDIV**FGGGTKVEIK
CL-41713		EIVLTQSPGTLSLSPGERATLSC**RASSGSIWYSFVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGINIDVV**FGGGTKVEIN
CL-41714		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDIV**FGGGTKVELS
CL-41720		EIVLTQIPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDIV**FGGGTKVEIK
CL-41725		EIVLTQSPGTLSLSPGERATLSC**ERSSGSNYDTYVS**WYQQKP GQAPRLLIY**ADDLRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGINIDVV**FGGGTKVEIK
CL-41727		EIVLTQSPGTLSLSPGERATLSC**RASSGSIWYSFVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYR**QSYGINIDVV**FGGGTKVEIK
CL-41729		EIVLTQSPGTLSLSPGERATLSC**RASSGSIWYSFVS**WYQQKP GQAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYGINIDVV**FGGGTKVEIK
CL-41732		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLVIY**ADDQRPI**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDIV**FGGGTKVEIK
CL-41735		EIVLTQSPGTLSLSPVERATLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDIV**FGGGTKVEIK
CL-41737		EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKP GQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDIV**FGGGTKVEIK
CL-41738		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPGQ APRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPEDFA VYYC**QQSWYDPLT**FGQGTKLEIK
CL-41739		EIVLTQSPATLSLSPGERAALSC**RASQSVSTHMH**WYQQKPGQ APRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPEDFA VYYC**QQSWYDPLT**FGQGTKLEIK
CL-41740		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPGQ APRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPEDFA VYYC**QQSRYDPLT**FGQGTKLEIK
CL-41742		EIVLTQSPGTLSLSPGERATLSC**RASQSVSTHMH**WYQQKPGQ APRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPEDFA VYYC**QQSWYDPLT**FGQGTKLEIK
CL-41751		AKLCXPVPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPGQ APRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPEDFA

Clone	SEQ ID NO:	VL
		VYYC**QQSWYDPLT**FGQGTKLEIK
CL-41752		EIVLTQSPATLSLSPGERATLSC**RASQSVSTHMH**WYQQKPGQ APRLLIY**GASNLES**GIPARFSGSGSGTDFTLTISSLEPEDFA VYYC**QQSWYDPLT**FGQGTKLRSN

Table 48. Amino Acid Residues Found In Each Position Of The Heavy Chain Variable Region During The Affinity Maturation Of Anti-PDGF-BB Antibody hBDI-9E8.4

hBDI-9E8.4-2|CL-22843 Heavy Chain Variable Region	
SEQ ID NO:	Sequence
XX	1 2 **3** 4 5 **6** 12345678901234567890123456**7890123456**7890123456789012**34567890** EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPPGKALEWLA**NIWWDDDKY** **I Y SEVSID**L **L DCYGEEH** **R A R L C NNGTC** **D A G HHVID** **T C V AQN** **M V E HVS** **R Y I YNA** **L R P NRF** **C T A QYG** **F E C SL** **W S G LM** **P C**
	7 8 9 10 **11** 12 **1234567**8901234567890123456789012345678**90123456789012**3456789012 **YNPSLKN**RLTISKDTSKNQVVLTMTNMDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS

hBDI-9E8.4-2l|CL-22843 Heavy Chain Variable Region	
SEQ ID NO:	Sequence
	SL NS LYQTGWPN E Y T T NVASPWS D LKYMFRK Y MYWVCIR A VLPLYFM C RDLFAAA N KGVNEME M FAEDLYI W CMKHVSV T TRFYSLL Q ESCTDGW G RRDP I Q KQ L K V P E N P E

Table 49. Amino Acid Residues Found In Each Position Of The Light Chain Variable Region During The Affinity Maturation Of Anti-PDGF Antibody hBDI-9E8.4

hBDI-9E8.4-2I|CL-22843 Light Chain Variable Region	
SEQ ID NO:	Sequence
XX	1 2 **3** 4 5 6 12345678901234567890123**4567890123456**7890123456789012**345678**90 EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKPGQAPRLVIY**ADDQRPS**GI F **RAY CSNWYTFFP**R R MH**GYGLQAI**R **KE VYTYQYLS** G **SA RP T** **S MSNMR WV H R** **MHKH T W G** **HGAN L Y** **DECC V M** **RSFA F K** **EKLD N D** **NFES P A** **CRWT E E** **ALD D N** **LCP V** **VAG S** **FP F** **T P** **Q** **K**
	7 8 9 **10** 11 12345678901234567890123456789**1234567890**1234567890 PDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QSYDINIDIV**FGGGTKVEIK

hBDI-9E8.4-2I|CL-22843 Light Chain Variable Region	
SEQ ID NO:	Sequence
	RKP GLFTNVT Q VDSPL H EEVAG TTDYT SIRGS QYEHN RCMEF NVLVA KSPLH GRFQR AANTQ CLK FG H K

Table 50. Variable Region Sequences of h9E8.4 Affinity Matured Clones Converted to IgG

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				12345678901234567890123456789O
	CL-33578 VH			EVTLRESGPALVKPTQTLTLTCTFS**G** **FSLSTYGMGVG**WIRQPPGKALEWLA**N** **IWWDDDKYYNPSLKN**RLTISKDTSKN QVVLTMTNMDPVDTATYYCAR**IQSGW** **TNYEFDY**WGQGTMVTVSS
	CL-33578	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTYGMGVG**
	CL-33578	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	CL-33578	CDR-H3	Residues 100-111 of SEQ ID NO.:	**IQSGWTNYEFDY**
	CL-33578 VL			EIVLTQSPGTLSLSPGERATLSC**ERS** **SGDIGDSYVS**WYQQKPGQAPRLVIY**A** **DDQRPS**GIPDRFSGSGSGTDFTLTIS RLEPEDFAVYYC**QSYDINIDIV**FGGG TKVEIK
	CL-33578	CDR-L1	Residues 24-36 of SEQ ID NO.:	**ERSSGDIGDSYVS**
	CL-33578	CDR-L2	Residues 52-58 of SEQ ID NO.:	**ADDQRPS**
	CL-33578	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYDINIDIV**
	CL-33587 VH			EVTLRESGPALVKPTQTLTLTCTFS**G** **FSLSTYGMGVG**WIRQPPGKALEWLA**N** **IWWDDDKYYNPSLKN**RLTISKDTSKN QVVLTMTNMDPVDTATYYCAR**IQSMW** **TRYDFDY**WGQGTMVTVSS
	CL-33587	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTYGMGVG**
	CL-33587	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	CL-33587	CDR-H3	Residues 100-111 of SEQ ID NO.:	**IQSMWTRYDFDY**
	CL-33587 VL			EIVLTQSPGTLSLSPGERATLSC**ERS** **SGDIGDSYVS**WYQQKPGQAPRLVIY**A** **DDQRPS**GIPDRFSGSGSGTDFTLTIS RLEPEDFAVYYC**QSYDINIDIV**FGGG TKVEIK
	CL-33587	CDR-L1	Residues 24-36 of SEQ ID NO.:	**ERSSGDIGDSYVS**
	CL-33587	CDR-L2	Residues 52-58 of SEQ ID NO.:	**ADDQRPS**
	CL-33587	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYDINIDIV**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				12345678901234567890123456789 0
	CL-33675 VH			EVTLRESGPALVKPTQTLTLTCTFS**G** **FSLSTYGMGVG**WIRQPPGKALEWLA**N** **IWWDDDKYYNPSLKN**RLTISKDTSKN QVVLTMTNMDPVDTATYYCAR**IESSG** **PKYSFDY**WGQGTMVTVSS
	CL-33675	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTYGMGVG**
	CL-33675	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	CL-33675	CDR-H3	Residues 100-111 of SEQ ID NO.:	**IESSGPKYSFDY**
	CL-33675 VL			EIVLTQSPGTLSLSPGERATLSC**RAS** **SGSIWYSFVS**WYQQKPGQAPRLLIY**A** **DDQRAS**GIPDRFSGSGSGTDFTLTIS RLEPEDFAVYYC**QSYGINIDVV**FGGG TKVEIK
	CL-33675	CDR-L1	Residues 24-36 of SEQ ID NO.:	**RASSGSIWYSFVS**
	CL-33675	CDR-L2	Residues 52-58 of SEQ ID NO.:	**ADDQRAS**
	CL-33675	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYGINIDVV**
	CL-33682 VH			EVTLRESGPALVKPTQTLTLTCTFS**G** **FSLSTYGMGVG**WIRQPPGKALEWLA**N** **IWWDDDKYYNPSLKN**RLTISKDTSKN QVVLTMTNMDPVDTATYYCAR**IESSW** **TSYSFDY**WGQGTMVTVSS
	CL-33682	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTYGMGVG**
	CL-33682	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	CL-33682	CDR-H3	Residues 100-111 of SEQ ID NO.:	**IESSWTSYSFDY**
	CL-33682 VL			EIVLTQSPGTLSLSPGERATLSC**ERS** **SGSNYDTYVS**WYQQKPGQAPRLLIY**A** **DDLRAS**GIPDRFSGSGSGTDFTLTIS RLEPEDFAVYYC**QSYGINIDVV**FGGG TKVEIK
	CL-33682	CDR-L1	Residues 24-36 of SEQ ID NO.:	**ERSSGSNYDTYVS**
	CL-33682	CDR-L2	Residues 52-58 of SEQ ID NO.:	**ADDLRAS**
	CL-33682	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYGINIDVV**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				12345678901234567890123456789 0
	CL-33683 VH			EVTLRESGPALVKPTQTLTLTCTFS**G** **FSLSTYGMGVG**WIRQPPGKALEWLA**N** **IWWDDDKYYNPSLKN**RLTISKDTSKN QVVLTMTNMDPVDTATYYCAR**IETIG** **PKYSFDY**WGQGTMVTVSS
	CL-33683	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTYGMGVG**
	CL-33683	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	CL-33683	CDR-H3	Residues 100-111 of SEQ ID NO.:	**IETIGPKYSFDY**
	CL-33683 VL			EIVLTQSPGTLSLSPGERATLSC**RAS** **SGSIWYSFVS**WYQQKPGQAPRLLIY**A** **DDQRAS**GIPDRFSGSGSGTDFTLTIS RLEPEDFAVYYC**QSYGINIDVV**FGGG TKVEIK
	CL-33683	CDR-L1	Residues 24-36 of SEQ ID NO.:	**RASSGSIWYSFVS**
	CL-33683	CDR-L2	Residues 52-58 of SEQ ID NO.:	**ADDQRAS**
	CL-33683	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYGINIDVV**
	CL-33699 VH			EVTLRESGPALVKPTQTLTLTCTFS**G** **FSLSTYGMGIG**WIRQPPGKALEWLA**N** **IWWDDDKYYNPSLKN**RLTISKDTSKN QVVLTMTNMDPVDTATYYCAR**IESMG** **PKYAFDY**WGQGTMVTVSS
	CL-33699	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTYGMGIG**
	CL-33699	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	CL-33699	CDR-H3	Residues 100-111 of SEQ ID NO.:	**IESMGPKYAFDY**
	CL-33699 VL			EIVLTQSPGTLSLSPGERATLSC**RAS** **SGSIWYSFVS**WYQQKPGQAPRLLIY**A** **DDQRAS**GIPDRFSGSGSGTDFTLTIS RLEPEDFAVYYC**QSYGINIDVV**FGGG TKVEIK
	CL-33699	CDR-L1	Residues 24-36 of SEQ ID NO.:	**RASSGSIWYSFVS**
	CL-33699	CDR-L2	Residues 52-58 of SEQ ID NO.:	**ADDQRAS**
	CL-33699	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYGINIDVV**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				12345678901234567890123456789 0
	CL-33701 VH			EVTLRESGPALVKPTQTLTLTCTFS**G** **FSLSTYGMGVG**WIRQPPGKALEWLA**N** **IWWDDDKYYNPSLKN**RLTISKDTSKN QVVLTMTNMDPVDTATYYCAR**IESLG** **TSYSFDY**WGQGTMVTVSS
	CL-33701	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTYGMGVG**
	CL-33701	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	CL-33701	CDR-H3	Residues 100-111 of SEQ ID NO.:	**IESLGTSYSFDY**
	CL-33701 VL			EIVLTQSPGTLSLSPGERATLSC**ERS** **SGDIWDYYVS**WYQQKPGQAPRLVIY**A** **DDQRPS**GIPDRFSGSGSGTDFTLTIS RLEPEDFAVYYC**QSYDLFIDVT**FGGG TKVEIK
	CL-33701	CDR-L1	Residues 24-36 of SEQ ID NO.:	**ERSSGDIWDYYVS**
	CL-33701	CDR-L2	Residues 52-58 of SEQ ID NO.:	**ADDQRPS**
	CL-33701	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYDLFIDVT**
	CL-33706 VH			EVTLRESGPALVKPTQTLTLTCTFS**G** **FSLSTYGMGVG**WIRQPPGKALEWLA**N** **IWWDDDKYYNPSLKN**RLTISKDTSKN QVVLTMTNMDPVDTATYYCAR**IETMG** **PKYSFDY**WGQGTMVTVSS
	CL-33706	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTYGMGVG**
	CL-33706	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	CL-33706	CDR-H3	Residues 100-111 of SEQ ID NO.:	**IETMGPKYSFDY**
	CL-33706 VL			EIVLTQSPGTLSLSPGERATLSC**RAS** **SGSIWYSFVS**WYQQKPGQAPRLLIY**A** **DDQRAS**GIPDRFSGSGSGTDFTLTIS RLEPEDFAVYYC**QSYGINIDVV**FGGG TKVEIK
	CL-33706	CDR-L1	Residues 24-36 of SEQ ID NO.:	**RASSGSIWYSFVS**
	CL-33706	CDR-L2	Residues 52-58 of SEQ ID NO.:	**ADDQRAS**
	CL-33706	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYGINIDVV**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				12345678901234567890123456789 0
	CL-33731 VH			EVTLRESGPALVKPTQTLTLTCTFS**G** **FSLSTYGMGVG**WIRQPPGKALEWLA**N** **IWWDDDKYYNPSLKN**RLTISKDTSKN QVVLTMTNMDPVDTATYYCAR**IESIP** **TSYSFDY**WGQGTMVTVSS
	CL-33731	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTYGMGVG**
	CL-33731	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	CL-33731	CDR-H3	Residues 100-111 of SEQ ID NO.:	**IESIPTSYSFDY**
	CL-33731 VL			EIVLTQSPGTLSLSPGERATLSC**ERS** **SGSIWQSYVS**WYQQKPGQAPRLVIY**A** **DDQRAT**GIPDRFSGSGSGTDFTLTIS RLEPEDFAVYYC**QSYDIDIDVV**FGGG TKVEIK
	CL-33731	CDR-L1	Residues 24-36 of SEQ ID NO.:	**ERSSGSIWQSYVS**
	CL-33731	CDR-L2	Residues 52-58 of SEQ ID NO.:	**ADDQRAT**
	CL-33731	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYDIDIDVV**
	CL-33737 VH			EVTLRESGPALVKPTQTLTLTCTFS**G** **FSLSTYGMGVG**WIRKPPGKALEWLA**N** **IWWDDDKYYNPSLKN**RLTISKDTSKN QVVLTMTNMDPVDTATYYCAR**IESSG** **PKYSFDY**WGQGTMVTVSS
	CL-33737	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTYGMGVG**
	CL-33737	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	CL-33737	CDR-H3	Residues 100-111 of SEQ ID NO.:	**IESSGPKYSFDY**
	CL-33737 VL			EIVLTQSPGTLSLSPGERATLSC**RAS** **SGSIWYSFVS**WYQQKPGQAPRLLIY**A** **DDQRAS**GIPDRFSGSGSGTDFTLTIS RLEPEDFAVYYC**QSYGINIDVV**FGGG TKVEIK
	CL-33737	CDR-L1	Residues 24-36 of SEQ ID NO.:	**RASSGSIWYSFVS**
	CL-33737	CDR-L2	Residues 52-58 of SEQ ID NO.:	**ADDQRAS**
	CL-33737	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYGINIDVV**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				12345678901234567890123456789 0
	CL-33759 VH			EVTLRESGPALVKPTQTLTLTCTFS**G** **FSLSTYGMGVG**WIRQPPGKALEWLA**N** **IWWDDDKYYNPSLKN**RLTISKDTSKN QVVLTMTNMDPVDTATYYCAR**IESVW** **TRYDFDY**WGQGTMVTVSS
	CL-33759	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTYGMGVG**
	CL-33759	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	CL-33759	CDR-H3	Residues 100-111 of SEQ ID NO.:	**IESVWTRYDFDY**
	CL-33759 VL			EIVLTQSPGTLSLSPGERATLSC**ERS** **SGDIWQTYVS**WYQQKPGQAPRLVIY**G** **DDQRAS**GIPDRFSGSGSGTDFTLTIS RLEPEDFAVYYC**QSYDIDIDIT**FGGG TKVEIK
	CL-33759	CDR-L1	Residues 24-36 of SEQ ID NO.:	**ERSSGDIWQTYVS**
	CL-33759	CDR-L2	Residues 52-58 of SEQ ID NO.:	**GDDQRAS**
	CL-33759	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYDIDIDIT**
	CL-33767 VH			EVTLRESGPALVKPTQTLTLTCTFS**G** **FSLSTYGMGVG**WIRQPPGKALEWLA**N** **IWWDDDKYYNPSLKN**RLTISKDTSKN QVVLTMTNMDPVDTATYYCAR**IESIG** **PKYSFDY**WGQGTMVTVSS
	CL-33767	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTYGMGVG**
	CL-33767	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	CL-33767	CDR-H3	Residues 100-111 of SEQ ID NO.:	**IESIGPKYSFDY**
	CL-33767 VL			EIVLTQSPGTLSLSPGERATLSC**RAS** **SGSIWYSFVS**WYQQKPGQAPRLLIY**A** **DDQRAS**GIPDRFSGSGSGTDFTLTIS RLEPEDFAVYYC**QSYGINIDVV**FGGG TKVEIK
	CL-33767	CDR-L1	Residues 24-36 of SEQ ID NO.:	**RASSGSIWYSFVS**
	CL-33767	CDR-L2	Residues 52-58 of SEQ ID NO.:	**ADDQRAS**
	CL-33767	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYGINIDVV**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				12345678901234567890123456789 0
	CL-33769 VH			EVTLRESGPALVKPTQTLTLTCTFS**G** **FSLSTYGMGVG**WIRQPPGKALEWLA**N** **IWWDDDKYYNPSLKN**RLTISKDTSKN QVVLTMTNMDPVDTATYYCAR**IESIG** **PKYSFDY**WGQGTMVTVSS
	CL-33769	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTYGMGVG**
	CL-33769	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	CL-33769	CDR-H3	Residues 100-111 of SEQ ID NO.:	**IESIGPKYSFDY**
	CL-33769 VL			EIVLTQSPGTLSLSPGERATLSC**RAS** **SGSIWYSFVS**WYQQKPGQAPRLLIY**A** **DDQRAS**GIPDRFSGSGSGTDFTLTIS RLEPEDFAVYYC**QSYGINIDVV**FGGG TKVEIK
	CL-33769	CDR-L1	Residues 24-36 of SEQ ID NO.:	**RASSGSIWYSFVS**
	CL-33769	CDR-L2	Residues 52-58 of SEQ ID NO.:	**ADDQRAS**
	CL-33769	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYGINIDVV**
	CL-33797 VH			EVTLRESGPALVKPTQTLTLTCTFS**G** **FSLSTYGMGVG**WIRQPPGKALEWLA**N** **IWWDDDKYYNPSLKN**RLTISKDTSKN QVVLTMTNMDPVDTATYYCAR**IESLG** **WSYSFDY**WGQGTMVTVSS
	CL-33797	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTYGMGVG**
	CL-33797	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	CL-33797	CDR-H3	Residues 100-111 of SEQ ID NO.:	**IESLGWSYSFDY**
	CL-33797 VL			EIVLTQSPGTLSLSPGERATLSC**ERS** **SGDIWDYYVS**WYQQKPGQAPRLVIY**A** **DDQRPS**GIPDRFSGSGSGTDFTLTIS RLEPEDFAVYYC**QSYDLFIDVT**FGGG TKVEIK
	CL-33797	CDR-L1	Residues 24-36 of SEQ ID NO.:	**ERSSGDIWDYYVS**
	CL-33797	CDR-L2	Residues 52-58 of SEQ ID NO.:	**ADDQRPS**
	CL-33797	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYDLFIDVT**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				12345678901234567890123456789 0
	CL-33803 VH			EVTLRESGPALVKPTQTLTLTCTFS**G** **FSLSTYGMGVG**WIRQPPGKALEWLA**N** **IWWDDDKYYNPSLKN**RLTISKDTSKN QVVLTMTNMDPVDTATYYCAR**IESLP** **TSYSFDY**WGQGTMVTVSS
	CL-33803	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTYGMGVG**
	CL-33803	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	CL-33803	CDR-H3	Residues 100-111 of SEQ ID NO.:	**IESLPTSYSFDY**
	CL-33803 VL			EIVLTQSPGTLSLSPGERATLSC**ERS** **SGDIWDTYVS**WYQQKPGQAPRLLIY**A** **DDQRPS**GIPDRFSGSGSGTDFTLTIS RLEPEDFAVYYC**QSYDIIIDIV**FGGG TKVEIK
	CL-33803	CDR-L1	Residues 24-36 of SEQ ID NO.:	**ERSSGDIWDTYVS**
	CL-33803	CDR-L2	Residues 52-58 of SEQ ID NO.:	**ADDQRPS**
	CL-33803	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYDIIIDIV**
	CL-33805 VH			EVTLRESGPALVKPTQTLTLTCTFS**G** **FSLSTYGMGVG**WIRQPPGKALEWLA**N** **IWWDDDKYYNPSLKN**RLTISKDTSKN QVVLTMTNMDPVDTATYYCAR**IESHW** **WSYAFDY**WGQGTMVTVSS
	CL-33805	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTYGMGVG**
	CL-33805	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	CL-33805	CDR-H3	Residues 100-111 of SEQ ID NO.:	**IESHWWSYAFDY**
	CL-33805 VL			EIVLTQSPGTLSLSPGERATLSC**ERS** **SGSNYDTYVS**WYQQKPGQAPRLLIY**A** **DDLRAS**GIPDRFSGSGSGTDFTLTIS RLEPEDFAVYYC**QSYGIETDIV**FGGG TKVEIK
	CL-33805	CDR-L1	Residues 24-36 of SEQ ID NO.:	**ERSSGSNYDTYVS**
	CL-33805	CDR-L2	Residues 52-58 of SEQ ID NO.:	**ADDLRAS**
	CL-33805	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYGIETDIV**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				12345678901234567890123456789 0
	CL-33811 VH			EVTLRESGPALVKPTQTLTLTCTFS**G** **FSLSTYGMGVG**WIRQPPGKALEWLA**N** **IWWDDDKYYNPSLKN**RLTISKDTSKN QVVLTMTNMDPVDTATYYCAR**IESSW** **TTYSFDY**WGQGTMVTVSS
	CL-33811	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTYGMGVG**
	CL-33811	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	CL-33811	CDR-H3	Residues 100-111 of SEQ ID NO.:	**IESSWTTYSFDY**
	CL-33811 VL			EIVLTQSPGTLSLSPGERATLSC**ERS** **SGSIWHSYVS**WYQQKPGQAPRLLIY**S** **DDQRAT**GIPDRFSGSGSGTDFTLTIS RLEPEDFAVYYC**QSYGIYIDVV**FGGG TKVEIK
	CL-33811	CDR-L1	Residues 24-36 of SEQ ID NO.:	**ERSSGSIWHSYVS**
	CL-33811	CDR-L2	Residues 52-58 of SEQ ID NO.:	**SDDQRAT**
	CL-33811	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYGIYIDVV**
	CL-33812 VH			EVTLRESGPALVKPTQTLTLTCTFS**G** **FSLSTYGMGVG**WIRQPPGKALEWLA**N** **IWWDDDKYYNPSLKN**RLTISKDTSKN QVVLTMTNMDPVDTATYYCAR**IESNP** **WKYSFDY**WGQGTMVTVSS
	CL-33812	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTYGMGVG**
	CL-33812	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	CL-33812	CDR-H3	Residues 100-111 of SEQ ID NO.:	**IESNPWKYSFDY**
	CL-33812 VL			EIVLTQSPGTLSLSPGERATLSC**ERS** **SGDIWQSYVS**WYQQKPGQAPRLVIY**S** **DDQRAS**GIPDRFSGSGSGTDFTLTIS RLEPEDFAVYYC**QSYGINIDVV**FGGG TKVEIK
	CL-33812	CDR-L1	Residues 24-36 of SEQ ID NO.:	**ERSSGDIWQSYVS**
	CL-33812	CDR-L2	Residues 52-58 of SEQ ID NO.:	**SDDQRAS**
	CL-33812	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYGINIDVV**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				12345678901234567890123456789 0
	CL-33820 VH			EVTLRESGPALVKPTQTLTLTCTFS**G** **FSLSTYGMGVG**WIRQPPGKALEWLA**N** **IWWDDDKYYNPSLKN**RLTISKDTSKN QVVLTMTNMDPVDTATYYCAR**IESSF** **TSYSFDY**WGQGTMVTVSS
	CL-33820	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTYGMGVG**
	CL-33820	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	CL-33820	CDR-H3	Residues 100-111 of SEQ ID NO.:	**IESSFTSYSFDY**
	CL-33820 VL			EIVLTQSPGTLSLSPGERATLSC**KRS** **SGSIYDTYVS**WYQQKPGQAPRLVIY**S** **DDQRPS**GIPDRFSGSGSGTDFTLTIS RLEPEDFAVYYC**QSYDLTIDIT**FGGG TKVEIK
	CL-33820	CDR-L1	Residues 24-36 of SEQ ID NO.:	**KRSSGSIYDTYVS**
	CL-33820	CDR-L2	Residues 52-58 of SEQ ID NO.:	**SDDQRPS**
	CL-33820	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYDLTIDIT**
	CL-33845 VH			EVTLRESGPALVKPTQTLTLTCTFS**G** **FSLSTYGMGVG**WIRQPPGKALEWLA**N** **IWWDDDKYYNPSLKN**RLTISKDTSKN QVVLTMTNMDPVDTATYYCAR**IVSDW** **TTYSFDY**WGQGTMVTVSS
	CL-33845	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTYGMGVG**
	CL-33845	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	CL-33845	CDR-H3	Residues 100-111 of SEQ ID NO.:	**IVSDWTTYSFDY**
	CL-33845 VL			EIVLTQSPGTLSLSPGERATLSC**RAS** **SGSIWYSFVS**WYQQKPGQAPRLLIY**A** **DDQRAS**GIPDRFSGSGSGTDFTLTIS RLEPEDFAVYYC**QSYGINIDVV**FGGG TKVEIK
	CL-33845	CDR-L1	Residues 24-36 of SEQ ID NO.:	**RASSGSIWYSFVS**
	CL-33845	CDR-L2	Residues 52-58 of SEQ ID NO.:	**ADDQRAS**
	CL-33845	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYGINIDVV**

SEQ ID NO:	Clone	Protein Region	Residues	V Region
				12345678901234567890123456789 0
	CL-33855 VH			EVTLRESGPALVKPTQTLTLTCTFS**G** **FSLSTYGMGVG**WIRQPPGKALEWLA**N** **IWWDDDKYYNPSLKN**RLTISKDTSKN QVVLTMTNMDPVDTATYYCAR**IETFG** **PKYSFDY**WGQGTMVTVSS
	CL-33855	CDR-H1	Residues 26-37 of SEQ ID NO.:	**GFSLSTYGMGVG**
	CL-33855	CDR-H2	Residues 52-67 of SEQ ID NO.:	**NIWWDDDKYYNPSLKN**
	CL-33855	CDR-H3	Residues 100-111 of SEQ ID NO.:	**IETFGPKYSFDY**
	CL-33855 VL			EIVLTQSPGTLSLSPGERATLSC**RAS** **SGSIWYSFVS**WYQQKPGQAPRLLIY**A** **DDQRAS**GIPDRFSGSGSGTDFTLTIS RLEPEDFAVYYC**QSYGINIDVV**FGGG TKVEIK
	CL-33855	CDR-L1	Residues 24-36 of SEQ ID NO.:	**RASSGSIWYSFVS**
	CL-33855	CDR-L2	Residues 52-58 of SEQ ID NO.:	**ADDQRAS**
	CL-33855	CDR-L3	Residues 91-100 of SEQ ID NO.:	**QSYGINIDVV**

Table 51. Summary of Protein Expression And Purification Of Affinity Matured Humanized Anti-Human PDGF-BB Antibodies

Name	Octet Titer (mg/L)[1]	~Yield (mg/L)[2]	SEC (% monomer)[3]
CL-33578-IgG	176.5	98.9	91.3
CL-33587-IgG	155.7	109.1	94.2
CL-33675-IgG	275.2	57.7	96.9
CL-33682-IgG	203.6	80.7	94.6
CL-33683-IgG	136.7	24.5	48.1
CL-33701-IgG	114.9	79.2	97.9
CL-33706-IgG	169.8	25.8	100.0
CL-33731-IgG	137.0	73.6	95.8
CL-33803-IgG	98.0	50.5	96.7
CL-33805-IgG	227.5	66.5	97.9
CL-33811-IgG	190.2	31.7	99.0
CL-33812-IgG	171.0	76.4	96.7
CL-33820-IgG	135.3	75.0	95.7
CL-33855-IgG	50.9	13.8	94.3
CL-33699-IgG	ND	10.5	81.7
CL-33737-IgG	ND	5.0	88.0
CL-33759-IgG	ND	18.5	100.0

Name	Octet Titer (mg/L)[1]	~Yield (mg/L)[2]	SEC (% monomer)[3]
CL-33767-IgG	ND	16.5	50.9
CL-33845-IgG	ND	0.8	60.6

ND = Not Determined

[1]Octet titer is the amount of IgG in the unpurified supernatant as determined by protein A binding compared to a standard curve using an Octet instrument.

[2]Yield is determined by the total amount of purified protein in mg divided by the total cell culture volume in liters.

[3]SEC % monomer is determined using HPLC size exclusion chromatography.

Table 52. Biacore Binding of Affinity-Matured Humanized Anti-PDGF Antibodies

Antibody	k_{on} (M-1 s-1)	k_{off} (M-1)	K_D (M)
CL-33578	≥ 9.0 E+07	2.70 E-05	≤ 3.0 E-13
CL-33587	≥ 9.0 E+07	2.00 E-05	≤ 2.2 E-13
CL-33675	3.60 E+07	2.20 E-05	6.10 E-13
CL-33682	≥ 9.0 E+07	2.20 E-05	≤ 2.4 E-13
CL-33683	1.90 E+07	8.20 E-06	4.40 E-13
CL-33701	7.30 E+07	1.80 E-05	2.40 E-13
CL-33706	1.80 E+07	1.20 E-05	6.90 E-13
CL-33731	8.10 E+07	1.60 E-05	2.00 E-13
CL-33803	≥ 9.0 E+07	1.40 E-05	≤ 1.6 E-13
CL-33805	6.80 E+07	1.50 E-05	2.10 E-13
CL-33811	2.70 E+07	1.20 E-05	4.50 E-13
CL-33812	6.30 E+07	1.90 E-05	3.00 E-13
CL-33820	≥ 9.8 E+07	1.60 E-05	≤ 1.6 E-13
CL-33855	2.00 E+07	≤ 1.0 E-06	≤ 5.0 E-14

*Heterogeneous off-rate

[0392] Affinity matured humanized anti-PDGF-BB antibodies were characterized for PDGF-BB binding and potency. Human PDGF-BB binding affinity was determined by Biacore analysis (Example 1.1). Potency was evaluated in both cell-based and ELISA formats. The ability to block binding of hPDGF-BB to hPDGF-Rβ was tested in a competition ELISA format (Example 1.13). Inhibition of human and cynomolgus PDGF-BB-induced cell proliferation was assessed using NIH-3T3 cells (Examples 1.15 and 1.16). The data is summarized in Table 53 below.

Table 53. Summary of Characterization of Affinity Matured Humanized Anti-Human PDGF-BB Antibodies

Affinity Matured Humanized IgG	PDGF-BB IC_{50} Potency (nM)

	hPDGF-BB NIH-3T3 Proliferation	cynoPDGF-BB NIH-3T3 Proliferation	hPDGF-BB /hPDGFR□ Competition
CL-33578-Ig	0.033	0.023	0.049
CL-33587-Ig	0.046	0.029	<0.1
CL-33675-Ig	0.04	0.024	0.054
CL-33682-Ig	0.03	0.019	0.069
CL-33683-Ig	0.029	0.028	0.126
CL-33699-Ig	0.033	0.016	0.072
CL-33706-Ig	0.035	0.019	0.081
CL-33731Ig	0.036	0.023	0.068
CL-33759-Ig	0.293	0.18	1.267
CL-33811-Ig	0.032	0.012	0.1
CL-33812-Ig	0.033	0.028	0.043
CL-33820-Ig	0.017	0.013	0.066
CL-33855-Ig	0.037	0.019	0.162
CL-33701-Ig	0.056	0.012	0.059
CL-33737-Ig	0.03	0.024	0.092
CL-33803-Ig	0.024	0.018	0.044
C-L33767-Ig	0.09	0.042	0.114
CL-33845-Ig	0.171	0.073	0.409
CL-33805-Ig	0.039	0.018	0.063

Example 9: Methods of Selecting Preferred Humanized Antibodies as DVD-Ig Building Blocks

Example 9.1. A Technique For Assessing The Stability Of Regions Of The Parental Antibodies Intended For DVD-Ig Protein Incorporation

[0393] The technique of differential scanning calorimetry (DSC) can be used to determine the thermal stabilities of the different domains of an antibody (e.g. CH2, CH3, CH1-CL, and VH-VL). The temperature of the highest peak in a DSC thermogram (plotted as heat capacity versus temperature) of an antibody has been shown to correspond to the midpoint of the unfolding transition or process of that antibody's VH-VL region due to increasing temperature. This may be interpreted as a measure of VH-VL thermal stability. VH-VL regions with high thermal stability in the antibody format will also likely have high thermal stability when incorporated into the DVD-Ig format as one of the binding domains. Therefore, antibodies can be screened to determine those with VH-VL regions of high thermal stability. Those regions can then be incorporated into the DVD-Ig format to increase the probability of generating a more stable DVD-Ig molecule.

Example 9.2. Determination of the Thermal Stability Of The VH-VL Regions Of Anti-VEGF mAbs and Anti-PDGF mAbs By Differential Scanning Calorimetry

[0394] A total of 73 mAbs (45 anti-VEGF and 28 anti-PDGF) were selected and analyzed by DSC (Example 2.2) and the thermal stabilities of their VH-VL regions were

quantitated by determining the temperature of the highest peak in the DSC thermograms as detailed in Example 9.1 (Table 54).

Table 54. Thermal Stability of Anti-VEGF and Anti-PDGF Antibodies

Name	Target Antigen	Temperature of highest peak in DSC thermogram (°C)
hBDB-4G8.1	VEGF	71.97
hBDB-4G8.2	VEGF	69.13
hBDB-4G8.3	VEGF	65.65
hBDB-4G8.4	VEGF	75.27
hBDB-4G8.5	VEGF	73.07
hBDB-4G8.6	VEGF	68.68
hBDB-4G8.7	VEGF	76.27
hBDB-4G8.8	VEGF	73.16
hBDB-4G8.9	VEGF	68.95
hBDB-4G8.10	VEGF	73.44
hBDB-4G8.11	VEGF	69.77
hBDB-4G8.12	VEGF	67.48
hBDB-4G8.13	VEGF	67.12
hBDB-4G8.14	VEGF	63.4
hBDB-4G8.15	VEGF	69.41
h4G8.3 EI	VEGF	68.31
h4G8 CL-32416	VEGF	68.95
h4G8 CL-34449	VEGF	72.7
h4G8 CL-34455	VEGF	70.69
h4G8 CL-34469	VEGF	70.23
h4G8 CL-34475	VEGF	70.69
h4G8 CL-34522	VEGF	67.49
h4G8 CL-34540	VEGF	69.87
h4G8 CL-34633	VEGF	69.22
h4G8 CL-34538	VEGF	71.15
h4G8 CL-34570	VEGF	66.84
h4G8 CL-34565	VEGF	71.15
hBEW-9A8.17	VEGF	64.56
hBEW-9A8.21	VEGF	54.25
hBEW-5C3.4	VEGF	66.94
hBEW-9E10.1	VEGF	71.88
hBEW-9E10.3	VEGF	71.24
hBEW-9E10.4	VEGF	71.77
hBEW-9E10.6	VEGF	71.24
hBEW-9A8.20	VEGF	61.85

hBEW-5C3.1	VEGF	63.15
hBEW-5C3.5	VEGF	64.83
hBEW-9E10.2	VEGF	71.37
hBEW-9E10.5	VEGF	71.24
hBEW-1B10.1	VEGF	87.95
hBEW-1B10.2	VEGF	86.38
hBEW-1E3.1	VEGF	62.74
hBEW-1E3.2	VEGF	66.29
hBEW-1E3.4	VEGF	66.11
hBEW-1E3.5	VEGF	68.83
hBDI-9E8.1	PDGF	77.6
hBDI-9E8.2	PDGF	76.28
hBDI-9E8.3	PDGF	87.4
hBDI-9E8.4	PDGF	84.2
hBDI-9E8.5	PDGF	77.69
hBDI-9E8.6	PDGF	75.91
hBDI-9E8.7	PDGF	87.4
hBDI-9E8.8	PDGF	84.29
hBDI-9E8.9	PDGF	82.09
hBDI-9E8.10	PDGF	83.37
hBDI-9E8.11	PDGF	80.9
hBDI-9E8.12	PDGF	82.64
hBDI-9E8.13	PDGF	85.39
CL-33578-IgG	PDGF	75.03
CL-33587-IgG	PDGF	76.37
CL-33675-IgG	PDGF	87.4
CL-33682-IgG	PDGF	78.52
CL-33683-IgG	PDGF	82.55
CL-33701-IgG	PDGF	73.62
CL-33706-IgG	PDGF	86.85
CL-33731-IgG	PDGF	77.33
CL-33803-IgG	PDGF	74.26
CL-33805-IgG	PDGF	80.35
CL-33811-IgG	PDGF	79.71
CL-33812-IgG	PDGF	78.15
CL-33820-IgG	PDGF	78.88
CL-33855-IgG	PDGF	82.18
hBFU-3E2.1	PDGF	68.31

Example 10: Generation of Anti-VEGF-A/Anti-PDGF-BB DVD-Ig Molecules

[0395] The variable domain sequences from humanized anti-human VEGF-A and anti-human PDGF-BB mAbs were used to design the VH and VL domains of anti-human VEGF-A/anti-human PDGF-BB DVD-Ig molecules. In some cases, variable regions were synthesized using two-step PCR. Primers were designed with homologous flanking regions to the cloning vector and the linker region between each DVD variable pair. In some cases, variable regions were generated using gene synthesis. Bacterial transformations were performed to identify positive clones and constructs were harvested and purified for use in mammalian transfection using standard protocols known in the art.

[0396] The variable domains of the heavy and light chain were cloned in-frame into mutant human IgG1 (L234, 235A) heavy-chain or mutant human IgG1 (L234, 235A, H435A) heavy-chain, and kappa light-chain constant regions, respectively, into pHybE vectors to generate anti-human VEGF-A/anti-human PDGF-BB DVD-Ig molecules.

Table 55. Amino Acid Sequences of DVD-Ig Linkers

Seq ID No	Name	Sequence
	HG-short	ASTKGP
	HG-long	ASTKGPSVFPLAP
	GS-H10	GGGGSGGGGS
	LK-short	RTVAAP
	LK-long	RTVAAPSVFIFPP
	GS-L10	RGGSGGGGSG
	GS-L10(dR)	GGSGGGGSGG
	GS-L11	RGGSGGGGSGG
		AKTTPKLEEGEFSEAR
		AKTTPKLEEGEFSEARV
		AKTTPKLGG
		SAKTTPKLGG
		SAKTTP
		RADAAP
		RADAAPTVS
		RADAAAAGGPGS
		RADAAAA$(G_4S)_4$
		SAKTTPKLEEGEFSEARV
		ADAAP
		ADAAPTVSIFPP
		TVAAP
		TVAAPSVFIFPP
		QPKAAP
		QPKAAPSVTLFPP
		AKTTPP
		AKTTPPSVTPLAP
		AKTTAP
		AKTTAPSVYPLAP
		ASTKGP
		ASTKGPSVFPLAP
		GGGGSGGGGSGGGGS

		GENKVEYAPALMALS
		GPAKELTPLKEAKVS
		GHEAAAVMQVQYPAS
		TVAAPSVFIFPPTVAAPSVFIFPP
		ASTKGPSVFPLAPASTKGPSVFPLAP
		GGGGSGGGGS
		GGSGGGGSG
		G/S based sequences (e.g., G4S and G4S repeats)

Table 56. Heavy (H) and Light Chain (L) Composition of Anti-VEGF-A/Anti-PDGF-BB DVD-Ig Molecules (first and second polypeptide chains are listed in alternating rows of the table)

SEQ ID NO	Corporate ID	DVD-Ig Variable Domain Name	Outer Variable Domain Name	Linker	Inner Variable Domain Name	SEQ ID NO VD1 – X1 – VD2 Formula
	NA	AB014-GS-9E8.4[a]	AB014 VH	GS-H10	hBDI-9E8.4 VH	
			AB014 VL	GS-L10	hBDI-9E8.4 VL	
	NA	9E8.4-GS-AB014[a]	hBDI-9E8.4 VH	GS-H10	AB014 VH	
			hBDI-9E8.4 VL	GS-L10	AB014 VL	
	NA	AB014-SS-9E8.4[a]	AB014 VH	HG-short	hBDI-9E8.4 VH	
			AB014 VL	LK-short	hBDI-9E8.4 VL	
	NA	9E8.4-SS-AB014[a]	hBDI-9E8.4 VH	HG-short	AB014 VH	
			hBDI-9E8.4 VL	LK-short	AB014 VL	
	NA	AB014-SL-9E8.4[a]	AB014 VH	HG-short	hBDI-9E8.4 VH	
			AB014 VL	LK-long	hBDI-9E8.4 VL	
	NA	9E8.4-SL-AB014[a]	hBDI-9E8.4 VH	HG-short	AB014 VH	
			hBDI-9E8.4 VL	LK-long	AB014 VL	
	NA	AB014-LS-9E8.4[a]	AB014 VH	HG-long	hBDI-9E8.4 VH	
			AB014 VL	LK-short	hBDI-9E8.4 VL	
	NA	9E8.4-LS-AB014[a]	hBDI-9E8.4 VH	HG-long	AB014 VH	
			hBDI-9E8.4 VL	LK-short	AB014 VL	
	PR-1563988	9E8.4-GS-4G8.3[a]	hBDI-9E8.4 VH	GS-H10	hBDB-4G8.3 VH	
			hBDI-9E8.4 VL	GS-L10	hBDB-4G8.3 VL	
	PR-1563990	9E8.4-SS-4G8.3[a]	hBDI-9E8.4 VH	HG-short	hBDB-4G8.3 VH	
			hBDI-9E8.4 VL	LK-short	hBDB-4G8.3 VL	
	PR-1563998	9E8.4-SL-4G8.3[a]	hBDI-9E8.4 VH	HG-short	hBDB-4G8.3 VH	
			hBDI-9E8.4 VL	LK-long	hBDB-4G8.3 VL	
	PR-1564009	9E8.4-LS-4G8.3[a]	hBDI-9E8.4 VH	HG-long	hBDB-4G8.3 VH	
			hBDI-9E8.4 VL	LK-short	hBDB-4G8.3 VL	
	PR-1564010	4G8.3-GS-9E8.4[a]	hBDB-4G8.3 VH	GS-H10	hBDI-9E8.4 VH	
			hBDB-4G8.3 VL	GS-H10	hBDI-9E8.4 VL	
	PR-1564011	4G8.3-SS-9E8.4[a]	hBDB-4G8.3 VH	HG-short	hBDI-9E8.4 VH	
			hBDB-4G8.3 VL	LK-short	hBDI-9E8.4 VL	
	PR-1564012	4G8.3-SL-9E8.4[a]	hBDB-4G8.3 VH	HG-short	hBDI-9E8.4 VH	
			hBDB-4G8.3 VL	LK-long	hBDI-9E8.4 VL	

	PR-1564013	4G8.3-LS-9E8.4[a]	hBDB-4G8.3 VH	HG-long	hBDI-9E8.4 VH	
			hBDB-4G8.3 VL	LK-short	hBDI-9E8.4 VL	
	PR-1569574	9E8.4-GS-4G8.3	hBDI-9E8.4 VH	GS-H10	hBDB-4G8.3 VH	
			hBDI-9E8.4 VL	GS-L10	hBDB-4G8.3 VL	
	PR-1569579	9E8.4-SL-4G8.3	hBDI-9E8.4 VH	HG-short	hBDB-4G8.3 VH	
			hBDI-9E8.4 VL	LK-long	hBDB-4G8.3 VL	
	PR-1575573	9E8.4-LS-4G8.3	hBDI-9E8.4 VH	HG-long	hBDB-4G8.3 VH	
			hBDI-9E8.4 VL	LK-short	hBDB-4G8.3 VL	
	PR-1572102	4G8.3-GS-9E8.4 (g)	hBDB-4G8.3 VH	GS-H10	hBDI-9E8.4 VH	
			hBDB-4G8.3 VL	GS-L10	hBDI-9E8.4 VL	
	PR-1572103	4G8.3-GS(11)-9E8.4 (g)	hBDB-4G8.3 VH	GS-H10	hBDI-9E8.4 VH	
			hBDB-4G8.3 VL	GS-L11	hBDI-9E8.4 VL	
	PR-1572104	4G8.3-GS(noR)-9E8.4 (g)	hBDB-4G8.3 VH	GS-H10	hBDI-9E8.4 VH	
			hBDB-4G8.3 VL	GS-L10(dR)	hBDI-9E8.4 VL	
	PR-1572105	4G8.3-SL-9E8.4 (g)	hBDB-4G8.3 VH	HG-short	hBDI-9E8.4 VH	
			hBDB-4G8.3 VL	LK-long	hBDI-9E8.4 VL	
	PR-1572106	4G8.3-LS-9E8.4 (g)	hBDB-4G8.3 VH	HG-long	hBDI-9E8.4 VH	
			hBDB-4G8.3 VL	LK-short	hBDI-9E8.4 VL	
	PR-1575832	4G8.3-GS-9E8.4E	hBDB-4G8.3 VH	GS-H10	hBDI-9E8.4E VH	
			hBDB-4G8.3 VL	GS-L10	hBDI-9E8.4E VL	
	PR-1575834	4G8.3-SL-9E8.4E	hBDB-4G8.3 VH	HG-short	hBDI-9E8.4E VH	
			hBDB-4G8.3 VL	LK-long	hBDI-9E8.4E VL	
	PR-1575835	4G8.3-LS-9E8.4E	hBDB-4G8.3 VH	HG-long	hBDI-9E8.4E VH	
			hBDB-4G8.3 VL	LK-short	hBDI-9E8.4E VL	
	PR-1577165	9A8.12-GS-9E8.4E	hBEW-9A8.12 VH	GS-H10	hBDI-9E8.4E VH	
			hBEW-9A8.12 VL	GS-L10	hBDI-9E8.4E VL	
	PR-1577166	9A8.12-SL-9E8.4E	hBEW-9A8.12 VH	HG-short	hBDI-9E8.4E VH	
			hBEW-9A8.12 VL	LK-long	hBDI-9E8.4E VL	
	PR-1577547	9A8.12-LS-9E8.4E	hBEW-9A8.12 VH	HG-long	hBDI-9E8.4E VH	
			hBEW-9A8.12 VL	LK-short	hBDI-9E8.4E VL	
	PR-1578137	9E8.4E-GS-9A8.12	hBDI-9E8.4E VH	GS-H10	hBEW-9A8.12 VH	
			hBDI-9E8.4E VL	GS-L10	hBEW-9A8.12 VL	
	PR-1577548	9E8.4E-SL-9A8.12	hBDI-9E8.4E VH	HG-short	hBEW-9A8.12 VH	
			hBDI-9E8.4E VL	LK-long	hBEW-9A8.12 VL	
	PR-1577550	9E8.4E-LS-9A8.12	hBDI-9E8.4E VH	HG-long	hBEW-9A8.12 VH	
			hBDI-9E8.4E VL	LK-short	hBEW-9A8.12 VL	
	PR-1598261	4G8.2-GS-9E8.4	hBDB-4G8.2 VH	GS-H10	hBDI-9E8.4 VH	
			hBDB-4G8.2 VL	GS-L10	hBDI-9E8.4 VL	
	PR-1598262	4G8.4-GS-9E8.4	hBDB-4G8.4 VH	GS-H10	hBDI-9E8.4 VH	
			hBDB-4G8.4 VL	GS-L10	hBDI-9E8.4 VL	
	PR-1598263	4G8.5-GS-9E8.4	hBDB-4G8.5 VH	GS-H10	hBDI-9E8.4 VH	
			hBDB-4G8.5 VL	GS-L10	hBDI-9E8.4 VL	
	PR-1598264	4G8.12-GS-9E8.4	hBDB-4G8.12 VH	GS-H10	hBDI-9E8.4 VH	

			hBDB-4G8.12 VL	GS-L10	hBDI-9E8.4 VL	
	PR-1598265	4G8.13-GS-9E8.4	hBDB-4G8.13 VH	GS-H10	hBDI-9E8.4 VH	
			hBDB-4G8.13 VL	GS-L10	hBDI-9E8.4 VL	
	PR-1598266	4G8.14-GS-9E8.4	hBDB-4G8.14 VH	GS-H10	hBDI-9E8.4 VH	
			hBDB-4G8.14 VL	GS-L10	hBDI-9E8.4 VL	
	PR-1613183	CL-34565_GS_CL-33675	CL-34565 VH	GS-H10	CL-33675 VH	
			CL-34565 VL	GS-L10(dR)	CL-33675 VL	
	PR-1613184	CL-34565_GS_9E8.4	CL-34565 VH	GS-H10	hBDI-9E8.4 VH	
			CL-34565 VL	GS-L10(dR)	hBDI-9E8.4 VL	
	PR-1613185	CL-34565_GS_3E2.1	CL-34565 VH	GS-H10	hBFU-3E2.1 VH	
			CL-34565 VL	GS-L10(dR)	hBFU-3E2.1 VL	
	PR-1611291	4G8.5_GS_CL-33675	hBDB-4G8.5 VH	GS-H10	CL-33675 VH	
			hBDB-4G8.5 VL	GS-L10(dR)	CL-33675 VL	
	PR-1612489	4G8.5_GS_9E8.4	hBDB-4G8.5 VH	GS-H10	hBDI-9E8.4 VH	
			hBDB-4G8.5 VL	GS-L10(dR)	hBDI-9E8.4 VL	
	PR-1610560	4G8.5_GS_3E2.1	hBDB-4G8.5 VH	GS-H10	hBFU-3E2.1 VH	
			hBDB-4G8.5 VL	GS-L10(dR)	hBFU-3E2.1 VL	
	PR-1610561	9E10.1_GS_CL-33675	hBEW-9E10.1 VH	GS-H10	CL-33675 VH	
			hBEW-9E10.1 VL	GS-L10(dR)	CL-33675 VL	
	PR-1612491	9E10.1_GS_9E8.4	hBEW-9E10.1 VH	GS-H10	hBDI-9E8.4 VH	
			hBEW-9E10.1 VL	GS-L10(dR)	hBDI-9E8.4 VL	
	PR-1610562	9E10.1_GS_3E2.1	hBEW-9E10.1 VH	GS-H10	hBFU-3E2.1 VH	
			hBEW-9E10.1 VL	GS-L10(dR)	hBFU-3E2.1 VL	
	PR-1612492	9E10.6_GS_CL-33675	hBEW-9E10.6 VH	GS-H10	CL-33675 VH	
			hBEW-9E10.6 VL	GS-L10(dR)	CL-33675 VL	
	PR-1612493	9E10.6_GS_9E8.4	hBEW-9E10.6 VH	GS-H10	hBDI-9E8.4 VH	
			hBEW-9E10.6 VL	GS-L10(dR)	hBDI-9E8.4 VL	
	PR-1610563	9E10.6_GS_3E2.1	hBEW-9E10.6 VH	GS-H10	hBFU-3E2.1 VH	
			hBEW-9E10.6 VL	GS-L10(dR)	hBFU-3E2.1 VL	
	PR-1611292	1B10.1_GS_CL-33675	hBEW-1B10.1 VH	GS-H10	CL-33675 VH	
			hBEW-1B10.1 VL	GS-L10(dR)	CL-33675 VL	
	PR-1612494	1B10.1_GS_9E8.4	hBEW-1B10.1 VH	GS-H10	hBDI-9E8.4 VH	
			hBEW-1B10.1 VL	GS-L10(dR)	hBDI-9E8.4 VL	
	PR-1610564	1B10.1_GS_3E2.1	hBEW-1B10.1 VH	GS-H10	hBFU-3E2.1 VH	
			hBEW-1B10.1 VL	GS-L10(dR)	hBFU-3E2.1 VL	
	PR-1611293	1E3.4_GS_CL-33675	hBEW-1E3.4 VH	GS-H10	CL-33675 VH	
			hBEW-1E3.4 VL	GS-L10(dR)	CL-33675 VL	

	PR-1611294	1E3.4_GS_9E8.4	hBEW-1E3.4 VH	GS-H10	hBDI-9E8.4 VH	
			hBEW-1E3.4 VL	GS-L10(dR)	hBDI-9E8.4 VL	
	PR-1612495	1E3.4_GS_3E2.1	hBEW-1E3.4 VH	GS-H10	hBFU-3E2.1 VH	
			hBEW-1E3.4 VL	GS-L10(dR)	hBFU-3E2.1 VL	
	PR-1613186	CL-33675_GS_CL-34565	CL-33675 VH	GS-H10	CL-34565 VH	
			CL-33675 VL	GS-L10(dR)	CL-34565 VL	
	PR-1612496	CL-33675_GS_4G8.5	CL-33675 VH	GS-H10	hBDB-4G8.5 VH	
			CL-33675 VL	GS-L10(dR)	hBDB-4G8.5 VL	
	PR-1611295	CL-33675_GS_9E10.1	CL-33675 VH	GS-H10	hBEW-9E10.1 VH	
			CL-33675 VL	GS-L10(dR)	hBEW-9E10.1 VL	
	PR-1611296	CL-33675_GS_9E10.6	CL-33675 VH	GS-H10	hBEW-9E10.6 VH	
			CL-33675 VL	GS-L10(dR)	hBEW-9E10.6 VL	
	PR-1612498	CL-33675_GS_1B10.1	CL-33675 VH	GS-H10	hBEW-1B10.1 VH	
			CL-33675 VL	GS-L10(dR)	hBEW-1B10.1 VL	
	PR-1611297	CL-33675_GS_1E3.4	CL-33675 VH	GS-H10	hBEW-1E3.4 VH	
			CL-33675 VL	GS-L10(dR)	hBEW-1E3.4 VL	
	PR-1613187	9E8.4_GS_CL-34565	hBDI-9E8.4 VH	GS-H10	CL-34565 VH	
			hBDI-9E8.4 VL	GS-L10(dR)	CL-34565 VL	
	PR-1613188	9E8.4_GS_4G8.5	hBDI-9E8.4 VH	GS-H10	hBDB-4G8.5 VH	
			hBDI-9E8.4 VL	GS-L10(dR)	hBDB-4G8.5 VL	
	PR-1611298	9E8.4_GS_9E10.1	hBDI-9E8.4 VH	GS-H10	hBEW-9E10.1 VH	
			hBDI-9E8.4 VL	GS-L10(dR)	hBEW-9E10.1 VL	
	PR-1611299	9E8.4_GS_9E10.6	hBDI-9E8.4 VH	GS-H10	hBEW-9E10.6 VH	
			hBDI-9E8.4 VL	GS-L10(dR)	hBEW-9E10.6 VL	
	PR-1611300	9E8.4_GS_1B10.1	hBDI-9E8.4 VH	GS-H10	hBEW-1B10.1 VH	
			hBDI-9E8.4 VL	GS-L10(dR)	hBEW-1B10.1 VL	
	PR-1611301	9E8.4_GS_1E3.4	hBDI-9E8.4 VH	GS-H10	hBEW-1E3.4 VH	
			hBDI-9E8.4 VL	GS-L10(dR)	hBEW-1E3.4 VL	
	PR-1613189	3E2.1_GS_CL-34565	hBFU-3E2.1 VH	GS-H10	CL-34565 VH	
			hBFU-3E2.1 VL	GS-L10(dR)	CL-34565 VL	
	PR-1612499	3E2.1_GS_4G8.5	hBFU-3E2.1 VH	GS-H10	hBDB-4G8.5 VH	
			hBFU-3E2.1 VL	GS-L10(dR)	hBDB-4G8.5 VL	
	PR-1612500	3E2.1_GS_9E10.1	hBFU-3E2.1 VH	GS-H10	hBEW-9E10.1 VH	
			hBFU-3E2.1 VL	GS-L10(dR)	hBEW-9E10.1 VL	
	PR-1612501	3E2.1_GS_9E10.6	hBFU-3E2.1 VH	GS-H10	hBEW-9E10.6	

					VH	
			hBFU-3E2.1 VL	GS-L10(dR)	hBEW-9E10.6 VL	
	PR-1612502	3E2.1_GS_1B10.1	hBFU-3E2.1 VH	GS-H10	hBEW-1B10.1 VH	
			hBFU-3E2.1 VL	GS-L10(dR)	hBEW-1B10.1 VL	
	PR-1613190	3E2.1_GS_1E3.4	hBFU-3E2.1 VH	GS-H10	hBEW-1E3.4 VH	
			hBFU-3E2.1 VL	GS-L10(dR)	hBEW-1E3.4 VL	
	PR-1629646	9E10.1_SL_CL-33675	hBEW-9E10.1 VH	HG-short	CL-33675 VH	
			hBEW-9E10.1 VL	LK-long	CL-33675 VL	
	PR-1629647	1B10.1_SL_CL-33675	hBEW-1B10.1 VH	HG-short	CL-33675 VH	
			hBEW-1B10.1 VL	LK-long	CL-33675 VL	
	PR-1629648	9E10.1_LS_CL-33675	hBEW-9E10.1 VH	HG-long	CL-33675 VH	
			hBEW-9E10.1 VL	LK-short	CL-33675 VL	
	PR-1629649	1B10.1_LS_CL-33675	hBEW-1B10.1 VH	HG-long	CL-33675 VH	
			hBEW-1B10.1 VL	LK-short	CL-33675 VL	
	PR-1564883	DVD3896[a]	hBDI-5H1.9 VH	HG-short	hBDB-4G8.13 VH	
			hBDI-5H1.9 VL	LK-long	hBDB-4G8.13 VL	
	PR-1564893	DVD3897[a]	hBDI-5H1.9 VH	HG-short	hBDB-4G8.14 VH	
			hBDI-5H1.9 VL	LK-long	hBDB-4G8.14 VL	
	PR-1564896	DVD3898[a]	hBDI-5H1.9 VH	HG-short	hBDB-4G8.15 VH	
			hBDI-5H1.9 VL	LK-long	hBDB-4G8.15 VL	
	PR-1564898	DVD3899[a]	hBDI-9E8.12 VH	HG-short	hBDB-4G8.14 VH	
			hBDI-9E8.12 VL	LK-long	hBDB-4G8.14 VL	
	PR-1564899	DVD3900[a]	hBDI-9E8.12 VH	HG-short	hBDB-4G8.15 VH	
			hBDI-9E8.12 VL	LK-long	hBDB-4G8.15 VL	
	PR-1565023	DVD3901[a]	hBDI-9E8.9 VH	HG-short	hBDB-4G8.13 VH	
			hBDI-9E8.9 VL	LK-long	hBDB-4G8.13 VL	
	PR-1565029	DVD3902[a]	hBDI-9E8.9 VH	HG-short	hBDB-4G8.14 VH	
			hBDI-9E8.9 VL	LK-long	hBDB-4G8.14 VL	
	PR-1565030	DVD3903[a]	hBDI-9E8.9 VH	HG-short	hBDB-4G8.15 VH	
			hBDI-9E8.9 VL	LK-long	hBDB-4G8.15 VL	
	PR-1565031	DVD3904[a]	hBDI-5H1.13 VH	HG-short	hBDB-4G8.14 VH	
			hBDI-5H1.13 VL	LK-long	hBDB-4G8.14 VL	
	PR-1565032	DVD3905[a]	hBDI-9E8.12 VH	HG-short	hBDB-4G8.15 VH	
			hBDI-9E8.12 VL	LK-long	hBDB-4G8.15 VL	

	PR-1565035	DVD3906[a]	hBDI-5H1.13 VH	HG-short	hBDB-4G8.15 VH	
			hBDI-5H1.13 VL	LK-long	hBDB-4G8.15 VL	
	PR-1565033	DVD3907[a]	hBDI-9E8.13 VH	HG-short	hBDB-4G8.15 VH	
			hBDI-9E8.13 VL	LK-long	hBDB-4G8.15 VL	

[a] These DVDs were made with Ig gamma-1 constant region L234A, L235A, all other DVDs made with Ig gamma-1 constant region L234A, L235A, and H435A.

Table 57. Heavy (H) and Light Chain (L) Amino Acid Composition of Some Anti-VEGF-A/Anti-PDGF-BB DVD-Ig Molecules

(Linker sequence in italics; CDR sequences in bold; HC = heavy chain and LC = light chain)

Sequence Identifier	DVD-Ig Variable Domain (Corporate ID)	Sequence
		12345678901234567890123456789012
SEQ ID NO:x	4G8.3-GS-9E8.4 HC (PR-1569574)	EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNY** **GMY**WVRQAPGQGLEWMG**WINTETGKPTYADDF** **KG**RFVFSLDTSVSTAYLQISSLKAEDTAVYYC AR**TNYYYRSYIFYFDY**WGQGTMVTVSS*GGGGS* *GGGGS*EVTLRESGPALVKPTQTLTLTCTFS**GF** **SLSTYGMGVG**WIRQPPGKALEWLA**NIWWDDDK** **YYNPSLKN**RLTISKDTSKNQVVLTMTNMDPVD TATYYCAR**IESIGTTYSFDY**WGQGTMVTVSSA STKGPSVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPK PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNAYTQ KSLSLSPGK
	4G8.3-GS-9E8.4 LC (PR-1569574)	DTVLTQSPATLSLSPGERATLSC**RASESVSTH** **MH**WYQQKPGQAPRLLIY**GASNLES**GVPARFSG SGSGTDFTLTISSLEPEDFAVYFC**QQSWNDPF** **T**FGQGTKLEIK*RGGSGGGGSG*EFVLTQSPGTL SLSPGERATLSC**ERSSGDIGDSYVS**WYQQKPG QAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTL TISRLEPEDFAVYYC**QSYDINIDIV**FGGGTKV EIKGTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQG LSSPVTKSFNRGEC
	4G8.3-SL-9E8.4 HC (PR-1569579)	EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNY** **GMY**WVRQAPGQGLEWMG**WINTETGKPTYADDF** **KG**RFVFSLDTSVSTAYLQISSLKAEDTAVYYC AR**TNYYYRSYIFYFDY**WGQGTMVTVSS*ASTKG* *P*EVTLRESGPALVKPTQTLTLTCTFS**GFSLST**

Sequence Identifier	DVD-Ig Variable Domain (Corporate ID)	Sequence
		123456789012345678901234567890123456789012
		YGMGVGWIRQPPGKALEWLA**NIWWDDDKYYNP SLKN**RLTISKDTSKNQVVLTMTNMDPVDTATY YCAR**IESIGTTYSFDY**WGQGTMVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDT LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVFSCSVMHEALHNAYTQKSLS LSPGK
	4G8.3-SL-9E8.4 LC (PR-1569579)	DTVLTQSPATLSLSPGERATLSC**RASESVSTH MH**WYQQKPGQAPRLLIY**GASNLES**GVPARFSG SGSGTDFTLTISSLEPEDFAVYFC**QQSWNDPF T**FGQGTKLEIK*RTVAAPSVFIFPP*EFVLTQSP GTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQ KPGQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTD FTLTISRLEPEDFAVYYC**QSYDINIDIV**FGGG TKVEIKGTVAAPSVFIFPPSDEQLKSGTASVV CLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDSTYSLSSTLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC
	4G8.3-LS-9E8.4 HC (PR-1575573)	EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNY GMY**WVRQAPGQGLEWMG**WINTETGKPTYADDF KG**RFVFSLDTSVSTAYLQISSLKAEDTAVYYC AR**TNYYYRSYIFYFDY**WGQGTMVTVSS*ASTKG PSVFPLAP*EVTLRESGPALVKPTQTLTLTCTF S**GFSLSTYGMGVG**WIRQPPGKALEWLA**NIWWD DDKYYNPSLKN**RLTISKDTSKNQVVLTMTNMD PVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTV SSASTKGPSVFPLAPSSKSTSGGTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV DKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNA YTQKSLSLSPGK
	4G8.3-LS-9E8.4 LC (PR-1575573)	DTVLTQSPATLSLSPGERATLSC**RASESVSTH MH**WYQQKPGQAPRLLIY**GASNLES**GVPARFSG SGSGTDFTLTISSLEPEDFAVYFC**QQSWNDPF T**FGQGTKLEIK*RTVAAP*EFVLTQSPGTLSLSP GERATLSC**ERSSGDIGDSYVS**WYQQKPGQAPR LVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISR

Sequence Identifier	DVD-Ig Variable Domain (Corporate ID)	Sequence
		123456789012345678901234567890 12
		LEPEDFAVYYC**QSYDINIDIV**FGGGTKVEIKG TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDST YSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC
	4G8.3-GS-9E8.4 (g) HC (PR-1572102)	EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNY GMY**WVRQAPGQGLEWMG**WINTETGKPTYADDF KG**RFVFSLDTSVSTAYLQISSLKAEDTAVYYC AR**TNYYYRSYIFYFDY**WGQGTMVTVSS*GGGGS GGGGS*EVTLRESGPALVKPTQTLTLTCTFS**GF SLSTYGMGVG**WIRQPPGKALEWLA**NIWWDDDK YYNPSLKN**RLTISKDTSKNQVVLTMTNMDPVD TATYYCAR**IESIGTTYSFDY**WGQGTMVTVSSA STKGPSVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPK PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNAYTQ KSLSLSPGK
	4G8.3-GS-9E8.4 (g) LC (PR-1572102)	DTVLTQSPATLSLSPGERATLSC**RASESVSTH MH**WYQQKPGQAPRLLIY**GASNLES**GVPARFSG SGSGTDFTLTISSLEPEDFAVYFC**QQSWNDPF T**FGQGTKLEIK*RGGSGGGGSG*EFVLTQSPGTL SLSPGERATLSC**ERSSGDIGDSYVS**WYQQKPG QAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTL TISRLEPEDFAVYYC**QSYDINIDIV**FGGGTKV EIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQG LSSPVTKSFNRGEC
	4G8.3-SL-9E8.4 (g) HC (PR-1572105)	EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNY GMY**WVRQAPGQGLEWMG**WINTETGKPTYADDF KG**RFVFSLDTSVSTAYLQISSLKAEDTAVYYC AR**TNYYYRSYIFYFDY**WGQGTMVTVSS*ASTKG P*EVTLRESGPALVKPTQTLTLTCTFS**GFSLST YGMGVG**WIRQPPGKALEWLA**NIWWDDDKYYNP SLKN**RLTISKDTSKNQVVLTMTNMDPVDTATY YCAR**IESIGTTYSFDY**WGQGTMVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDT LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKALPAPIEKTISKAKGQPREP

Sequence Identifier	DVD-Ig Variable Domain (Corporate ID)	Sequence
		12345678901234567890123456789012
		QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVFSCSVMHEALHNAYTQKSLS LSPGK
	4G8.3-SL-9E8.4 (g) LC (PR-1572105)	DTVLTQSPATLSLSPGERATLSC**RASESVSTH MH**WYQQKPGQAPRLLIY**GASNLES**GVPARFSG SGSGTDFTLTISSLEPEDFAVYFC**QQSWNDPF T**FGQGTKLEIK*RTVAAPSVFIFPP*EFVLTQSP GTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQ KPGQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTD FTLTISRLEPEDFAVYYC**QSYDINIDIV**FGGG TKVEIKrTVAAPSVFIFPPSDEQLKSGTASVV CLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDSTYSLSSTLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC
	9E10.1_GS_CL-33675 HC (PR-1610561)	EIQLVQSGSELKKPGASVKVSCKAS**GYTFTNY GMY**WVKQAPGQGLEYMG**WIDTETGRPTYADDF KG**RFVFSLDTSVSTAYLQISSLKAEDTAVYFC AR**WSGDTTGIRGPWFAY**WGQGTLVTVSS*GGGG SGGGGS*EVTLRESGPALVKPTQTLTLTCTFS**G FSLSTYGMGVG**WIRQPPGKALEWLA**NIWWDDD KYYNPSLKN**RLTISKDTSKNQVVLTMTNMDPV DTATYYCAR**IESSGPKYSFDY**WGQGTMVTVSS ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPP KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFF LYSKLTVDKSRWQQGNVFSCSVMHEALHNAYT QKSLSLSPGK
	9E10.1_GS_CL-33675 LC (PR-1610561)	DIRMTQSPSSLSASVGDRVTIEC**LASEDIYSD LA**WYQQKPGKSPKLLIY**NANGLQN**GVPSRFSG SGSGTDYSLTISSLQPEDVATYFC**QQYNYFPG T**FGQGTKLEIK*GGSGGGGSGG*EIVLTQSPGTL SLSPGERATLSC**RASSGSIWYSFVS**WYQQKPG QAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTL TISRLEPEDFAVYYC**QSYGINIDVV**FGGGTKV EIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQG LSSPVTKSFNRGEC
	1B10.1_GS_CL-33675 HC (PR-1611292)	EVQLVESGGGLVQPGGSLRLSCAAS**GFSFSKY DMA**WFRQAPGKGLEWVA**SITTSGVGTYYRDSV KG**RFTVSRDNAKSTLYLQMNSLRAEDTAVYYC AR**GYGAMDA**WGQGTTVTVSSGGGGSGGGGSEV TLRESGPALVKPTQTLTLTCTFS**GFSLSTYGM**

Sequence Identifier	DVD-Ig Variable Domain (Corporate ID)	Sequence
		12345678901234567890123456789012
		GVGWIRQPPGKALEWLA**NIWWDDDKYYNPSLK** **N**RLTISKDTSKNQVVLTMTNMDPVDTATYYCA R**IESSGPKYSFDY**WGQ GTMVTVSSASTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVMHEALHNAYTQKSLSLSP GK
	1B10.1_GS_CL-33675 LC (PR-1611292)	DIQMTQSPSSLSASVGDRVTITC**KASQDIDDY** **LS**WYQQKPGKSPKLVIY**AATRLAD**GVPSRFSG SGSGTDYTLTISSLQPEDFATYYC**LQSSSTPW** **T**FGGGTKVEIKGGSGGGGSGGEIVLTQSPGTL SLSPGERATLSC**RASSGSIWYSFVS**WYQQKPG QAPRLLIY**ADDQRAS**GIPDRFSGSGSGTDFTL TISRLEPEDFAVYYC**QSYGINIDVV**FGGGTKV EIKRTVAAPSVFIFPP SDEQLKSGTASVVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Example 11: Generation of CO-DVD-Ig Molecules

[0397] Cross-over DVD-Ig binding proteins are constructed as shown below. Each of VD1, VD2, VD3 and VD4 could be the VH or VL from a mAb. In cross-over DVD-Ig, VD1 and VD4 form one antigen binding domain. VD2 and VD3 form another binding domain.

Table 58. Heavy Chain and Light Chain Amino Acid Sequences of Anti-Human VEGF-A/Anti-Human PDGF-BB Cross-over DVD-Ig Molecules (Linker sequence in italics; CDR sequences in bold)

Seq ID No	Name (Corporate ID)	Sequence
		12345678901234567890123456789012345678901234567890

	CODV001 HC (PR-1565040)	EVQLVESGGGLVQPGGSLRLSCAAS**GYTFTNYGMN**WVRQA PGKGLEWVG**WINTYTGEPTYAADFKR**RFTFSLDTSKSTAY LQMNSLRAEDTAVYYCAK**YPHYYGSSHWYFDV**WGQGTLVT VSS*G*EVTLKESGPALVKPTQTLTLTCTFS**GFSLSTFGMGV G**WIRQPPGKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTS KNQAVLTITNMDPVDTATYYCAR**ISTGISSYYVMDA**WGQG TTVTVSS*GG*ASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTV PSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP CPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPGK
	CODV001 LC (PR-1565040)	DFQLTQSPSSLSASVGDRVTITC**ERSSGDIGDTYVS**WYQQ KPGKAPKNVIY**GNDQRPS**GVPSRFSGSGSGNSATLTISSL QPEDFATYFC**QSYDSDIDIV**FGQGTKVEIK*GGGSGGG*DIQ MTQSPSSLSASVGDRVTITC**SASQDISNYLN**WYQQKPGKA PKVLIY**FTSSLHS**GVPSRFSGSGSGTDFTLTISSLQPEDF ATYYC**QQYSTVPWT**FGQGTKVEIK*GGGSG*RTVAAPSVFIF PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC
	CODV002 HC (PR-1565042)	EVTLKESGPALVKPTQTLTLTCTFS**GFSLSTFGMGVG**WIR QPPGKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQA VLTITNMDPVDTATYYCAR**ISTGISSYYVMDA**WGQGTTVT VSS*G*EVQLVESGGGLVQPGGSLRLSCAAS**GYTFTNYGMN**W VRQAPGKGLEWVG**WINTYTGEPTYAADFKR**RFTFSLDTSK STAYLQMNSLRAEDTAVYYCAK**YPHYYGSSHWYFDV**WGQG TLVTVSS*GG*ASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTV PSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP CPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPGK
	CODV002 LC (PR-1565042)	DIQMTQSPSSLSASVGDRVTITC**SASQDISNYLN**WYQQKP GKAPKVLIY**FTSSLHS**GVPSRFSGSGSGTDFTLTISSLQP EDFATYYC**QQYSTVPWT**FGQGTKVEIK*GGGSGGG*DFQLTQ SPSSLSASVGDRVTITC**ERSSGDIGDTYVS**WYQQKPGKAP KNVIY**GNDQRPS**GVPSRFSGSGSGNSATLTISSLQPEDFA TYFC**QSYDSDIDIV**FGQGTKVEIK*GGGSG*RTVAAPSVFIF PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC
	CODV003 HC (PR-1565044)	EVQLVESGGGLVQPGGSLRLSCAAS**GYTFTNYGMN**WVRQA PGKGLEWVG**WINTYTGEPTYAADFKR**RFTFSLDTSKSTAY LQMNSLRAEDTAVYYCAK**YPHYYGSSHWYFDV**WGQGTLVT VSS*G*EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGV G**WIRQPPGKGLEWLA**NIWWDDDKYYNPSLKN**RLTISKDTS KNQAVLTITNMDPVDTATYYCAR**IESIGTTYSFDY**WGQGT MVTVSS*GG*ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY

		FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK
	CODV003 LC (PR-1565044)	DFQLTQSPSSLSASVGDRVTITC**ERSSGDIGDSYVS**WYQQ KPGKAPKNVIY**ADDQRPS**GVPSRFSGSGSGNSASLTISSL QPEDFATYFC**QSYDINIDIV**FGQGTKVEIK*GGGSGGG*DIQ MTQSPSSLSASVGDRVTITC**SASQDISNYLN**WYQQKPGKA PKVLIY**FTSSLHS**GVPSRFSGSGSGTDFTLTISSLQPEDF ATYYC**QQYSTVPWT**FGQGTKVEIK*GGGSG*RTVAAPSVFIF PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC
	CODV004 HC (PR-1565051)	EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIR QPPGKGLEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQA VLTITNMDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTV SS*G*EVQLVESGGGLVQPGGSLRLSCAAS**GYTFTNYGMN**WV RQAPGKGLEWVG**WINTYTGEPTYAADFKR**RFTFSLDTSKS TAYLQMNSLRAEDTAVYYCAK**YPHYYGSSHWYFDV**WGQGT LVTVSS*GG*ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK
	CODV004 LC (PR-1565051)	DIQMTQSPSSLSASVGDRVTITC**SASQDISNYLN**WYQQKP GKAPKVLIY**FTSSLHS**GVPSRFSGSGSGTDFTLTISSLQP EDFATYYC**QQYSTVPWT**FGQGTKVEIK*GGGSGGG*DFQLTQ SPSSLSASVGDRVTITC**ERSSGDIGDSYVS**WYQQKPGKAP KNVIY**ADDQRPS**GVPSRFSGSGSGNSASLTISSLQPEDFA TYFC**QSYDINIDIV**FGQGTKVEIK*GGGSG*RTVAAPSVFIF PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC
	CODV005 HC (PR-1565083)	EVQLVESGGGLVQPGGSLRLSCAAS**GYTFTNYGMY**WVKQA PGKGLEYMG**WINTETGKPTYADDFKG**RFTFSLDTSKSTAY LQMNSLRAEDTAVYFCAR**TNYYYRSYIFYFDY**WGQGTLVT VSS*G*EVTLKESGPALVKPTQTLTLTCTFS**GFSLSTFGMGV G**WIRQPPGKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTS KNQAVLTITNMDPVDTATYYCAR**ISTGISSYYVMDA**WGQG TTVTVSS*GG*ASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTV PSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP CPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM

		HEALHNHYTQKSLSLSPGK
	CODV005 LC (PR-1565083)	DFQLTQSPSSLSASVGDRVTITC**ERSSGDIGDTYVS**WYQQ KPGKAPKNVIY**GNDQRPS**GVPSRFSGSGSGNSATLTISSL QPEDFATYFC**QSYDSDIDIV**FGQGTKVEIK*GGGSGGG*DTQ LTQSPSSLSASVGDRVTISC**RASESVSTHMH**WYQQKPGKA PKLLIY**GASNLES**GVPSRFSGSGSGTDFTLTISSLQPEDF ATYFC**QQSWNDPFT**FGQGTKVEIK*GGGSG*RTVAAPSVFIF PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC
	CODV006 HC (PR-1565084)	EVTLKESGPALVKPTQTLTLTCTFS**GFSLSTFGMGVG**WIR QPPGKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQA VLTITNMDPVDTATYYCAR**ISTGISSYYVMDA**WGQGTTVT VSS*G*EVQLVESGGGLVQPGGSLRLSCAAS**GYTFTNYGMY**W VKQAPGKGLEYMG**WINTETGKPTYADDFKG**RFTFSLDTSK STAYLQMNSLRAEDTAVYFCAR**TNYYYRSYIFYFDY**WGQG TLVTVSS*GG*ASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTV PSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP CPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPGK
	CODV006 LC (PR-1565084)	DTQLTQSPSSLSASVGDRVTISC**RASESVSTHMH**WYQQKP GKAPKLLIY**GASNLES**GVPSRFSGSGSGTDFTLTISSLQP EDFATYFC**QQSWNDPFT**FGQGTKVEIK*GGGSGGG*DFQLTQ SPSSLSASVGDRVTITC**ERSSGDIGDTYVS**WYQQKPGKAP KNVIY**GNDQRPS**GVPSRFSGSGSGNSATLTISSLQPEDFA TYFC**QSYDSDIDIV**FGQGTKVEIK*GGGSG*RTVAAPSVFIF PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC
	CODV007 HC (PR-1565085)	EVQLVESGGGLVQPGGSLRLSCAAS**GYTFTNYGMY**WVKQA PGKGLEYMG**WINTETGKPTYADDFKG**RFTFSLDTSKSTAY LQMNSLRAEDTAVYFCAR**TNYYYRSYIFYFDY**WGQGTLVT VSS*G*EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGV G**WIRQPPGKGLEWLA**NIWWDDDKYYNPSLKN**RLTISKDTS KNQAVLTITNMDPVDTATYYCAR**IESIGTTYSFDY**WGQGT MVTVSS*GG*ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK
	CODV007 LC (PR-1565085)	DFQLTQSPSSLSASVGDRVTITC**ERSSGDIGDSYVS**WYQQ KPGKAPKNVIY**ADDQRPS**GVPSRFSGSGSGNSASLTISSL QPEDFATYFC**QSYDINIDIV**FGQGTKVEIK*GGGSGGG*DTQ LTQSPSSLSASVGDRVTISC**RASESVSTHMH**WYQQKPGKA PKLLIY**GASNLES**GVPSRFSGSGSGTDFTLTISSLQPEDF ATYFC**QQSWNDPFT**FGQGTKVEIK*GGGSG*RTVAAPSVFIF

		PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC
	CODV008 HC (PR-1565086)	EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIR QPPGKGLEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQA VLTITNMDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTV SS*G*EVQLVESGGGLVQPGGSLRLSCAAS**GYTFTNYGMY**WV KQAPGKGLEYMG**WINTETGKPTYADDFKG**RFTFSLDTSKS TAYLQMNSLRAEDTAVYFCAR**TNYYYRSYIFYFDY**WGQGT LVTVSS*GG*ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK
	CODV008 LC (PR-1565086)	DTQLTQSPSSLSASVGDRVTISC**RASESVSTHMH**WYQQKP GKAPKLLIY**GASNLES**GVPSRFSGSGSGTDFTLTISSLQP EDFATYFC**QQSWNDPFT**FGQGTKVEIK*GGGSGGG*DFQLTQ SPSSLSASVGDRVTITC**ERSSGDIGDSYVS**WYQQKPGKAP KNVIY**ADDQRPS**GVPSRFSGSGSGNSASLTISSLQPEDFA TYFC**QSYDINIDIV**FGQGTKVEIK*GGGSG*RTVAAPSVFIF PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC
	CODV009 HC (PR-1571821)	EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQA PGQGLEWMG**WINTETGKPTYADDFKG**RFVFSLDTSVSTAY LQISSLKAEDTAVYYCAR**TNYYYRSYIFYFDY**WGQGTMVT VSS*G*EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGV G**WIRQPPGKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTS KNQVVLTMTNMDPVDTATYYCAR**IESIGTTYSFDY**WGQGT MVTVSS*GG*ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH EALHNAYTQKSLSLSPGK
	CODV009 LC (PR-1571821)	EFVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQ KPGQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRL EPEDFAVYYC**QSYDINIDIV**FGGGTKVEIK*GGGSGGG*DTV LTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPGQA PRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPEDF AVYFC**QQSWNDPFT**FGQGTKLEIK*GGGSG*RTVAAPSVFIF PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC
	CODV010 HC (PR-1571823)	EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIR QPPGKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQV VLTMTNMDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTV SS*G*EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WV

		RQAPGQGLEWMG**WINTETGKPTYADDFKG**RFVFSLDTSVS TAYLQISSLKAEDTAVYYCAR**TNYYYRSYIFYFDY**WGQGT MVTVSS*GG*ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH EALHNAYTQKSLSLSPGK
	CODV010 LC (PR-1571823)	DTVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKP GQAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEP EDFAVYFC**QQSWNDPFT**FGQGTKLEIK*GGGSGGG*EFVLTQ SPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKPGQAP RLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPEDFA VYYC**QSYDINIDIV**FGGGTKVEIK*GGGSG*RTVAAPSVFIF PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC
	CODV011 HC (PR-1575521)	EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQA PGQGLEWMG**WINTETGKPTYADDFKG**RFVFSLDTSVSTAY LQISSLKAEDTAVYYCAR**TNYYYRSYIFYFDY**WGQGTMVT VSS*GGGGSGGGGS*EFVLTQSPGTLSLSPGERATLSC**ERSS GDIGDSYVS**WYQQKPGQAPRLVIY**ADDQRPS**GIPDRFSGS GSGTDFTLTISRLEPEDFAVYYC**QSYDINIDIV**FGGGTKV EIK*GGGSG*ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH EALHNAYTQKSLSLSPGK
	CODV011 LC (PR-1575521)	EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIR QPPGKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQV VLTMTNMDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTV SS**GGGGSGGGGS**DTVLTQSPATLSLSPGERATLSC**RASES VSTHMH**WYQQKPGQAPRLLIY**GASNLES**GVPARFSGSGSG TDFTLTISSLEPEDFAVYFC**QQSWNDPFT**FGQGTKLEIK*G GGSG*RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSK ADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
	CODV012 HC (PR-1571824)	EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQA PGQGLEWMG**WINTETGKPTYADDFKG**RFVFSLDTSVSTAY LQISSLKAEDTAVYYCAR**TNYYYRSYIFYFDY**WGQGTMVT VSS*GGGGSGGG*EFVLTQSPGTLSLSPGERATLSC**ERSSGD IGDSYVS**WYQQKPGQAPRLVIY**ADDQRPS**GIPDRFSGSGS GTDFTLTISRLEPEDFAVYYC**QSYDINIDIV**FGGGTKVEI K**GGGSG**ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS SLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA PEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ

		DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNAYTQKSLSLSPGK
	CODV012 LC (PR-1571824)	EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIR QPPGKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQV VLTMTNMDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTV SS*GGGGSGGG*DTVLTQSPATLSLSPGERATLSC**RASESVS THMH**WYQQKPGQAPRLLIY**GASNLES**GVPARFSGSGSGTD FTLTISSLEPEDFAVYFC**QQSWNDPFT**FGQGTKLEIK*GGG SG*RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAK VQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKAD YEKHKVYACEVTHQGLSSPVTKSFNRGEC
	CODV013 HC (PR-1571825)	EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQA PGQGLEWMG**WINTETGKPTYADDFKG**RFVFSLDTSVSTAY LQISSLKAEDTAVYYCAR**TNYYYRSYIFYFDY**WGQGTMVT VSS*GGGGSGGG*EFVLTQSPGTLSLSPGERATLSC**ERSSGD IGDSYVS**WYQQKPGQAPRLVIY**ADDQRPS**GIPDRFSGSGS GTDFTLTISRLEPEDFAVYYC**QSYDINIDIV**FGGGTKVEI K*GGS*ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE AAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH NAYTQKSLSLSPGK
	CODV013 LC (PR-1571825)	EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIR QPPGKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQV VLTMTNMDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTV SS*GGGGSGGG*DTVLTQSPATLSLSPGERATLSC**RASESVS THMH**WYQQKPGQAPRLLIY**GASNLES**GVPARFSGSGSGTD FTLTISSLEPEDFAVYFC**QQSWNDPFT**FGQGTKLEIK*GGG SG*RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAK VQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKAD YEKHKVYACEVTHQGLSSPVTKSFNRGEC
	CODV014 HC (PR-1571826)	EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQA PGQGLEWMG**WINTETGKPTYADDFKG**RFVFSLDTSVSTAY LQISSLKAEDTAVYYCAR**TNYYYRSYIFYFDY**WGQGTMVT VSS*GGGGS*EFVLTQSPGTLSLSPGERATLSC**ERSSGDIGD SYVS**WYQQKPGQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTD FTLTISRLEPEDFAVYYC**QSYDINIDIV**FGGGTKVEIK*GG S*ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQ TYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNAY TQKSLSLSPGK
	CODV014 LC (PR-1571826)	EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIR QPPGKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQV VLTMTNMDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTV

		SS*GGGGSGGG*DTVLTQSPATLSLSPGERATLSC**RASESVS THMH**WYQQKPGQAPRLLIY**GASNLES**GVPARFSGSGSGTD FTLTISSLEPEDFAVYFC**QQSWNDPFT**FGQGTKLEIK*GGG SG*RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAK VQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKAD YEKHKVYACEVTHQGLSSPVTKSFNRGEC
	CODV015 HC (PR-1571827)	EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQA PGQGLEWMG**WINTETGKPTYADDFKG**RFVFSLDTSVSTAY LQISSLKAEDTAVYYCAR**TNYYYRSYIFYFDY**WGQGTMVT VSS*GGGGSGGG*EFVLTQSPGTLSLSPGERATLSC**ERSSGD IGDSYVS**WYQQKPGQAPRLVIY**ADDQRPS**GIPDRFSGSGS GTDFTLTISRLEPEDFAVYYC**QSYDINIDIV**FGGGTKVEI K*GGGSG*ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS SLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA PEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNAYTQKSLSLSPGK
	CODV015 LC (PR-1571827)	EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIR QPPGKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQV VLTMTNMDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTV SS*GGGGSGGG*DTVLTQSPATLSLSPGERATLSC**RASESVS THMH**WYQQKPGQAPRLLIY**GASNLES**GVPARFSGSGSGTD FTLTISSLEPEDFAVYFC**QQSWNDPFT**FGQGTKLEIK*GGS* RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
	CODV016 HC (PR-1571828)	EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQA PGQGLEWMG**WINTETGKPTYADDFKG**RFVFSLDTSVSTAY LQISSLKAEDTAVYYCAR**TNYYYRSYIFYFDY**WGQGTMVT VSS*GGGGSGGG*EFVLTQSPGTLSLSPGERATLSC**ERSSGD IGDSYVS**WYQQKPGQAPRLVIY**ADDQRPS**GIPDRFSGSGS GTDFTLTISRLEPEDFAVYYC**QSYDINIDIV**FGGGTKVEI K*GGGSG*ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS SLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA PEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNAYTQKSLSLSPGK
	CODV016 LC (PR-1571828)	EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIR QPPGKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQV VLTMTNMDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTV SS*GGGGS*DTVLTQSPATLSLSPGERATLSC**RASESVSTHM H**WYQQKPGQAPRLLIY**GASNLES**GVPARFSGSGSGTDFTL TISSLEPEDFAVYFC**QQSWNDPFT**FGQGTKLEIK*GGS*RTV AAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKV DNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHK VYACEVTHQGLSSPVTKSFNRGEC
	CODV017 HC	DTVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKP

	(PR-1571830)	GQAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEP EDFAVYFC**QQSWNDPFT**FGQGTKLEIK*GGGSGGG*EFVLTQ SPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKPGQAP RLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPEDFA VYYC**QSYDINIDIV**FGGGTKVEIK*GGGSG*ASTKGPSVFPL APSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNAYTQKSLSLSPGK
	CODV017 LC (PR-1571830)	EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIR QPPGKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQV VLTMTNMDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTV SS*G*EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WV RQAPGQGLEWMG**WINTETGKPTYADDFKG**RFVFSLDTSVS TAYLQISSLKAEDTAVYYCAR**TNYYYRSYIFYFDY**WGQGT MVTVSS*GGR*TVAAPSVFIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
	CODV018 HC (PR-1571831)	EFVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQ KPGQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRL EPEDFAVYYC**QSYDINIDIV**FGGGTKVEIK*GGGSGGG*DTV LTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKPGQA PRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEPEDF AVYFC**QQSWNDPFT**FGQGTKLEIK*GGGSG*ASTKGPSVFPL APSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNAYTQKSLSLSPGK
	CODV018 LC (PR-1571831)	EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQA PGQGLEWMG**WINTETGKPTYADDFKG**RFVFSLDTSVSTAY LQISSLKAEDTAVYYCAR**TNYYYRSYIFYFDY**WGQGTMVT VSS*G*EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGV** **G**WIRQPPGKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTS KNQVVLTMTNMDPVDTATYYCAR**IESIGTTYSFDY**WGQGT MVTVSS*GG*RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
	CODV019 HC (PR-1571832)	DTVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKP GQAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEP EDFAVYFC**QQSWNDPFT**FGQGTKLEIK*GGGSGGGG*EVTLR ESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPPGK ALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMT NMDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS*LGG* *CGGGS*ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP EAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE

		VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNAYTQKSLSLSPGK
	CODV019 LC (PR-1571832)	EFVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQ KPGQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRL EPEDFAVYYC**QSYDINIDIV**FGGGTKVEIK*GGGSGGGG*EV QLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPG QGLEWMG**WINTETGKPTYADDFKG**RFVFSLDTSVSTAYLQ ISSLKAEDTAVYYCAR**TNYYYRSYIFYFDY**WGQGTMVTVS S*LGGCGGGS*RTVAAPSVFIFPPSDEQLKSGTASVVCLLNN FYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
	CODV020 HC (PR-1571836)	EFVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQ KPGQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRL EPEDFAVYYC**QSYDINIDIV**FGGGTKVEIK*GGGSGGGG*EV QLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQAPG QGLEWMG**WINTETGKPTYADDFKG**RFVFSLDTSVSTAYLQ ISSLKAEDTAVYYCAR**TNYYYRSYIFYFDY**WGQGTMVTVS S*LGGCGGGS*ASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTV PSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP CPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNAYTQKSLSLSPGK
	CODV020 LC (PR-1571836)	DTVLTQSPATLSLSPGERATLSC**RASESVSTHMH**WYQQKP GQAPRLLIY**GASNLES**GVPARFSGSGSGTDFTLTISSLEP EDFAVYFC**QQSWNDPFT**FGQGTKLEIK*GGGSGGGG*EVTLR ESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPPGK ALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMT NMDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS*LGG CGGGS*RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLS KADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
	CODV021 HC (PR-1577053)	EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQA PGQGLEWMG**WINTETGKPTYADDFKG**RFVFSLDTSVSTAY LQISSLKAEDTAVYYCAR**TNYYYRSYIFYFDY**WGQGTMVT VSS*GGGGSGGG*EFVLTQSPGTLSLSPGERATLSCERSSGD IGESYVSWYQQKPGQAPRLVIY**ADDQRPS**GIPDRFSGSGS GTDFTLTISRLEPEDFAVYYC**QSYDINIDIV**FGGGTKVEI K*GGGSG*ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS SLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA PEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNAYTQKSLSLSPGK
	CODV021 LC (PR-1577053)	EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIR QPPGKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQV

		VLTMTNMDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTV SS*GGGGSGGG*DTVLTQSPATLSLSPGERATLSC**RASESVS THMH**WYQQKPGQAPRLLIY**GASNLES**GVPARFSGSGSGTD FTLTISSLEPEDFAVYFC**QQSWNDPFT**FGQGTKLEIK*GGS* RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
	CODV022 HC (PR-1577056)	EVQLVQSGSELKKPGASVKVSCKAS**GYTFTNYGMY**WVRQA PGQGLEWMG**WINTETGKPTYADDFKG**RFVFSLDTSVSTAY LQISSLKAEDTAVYYCAR**TNYYYRSYIFYFDY**WGQGTMVT VSS*GGGGSGGG*EFVLTQSPGTLSLSPGERATLSCERSSGD IGESYVSWYQQKPGQAPRLVIY**ADDQRPS**GIPDRFSGSGS GTDFTLTISRLEPEDFAVYYC**QSYDINIDIV**FGGGTKVEI K*GGGSG*ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS SLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA PEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNAYTQKSLSLSPGK
	CODV022 LC (PR-1577056)	EVTLRESGPALVKPTQTLTLTCTFS**GFSLSTYGMGVG**WIR QPPGKALEWLA**NIWWDDDKYYNPSLKN**RLTISKDTSKNQV VLTMTNMDPVDTATYYCAR**IESIGTTYSFDY**WGQGTMVTV SS*GGGGS*DTVLTQSPATLSLSPGERATLSC**RASESVSTHM H**WYQQKPGQAPRLLIY**GASNLES**GVPARFSGSGSGTDFTL TISSLEPEDFAVYFC**QQSWNDPFT**FGQGTKLEIK*GGS*RTV AAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKV DNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHK VYACEVTHQGLSSPVTKSFNRGEC

Example 12: Generation of scFv-IgG Fusion Proteins

[0398] All Ig-scFv molecules used the same anti-VEGF-A mAb AB014 as the IgG molecule. A single chain Fv (scFv) anti-PDGF-BB antibody was fused to the C-terminus of AB014 heavy chain using various length of GS linker using standard molecular cloning techniques. Four different heavy chains and one common light chain were made, as shown in the table below. Each heavy chain and the common light chain were co-transfected into HEK293 cells and the resulting Ig-scFv fusion proteins were purified using rProtein-A chromatography.

Table 59: Heavy Chain and Light Chain Amino Acid Sequences of Anti-human VEGF-A/anti-human PDGF-BB Ig-scFv Molecules (Linker sequence in italics; CDR sequences in bold)

Seq ID No	Name (Corporate ID)	Sequence
		12345678901234567890123456789012345678 90
	AB014-GS6-9E8.4 VH-VK HC (PR-1599234)	EVQLVESGGGLVQPGGSLRLSCAAS**GYTFTNYGMN**WVRQA PGKGLEWVG**WINTYTGEPTYAADFKR**RFTFSLDTSKSTAY LQMNSLRAEDTAVYYCAK**YPHYYGSSHWYFDV**WGQGTLVT

		VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEA AGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN AYTQKSLSLSPGK*GGSGGG*EVTLRESGPALVKPTQTLTLT CTFS**GFSLSTYGMGVG**WIRQPPGKALEWLA**NIWWDDDKYY** **NPSLKN**RLTISKDTSKNQVVLTMTNMDPVDTATYYCAR**IE** **SIGTTYSFDY**WGQGTMVTVSS*GGGGSGGGGSGGGGS*EIVL TQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQKPGQ APRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRLEPED FAVYYC**QSYDINIDIV**FGGGTKVEIK
	AB014-GS10-9E8.4 VH-VK HC (PR-1599236)	EVQLVESGGGLVQPGGSLRLSCAAS**GYTFTNYGMN**WVRQA PGKGLEWVG**WINTYTGEPTYAADFKR**RFTFSLDTSKSTAY LQMNSLRAEDTAVYYCAK**YPHYYGSSHWYFDV**WGQGTLVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEA AGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN AYTQKSLSLSPGK*GGSGGGGSGGG*EVTLRESGPALVKPTQT LTLTCTFS**GFSLSTYGMGVGW**IRQPPGKALEWLA**NIWWDD** **DKYYNPSLKN**RLTISKDTSKNQVVLTMTNMDPVDTATYYC AR**IESIGTTYSFDY**WGQGTMVTVSS*GGGGSGGGGSGGGGS* EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYVS**WYQQ KPGQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTLTISRL EPEDFAVYYC**QSYDINIDIV**FGGGTKVEIK
	AB014-GS15-9E8.4 VH-VK HC (PR-1599239)	EVQLVESGGGLVQPGGSLRLSCAAS**GYTFTNYGMN**WVRQA PGKGLEWVG**WINTYTGEPTYAADFKR**RFTFSLDTSKSTAY LQMNSLRAEDTAVYYCAK**YPHYYGSSHWY**FDVWGQGTLVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEA AGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN AYTQKSLSLSPGK*GGSGGGGSGGGGSGG*EVTLRESGPALV KPTQTLTLTCTFS**GFSLSTYGMGVGW**IRQPPGKALEWLA**N** **IWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTNMDPVDT ATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS*GGGGSGGGGS* *GGGGS*EIVLTQSPGTLSLSPGERATLSC**ERSSGDIGDSYV** **S**WYQQKPGQAPRLVIY**ADDQRPS**GIPDRFSGSGSGTDFTL TISRLEPEDFAVYYC**QSYDINIDIV**FGGGTKVEIK
	AB014-GS10-9E8.4 VK-VH HC (PR-1599240)	EVQLVESGGGLVQPGGSLRLSCAAS**GYTFTNYGMN**WVRQA PGKGLEWVG**WINTYTGEPTYAADFKR**RFTFSLDTSKSTAY LQMNSLRAEDTAVYYCAK**YPHYYGSSHWYFDV**WGQGTLVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV

		TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEA AGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN AYTQKSLSLSPGK*GGSGGGGSGG*EIVLTQSPGTLSLSPGE RATLSC**ERSSGDIGDSYVS**WYQQKPGQAPRLVIY**ADDQRP** **S**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QSYDINI** **DIV**FGGGTKVEIKGGGGSGGGGSGGGGSEVTLRESGPALV KPTQTLTLTCTFS**GFSLSTYGMGVG**WIRQPPGKALEWLA**N** **IWWDDDKYYNPSLKN**RLTISKDTSKNQVVLTMTNMDPVDT ATYYCAR**IESIGTTYSFDY**WGQGTMVTVSS
	AB014 LC	DIQMTQSPSSLSASVGDRVTITC**SASQDISNYLN**WYQQKP GKAPKVLIY**FTSSLHS**GVPSRFSGSGSGTDFTLTISSLQP EDFATYYC**QQYSTVPWT**FGQGTKVEIKRTVAAPSVFIFPP SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQG LSSPVTKSFNRGEC

All HC use the exact same LC (last sequence in Table 59). The naming of the HC follows the following convention: VH name - Linker length (between Fc and scFv) - scFv name with orientation of scFv.

Example 13: In vitro Characterization of Anti-VEGF-A/Anti-PDGF-BB DVD-Ig Molecules and Other Bispecific Molecules

Example 13.1: Expression and Purification of Anti-VEGF-A/Anti-PDGF-BB DVD-Ig Molecules and CO-DVD-Ig Molecules

[0399] All variants were transiently transfected into 200 - 500 mls of HEK 293 6e suspension cell cultures in a ratio of 60% to 40% light to heavy chain construct. 1 mg/ml PEI was used to transfect the cells. Alternatively variants were transiently transfected into 500 mls of Expi293 suspension cell cultures using the ExpiFectamine kit (LifeTechnologies A14524). Supernatants were harvested after six days in shaking flasks, spun down to pellet cells, and filtered through 0.22 μm filters to separate IgG from culture contaminates. All was purified via gravity flow using 1-2 ml of rProteinA sepharose fast flow beads (GE Healthcare, 17-1279-04) over poly prep chromatography columns (Bio Rad, 731-1550). Once supernatants had passed through the columns the beads were washed with 10 column volumes of binding buffer, and IgG was eluted with Immunopure IgG elution buffer (Pierce, 185 1520) and collected in 1 ml aliquots. Fractions containing DVD-Ig were pooled and dialyzed in PBS or 15mM Histidine pH 6 overnight at 4°C.

Table 60. Expression Level and SEC Profile of Anti-VEGF-A/Anti-PDGF-BB DVD-Ig, CO-DVD-Ig and IgG-scFv Fusion Proteins

Name	Corporate ID	Octet Titer (mg/L)	Yield (mg/L)	SEC (% monomer)
AB014-GS-9E8.4	NA	4.2	ND	ND
9E8.4-GS-AB014	NA	1.2	ND	ND
AB014-SS-9E8.4	NA	3.5	0.4	ND
9E8.4-SS-AB014	NA	3.5	0.6	ND
AB014-SL-9E8.4	NA	2.0	ND	ND
9E8.4-SL-AB014	NA	2.8	0.1	ND
AB014-LS-9E8.4	NA	3.3	ND	ND
9E8.4-LS-AB014	NA	3.6	ND	ND
9E8.4-GS-4G8.3	PR-1563988	6.5	2.8	94.5
9E8.4-SS-4G8.3	PR-1563990	5.9	4.5	92.1
9E8.4-SL-4G8.3	PR-1563998	3.4	2.0	94.0
9E8.4-LS-4G8.3	PR-1564009	10.7	8.0	93.3
4G8.3-GS-9E8.4	PR-1564010	3.6	2.1	98.4
4G8.3-SS-9E8.4	PR-1564011	5.7	3.1	99.4
4G8.3-SL-9E8.4	PR-1564012	2.6	0.7	99.4
4G8.3-LS-9E8.4	PR-1564013	6.7	3.1	99.2
DVD3896	PR-1564883	ND	2.8	100.0
DVD3897	PR-1564893	ND	2.7	79.1
DVD3898	PR-1564896	ND	22.0	93.0
DVD3899	PR-1564898	ND	14.7	87.4
DVD3900	PR-1564899	ND	12.1	72.4
DVD3901	PR-1565023	ND	1.3	99.1
DVD3902	PR-1565029	ND	3.2	98.3
DVD3903	PR-1565030	ND	2.9	98.0
DVD3904	PR-1565031	ND	13.8	97.8
DVD3905	PR-1565032	ND	15.1	92.5
DVD3906	PR-1565035	ND	28.2	85.5
DVD3907	PR-1565033	ND	0.5	ND
CODV001	PR-1565040	ND	88.4	87.6
CODV002	PR-1565042	ND	46.5	97.0
CODV003	PR-1565044	ND	37.3	77.3
CODV004	PR-1565051	ND	75.8	77.4
CODV005	PR-1565083	ND	104.5	86.9
CODV006	PR-1565084	ND	83.9	96.4
CODV007	PR-1565085	ND	43.9	77.4
CODV008	PR-1565086	ND	44.5	75.5
CODV009	PR-1571821	2.0	1.2	86.6
CODV010	PR-1571823	4.5	3.6	94.8
CODV011	PR-1575521	3.7	2.0	100.0
CODV012	PR-1571824	2.0	0.7	98.9

Name	Corporate ID	Octet Titer (mg/L)	Yield (mg/L)	SEC (% monomer)
CODV013	PR-1571825	0.7	0.4	90.6
CODV014	PR-1571826	4.5	0.5	89.6
CODV015	PR-1571827	0.7	0.9	91.7
CODV016	PR-1571828	2.6	1.4	93.6
CODV017	PR-1571830	4.2	2.6	99.8
CODV018	PR-1571831	2.6	1.5	88.8
CODV019	PR-1571832	0.4	0.2	87.1
CODV020	PR-1571836	2.1	0.3	58.1
4G8.3-GS-9E8.4	PR-1569574	4.4	4.3	ND
4G8.3-SL-9E8.4	PR-1569579	0.7	0.5	ND
4G8.3-LS-9E8.4	PR-1575573	3.8	2.7	ND
4G8.3-GS-9E8.4 (g)	PR-1572102	2.5	0.4	98.8
4G8.3-GS(11)-9E8.4 (g)	PR-1572103	5.3	1.4	100.0
4G8.3-GS(noR)-9E8.4 (g)	PR-1572104	4.1	0.7	99.5
4G8.3-SL-9E8.4 (g)	PR-1572105	1.4	0.3	98.6
4G8.3-LS-9E8.4 (g)	PR-1572106	4.0	0.8	100.0
4G8.3-GS-9E8.4E	PR-1575832	9.8	8.1	99.2
4G8.3-SL-9E8.4E	PR-1575834	4.5	2.6	99.0
4G8.3-LS-9E8.4E	PR-1575835	16.0	9.7	99.6
CODV021	PR-1577053	2.6	0.3	92.8
CODV022	PR-1577056	2.0	0.2	93.2
9A8.12-GS-9E8.4E	PR-1577165	3.3	2.4	82.99
9A8.12-SL-9E8.4E	PR-1577166	1.1	0.2	51.54
9A8.12-LS-9E8.4E	PR-1577547	10.6	1.1	97.35
9E8.4E-GS-9A8.12	PR-1578137	12.0	3.8	97.3
9E8.4E-SL-9A8.12	PR-1577548	5.0	1.7	97.51
9E8.4E-LS-9A8.12	PR-1577550	2.5	2.5	96.96
AB014-GS6-9E8.4 VH-VK	PR-1599234	70.0	25.6	33.8
AB014-GS10-9E8.4 VH-VK	PR-1599236	70.0	24.3	34.7
AB014-GS15-9E8.4 VH-VK	PR-1599239	70.0	29.3	39.3
AB014-GS10-9E8.4 VK-VH	PR-1599240	47.0	21.4	33.2
4G8.2-GS-9E8.4	PR-1598261	29.4	10.3	98.31
4G8.4-GS-9E8.4	PR-1598262	61.0	20.4	87.65
4G8.5-GS-9E8.4	PR-1598263	31.3	11.5	98.5
4G8.12-GS-9E8.4	PR-1598264	44.0	15.1	93.12
4G8.13-GS-9E8.4	PR-1598265	6.3	2.6	83.58
4G8.14-GS-9E8.4	PR-1598266	19.3	9.9	96.52
CL-34565_GS_CL-33675	PR-1613183	101.4	27.7	88.2
CL-34565_GS_9E8.4	PR-1613184	49.3	31.3	95.9
CL-34565_GS_3E2.1	PR-1613185	109.8	82.5	96.3
4G8.5_GS_CL-33675	PR-1611291	91.1	10.4	96.9

Name	Corporate ID	Octet Titer (mg/L)	Yield (mg/L)	SEC (% monomer)
4G8.5_GS_9E8.4	PR-1612489	39.0	23.0	97.0
4G8.5_GS_3E2.1	PR-1610560	127.0	13.9	100.0
9E10.1_GS_CL-33675	PR-1610561	136.0	19.2	92.9
9E10.1_GS_9E8.4	PR-1612491	86.0	50.1	95.0
9E10.1_GS_3E2.1	PR-1610562	44.0	10.2	96.0
9E10.6_GS_CL-33675	PR-1612492	152.0	65.7	89.0
9E10.6_GS_9E8.4	PR-1612493	96.0	50.1	93.0
9E10.6_GS_3E2.1	PR-1610563	122.0	18.0	95.0
1B10.1_GS_CL-33675	PR-1611292	233.0	22.7	75.4
1B10.1_GS_9E8.4	PR-1612494	123.0	52.1	77.0
1B10.1_GS_3E2.1	PR-1610564	142.0	23.3	93.7
1E3.4_GS_CL-33675	PR-1611293	54.0	9.3	83.7
1E3.4_GS_9E8.4	PR-1611294	67.5	11.6	72.1
1E3.4_GS_3E2.1	PR-1612495	101.0	29.6	97.0
CL-33675_GS_CL-34565	PR-1613186	73.5	17.7	87.6
CL-33675_GS_4G8.5	PR-1612496	36.0	8.6	94.0
CL-33675_GS_9E10.1	PR-1611295	148.5	2.3	95.9
CL-33675_GS_9E10.6	PR-1611296	185.3	4.9	95.8
CL-33675_GS_1B10.1	PR-1612498	19.0	7.0	65.0
CL-33675_GS_1E3.4	PR-1611297	72.8	3.5	95.9
9E8.4_GS_CL-34565	PR-1613187	67.5	53.6	79.0
9E8.4_GS_4G8.5	PR-1613188	95.2	73.6	81.7
9E8.4_GS_9E10.1	PR-1611298	237.5	21.5	73.3
9E8.4_GS_9E10.6	PR-1611299	179.0	19.1	71.9
9E8.4_GS_1B10.1	PR-1611300	93.7	12.9	71.7
9E8.4_GS_1E3.4	PR-1611301	87.9	12.2	66.4
3E2.1_GS_CL-34565	PR-1613189	76.1	65.7	93.3
3E2.1_GS_4G8.5	PR-1612499	98.0	46.9	95.0
3E2.1_GS_9E10.1	PR-1612500	126.0	59.2	85.0
3E2.1_GS_9E10.6	PR-1612501	141.0	61.0	86.5
3E2.1_GS_1B10.1	PR-1612502	141.0	61.0	97.0
3E2.1_GS_1E3.4	PR-1613190	107.8	79.9	96.5
9E10.1_SL_CL-33675	PR-1629646	7.6	1.0	98.7
1B10.1_SL_CL-33675	PR-1629647	157.0	111.7	63.3
9E10.1_LS_CL-33675	PR-1629648	64.4	36.4	92.9
1B10.1_LS_CL-33675	PR-1629649	218.4	157.7	65.4

Example 13.2: Binding Affinity of Anti-VEGF-A/Anti-PDGF-BB DVD-Ig Molecules and CO-DVD-Ig Molecules

[0400] The binding affinity of anti-VEGF-A/anti-PDGF-BB DVD-Ig molecules and CO-DVD-Ig molecules to VEGF-A and PDGF-BB were measured by Biacore using the method described in Example 1.1 and the data is summarized in Tables 61 and 62 below.

Table 61. Biacore Binding of Anti-VEGF/anti-PDGF DVD-Ig Molecules

		VEGF			PDGF		
DVD Name	**Corporate ID**	**k_{on} (M-1 s-1)**	**k_{off} (M-1)**	**K_D (M)**	**k_{on} (M-1 s-1)**	**k_{off} (M-1)**	**K_D (M)**
9E8.4-GS-4G8.3	PR-1563988	2.2 E+05	6.3 E-05	2.9 E-10	1.0 E+07	2.0 E-04	2.0 E-11
9E8.4-SS-4G8.3	PR-1563990	1.6 E+05	1.2 E-04	7.8 E-10	1.0 E+07	2.0 E-04	2.0 E-11
9E8.4-SL-4G8.3	PR-1563998	7.0 E+05	8.0 E-05	1.2 E-10	1.0 E+07	1.9 E-04	1.9 E-11
9E8.4-LS-4G8.3	PR-1564009	2.7 E+05	5.5 E-05	2.0 E-10	1.0 E+07	2.0 E-04	2.0 E-11
4G8.3-GS-9E8.4	PR-1564010	3.3 E+06	5.7 E-05	1.7 E-11	1.0 E+07	1.4 E-04	1.3 E-11
4G8.3-SS-9E8.4	PR-1564011	3.1 E+06	4.1 E-05	1.3 E-11	7.5 E+06	1.5 E-04	1.9 E-11
4G8.3-SL-9E8.4	PR-1564012	3.1 E+06	4.1 E-05	1.3 E-11	1.4 E+07	1.4 E-04	9.9 E-12
4G8.3-LS-9E8.4	PR-1564013	3.1 E+06	3.9 E-05	1.2 E-11	1.7 E+07	1.4 E-04	8.6 E-12
DVD3904	PR-1565031	6.1 E+05	1.1 E-04	1.9 E-10	1.0 E+07	9.0 E-04	9.0 E-11
DVD3905	PR-1565032	1.1 E+06	1.0 E-04	9.4 E-11	1.0 E+07	1.8 E-03	1.8 E-10
DVD3906	PR-1565035	9.2 E+05	9.3 E-05	1.0 E-10	1.0 E+07	7.2 E-03	7.2 E-10
4G8.3-GS(9)-9E8.4 (g)	PR-1572102	6.0 E+06	7.6 E-05	1.3 E-11	1.3 E+07	1.7 E-04	1.3 E-11
4G8.3-GS(11)-9E8.4 (g)	PR-1572103	6.3 E+06	7.5 E-05	1.2 E-11	1.4 E+07	1.7 E-04	1.3 E-11
4G8.3-GS(noR)-9E8.4 (g)	PR-1572104	6.1 E+06	6.9 E-05	1.1 E-11	1.5 E+07	1.4 E-04	8.9 E-12
4G8.3-SL-9E8.4 (g)	PR-1572105	5.6 E+06	6.1 E-05	1.1 E-11	1.3 E+07	1.7 E-04	1.3 E-11
4G8.3-LS-9E8.4 (g)	PR-1572106	6.3 E+06	5.1 E-05	8.1 E-12	1.8 E+07	2.0 E-04	1.1 E-11
4G8.3-GS-9E8.4E	PR-1575832	6.1 E+06	8.0 E-05	1.3 E-11	1.3 E+07	2.7 E-04	2.0 E-11
4G8.3-SL-9E8.4E	PR-1575834	6.2 E+06	6.3 E-05	1.0 E-11	1.7 E+07	2.5 E-04	1.5 E-11
4G8.3-LS-9E8.4E	PR-1575835	5.8 E+06	5.9 E-05	1.0 E-11	2.0 E+07	2.8 E-04	1.4 E-11
9A8.12-GS-9E8.4E	PR-1577165	7.7 E+05	1.4 E-04	1.8 E-10	3.3 E+07	2.6 E-04	8.1 E-12
9A8.12-SL-9E8.4E	PR-1577166	2.5 E+05	1.2 E-04	4.7 E-10	2.7 E+07	2.3 E-04	8.3 E-12
9A8.12-LS-9E8.4E	PR-1577547	2.7 E+05	9.3 E-05	3.5 E-10	3.6 E+07	2.3 E-04	6.5 E-12
9E8.4E-SL-9A8.12	PR-1577548	2.2 E+06	3.4 E-04	1.6 E-10	5.0 E+07	3.2 E-04	6.4 E-12
9E8.4E-LS-9A8.12	PR-1577550	6.4 E+05	1.5 E-04	2.3 E-10	5.0 E+07	2.5 E-04	5.0 E-12
9E8.4E-GS-9A8.12	PR-1578137	4.7 E+05	1.8 E-04	3.8 E-10	5.0 E+07	4.4 E-04	8.8 E-12
CL-34565_GS_CL-33675	PR-1613183	1.2 E+07	2.0 E-05	1.7 E-12	6.0 E+07	1.1 E-05	1.9 E-13
CL-34565_GS_9E8.4	PR-1613184	1.5 E+07	1.6 E-05	1.1 E-12	3.5 E+07	1.9 E-04	5.4 E-12
CL-34565_GS_3E2.1	PR-1613185	1.2 E+07	1.7 E-05	1.4 E-12	4.5 E+07	5.2 E-04	1.2 E-11
4G8.5_GS_CL-33675	PR-1611291	4.7 E+06	3.1 E-05	6.6 E-12	1.6 E+07	1.2 E-05	7.4 E-13
4G8.5_GS_9E8.4	PR-1612489	5.4 E+06	4.6 E-05	8.5 E-12	5.8 E+06	1.6 E-04	2.8 E-11
4G8.5_GS_3E2.1	PR-1610560	4.8 E+06	4.2 E-05	8.7 E-12	4.1 E+07	5.5 E-04	1.3 E-11
9E10.1_GS_CL-33675	PR-1610561	9.7 E+06	1.7 E-05	1.8 E-12	2.0 E+07	9.1 E-06	4.5 E-13
9E10.1_GS_9E8.4	PR-1612491	1.1 E+07	2.5 E-05	2.2 E-12	6.8 E+06	1.7 E-04	2.5 E-11
9E10.1_GS_3E2.1	PR-1610562	9.3 E+06	2.3 E-05	2.4 E-12	4.1 E+07	8.5 E-04	2.1 E-11
9E10.6_GS_CL-33675	PR-1612492	1.1 E+07	2.2 E-05	2.0 E-12	2.4 E+07	2.8 E-05	1.2 E-12
9E10.6_GS_3E2.1	PR-1610563	8.6 E+06	2.5 E-05	3.0 E-12	5.8 E+06	2.1 E-04	3.6 E-11
1B10.1_GS_CL-33675	PR-1611292	2.1 E+06	1.3 E-04	6.2 E-11	2.2 E+07	1.2 E-05	5.4 E-13
1E3.4_GS_3E2.1	PR-1612495	5.3 E+06	5.2 E-05	9.8 E-12	4.5 E+07	5.1 E-04	1.2 E-11
CL-33675_GS_4G8.5	PR-1612496	2.3 E+05	4.0 E-05	1.8 E-10	3.8 E+07	9.0 E-06	2.3 E-13
3E2.1_GS_4G8.5	PR-1612499	2.4 E+05	3.9 E-05	1.7 E-10	≥ 9.0 E+07	3.4 E-04	≤ 3.8 E-12
3E2.1_GS_9E10.1	PR-1612500	6.3 E+05	1.2 E-05	1.9 E-11	≥ 9.0 E+07	3.9 E-04	≤ 4.3 E-12
3E2.1_GS_9E10.6	PR-1612501	5.7 E+05	2.3 E-05	4.1 E-11	≥ 9.0 E+07	4.5 E-04	≤ 5.3 E-

							12
3E2.1_GS_1B10.1	PR-1612502	3.5 E+05	1.2 E-04	3.2 E-10	8.4 E+07	1.5 E-04	1.8 E-12
3E2.1_GS_1E3.4	PR-1613190	3.6 E+05	9.2 E-05	2.6 E-10	≥ 9.0 E+07	4.8 E-04	≤ 5.3 E-12

Table 62. Biacore Binding of Anti-VEGF/anti-PDGF CO-DVD-Ig Molecules

		VEGF			PDGF		
CO-DVD-Ig Name	**Corporate ID**	**k_{on} (M-1 s-1)**	**k_{off} (M-1)**	**K_D (M)**	**k_{on} (M-1 s-1)**	**k_{off} (M-1)**	**K_D (M)**
CODV003	PR-1565044	no binding			2.3 E+07	2.5 E-04	1.1 E-11
CODV004	PR-1565051	no binding			1.0 E+07	8.7 E-04	8.7 E-11
CODV005	PR-1565083			3.5 E-08	1.2 E+07	1.3 E-04	1.1 E-11
CODV006	PR-1565084	no binding			2.2 E+07	2.1 E-04	9.7 E-12
CODV007	PR-1565085			2.2 E-08	2.9 E+07	2.2 E-04	7.3 E-12
CODV008	PR-1565086	no binding			1.7 E+07	1.3 E-04	7.4 E-12
CODV009	PR-1571821			2.6 E-08	3.5 E+07	2.0 E-04	5.6 E-12
CODV010	PR-1571823	5.7 E+04	3.7 E-04	6.6 E-09	4.1 E+07	1.6 E-04	4.0 E-12
CODV011	PR-1575521	1.1 E+06	4.0 E-05	3.8 E-11	3.8 E+07	6.9 E-05	1.8 E-12
CODV012	PR-1571824	2.7 E+06	7.6 E-05	2.8 E-11	7.0 E+07	1.0 E-04	1.5 E-12
CODV014	PR-1571826	2.2 E+06	7.7 E-05	3.6 E-11	5.5 E+07	1.3 E-04	2.4 E-12
CODV015	PR-1571827	2.7 E+06	6.5 E-05	2.4 E-11	7.0 E+07	9.1 E-05	1.3 E-12
CODV016	PR-1571828	2.9 E+06	5.9 E-05	2.0 E-11	4.6 E+07	1.1 E-04	2.5 E-12
CODV017	PR-1571830	-	-	5.7 E-08	3.0 E+07	2.0 E-04	6.5 E-12
CODV018	PR-1571831	-	-	3.1 E-08	3.5 E+07	1.9 E-04	5.3 E-12
CODV019	PR-1571832	2.9 E+06	1.4 E-04	5.0 E-11	3.9 E+07	1.7 E-04	4.4 E-12
CODV020	PR-1571836	3.1 E+06	1.0 E-04	3.3 E-11	4.6 E+07	1.6 E-04	3.5 E-12
CODV021	PR-1577053	3.8 E+06	6.8 E-05	1.8 E-11	6.1 E+07	1.2 E-04	1.9 E-12
CODV022	PR-1577056	4.5 E+06	5.6 E-05	1.3 E-11	3.2 E+07	1.3 E-04	4.2 E-12

Example 13.2.1: Binding of Anti-VEGF/anti-PDGF DVD-Ig Molecule (PR-1610561) to Various VEGF-A Isoforms and VEGF-A and PDGF-BB of Different Species

[0401] Binding of anti-VEGF/anti-PDGF DVD-Ig molecule (PR-1610561) and their parental monoclonal antibodies to various VEGF-A isoforms and VEGF-A and PDGF-BB of different species were measured by Biacore using the method described in Example 1.1 and the data is summarized in Table 63 below. Tables 63A-B summarize the high affinity for VEGF-A_{165} (65 pM), VEGF-A_{121} (230 pM), VEGF-A_{111} (290 pM), isoforms and the high affinity for soluble PDGF-BB (5 pM), observed for PR-1610561. The data shows that PR-1610561binds to both soluble and extracellular-matrix (ECM) bound forms of PDGF-BB.

Table 63. Binding of Anti-VEGF/Anti-PDGF DVD-Ig Molecule (PR-1610561) and Parental mAbs to VEGF-A Isoforms and PDGF

				human VEGF 165 PR-1350437, 1925483			human PDGF-B PR-1373790, 1926007		
No		PR-	lot	K_a($M^{-1}s^{-1}$)	K_d(s^{-1})	K_D(M)	K_a($M^{-1}s^{-1}$)	K_d(s^{-1})	K_D(M)
1	**9E10.1-GS-33675**	PR-1610561	2213329	5.2E+05	3.4E-05	6.5E-11	≥1.0E+07	5.2E-05	≤5.2E-12
2	**AB014 (Avastin)**	PR-1545939	2129911	5.5E+05	4.1E-05	7.6E-11			
3	**AB642 (9E10.1)**	PR-1594047	2169800	1.6E+07	2.8E-05	1.8E-12			
4	**CL-33675**	PR-1593725	2178826				≥1.0E+07	5.8E-06	≤5.8E-13
				human VEGF 121 PR-1515941, 2069355					
No		PR-	lot	K_a($M^{-1}s^{-1}$)	K_d(s^{-1})	K_D(M)			
1	**9E10.1-GS-33675**	PR-1610561	2213329	1.8E+05	4.1E-05	2.3E-10			
2	**AB014 (Avastin)**	PR-1545939	2129911	1.8E+05	5.1E-05	2.8E-10			
3	**AB642 (9E10.1)**	PR-1594047	2169800	3.2E+06	6.8E-05	2.1E-11			
4	**CL-33675**	PR-1593725	2178826						
				human VEGF 111 PR-1520687, 2074657					
No		PR-	lot	K_a($M^{-1}s^{-1}$)	K_d(s^{-1})	K_D(M)			
1	**9E10.1-GS-33675**	PR-1610561	2213329	1.5E+05	4.3E-05	2.9E-10			
2	**AB014 (Avastin)**	PR-1545939	2129911	1.4E+05	5.3E-05	3.8E-10			
3	**AB642 (9E10.1)**	PR-1594047	2169800	1.8E+06	1.0E-04	5.8E-11			
4	**CL-33675**	PR-1593725	2178826						
				cyno VEGF has similar sequence as human			cyno PDGF-B PR-1575400, 2154322		
No		PR-	lot				K_a($M^{-1}s^{-1}$)	K_d(s^{-1})	K_D(M)
1	**9E10.1-GS-33675**	PR-1610561	2213329				≥1.0E+07	8.1E-06	≤8.1E-13
2	**AB014 (Avastin)**	PR-1545939	2129911						
3	**AB642 (9E10.1)**	PR-1594047	2169800						
4	**CL-33675**	PR-1593725	2178826				≥1.0E+07	1.3E-05	≤1.3E-12
				mouse VEGF PR-1578904, 2150241			mouse PDGF-B PR-1577160, 2147923		
No		PR-	lot	K_a($M^{-1}s^{-1}$)	K_d(s^{-1})	K_D(M)	K_a($M^{-1}s^{-1}$)	K_d(s^{-1})	K_D(M)
1	**9E10.1-GS-33675**	PR-1610561	2213329			potentially very weak binding	≥1.0E+07	5.2E-05	≤5.2E-12
2	**AB014 (Avastin)**	PR-1545939	2129911			no binding			
3	**AB642 (9E10.1)**	PR-1594047	2169800			potentially very weak binding			

4	**CL-33675**	PR-1593725	2178826				≥1.0E+07	5.8E-06	≤5.8E-13
				rat VEGF PR-1645045, 2235296			**rat PDGF-B PR-1645048, 2235300**		
No		**PR-**	**lot**	K_a(M^{-1}s^{-1})	K_d(s^{-1})	K_D(M)	K_a(M^{-1}s^{-1})	K_d(s^{-1})	K_D(M)
1	**9E10.1-GS-33675**	PR-1610561	2213329			potentially very weak binding	≥1.0E+07	5.2E-05	≤5.2E-12
2	**AB014 (Avastin)**	PR-1545939	2129911			no binding			
3	**AB642 (9E10.1)**	PR-1594047	2169800			potentially very weak binding			
4	**CL-33675**	PR-1593725	2178826				≥1.0E+07	5.8E-06	≤5.8E-13
				rabbit VEGF PR-1563693, 2130027			**rabbit PDGF-B has similar sequence as rat**		
No		**PR-**	**lot**	K_a(M^{-1}s^{-1})	K_d(s^{-1})	K_D(M)			
1	**9E10.1-GS-33675**	PR-1610561	2213329	9.6E+05	4.0E-05	4.1E-11			
2	**AB014 (Avastin)**	PR-1545939	2129911	9.4E+05	4.4E-05	4.7E-11			
3	**AB642 (9E10.1)**	PR-1594047	2169800	1.6E+07	2.8E-05	1.8E-12			
4	**CL-33675**	PR-1593725	2178826						

Table 63A. Affinity of PR-1610561 to Various Isoforms of Human VEGF-A

Human VEGF-A Isoforms	A_{165}	A_{121}	A_{111}
Affinity K_D (pM)	65	230	290

Table 63B. Affinity of PR-1610561 to Human PDGF-BB

Human PDGF-BB Forms	Soluble	ECM-associated
Affinity K_D (pM)	5	n/t
Cell Staining	n/t	+

Example 13.3: Neutralization Potencies of Anti-VEGF-A/anti-PDGF-BB DVD-Ig Molecules and CO-DVD-Ig Molecules

[0402] The DVD-Ig molecules and CO-DVD-Ig molecules were evaluated for their potencies to block $VEGF_{165}$/VEGFR2 interaction (Example 1.4) and neutralize $VEGF_{165}$ activity in HMVEC-d or VEGFR2-3T3 proliferation assays (Examples 1.10 and 1.7). The molecules were also characterized for the ability to block PDGF-BB/PDGF-Rβ interaction (Example 1.13) and inhibition of PDGF-BB induced proliferation of NIH-3T3 cells (Example 1.15). The data is summarized in Table 64 below. PR-1610561 exhibited neutralization activity against human VEGF-A (IC_{50} of 145 pM) and human PDGF-BB (IC_{50} of 34 pM), as summarized in Table 64A.

Table 64. Human VEGF-A and Human PDGF-BB Neutralization Potency of Anti-VEGF-A/anti-PDGF-BB DVD-Ig and CO-DVD-Ig Proteins

DVD-Ig	Corporate ID	Potency IC50 (nM)				
		HMVEC-d $hVEGF_{165}$	VEGFR2-3T3 $hVEGF_{165}$	NIH-3T3 hPDGF-BB	hVEGFR2 Competition ELISA IC_{50} nM	hPDGF β Competition ELISA IC_{50} nM
9E8.4-GS-4G8.3	PR-1563988	2.643	>5	0.076	NT	NT
9E8.4-SS-4G8.3	PR-1563990	NT	>5	0.094	NT	NT
9E8.4-SL-4G8.3	PR-1563998	NT	>5	0.091	NT	NT
9E8.4-LS-4G8.3	PR-1564009	NT	>5	0.104	NT	NT
4G8.3-GS-9E8.4	PR-1564010	0.096	NT	NT	0.126	NT
4G8.3-GS-9E8.4E	PR-1575832	NT	2.953	>5	NT	NT
4G8.3-SS-9E8.4	PR-1564011	NT	0.747	5.511	NT	NT

4G8.3-SL-9E8.4	PR-1564012	NT	NT	0.365	0.086	NT
4G8.3-SL-9E8.4E	PR-1575834	NT	3.090	0.572	NT	NT
4G8.3-LS-9E8.4	PR-1564013	0.060	NT	0.152	0.092	NT
CODV009	PR-1571821	NT	>5	>5	NT	NT
CODV010	PR-1571823	NT	>5	2.139	NT	NT
CODV011	PR-1575521	NT	2.553	0.043	NT	NT
CODV012	PR-1571824	NT	1.424	0.182	NT	NT
CODV013	PR-1571825	NT	0.785	0.11	NT	NT
CODV014	PR-1571826	NT	3.768	0.469	NT	NT
CODV015	PR-1571827	0.104	0.407	0.075	NT	NT
CODV021	PR-1577053	NT	>5	0.056	NT	NT
CODV016	PR-1571828	0.115	0.503	0.096	NT	NT
CODV022	PR-1577056	NT	1.462	0.059	NT	NT
CODV017	PR-1571830	NT	>5	>5	NT	NT
CODV018	PR-1571831	NT	>5	>5	NT	NT
DVD3904	PR-1565031	NT	>5	>5	NT	NT
DVD3905	PR-1565032	NT	>5	>5	NT	NT
DVD3906	PR-1565035	NT	>5	>5	NT	NT
CODV003	PR-1565044	NT	>5	>5	NT	NT
CODV004	PR-1565051	NT	>5	>5	NT	NT
CODV005	PR-1565083	NT	>5	>5	NT	NT
CODV006	PR-1565084	NT	>5	>5	NT	NT
CODV007	PR-1565085	NT	>5	>5	NT	NT
CODV008	PR-1565086	NT	>5	>5	NT	NT
4G8.3-GS(9)-9E8.4 (g)	PR-1572102	0.417	0.986	.528	0.157	>5
4G8.3-GS(11)-9E8.4 (g)	PR-1572103	NT	0.318	0.298	NT	NT

4G8.3-GS(noR)-9E8.4 (g)	PR-1572104	NT	0.217	0.095	NT	NT
4G8.3-SL-9E8.4 (g)	PR-1572105	0.347	1.603	0.290	0.111	>5
4G8.3-LS-9E8.4 (g)	PR-1572106	NT	0.203	0.109	NT	NT
4G8.3-LS-9E8.4E	PR-1575835	NT	2.852	0.176	NT	NT
9A8.12-GS-9E8.4E	PR-1577165	NT	2.992	0.204	NT	NT
9A8.12-SL-9E8.4E	PR-1577166	NT	5.536	0.148	NT	NT
9A8.12-LS-9E8.4E	PR-1577547	NT	4.13	0.133	NT	NT
9E8.4E-SL-9A8.12	PR-1577548	NT	>5	0.147	NT	NT
9E8.4E-LS-9A8.12	PR-1577550	NT	>5	0.066	NT	NT
9E8.4E-GS-9A8.12	PR-1578137	NT	>5	0.327	NT	NT
hVEGF 4G8.3-GS-hPDGF 9E8.4 [hu IgG1/k] mut(234,235) H435A	PR-1569574	0.341	1.02	0.630	0.137	>5
hVEGF 4G8.3-SL-hPDGF 9E8.4 [hu IgG1/k] mut(234,235) H435A	PR-1569579	0.36	1.178	0.427	0.133	>5
hVEGF 4G8.3-LS-hPDGF 9E8.4 [hu IgG1/k] mut(234,235) H435A	PR-1575573	NT	NT	NT	0.131	>5
AB014-GS6-9E8.4 VH-VK	PR-1599234	0.124	NT	0.222	NT	NT
AB014-GS10-9E8.4 VH-VK	PR-1599236	0.095	NT	0.063	NT	NT
AB014-GS15-9E8.4 VH-VK	PR-1599239	0.13	NT	0.066	NT	NT
AB014-GS10-9E8.4 VK-VH	PR-1599240	0.086	NT	0.074	NT	NT
4G8.2-GS10-9E8.4	PR-1598261	0.221	NT	>5	NT	NT
4G8.4-GS10-9E8.4	PR-1598262	0.281	NT	1.327	NT	NT
4G8.5-GS10-9E8.4	PR-1598263	0.079	NT	>5	NT	NT
4G8.12-GS10-9E8.4	PR-1598264	0.079	NT	0.227	NT	NT
4G8.13-GS10-9E8.4	PR-1598265	0.907	NT	0.255	NT	NT
4G8.14-GS10-9E8.4	PR-1598266	0.113	NT	0.459	NT	NT
4G8.5_GS_CL-33675	PR-1611291	0.076	NT	0.05	NT	NT

4G8.5_GS_3E2.1	PR-1610562	0.072	NT	1.398	NT	NT
9E10.1_GS_CL-33675	PR-1610561	0.145	0.433	0.034	0.045	0.09
9E10.1_GS_3E2.1	PR-1610562	0.054	NT	5.724	NT	NT
9E10.6_GS_3E2.1	PR-1610563	0.06	NT	1.317	NT	NT
1B10.1_GS_CL-33675	PR-1611292	0.05	NT	0.037	NT	NT
1B10.1_GS_3E2.1	PR-1610564	0.084	NT	1.545	NT	NT
1E3.4_GS_CL-33675	PR-1611293	0.067	NT	0.037	NT	NT
1E3.4_GS_9E8.4	PR-1611294	0.092	NT	0.329	NT	NT
CL-33675_GS_9E10.1	PR-1611295	0.064	NT	0.031	NT	NT
CL-33675_GS_9E10.6	PR-1611296	0.082	NT	0.037	NT	NT
CL-33675_GS_1E3.4	PR-1611297	0.372	NT	0.039	NT	NT
9E8.4_GS_9E10.1	PR-1611298	0.073	NT	0.317	NT	NT
9E8.4_GS_9E10.6	PR-1611299	0.132	NT	0.213	NT	NT
9E8.4_GS_1B10.1	PR-1611300	0.391	NT	0.109	NT	NT
9E8.4_GS_1E3.4	PR-1611301	0.897	NT	0.131	NT	NT
4G8.5_GS_9E8.4	PR-1612489	0.069	NT	4.829	NT	NT
9E10.1_GS_9E8.4	PR-1612491	0.059	NT	1.913	NT	NT
9E10.6_GS_CL-33675	PR-1612492	0.05	NT	0.037	NT	NT
9E10.6_GS_9E8.4	PR-1612493	0.049	NT	1.14	NT	NT
1B10.1_GS_9E8.4	PR-1612494	0.127	NT	0.678	NT	NT
1E3.4_GS_3E2.1	PR-1612495	0.043	NT	6.253	NT	NT
CL-33675_GS_4G8.5	PR-1612496	0.219	NT	0.035	NT	NT
CL-33675_GS_1B10.1	PR-1612498	0.265	NT	0.11	NT	NT
3E2.1_GS_4G8.5	PR-1612499	0.743	NT	0.38	NT	NT
3E2.1_GS_9E10.1	PR-1612500	0.133	NT	0.394	NT	NT
3E2.1_GS_9E10.6	PR-1612501	0.188	NT	0.377	NT	NT

3E2.1_GS_1B10.1	PR-1612502	1.78	NT	0.187	NT	NT
CL-34565_GS_CL-33675	PR-1613183	0.059	NT	0.052	NT	NT
CL-34565_GS_9E8.4	PR-1613184	0.065	NT	0.323	NT	NT
CL-34565_GS_3E2.1	PR-1613185	0.053	NT	6.005	NT	NT
CL-33675_GS_CL-34565	PR-1613186	0.05	NT	0.043	NT	NT
9E8.4_GS_CL-34565	PR-1613187	0.058	NT	0.134	NT	NT
9E8.4_GS_4G8.5	PR-1613188	0.354	NT	0.108	NT	NT
3E2.1_GS_CL-34565	PR-1613189	0.063	NT	1.157	NT	NT
3E2.1_GS_1E3.4	PR-1613190	0.709	NT	0.896	NT	NT

NT – Not tested

Table 64A. Neutralization Activities in Cellular Assays

Protein	**Human VEGF-A**	**Human PDGF-BB**
Potency IC_{50} (pM)	145	34

[0403] Selected DVD-Ig molecules were further characterized for the ability to neutralize human $VEGF_{111}$ and human $VEGF_{121}$, isoforms of human VEGF-A. The molecules were tested for inhibition of $VEGF_{111}$ and human $VEGF_{121}$ induced proliferation of VEGFR2-3T3 cells (Example 1.8). Neutralization of non-human VEGF-A species was also evaluated. Molecules were tested for inhibition of rabbit $VEGF_{165}$ induced proliferation of VEGFR2-3T3 cells (Example 1.9). The data is summarized in Table 65 below. As noted, the amino acid sequence of cynomolgus monkey VEGF-A is identical to human VEGF-A. Parental antibodies had previously been examined for mouse $VEGF_{164}$ cross-reactivity in a competition ELISA and no blocking was observed (Example 1.5).

Table 65. Neutralization of Different VEGF-A Isoforms by Anti-VEGF-A/Anti-PDGF-BB DVD-Ig Molecules

DVD-Ig and Controls	Corporate ID	Potency IC50 (nM)		
		human $VEGF_{111}$	human $VEGF_{121}$	rabbit $VEGF_{165}$
4G8.3-GS(9)-9E8.4 (g)	PR-1572102	0.771	0.182	0.869
4G8.3-SL-9E8.4 (g)	PR-1572105	0.654	0.139	1.194
4G8.3-LS-9E8.4 (g)	PR-1572106	0.431	0.148	0.601

4G8.3-LS-9E8.4E	PR-1575835	NT	NT	1.534
hVEGF 4G8.3-GS-hPDGF 9E8.4 [hu IgG1/k] mut(234,235) H435A	PR-1569574	0.674	0.124	0.841
hVEGF 4G8.3-SL-hPDGF 9E8.4 [hu IgG1/k] mut(234,235) H435A	PR-1569579	0.576	0.154	1.213
9E10.1_GS_CL-33675	PR-1610561	0.213	0.097	0.520

NT – Not tested

[0404] Selected DVD-Ig molecules were further evaluated for their potencies to neutralize PDGF-BB of different species using the assay described in Examples 1.15-1.18. The data is summarized in Table 66 below. As noted, the amino acid sequence of rabbit PDGF-BB is identical to rat PDGF-BB.

Table 66. Neutralization of Different PDGF-BB Species by Anti-VEGF-A/Anti-PDGF-BB DVD-Ig Molecules

DVD-Ig and Controls	Corporate ID	Potency IC50 (nM)		
		cynoPDGF-BB	mPDGF-BB	ratPDGF-BB
4G8.3-GS-9E8.4	PR-1564010	NT	0.440	1.359
4G8.3-SL-9E8.4	PR-1564012	NT	0.290	0.650
4G8.3-SL-9E8.4E	PR-1575834	NT	0.772	NT
4G8.3-LS-9E8.4	PR-1564013	NT	0.110	0.210
4G8.3-GS(9)-9E8.4 (g)	PR-1572102	0.139	0.174	2.202
4G8.3-SL-9E8.4 (g)	PR-1572105	0.142	0.096	1.296
4G8.3-LS-9E8.4 (g)	PR-1572106	0.094	0.14	NT
hVEGF 4G8.3-GS-hPDGF 9E8.4 [hu IgG1/k] mut(234,235) H435A	PR-1569574	0.139	0.134	1.514
hVEGF 4G8.3-SL-hPDGF 9E8.4 [hu IgG1/k] mut(234,235) H435A	PR-1569579	0.144	0.150	0.994
9E10.1_GS_CL-33675	PR-1610561	0.035	0.032	0.038

NT – Not tested

[0405] Selected DVD-Ig molecules were evaluated for their ability to neutralize in the presence of a second ligand. To evaluate hPDGF-BB potency, the DVD-Ig molecules were pre-incubated with an excess of human $VEGF_{165}$ prior to testing in the NIH-3T3 proliferation assay (Example 1.21). To evaluate $hVEGF_{165}$ potency, the DVD-Ig molecules were pre-incubated with

an excess of human hPDGF-BB prior to testing in the VEGFR2-3T3 (KDR/Flk-1) phosphorylation assay (Example 1.20). The data is summarized in Table 67 below.

Table 67. Simultaneous binding to VEGF and PDGF

DVD-Ig	Corporate ID	Co-incubation Potency IC50 (nM)	
		hPDGF-BB	$hVEGF_{165}$
9E8.4-GS-4G8.3	PR-1563988	NT	NT
9E8.4-SS-4G8.3	PR-1563990	NT	NT
9E8.4-SL-4G8.3	PR-1563998	NT	NT
9E8.4-LS-4G8.3	PR-1564009	NT	NT
4G8.3-GS-9E8.4	PR-1564010	NT	NT
4G8.3-SS-9E8.4	PR-1564011	NT	NT
4G8.3-SL-9E8.4	PR-1564012	NT	NT
4G8.3-LS-9E8.4	PR-1564013	NT	NT
4G8.3-GS(9)-9E8.4 (g)	PR-1572102	0.051	0.701
4G8.3-SL-9E8.4 (g)	PR-1572105	0.047	0.773
hVEGF 4G8.3-GS-hPDGF 9E8.4 [hu IgG1/k] mut(234,235) H435A	PR-1569574	0.032	0.594
hVEGF 4G8.3-SL-hPDGF 9E8.4 [hu IgG1/k] mut(234,235) H435A	PR-1569579	0.038	0.789
9E10.1_GS_CL-33675	PR-1610561	0.04	0.464

NT – Not tested

[0406] Selected DVD-Ig molecules were further evaluated for their ability to bind naturally derived human $VEGF_{165}$ (Example 1.11) and naturally derived human PDGF-BB (Example 1.19). The data is summarized in Table 68 below.

Table 68. Binding of Anti-VEGF-A/Anti-PDGF-BB DVD-Ig Molecules to $hVEGF_{165}$ and hPDGF-BB by ELISA

DVD-Ig	Corporate ID	Binding	
		Platelet derived hPDGF-BB	Y-79 derived $hVEGF_{165}$
4G8.3-GS(9)-9E8.4 (g)	PR-1572102	Yes	NT
4G8.3-SL-9E8.4 (g)	PR-1572105	Yes	NT
hVEGF 4G8.3-GS-hPDGF 9E8.4 [hu IgG1/k] mut(234,235) H435A	PR-1569574	Yes	NT
hVEGF 4G8.3-SL-hPDGF 9E8.4 [hu IgG1/k] mut(234,235) H435A	PR-1569579	Yes	NT
9E10.1_GS_CL-33675	PR-1610561	Yes	Yes

NT – Not tested

Example 13.4: Species cross-reactivity of an Anti-VEGF/anti-PDGF DVD-Ig Molecule (PR-1610561)

[0407] PR-1610561 was further evaluated for its ability to cross-react with cynomolgus monkey, mouse, rat, and rabbit using cell-based proliferation assays (Examples 1.6, 1.17, 1.18, and 1.25). The data is summarized in Table 69 below.

Table 69. Species Cross-Reactivity of Anti-VEGF/anti-PDGF DVD-Ig Molecule (PR-1610561)

Protein	**VEGF**				**PDGF**			
	cyno	mo	rat	rab	cyno	mo	rat	rab
Affinity K_D (pM)	65	-	-	41	0.8	0.3	3	3

Example 13.5: Reactivity of Anti-PDGF-BB Antibodies and Anti-VEGF-A/Anti-PDGF-BB DVD-Ig Molecules to ECM-Associated PDGF-BB

[0408] As described in Example 1.27, first recombinant cell line HEK293 cells over-expressing PDGFBB-RM and then HUVEC naturally expressing ECM-associated PDGF-BB cells were used for staining:

[0409] **HEK293 Cell Staining:** PDGFB-RM transient transfected HEK 293 cells and parental HEK293 cells were re-suspended at 1E6 cells/mL in PBS and fixed in 4% paraformaldehyde at RT for 10 minutes, washed with PBS and 2E5 cells/tube were incubated in blocking buffer (10% goat serum in PBS) for one hour on ice. Cells were washed with PBS and

incubated with primary antibody or DVD at 33nM in antibody dilution buffer (5% goat serum in PBS) for one hour on ice. Cells were washed three times with PBS and incubated with Alexa Fluo 488 conjugated Goat anti-Human IgG (Jackson Immune, code: 109-546-098; lot: 108427) 1 : 400 dilution in antibody dilution buffer, incubate on ice for 45 minutes. Cells were washed three times with PBS and cytospin onto glass slides and mounted with mounting media with DAPI. Pictures were taken by fluorescent microscopy. Anti-PDGF-BB parental and affinity matured mAbs and three DVD-Ig molecules all showed positive staining on PDGFB-RM transient transfected 293 cells (Figure 2A) and no staining on parental HEK 293 cells except for the slightly positive staining of affinity matured anti-PDGF-BB mAb. It is unclear if parental HEK 293 cells express low level of PDGF-BB endogenously

[0410] **HUVEC Staining:** HUVEC cells secrete PDGF-BB, and low level of PDGF-BB may be captured on the cell surface as ECM-associated PDGF-BB. Affinity matured anti-PDGF-BB mAb and anti-VEGF/anti-PDGF DVD-Ig built with affinity-matured anti-PDGF-BB mAb was further assessed for its staining on naturally derived ECM-associated PDGF-BB on HUVEC cells. HUVECs (Lonza, cat#: C2519A lot: 181607) were trypsinized, resuspended at 2E4 cells/mL in culture media (Lonza, EGM2 MV Bulletkit: CC-3202). Cells were plated at 10,000 cells / 500 µl / well in 8-chamber glass slide and incubated for 16 hours at 37°C, 5% CO_2. After incubation, cells were fixed with 200 µl 4% paraformaldehyde at RT for 10 minutes, washed with PBS and incubated in blocking buffer (10% goat serum in PBS) for one hour on ice. Cells were washed with PBS 3X and incubated with primary antibodies or DVD-Ig molecules at 33 nM in antibody dilution buffer (5% goat serum in PBS) for one hour on ice. Cells were washed three times with PBS and incubated with Alexa Fluo 488 conjugated Goat anti-Human IgG (JacksonImmune, code: 109-546-098; lot: 108427) 1 : 400 dilution in antibody dilution buffer, incubate on ice for 45 minutes . Cells were washed three times with PBS and mounted with mounting media with DAPI. Pictures were taken by fluorescent microscopy. As shown in Figure 2B, affinity matured anti-PDGF-BB mAb showed positive staining on HUVEC cells while the staining of parental anti-PDGF-BB mAb on HUVEC cells is not evident (Figure 2B). Anti-VEGF/anti-PDGF DVD-Ig (PR-1610561) built with affinity-matured anti-PDGF-BB mAb showed positive staining on HUVEC cells but control anti-tetanus toxoid DVD-Ig molecule also showed some weak staining which may be due to the background issue.

Example 13.6: Inhibition of Sprouting in HUVEC/MSC Co-culture Sprouting Assay by Anti-VEGF-A/Anti-PDGF-BB DVD-Ig Molecules

[0411] As described in Example 1.28, in early therapeutic treatment mode, Cytodex-3 beads (Sigma-Aldrich, cat# C3275) were coated with HUVEC cells (Lonza) overnight, and then embedded (100 beads/well) with human mesenchymal stem cells (Lonza, 20,000 cells/well) in fibrin gel in 24-well tissue culture plates. A 1:1 mixture of fresh EGM-2 complete media (Lonza)

and fibroblast (Lonza) conditioned EGM-2 media were added on top of the fibrin gel along with 2 ng/mL of recombinant human HGF. Medium was replaced every 2-3 days till the end of the experiment. After EC sprouts and pericyte coverings were formed, usually on day 4, anti-VEGF-A (4G8.4), anti-PDGFBB (9E8.) or anti-PDGFBB/VEGF-A DVD-Ig were added to the culture medium at 10 nM. 10 days later cells were fixed in 4% PFA overnight at 4°C. Endothelial cells were stained with anti-PECAM (Abcam, ab32457), followed by fluorescence-conjugated secondary antibody, and pericytes were labeled with anti-αSMA-Cy3 (Sigma, C6198). Cells were then viewed by an inverted fluorescence microscope and 5 × images were captured (Figure 3). As seen in the pictures, DVD-Ig molecules as well as the combination of anti-VEGF and anti-PDGF mAbs are able to prevent sprouting formation greater than that of anti-VEGF mAb alone. Neither anti-PDGF mAb or anti-PDGF aptamer alone appear to have any significant inhibition of sprouting formation (Figure 3). Similar experiments were also conducted in prophylactic and later therapeutic treatment modes and the results clearly demonstrated that anti-VEGF/anti-PDGF DVD-Ig (PR-1610561) strongly inhibited sprouting formation in this 3D co-culture assay.

Example 13.7: Characterization of FcRn and FcγRs Binding

[0412] Anti-VEGF/anti-PDGF DVD-Ig molecules, including 4G8.3-GS-9E8.4, 4G8.3-SL-9E8.4, 4G8.3-GS-9E8.4(g), 4G8.3-SL-9E8.4(g), 9E10.1GS_CL-33675, are human IgG1/κ isotype with L234A, L235A mutations to attenuate FcγRs binding and H435A mutation to eliminate FcRn binding. The binding of DVD-Ig molecules to FcRn from various species and the binding of DVD-Ig molecules to various FcγRs were characterized by Biacore using the method described in Example 1.2. The data is summarized in Tables 70 and 71 below.

Table 70. Binding of Anti-VEGF-A/Anti-PDGF-BB DVD-Ig Molecules to FcRn from Different Species, Measured by Biacore

	Steady State			1:1 Binding fit					
	huFcRn	cynoFcRn	rabbitFcRn	ratFcRn			muFcRn		
Immobilized	K_D (M)	K_D (M)	K_D (M)	ka (1/Ms)	kd (1/s)	K_D (M)	ka (1/Ms)	kd (1/s)	K_D (M)
4G8.3-GS-9E8.4(g) PR-1572102	NSB	NSB	NSB	n/a	n/a	NSB	n/a	n/a	NSB
4G8.3-SL-9E8.4(g) PR-1572105	NSB	NSB	NSB	n/a	n/a	NSB	n/a	n/a	NSB
9E10.1_GS_CL-33675 PR-1610561	NSB	NSB	NSB	n/a	n/a	NSB	n/a	n/a	NSB
4G8.3-GS-9E8.4 PR-1569574	NSB	NSB	NSB	n/a	n/a	NSB	n/a	n/a	NSB
4G8.3-SL-9E8.4 PR-1569579	NSB	NSB	NSB	n/a	n/a	NSB	n/a	n/a	NSB

* NSB = No significant binding at the concentration tested; n/a = not available

Table 71. Binding of Anti-VEGF-A/Anti-PDGF-BB DVD-Ig Molecules to Various Human FcγRs, Measured by Biacore

	huFcRIIb	huFcRIIa 131H	huFcRIIa 131R	huFcRIIIa 158F	huFcRIIIa 158V			Fit
Sample	K_D (M)	K_D (M)	K_D (M)	K_D (M)	ka (1/Ms)	kd (1/s)	K_D (M)	
4G8.3-GS-9E8.4(g) PR-1572102	NSB	NSB	NSB	NSB	n/a	n/a	7.40E-06	steady state
4G8.3-SL-9E8.4(g) PR-1572105	NSB	NSB	NSB	NSB	n/a	n/a	6.20E-06	steady state
9E10.1_GS_CL-33675 PR-1610561	NSB	NSB	NSB	NSB	n/a	n/a	1.1E-05*	steady state
4G8.3-GS-9E8.4 PR-1569574	NSB	NSB	NSB	NSB	n/a	n/a	1.6E-05*	steady state
4G8.3-SL-9E8.4 PR-1569579	NSB	NSB	NSB	NSB	n/a	n/a	1.2E-05*	steady state

* NSB = No significant binding at the concentration tested; n/a = not available

Example 14: Physicochemical Properties of Anti-VEGF-A/Anti-PDGF-BB DVD-Ig Molecules

Example 14.1: Assessment of Physicochemical Properties of Anti-VEGF-A/Anti-PDGF-BB DVD-Ig Molecules.

[0413] Twenty one DVD-Ig molecules were selected for a screen of their solubility and stability profiles. Samples were prepped and evaluated according to Example 2.4. The DVD-Ig proteins were prepared in a formulation buffer and stored at 40°C and 5°C for up to 21 days. Samples were pulled and analyzed by SEC to determine changes in aggregation (Table 72). The molecules were evaluated at the listed concentrations. SEC was used to quantitate the aggregation percentage.

Table 72. Aggregation and Solubility Screening Of Selected DVD-Ig Molecules Stored At 40°C and 5°C for 21 Days in a Formulation Buffer

DVD-Ig Molecule	Concentration (mg/ml)	% Aggregation Change from T0	
		T21d 5°C	T21d 40°C
4G8.3-GS-9E8.4	100	0.24	*
4G8.3-SL-9E8.4	100	0.27	*
CL-34565_GS_CL-33675	48.7	0.20	0.25
CL-34565_GS_9E8.4	4.3	-0.30	0.05
CL-34565_GS_3E2.1	10.9	-1.12	-0.89
4G8.5_GS_CL-33675	50	-0.09	*

4G8.5_GS_9E8.4	50	-0.09	12.50
4G8.5_GS_3E2.1	50	0.53	14.63
9E10.1_GS_CL-33675	50	-2.08	-3.09
9E10.1_GS_9E8.4	50.7	2.95	-0.39
9E10.1_GS_3E2.1	43.2	-6.16	-9.05
9E10.6_GS_CL-33675	50	3.17	1.87
9E10.6_GS_3E2.1	34.9	-0.63	-0.65
1B10.1_GS_CL-33675	50	0.72	1.10
1E3.4_GS_3E2.1	50	0.17	*
CL-33675_GS_4G8.5	38.7	0.15	2.34
3E2.1_GS_4G8.5	50	16.15	*
3E2.1_GS_9E10.1	30.4	*	*
3E2.1_GS_9E10.6	50	0.17	5.55
3E2.1_GS_1B10.1	38.6	-6.33	*
3E2.1_GS_1E3.4	50	10.12	*

* Samples were too degraded or compromised to evaluate with SEC (e.g. gelled, precipitated).

Example 14.2: Further Assessment of Physicochemical Properties of Anti-VEGF-A/Anti-PDGF-BB DVD-Ig Molecules (Stability During Storage at 40°C, 25°C, and 5°C)

[0414] Based on the physicochemical screen discussed above (Example 14.1), three anti-VEGF-A/anti-PDGF-BB DVD-Ig molecules (4G8.3-GS-9E8.4, 4G8.3-SL-9E8.4, and 9E10.1-GS-33675) were selected for further characterization. Sample prep and analysis was performed according to Example 2.4.

[0415] Briefly, the molecules were prepared in a formulation buffer at 100 ± 10 mg/ml and stored at 40°C, 25°C, and 5°C for 84 days. Samples were periodically pulled for characterization (Tables 73-75 below).

[0416] As mentioned in Example 2.4, both 25°C (room temperature) and 5°C (storage temperature) are typical temperatures at which the samples would be subjected either during preparation and storage for manufacture or as part of the final drug product presentation. Also, storage at 40°C is considered an accelerated stability condition which provides an indication of long-term stability prospects.

Table 73. Stability of 4G8.3-GS-9E8.4 During Storage. Aggregate, Monomer, And Fragment Percentages Were Quantitated By SEC

	% Aggregate	% Monomer	% Fragment	Area Under SEC Chromatogram Signal Relative to T0
T0	1.8	97.3	0.9	1.00
T7d 40°C	*	*	*	*
T7d 25°C	2.2	97.0	0.9	0.91
T7d 5°C	1.9	97.2	0.9	0.92
T21d 40°C	*	*	*	*
T21d 25°C	3.0	96.4	0.6	0.84
T21d 5°C	1.8	97.8	0.5	0.90
T42d 40°C	*	*	*	*
T42d 25°C	3.4	95.6	1.0	0.88
T42d 5°C	2.0	97.3	0.7	1.00
T63d 40°C	*	*	*	*
T63d 25°C	4.2	94.7	1.0	0.85
T63d 5°C	2.1	97.4	0.5	0.92
T84d 40°C	*	*	*	*
T84d 25°C	5.0	93.7	1.3	0.79
T84d 5°C	2.2	97.3	0.6	0.85

* Samples were too degraded or compromised to evaluate with SEC (e.g. gelled, precipitated).

Table 74. Stability of 4G8.3-SL-9E8.4 During Storage. Aggregate, Monomer, And Fragment Percentages Were Quantitated by SEC

	% Aggregate	% Monomer	% Fragment	Area Under SEC Chromatogram Signal Relative to T0
T0	4.2	94.7	1.1	1.00
T7d 40°C	*	*	*	*
T7d 25°C	6.6	92.2	1.3	0.86
T7d 5°C	4.3	94.7	1.0	0.82
T21d 40°C	*	*	*	*
T21d 25°C	8.5	90.5	1.1	0.77
T21d 5°C	3.9	95.3	0.8	0.87

T42d 40°C	*	*	*	*
T42d 25°C	13.2	85.6	1.3	0.80
T42d 5°C	4.5	94.4	1.1	0.97
T63d 40°C	*	*	*	*
T63d 25°C	13.2	85.3	1.5	0.73
T63d 5°C	4.3	95.0	0.7	0.87
T84d 40°C	*	*	*	*
T84d 25°C	10.3	88.1	1.6	0.62
T84d 5°C	4.5	94.7	0.7	0.80

* Samples were too degraded or compromised to evaluate with SEC (e.g. gelled, precipitated).

Table 75. Stability of 9E10.1-GS-33675 During Storage. Aggregate, Monomer, And Fragment Percentages Were Quantitated by SEC.

	% Aggregate	% Monomer	% Fragment	Area Under SEC Chromatogram Signal Relative to T0
T0	0.8	98.4	0.7	1.00
T7d 40°C	5.3	93.8	0.8	0.84
T7d 25°C	4.8	94.6	0.6	0.89
T7d 5°C	3.7	95.5	0.8	0.92
T21d 40°C	6.1	92.5	1.4	0.77
T21d 25°C	4.4	95.0	0.6	0.82
T21d 5°C	6.7	92.8	0.5	0.89
T42d 40°C	13.8	83.9	2.3	0.76
T42d 25°C	4.7	94.6	0.8	0.85
T42d 5°C	7.7	91.7	0.5	0.92
T63d 40°C	19.8	77.0	3.2	0.77
T63d 25°C	4.8	94.4	0.8	0.84
T63d 5°C	8.4	91.2	0.4	0.94
T84d 40°C	22.8	73.2	4.0	0.68
T84d 25°C	5.3	93.7	1.0	0.80
T84d 5°C	8.1	91.5	0.4	0.88

[0417] Both 4G8.3-GS-9E8.4 and 4G8.3-SL-9E8.4 formed a white precipitate when stored at 40°C after 7 days and thus could not be analyzed by SEC. The samples are assumed to be completely aggregated. At 25°C, there was an observable increase in aggregation for both

molecules. The aggregation was less rapid for 4G8.3-GS-9E8.4 than for 4G8.3-SL-9E8.4. Aggregation of the former increased from 1.8% to 5.0% after 84 days while that of the latter started at 4.2% and reached as high as 13.2% over the course of 84 days. At 5°C, there is no noticeable aggregate increase for the two molecules.

[0418] For 9E10.1-GS-33675, aggregation at 5°C increased from 0.8% to 6.7% by 21 days and levelled off at ~ 8% from 42 to 84 days. At 25°C, aggregation increased from 0.8% to 4.7% by 7 days and levelled off at that value up to 84 days. Finally, aggregation at 40°C increased from 0.8% to 22.8% in an apparently linear fashion over the course of 84 days. The aggregation at 40°C for 9E10.1-GS-33675 is much less that that observed for the other two DVD-Ig molecules. This may be the result of the universal formulation buffer used.

[0419] There was no apparent change in fragmentation for all three DVD-Ig molecules at 25°C or 5°C. At 40°C, an apparent and expected increase in fragmentation was observed for 9E10.1-GS-33675 after 21 days.

Example 14.3: Further Assessment of Physicochemical Properties of Anti-VEGF-A/Anti-PDGF-BB DVD-Ig Molecules (Stability to Freeze-Thaw Stress)

[0420] Based on the earlier physicochemical screen (Example 14.1), three anti-VEGF-A/anti-PDGF-BB DVD-Ig molecules (4G8.3-GS-9E8.4, 4G8.3-SL-9E8.4, and 9E10.1-GS-33675) were selected for further characterization. Sample prep, stress, and analysis were performed according to Example 2.5. Briefly, the molecules were prepared in a formulation buffer at concentrations of 100 ± 10 mg/ml or 1 mg/ml and subjected to four cycles of freezing (-80°C) and thawing (30°C). Samples were characterized after the second and fourth thaw (Tables 76-81 below).

[0421] As mentioned in Example 2.5, protein samples are typically frozen at -80°C for long term storage as well as shipping to remote manufacturing sites. The samples are then thawed in order to complete the drug product manufacturing process.

Table 76. Stability of 4G8.3-GS-9E8.4 at 100 ± 10 mg/ml When Subjected To Freeze-Thaw Stress (-80°C / 30°C). Aggregate, Monomer, And Fragment Percentages Were Quantitated by SEC.

	% Aggregate	% Monomer	% Fragment	Area Under SEC Chromatogram Signal Relative to T0
F/T 0	1.8	97.3	0.9	1.00
F/T 2	1.8	97.4	0.8	0.90
F/T 4	2.2	96.9	0.9	0.92

Table 77. Stability of 4G8.3-SL-9E8.4 at 100 ± 10 mg/ml When Subjected To Freeze-Thaw stress (-80°C / 30°C). Aggregate, Monomer, And Fragment Percentages Were Quantitated by SEC

	% Aggregate	% Monomer	% Fragment	Area Under SEC Chromatogram Signal Relative to T0
F/T 0	4.2	94.7	1.1	1.00
F/T 2	4.1	95.2	0.7	0.83
F/T 4	4.3	94.4	1.3	0.82

Table 78. Stability of 9E10.1-GS-33675 at 100 ± 10 mg/ml when Subjected To Freeze-Thaw Stress (-80°C / 30°C). Aggregate, Monomer, And Fragment Percentages Were Quantitated by SEC.

	% Aggregate	% Monomer	% Fragment	Area Under SEC Chromatogram Signal Relative to T0
F/T 0	0.8	98.4	0.7	1.00
F/T 2	1.1	98.5	0.4	0.91
F/T 4	1.8	97.6	0.6	0.88

Table 79. Stability of 4G8.3-GS-9E8.4 at 1 mg/ml When Subjected To Freeze-Thaw Stress (-80°C / 30°C). Aggregate, Monomer, And Fragment Percentages Were Quantitated by SEC.

	% Aggregate	% Monomer	% Fragment	Area Under SEC Chromatogram Signal Relative to T0
F/T 0	1.8	97.3	0.9	1.00
F/T 2	1.9	97.5	0.6	0.95
F/T 4	2.0	97.1	0.9	0.96

Table 80. Stability of 4G8.3-SL-9E8.4 at 1 mg/ When Subjected To Freeze-Thaw Stress (-80°C / 30°C). Aggregate, Monomer, And Fragment Percentages Were Quantitated by SEC.

	% Aggregate	% Monomer	% Fragment	Area Under SEC Chromatogram Signal Relative to T0
F/T 0	4.2	94.7	1.1	1.00
F/T 2	3.9	95.4	0.7	0.94

F/T 4	4.1	94.9	1.0	0.94

Table 81. Stability of 9E10.1-GS-33675 at 1 mg/ml When Subjected To Freeze-Thaw Stress (-80°C / 30°C). Aggregate, Monomer, And Fragment Percentages Were Quantitated by SEC.

	% Aggregate	% Monomer	% Fragment	Area Under SEC Chromatogram Signal Relative to T0
F/T 0	0.8	98.4	0.7	1.00
F/T 2	1.0	98.6	0.5	0.98
F/T 4	1.2	98.2	0.6	0.98

[0422] For all three DVD-Igs, at either 100 ± 10 mg/ml or 1 mg/ml, no apparent increase in aggregation was observed due to freeze-thaw stress after two cycles.

Example 14.4: Further Assessment of Physicochemical Properties of Anti-VEGF-A/Anti-PDGF-BB DVD-Ig Molecules (Viscosity Determination)

[0423] Based on the earlier physicochemical screen (Example 14.1), three anti-VEGF-A/anti-PDGF-BB DVD-Ig molecules (4G8.3-GS-9E8.4, 4G8.3-SL-9E8.4, and 9E10.1-GS-33675) were selected for further characterization. The molecules were prepared in a formulation buffer at 100 ± 10 mg/ml and the viscosities were measured at room temperature (Example 2.6). The viscosities were 5.1, 7.2, and 7.2 centipoise, respectively. The values are within the range that enables ease of administration via a small diameter needle attached to a syringe.

Example 14.5: Further Assessment of Physicochemical Properties of Anti-VEGF-A/Anti-PDGF-BB DVD-Ig Molecules (Thermal Stability Assessment)

[0424] Based on the earlier physicochemical screen (Example 14.1), three anti-VEGF-A/anti-PDGF-BB DVD-Ig molecules (4G8.3-GS-9E8.4, 4G8.3-SL-9E8.4, and 9E10.1-GS-33675) were selected for further characterization. The molecules were prepared in a formulation buffer at 1 mg/ml according to Example 2.3 and the thermal stabilities were determined according to Example 2.2. The midpoint temperatures of the first transition of unfolding are 52°C, 51°C, and 62°C, respectively. The temperatures at which the first transitions began to appear are 44°C, 42°C, and 62°C, respectively. The data indicate that 9E10.1-GS-33675 has a significantly greater thermal stability than the other two DVD-Ig molecules.

Example 14.6: Physicochemical Properties of an Anti-VEGF/anti-PDGF DVD-Ig Molecule (PR-1610561)

[0425] Testing of PR-1610561 revealed high thermostability (T_{onset} = 62°C), solubility at least at 76 mg/ml, and a viscosity at 100 mg/ml at room temperature of 7.2 centipoise, which is within the range that enables ease of administration via a small diameter needle attached to a syringe. PR-1610561 has appropriate storage stability in a universal buffer and freeze-thaw stability.

Example 14.76: Intact and Reduced Molecular Weight Determination

[0426] Q-TOF LC-MS can detect mass differences between proteins that can result from mis-sense mutations, post-translational modifications, truncations, and other covalent changes that affect protein molecular weight. Table 82 shows the intact molecular weight and deglycosylated intact molecular weight of all three DVD-Ig molecules. Table 83 shows the molecular weights of light chain, heavy chain and deglycosylated heavy chain. The observed molecular weights of the three DVD-Ig molecules match well with the theoretical values with difference of less than 3 Dalton, which is well within the expected range of the error for the instrument.

Table 82. Intact molecular weight

	Intact MW		Deglycosylated Intact MW	
	Theoretical	Observed	Theoretical	Observed
PR-1572102	203220	203219	200330	200330
PR-1572105	204350	204348	201460	201460
PR-1610561	202452	202450	199562	199562

Table 83. Reduced molecular weight

	Light Chain MW		Heavy Chain MW		Deglycosylated HC MW	
	Theoretical	Observed	Theoretical	Observed	Theoretical	Observed
PR-1572102	36080	36080	65533	65533	64088	64091
PR-1572105	36735	36734	65444	65444	63999	64002
PR-1610561	36006	36005	65224	65224	63779	63780

Example 14.8: Oligosaccharide Profiles By Fc Molecular Weight

[0427] DVD-Ig molecules contain N-linked oligosaccharides in the Fc region of the heavy chain. Fc molecular weight measurement can provide a semi-quantitative analysis of the oligosaccharide profiles. Table 84 shows the results of oligosaccharide profiles by Fc molecular weight. The oligosaccharide profiles of all three DVD-Ig molecules were similar to what is

normally observed for mAbs, with 70-73% Gal 0F and 21-24% Gal 1F. The level of high mannose species was very low in all three samples. No significant level of aglycosylated species was detected.

Table 84. Oligosaccharide Profiles By Fc Molecular Weight

Species	PR-1572102	PR-1572105	PR-1610561
Man 5	1.0	1.1	0.4
Gal 0F-GlcNAc	0.5	0.4	0.0
Gal 0	0.5	0.2	0.7
Gal 0F	73.4	73.4	70.8
Lys-1	0.8	0.3	0.8
Gal 1F	21.0	21.2	23.8
Gal 2F	2.8	3.3	3.6

Example 14.9: Charge Heterogeneity by Weak Cation Exchange Chromatography and Imaged Isoelectric Focusing

[0428] Weak cation exchange (WCX) chromatography separates molecules on the basis of the differences in their net surface charge. Variation in the extent of C terminal processing and certain post-translational modifications can lead to different species of an antibody with different charge distributions. Molecules that vary in their charge properties will exhibit different degrees of interaction with ion exchange resins, thus different elution profiles. Each chromatogram is characterized by a predominant peak ("main") and species eluting before ("acidic") or after ("basic"). The relative abundances of these species types are shown in Table 85.

Table 85. Results of Weak Cation Exchange Chromatography Analysis

	Acidic (%)	Main (%)	Basic (%)
PR-1572102	9.2	63.9	26.9
PR-1572105	14.9	52.4	32.7
PR-1610561	17.7	56.5	25.8

[0429] Imaged capillary isoelectric focusing (icIEF) is a technique that separates proteins on the basis of their isoelectric points or pI values. Different proteins have different pI and peak profiles, which makes icIEF an ideal identity assay. In icIEF, proteins with different pI values focus into distinctive bands in a linear pH gradient formed by ampholytes after applying high voltage. Table 86 shows the theoretical pI (calculated based on amino acid sequence) and

the observed pI values measured by imaged icIEF. Also shown in Table 86 are the relative abundances of different charge species detected by imaged icIEF.

Table 86. Results of Imaged Isoelectric Focusing

	Thoe. pI	pI by icIEF	Acidic (%)	Main (%)	Basic (%)
PR- 1572102	6.13	6.78	14.3	71.6	14.1
PR-1572105	6.13	6.74	25.3	60.2	14.4
PR-1610561	6.67	7.27	27.2	63.2	9.6

Example 15: Pharmacokinetic Properties of Anti-VEGF-A/Anti-PDGF-BB DVD-Ig Molecules

Example 15.1: Pharmacokinetic Properties of Anti-VEGF-A/Anti-PDGF-BB DVD-Ig Molecules Intravenously Administered In huFcRN Transgenic Mice

[0430] Studies were conducted in accordance with the AbbVie IACUC guidelines. Anti-VEGF/anti-PDGF DVD-Ig molecules PR-1572102 (lot 2211502), PR-1572105 (lot 2211597), or PR-1610561 (lot 2213329) were administered to huFcRn B6.Cg transgenic mice (5/group) at 5 mg/kg by slow intravenous bolus dose injection. Blood samples were collected from each mouse at 1, 24 and 96 hours and 7, 10, 14 and 21 days post dose. All samples were stored at -80°C until analysis. DVD-Ig serum concentrations were measured using a Meso Scale Discovery (MSD) electrochemiluminescence (ECL) Ligand Binding Assay. Biotinylated VEGF ligand was coated onto streptavidin MSD plates for capture of anti-VEGF-A/anti-PDGF-BB DVD-Ig molecules from blood samples, and detection was achieved with a sulfo-tag goat anti-human IgG antibody. Concentrations were calculated by four-parameter logistic fit using XLfit4. Pharmacokinetic parameters were calculated with Non-compartmental analysis using Pharmacokinetics Laboratory Automation Software for Management and Analysis (PLASMA) (Version 2.6.12, SParCS, AbbVie).

[0431] All three anti-VEGF/PDGF DVD-Ig molecules carrying the H435A substitution had serum concentrations rapidly clear, with measurable concentrations only to 24 hours. These results are in agreement with the rapid clearance observed with other H435A modified antibody and DVD-Ig molecules in human FcRn transgenic mice.

Example 15.2: Pharmacokinetic Properties of Anti-VEGF-A/Anti-PDGF-BB DVD-Ig Molecules Intravitreously Administered in Rabbit

[0432] Studies were conducted in accordance with the Abbott IACUC guidelines. Female New Zealand White rabbits were used for the ocular pharmacokinetic characterization of Anti-VEGF-A/anti-PDGF-BB DVD-Igs: PR-1572102, PR-1572105 and PR-1610561. Animals (4 animals) were split into two cohorts of two for determination of ocular pharmacokinetics.

Samples of aqueous humour were taken at 4, 24, 48, 72, 120, 168, 336 and 504 hours post dosing. With cohort 1 providing samples at 4, 48, 120 and 168 hours, and cohort 2 providing samples at 24, 72, 336 and 504 hours, post dosing. Drug levels in the eye were determined from concentrations in aqueous humour as a surrogate for the vitreous concentrations. Vitreous was harvested from each animal as a terminal sample after their last aqueous humour sample. The proportion of aqueous to vitreous concentration was determined from these terminal time points. Blood samples for the harvest of serum used to estimate systemic exposure after vitreous dosing were also collected at 4, 24, 48, 72, 120, and 168 hours post dosing from all animals, and at 336 and 504 hours from the animals in cohort 2. Test articles were dosed into the vitreous compartment at a range of 0.25 to 0.50 mg per eye with a dose volume of no more than 0.050 mL. Only the right eye of each animal was dosed. Prior to dosing, animals were anesthetized with xylazine/ketamine. The eye was prepared by first applying topical analgesic drops (procaine HCl Ophthalmic solution, 0.5%), then the injections site was swabbed with a saturated povidone-iodine swabstick (10% solution equivalent to 1% available iodine) prior to injection. The intravitreal dose was administered with a 26 gauge needle. The point of entry for the injection was 1-2 mm from the limbus through the sclera. After injection, a sterile cotton eye spear was placed on the injection site and held for 30 seconds to prevent leakage. Animals were anesthetized for aqueous fluid collection. At the selected time points after dosing, the aqueous fluid was collected using a 30 gauge needle inserted through the cornea. The needle was advanced just past the bevel and fluid was collected. The samples provided approximately 0.05-0.1 mL of aqueous humour per sampling period. At the selected time points after dosing, blood samples were obtained from an ear vein or artery. Hemostasis following collection was achieved by the application of manual pressure and topical clotting factor or tissue glue as needed. The samples were from 0.5-1 ml in volume, and were allowed to clot for harvest of serum. Aqueous, vitreous and serum samples were stored at -80°C, and submitted for drug level determinations.

[0433] All DVD-Ig serum concentrations were measured using a GYROS method employing biotinylated VEGF ligand for capture, and Alexa Flour 647 goat anti-human IgG detection. Concentrations were calculated by four-parameter logistic fit using XLfit4. Pharmacokinetic parameters were calculated with Non-compartmental analysis using Pharmacokinetics Laboratory Automation Software for Management and Analysis (PLASMA) (Version 2.6.12, SParCS, AbbVie).

Table 87. Ocular Half Lives in Rabbit from Analysis of Aqueous Humor

Experiment	Test Article	Corporate ID	Half life (hours)
#1	9E10.1_GS_CL-33675	PR-1610561	111
#2	9E10.1_GS_CL-33675	PR-1610561	Pending

Example 15.3: Pharmacokinetic Properties of Anti-VEGF-A/anti-PDGF-BB DVD-Ig Molecules Intravenously Administered in Cynomolgus Monkey

[0434] Studies are conducted in accordance with the AbbVie IACUC guidelines. Female cynomolgus are used for the systemic pharmacokinetic characterization of Anti-VEGF-A/anti-PDGF-BB DVD-Igs, including PR-1572102, PR-1572105 and PR-1610561 after intravenous dosing. Monkeys are dosed intravenously at 5 mg/kg by slow bolus into the saphenous vein over approximately 2 minutes with a volume of 0.5 mL/kg. Samples are taken for determination of the pharmacokinetics of the test compounds at 0, 0.08, 4, 8, 24, 72, 168, 240, 336, 504 and 672 hours post dosing. At the selected time points after dosing, blood samples are obtained from a femoral vein. Hemostasis following collection is achieved by the application of manual pressure and topical clotting factor or tissue glue as needed. The samples may be approximately 1 ml in volume, and are allowed to clot for harvest of serum. Serum samples are stored at -80°C, and submitted for drug level determinations.

[0435] DVD-Ig serum concentrations are measured using either a GYROS or a MSD method. GYROS employs biotinylated VEGF ligand for capture, and Alexa Flour 647 goat anti-human IgG detection. MSD employs biotinylated VEGF ligand for capture, and Sulfo-tag goat anti-human IgG or sulfo-tag VEGF for detection. Concentrations are calculated by four-parameter logistic fit using XLfit4. Pharmacokinetic parameters are calculated with Non-compartmental analysis using Pharmacokinetics Laboratory Automation Software for Management and Analysis (PLASMA) (Version 2.6.12, SParCS, AbbVie).

Example 15.4: Pharmacokinetic Properties of Anti-VEGF-A/Anti-PDGF-BB DVD-Ig Molecules Intravitreously Administered in Cynomolgus Monkey.

[0436] Studies are conducted in accordance with the AbbVie IACUC guidelines. Female cynomolgus are used for the ocular pharmacokinetic characterization of Anti-VEGF-A/anti-PDGF-BB DVD-Igs, including PR-1572102, PR-1572105 and PR-1610561. Animals (4 animals) are split into two cohorts of two for determination of ocular pharmacokinetics. Samples of aqueous humour are taken at 4, 24, 48, 72, 120, 168, 336 and 504 hours post dosing. With cohort 1 providing samples at 4, 48, 120 and 168 hours, and cohort 2 providing samples at 24, 72, 336 and 504 hours, post dosing. Drug levels in the eye are determined from concentrations in aqueous humour as a surrogate for the vitreous concentrations. Blood samples for the harvest of serum used to estimate systemic exposure after vitreous dosing are also collected at 4, 24, 48, 72, 120, and 168 hours post dosing from all animals, and at 336 and 504 hours from the animals in cohort 2. Test articles are dosed into the vitreous compartment at a range of 0.25 to 0.50 mg per eye with a dose volume of no more than 0.050 mL. Only the right eye of each animal is dosed. Prior to dosing, animals are anesthetized with xylazine/ketamine. The eye is prepared by first applying topical analgesic drops (procaine HCl Ophthalmic solution, 0.5%), then the injections

site is swabbed with a saturated povidone-iodine swabstick (10% solution equivalent to 1% available iodine) prior to injection. The intravitreal dose is administered with a 26 gauge needle. The point of entry for the injection is 1-2 mm from the limbus through the sclera. After injection, a sterile cotton eye spear is placed on the injection site and held for 30 seconds to prevent leakage. Animals are anesthetized for aqueous fluid collection. At the selected time points after dosing, the aqueous fluid is collected using a 30 gauge needle inserted through the cornea. The needle is advanced just past the bevel and fluid was collected. The samples provide approximately 0.05-0.1 mL of aqueous humour per sampling period. At the selected time points after dosing, blood samples are obtained from an ear vein or artery. Hemostasis following collection is achieved by the application of manual pressure and topical clotting factor or tissue glue as needed. The samples are approximately 1 ml in volume, and are allowed to clot for harvest of serum. Aqueous, vitreous and serum samples are stored at -80°C, and submitted for drug level determinations.

[0437] DVD-Ig serum concentrations are measured using either a GYROS or a MSD method. GYROS employs biotinylated VEGF ligand for capture, and Alexa Flour 647 goat anti-human IgG detection. MSD employs biotinylated VEGF ligand for capture, and Sulfo-tag goat anti-human IgG or sulfo-tag VEGF for detection. Concentrations are calculated by four-parameter logistic fit using XLfit4. Pharmacokinetic parameters are calculated with Non-compartmental analysis using Pharmacokinetics Laboratory Automation Software for Management and Analysis (PLASMA) (Version 2.6.12, SParCS, AbbVie).

Example 16: Efficacy of Anti-VEGF-A/Anti-PDGF-BB DVD-Ig Molecules Human VEGF Transgenic Mice

Example 16.1: Efficacy of Anti-VEGF-A/Anti-PDGF-BB DVD-Ig Molecules to Inhibit Subretinal Neovascularization in Rho/huVEGF Transgenic Mice

[0438] Transgenic mice in which the rhodopsin promoter drives expression of human $VEGF_{165}$ in photoreceptors (Rho-VEGF mice) have onset of VEGF expression at P7 and starting at P10, develop sprouts of NV from the deep capillary bed of the retina that grow through the photoreceptor layer and form an extensive network of new vessels in the subretinal space. Since the new vessels originate from retinal capillaries and not choroidal vessels, it is technically a model of retinal angiomatous proliferation (RAP) which occurs in roughly 30% of patients with neovascular AMD, but in general it mimics critical features of wet AMD. At P14, hemizygous Rho-VEGF mice were given an intraocular injection of test reagents. At P21, the mice were euthanized, and eyes were fixed in 10% phosphate-buffered formalin for 2 hours. Retinas were dissected, blocked with 5% normal swine serum in PBS for 1 hour, stained with FITC-conjugated GSA, a vascular stain, for 2 hours to stain vascular cells, flat mounted with the photoreceptor side up, and examined by fluorescence microscopy. The area of subretinal NV was measured with

image analysis by an investigator blinded with respect to treatment group. The other eye will provide information regarding systemic effect of an intraocular injection.

[0439] In the study below, nine treatment groups were evaluated: DVD-Ig Control (DVD 889), Eylea, Anti VEGF mAb, Anti PDGF mAb, Anti VEGF + Anti PDGF (combination Ab treatment), Anti-VEGF/anti-PDGF DVD-Ig. Only eye measurements in the experimental eye were analyzed and reported here using one way ANOVA analysis. Posthoc comparison of treatment vs the DVD control groups was analysed by Dunnett's test. Results are shown in See Fig. 4 and in Table 88 below. Further, differences in PDGF neutralization potencies and the molecular size of the DVD-Ig versus IgG did not have an effect in this model.

[0440] An overall ANOVA F-test for significance was used and the data was shown to be significant ($p<.0001$). Comparison of the test groups to the DVD-Ig control group shows that the difference from all the groups was significant (Dunnet test $p<.0001$). PR-1610561 was significantly more effective at inhibiting subretinal neovascularization in Rho/huVEGF transgenic mice than Eylea (Tukey HSD test pvalue = 0.0031). PR-1610561 was more effective, but not significantly different from, the anti-VEGF and anti-PDGF (potency matched mAbs) combination group.

Table 88. Inhibition Efficacy of Anti-VEGF-A, Anti-PDGF-BB, Anti-VEGF-A + Anti-PDGF-BB, and Anti-VEGF-A/Anti-PDGF-BB DVD-Ig Molecules to Subretinal Neovascularization in Rho/huVEGF Transgenic Mice

Groups	Corporate ID#	N (# of animals)	Mean	Std Dev	Std Err	CV (%)
DVD negative control	PR-1250499	8	0.0892	0.0665	0.0235	74
Eylea	-	19	0.0198	0.0224	0.0051	113
Anti VEGF	-	7	0.0164	0.0088	0.0033	54
Anti PDGF	-	16	0.0297	0.0265	0.0066	89
Anti VEGF + Anti PDGF	-	10	0.0119	0.0182	0.0058	153
Anti-VEGF/anti-PDGF DVD-Ig	PR-1610561	9	0.0033	0.0038	0.0013	115

Example 16.2: Efficacy of Anti-VEGF-A/Anti-PDGF-BB DVD-Ig Molecules in Tet-Opsin-Human $VEGF_{165}$ Double–Transgenic Mice

[0441] When given injections of doxycycline, Tet-opsin-VEGF double-transgenic mice with Dox-inducible expression of VEGF express 10-fold higher levels of human $VEGF_{165}$ than Rho-VEGF–transgenic mice and develop severe NV and exudative retinal detachments within 3 to 5 days. Tet-opsin-VEGF mice provide a severe model where mice develop exudative retinal detachments and only the most effective agents have a significant impact. Double-hemizygous Tet-opsin-VEGF mice were given intraocular injections of test reagent in the right eyes. For the

next 3 days, the mice were also administered a daily subcutaneous injection of 50 mg/kg doxycycline. At the 4th day, mice were euthanized and fundus photographs taken with Micron III retinal imaging microscope (Phoenix Research Laboratories, Pleasanton, CA). Also, OCT images were taken by Bioptigen Image-guided OCT (Envisu R4110, Bioptigen Inc. Morrisville, NC). Then eyes were frozen in optimal cutting temperature embedding solution. Ten-micron ocular serial sections were cut through the entire eye, stained with H&E stain and examined by light microscopy. After that mean length of the retinal detachment per section was measured with image analysis by an investigator blinded with respect to treatment group. The percentage of the detached retina was computed. Retinal detachment was graded as no detachment (0); partial retinal detachment (1); or total retinal detachment (2).

[0442] Anti-VEGF-A, anti-PDGF-BB, and the combination of anti-VEGF-A and anti-PDGF-BB were tested for their ability to suppress retinal detachment (RD) in tet-opsin-VEGF double transgenic mice. Results showed differences among the 3 test groups (P=0.01, Kruskal-Wallis test). Based on the RD number, the combination of anti-VEGF-A and anti-PDGF-BB (7 NRD, 1 PRD, 0 TRD), and the anti-VEGF-A alone (5 NRD, 0 PRD, 0 TRD) groups were more effective than anti-PDGF-BB alone (2 NRD, 2 PRD, 2 TRD) in preventing RD in Tet-opsin-VEGF double transgenic mice.

[0443] The differences in efficacy between PR-1610561, Eylea, and control IgG were compared next in tet-opsin-VEGF mice. Differences were also found among the 3 groups (P=0.01, Kruskal-Wallis test). PR-1610561 (10 NRD, 0 PRD, 1 TRD) and Eylea (4 NRD, 3 PRD, 1 TRD) were more effective than IgG control (2 NRD, 2 PRD, 2 TRD) in preventing RD in Tet-opsin-VEGF double transgenic mice. The data is summarized in Table 89 below.

Table 89. The efficacy of test articles in tet-opsin-VEGF double transgenic mice

Grade	IgG control	Anti-VEGF mAb	Anti-PDGF mAb	Anti-VEGF+ Anti-PDGF	PR-1610561	Eylea
0 (NRD)	2	5	2	7	10	4
1 (PRD)	1	0	2	1	0	3
2 (TRD)	6	0	3	0	1	1
Total eyes	9	5	7	8	11	8

[0444] The effects of PR-1610561 in a tet/opsin/huVEGF double transgenic mouse retinal detachment model were also analyzed by another grading system (Table 89A). 1 μl of reagent was injected into one eye, followed by subcutaneous injection of doxycycline at 500 mg/kg once a day for three days, and then fundus images and OCTs were done at day 4. Retinal

detachment was graded as no detachment (0); no retinal detachment but at least one sign selected from dilated retinal vessels, retinal edema, or hemorrhage (1); one or less than one quadrant of retinal detachment (2); two or three quandrants of retinal detachment or shallow pan retinal detachment (3); or severe bullous retinal detachment (4).

Table 89A. Efficacy of Anti-VEGF, Anti-PDGF, Anti-VEGF + Anti-PDGF, and Anti-VEGF/Anti-PDGF DVD-Ig Molecules in Tet/Opsin/huVEGF Double Transgenic Mice

Grade	DVD889	Anti-VEGF	Anti-PDGF	Combo	PR-1610561	Aflibercept
0	1	4	1	4	3	1
1	1	1	1	2	7	3
2	1	0	2	0	0	1
3	0	0	0	1	1	1
4	6	0	3	0	0	1
Total eyes evaluated	9	5	7	8	11	7

[0445] The results in the tables above show that PR-1610561 has similar efficacy to a combination of anti-VEGF-A and anti-PDGF-BB, and is superior to Aflibercept alone in suppressing subretinal neovascularization in Rho/huVEGF transgenic mice. PR-1610561 is also superior to the combination of Aflibercept and anti-PDGF-BB in the prevention of vascular leakage in Rho/huVEGF transgenic mice.

Example 16.3: Effects of Anti-VEGF/Anti-PDGF on Ocular Neovascularization and Vascular Permeability/Perfusion

[0446] This study compared the effects of intraocular injections of anti-VEGF/anti-PDGF DVD-Ig molecules, anti-VEGF mAb alone, anti-PDGF alone, and a combination of antibodies.

[0447] DVD-Ig molecules and DVD-Ig Fab fragments were selected for evaluation, first in Rho/VEGF mice and then in Tet/opsin/VEGF double transgenic mice.

[0448] Studies used rho/VEGF and Tet/opsin/VEGF mouse models as described in Example 16.1. The compounds evaluated are shown in Table 90 below. About 20 mice were included per experiment, where one eye was injected with agent and the other eye was not injected.

Table 90. Study Agents

4G8.3-GS-9E8.4 (PR-1572102; DVD-Ig-1)
4G8.3-LS-9E8.4 (PR- PR-1575573; DVD-Ig-2)
4G8.3-SL-9E8.4 (PR-1572105; DVD-Ig-3)

DVD 889(IgG control)
Anti-VEGF IgG 4G83
Anti-PDGF-BB IgG 9E8.4
Anti-VEGF IgG 24 μg + Anti-PDGF-BB IgG
Avastin 24 μg
Anti-PDGF-BB aptamer E10030.1
Avastin 24 μg + Anti-PDGF-BB aptamer

[0449] Transgenic mice in which the rhodopsin promoter drives expression of VEGF in photoreceptors (rho/VEGF mice) develop retinal angiomatous proliferation (RAP) which originates from the deep capillary bed of the retina and grows through the photoreceptor layer to reach the subretinal spaces. The transgenic mice were utilized to determine the effects of DVD-Ig molecules on subretinal neovascularization. The rho/VEGF mice have an onset of VEGF expression at P7 and, starting at P10, develop sprouts of NV from the deep capillary bed of the retina that grow through the photoreceptor layer and form an extensive network of new vessels in the subretinal space. At P14, hemizygous Rho-VEGF mice were given an intraocular injection of test reagents. At P21, the mice were euthanized, and eyes were fixed in 10% phosphate-buffered formalin for 2 hours. Retinas were dissected, blocked with 5% normal swine serum in PBS for 1 hour, stained with FITC-conjugated GSA for 2 hours to stain vascular cells, flat mounted with the photoreceptor side up, and examined by fluorescence microscopy. The area of subretinal NV was measured with image analysis by an investigator blinded with respect to treatment group.

[0450] Compared with the control DVD-Ig molecule, DVD-Ig-1 and DVD-Ig-3 significantly decreased choroidal neovascularization (CNV) ($p=0.02$, 0.04), whereas DVD-Ig-2 did not show much effect. Compared with the IgG control, the combined administration of anti-VEGF IgG and anti-PDGF-BB IgG significantly decreased CNV ($p=0.045$), while administration of anti-VEGF IgG or anti-PDGF IgG alone did not significantly reduce subretinal NV. No other difference was observed in eyes injected with Avastin, anti-PDGF-BB aptamer, or a mixture of Avastin and anti-PDGF-BB aptamer. Significantly decreased subretinal NV was found after administration of DVD-Ig-1 and DVD-Ig-3, when compared to the mixture of Avastin and the anti-PDGF-BB aptamer. No other difference was found between DVD-Ig reagents and the combined administration of anti-VEGF-IgG and anti-PDGF IgG. Fig. 5.

[0451] No difference was found in the untreated eyes of mice injected with anti-VEGF/anti-PDGF DVD-Ig molecules, control DVD-Ig, anti-VEGF mAb alone, anti-PDGF alone, and a combination of antibodies (ANOVA, $P>0.05$), indicating there was no clear systemic effect of intraocular injection. Fig. 6.

[0452] Tet/opsin/VEGF mice express higher levels of VEGF in photoreceptors than rho/VEGF mice, resulting in severe NV and vascular leakage with exudative retinal detachment. The efficacy of intraocular injections of anti-VEGF/anti-PDGF DVD-Ig molecules in this transgenic mouse was also evaluated. Mice were given intraocular injections of test reagent in the

right eye. For the next 3 days, the mice were also administered a daily subcutaneous injection of 50 mg/kg doxycycline. At the 4th days, mice were euthanized and fundus photographs were taken with Micron III retinal imaging microscope (Phoenix Research Laboratories, Pleasanton, CA). OCT images were taken by Bioptigen Image-guided OCT (Envisu R4110, Bioptigen Inc. Morrisville, NC). Then eyes were frozen in optimal cutting temperature embedding solution. Ten-micron ocular serial sections were cut through the entire eye, stained with H&E stain and examined by light microscopy. Mean length of the retinal detachment per section was measured with image analysis by an investigator blinded with respect to treatment group. The percentage of the retina that was detached was computed.

[0453] Five mice in each test group were injected with DVD-Ig reagents separately. In DVD-Ig-1 injected eyes, two were not detached and three were partially detached, while three eyes were totally detached and two partially detached in the uninjected eye. In DVD-Ig-3 injected eyes, one was not detached, two were partially detached, and two were totally detached, while all the uninjected eyes were totally detached. In the DVD-Ig-2 injected eyes, one was not detached and four were totally detached, while one eye was partially detached and four eyes were totally detached in the uninjected eye. In the IgG control group, one injected eye was not detached, one eye was partially detached, and three eyes were totally detached, while all eyes were totally detached in the uninjected eye. Fig. 7.

[0454] Thus, DVD-Ig-1 and DVD-Ig-3 appeared to perform at least as well as a combination of anti-VEGF mAb and anti-PDGF mAb for the measured parameters, while requiring the administration of only one compound.

Example 17: Generation and Identification of Various Molecular Formats Optimal for Applications in Ocular Diseases

[0455] Several attributes were considered in the design of a therapeutic biologic for the treatment of wet AMD:

[0456] **PK, efficacy and frequency of administration:** Longer ocular duration may support less frequent intravitreous injection. The size of the administered molecule may play a role in determining ocular half-life. This is supported by consistently longer ocular half-life for the current anti-VEGF agents with larger molecular size in humans and in experimental animals. Bevacizumab, which has a larger molecular size (150 kDa) than ranibizumab (49 kDa), also seems to have more robust duration of efficacy in both Rho/huVEGF and tet/huVEGF transgenic mice, the two models used for preclinical efficacy.

[0457] **FcRn and FcγR binding and safety:** Fc neonatal receptor (FcRn), which plays a role for long circulating half-life of IgG molecules in serum, may or may not play an important role in determining ocular half-life. The molecules with wild type FcRn binding, however, will have long systemic half-life and may increase safety risk due to unnecessary systemic exposure of intravitreously injected molecules. FcRn is also perceived to play a role in active efflux of IgGs

across blood-retina barrier. This may lead to shortened ocular retention time for the intravitreously inject molecules. Effector functions are not needed for the efficacy of anti-wet AMD agents. But both VEGF-A and PDGF-BB may be associated with extracellular matrix when they are initially synthesized and secreted. The ECM-associated VEGF-A and PDGF-BB therefore may potentially mediate effector functions.

[0458] **Affinity, valency and potency:** Both VEGF-A and PDGF-BB are homodimeric molecules. If a monovalent molecular format similar to that of ranibizumab (Fab) is used for bispecific molecules targeting VEGF and PDGF for the treatment of wet AMD, high affinity may be needed to maintain binding and potent neutralization of both VEGF-A and PDGF-BB.

[0459] **Manufacturability:** Any viable format needs to have acceptable expression, purification, formulation properties to accommodate DS and DP manufacturing.

[0460] Various binding protein formats disclosed herein may satisfy these characteristics:

(1) Full length DVD-Ig [L234A, L235A] (200 kDa, lacks binding to FcgRs)
(2) Full length DVD-Ig [L234A, L235A, H435A] (200 kDa, lacks binding to FcgRs and FcRn)
(3) Half DVD-Ig (100 kDa, lacks binding to FcgRs and FcRn)
(4) DVD-Fab (75 kDa, no Fc)

Example 17.1: Generation of Various Molecular Formats Including DVD-Ig [L234A, L235A], DVD-Ig [L234A, L235A and H435A], DVD-Ig [L234A, L235A and H435R], Half DVD-Ig and DVD-Fab

[0461] This example evaluates the impact of Fc mutations on the PK properties of DVD-Ig binding proteins. DVD-038 was used a tool molecule to study various DVD-Ig formats, including a half-DVD-Ig (DVD038 [L234A, L235A] Half-DVD), full DVD-Ig binding proteins having three constant domain mutations (DVD038 [L234A, L235A and H435A] and DVD038 [L234A, L235A and H435R]), and a full DVD-Ig binding protein having two constant domain mutations (DVD038 [L234A, L235A]). The data below was used to evaluate options for producing a VEGF/PDGF binding protein structure with good drug-like properties and exhibiting high ocular duration but low systemic circulation. DVD038 is a dual variable domain binding protein that binds HER2 and VEGF.

[0462] To prepare mutants of DVD038, overlapping PCR was used with primers designed to include the desired mutations. PCR products were digested and ligated into the cloning vector. Bacterial transformation was performed to identify positive clones and constructs were harvested and purified for use in mammalian transfection using standard protocols known in the art.

[0463] All variants were transiently transfected into 10L of HEK 293 6E suspension cell cultures in a Wave-bag with a ratio of 60% to 40% light to heavy chain construct. 0.5 mg/mL PEI was used to transfect the cells. Supernatants were harvested after 11 days by centrifugation at 16000g for 20 minutes followed by filtration using Pall Serum Capsule and Pall AcroPak 1000. All except DVD-Fab were purified on MabSelectSuRe resin (GE Healthcare, 17-5438-04). Following equilibration with PBS pH 7.4, the supernatant was loaded on the resin and washed with PBS pH 7.4. DVD-Ig protein was eluted with 50 mM Glycine, 50 mM NaCl pH 3.5. DVD-Fab was purified using Protein G Sepharose 4 FF resin (GE Healthcare, 17-0618-04). Elution was performed with Immunopure IgG elution buffer (Pierce, 185 1520). Fractions containing DVD-Ig were pooled and dialyzed in 30 mM Histidine pH 6, 8% sucrose overnight at 4°C.

Example 17.2: Binding of Various Formats to FcRns from Different Species

[0464] As described in Example 1.2, all variants of DVD038, except for DVD038 Fab which does not have an Fc region, were analyzed for their binding to FcRns from different species. The data is summarized in Table 91 below.

Table 91. Binding of Various Formats to FcRns from Different Species

Test Articles	Corporate ID	Hu FcRn	Cyno FcRn	Rabbit FcRn	Rat FcRn		
		KD (M)	KD (M)	KD (M)	ka (1/Ms)	kd (1/s)	KD (M)
DVD038 (L234A, L235A) Half DVD-Ig	PR-1578399	6.26E-06	3.13E-06	6.76E-07	3.06E+04	2.57E-02	8.40E-07
DVD038 (L234A ,L235A, H435R)	PR-1564681	7.96E-06	2.57E-06	3.98E-07	5.15E+04	5.53E-02	1.07E-06
DVD038 (L234A, L235A)	PR-1565009	4.90E-06	1.74E-06	2.75E-07	3.66E+04	1.94E-02	5.31E-07
DVD038 (L234A, L235A, H435A)	PR-1565689	NSB	NSB	NSB	NSB		
HERCEPTIN	-	4.53E-06	2.62E-06	4.69E-07	3.27E+04	1.81E-02	5.55E-07

* NSB = no significant binding

Example 17.3: Pharmacokinetic Properties of Different Formats in huFcRn Transgenic Mice Administered Intravenously

[0465] Studies were conducted in accordance with the Abbott IACUC guidelines. DVD038 (L234A, L235A) (PR-1565009), DVD038 (L234A, L235A, H435R) (PR-1564681), and DVD038 (L234A, L235A, H435A) (PR-1565689) were administered to huFcRn transgenic mice (5/group) at 6.7 mg/kg by slow intravenous bolus dose injection. Blood samples were collected from each mouse at 1, 24 and 96 hours and 7, 10, 14 and 21 days post dose. All samples were stored at -80°C until analysis. DVD-Ig serum concentrations were measured using a Meso Scale Discovery (MSD) electrochemiluminescence (ECL) Ligand Binding Assay. Biotinylated VEGF ligand was coated onto streptavidin MSD plates for capture of anti-VEGF-A/anti-PDGF-BB DVD-Ig molecules from blood samples, and detection was achieved with a sulfo-tag goat anti-

human IgG antibody. Concentrations were calculated by four-parameter logistic fit using XLfit4. Pharmacokinetic parameters were calculated with Non-compartmental analysis using Pharmacokinetics Laboratory Automation Software for Management and Analysis (PLASMA) (Version 2.6.12, SParCS, AbbVie).

Table 92. PK in huFcRn Transgenic Mice

Test Articles	Corporate ID	T1/2 (d)	CL (mL/h/kg)
DVD038 (L234A, L235A)	PR-1565009	2.8	0.81
DVD038 (L234A ,L235A, H435R)	PR-1564681	1.8	1.25
DVD038 (L234A, L235A, H435A)	PR-1565689	0.6	1.58

The results demonstrate a trend for increased clearance and shorter half-life for DVD constructs with reduced or lack of Fc binding in huFcRn transgenic mice.

Example 17.4: Pharmacokinetic Properties of Different Formats in CD-1 Mice Administered Intravenously

[0466] Studies were conducted in accordance with the Abbott IACUC guidelines. DVD038 (L234A, L235A) (PR-1565009), DVD038 (L234A, L235A, H435R) (PR-1564681), DVD038 (L234A, L235A, H435A) (PR-1565689), DVD038 half DVD-Ig (L234A, L235A) (PR-1578399) and DVD-Fab (PR-1574215) were administered to CD-1 mice (5/group) at 6.7 mg/kg by slow intravenous bolus dose injection. Blood samples were collected from each mouse at 1, 24 and 96 hours and 7, 10, 14 and 21 days post dose. All samples were stored at -80°C until analysis. DVD-Ig serum concentrations were measured using a Meso Scale Discovery (MSD) electrochemiluminescence (ECL) Ligand Binding Assay. Biotinylated VEGF ligand was coated onto streptavidin MSD plates for capture of anti-VEGF-A/anti-PDGF-BB DVD-Ig molecules from blood samples, and detection was achieved with a sulfo-tag goat anti-human IgG antibody. Concentrations were calculated by four-parameter logistic fit using XLfit4. Pharmacokinetic parameters were calculated with Non-compartmental analysis using Pharmacokinetics Laboratory Automation Software for Management and Analysis (PLASMA) (Version 2.6.12, SParCS, AbbVie).

Table 93. PK in CD-1 Mice

Test Articles	Corporate ID	T1/2 (d)	CL (mL/h/kg)
DVD038 (L234A, L235A)	PR-1565009	7.6	0.46
DVD038 (L234A ,L235A, H435R)	PR-1564681	6.4	0.29
DVD038 (L234A, L235A, H435A)	PR-1565689	2.7	0.73
DVD038 Half DVD-Ig (L234A, L235A)	PR-1578399	0.4	8.86
DVD038 DVD-Fab	PR-1574215	0.2	20.76

Results demonstrate a trend for increased clearance and shorter half-life for DVD constructs with reduced or lack of Fc binding in CD-1 mice. Molecules composed of a fragment of immunoglobulin structure are cleared fastest.

Example 17.5: Pharmacokinetic Properties of Different Formats in Rabbits Administered Intravitreously

[0467] Studies were conducted in accordance with the AbbVie IACUC guidelines. Female New Zealand White rabbits were used for the ocular pharmacokinetic characterization of formats DVD038 (PR-1565009, lot 2131983), DVD038 H435A (PR-1565689, lot 2131481), DVD038 Dhab (PR-1578399, lot 2149586) and DVDFab (PR-1574215, lot 2143755). Animals (4 animals) were split into two cohorts of two for determination of ocular pharmacokinetics. Samples of aqueous humour were taken at 48, 168, 336 and 504 hours post dosing. With cohort 1 providing samples at 48 and 168 hours, and cohort 2 providing samples at 336 and 504 hours, post dosing. Drug levels in the eye were determined from concentrations in aqueous humour. Blood samples for the harvest of serum used to estimate systemic exposure after vitreous dosing were also collected at 4, 24, 48, 72, 120, 168 hours post dosing from all animals, and at 336 and 504 hours from the animals in cohort 2. Test articles were dosed into the vitreous compartment at 0.50 mg per eye with a volume of no more than 0.050 mL. Only the right eye of each animal was dosed. Prior to dosing, animals were anesthetized with xylazine/ketamine. The eye was prepared by first applying topical analgesic drops (procaine HCl Ophthalmic solution, 0.5%), then the injections site was swabbed with a saturated povidone-iodine swab stick (10% solution equivalent to 1% available iodine) prior to injection. The intravitreal dose was administered with a 26 gauge needle. The point of entry for the injection was 1-2 mm from the limbus through the sclera. After injection, a sterile cotton eye spear was placed on the injection site and held for 30 seconds to prevent leakage. Animals were anesthetized for aqueous fluid collection. At the selected time points after dosing, the aqueous fluid was collected using a 30 gauge needle inserted through the cornea. The needle was advanced just past the bevel and fluid was collected. The samples provided approximately 0.05-0.1 mL of aqueous humour per sampling period. At the selected time points after dosing, blood samples were obtained from an ear vein or artery. Hemostasis following collection was achieved by the application of manual pressure and topical clotting factor or tissue glue as needed. The samples were from 0.5-1 ml in volume, and were allowed to clot for harvest of serum. Aqueous, vitreous and serum samples were stored at -80°C, and submitted for drug level determinations.

[0468] The serum, and aqueous humour concentrations for these molecules were measured using either a GYROS or a MSD method. GYROS employs a biotinylated VEGF ligand for capture, and Alexa Flour 647 goat anti-human IgG detection. MSD employs

biotinylated VEGF ligand for capture, and Sulfo-tag goat anti-human IgG or sulfo-tag VEGF for detection. Results were comparable between the two methods. Concentrations were calculated by four-parameter logistic fit using XLfit4. Pharmacokinetic parameters were calculated with Non-compartmental analysis using Pharmacokinetics Laboratory Automation Software for Management and Analysis (PLASMA) (Version 2.6.12, SParCS, AbbVie). Results from the experiment are shown in Table 94.

Table 94. Ocular Half Lives in Rabbit from Analysis of Aqueous Humor

Test Articles	Corporate ID	Half life
DVD038 (L234A, L235A)	PR-1565009	151
DVD038 (L234A, L235A, H435A)	PR-1565689	157
DVD038 Half DVD-Ig (L234A, L235A)	PR-1578399	90
DVD038 DVD-Fab	PR-1574215	110

[0469] Population analysis of the pooled data sets was performed on the composite profile from multiple animals at each dose level. The analysis provided parameter estimates with reasonable variability (CV<30%). The larger molecular weight constructs show a weak trend towards a longer ocular half-life.

Table 95. Exemplary DVD-Ig Binding Proteins And Component Subunits

SEQ ID NO	DVD-Ig	Outer VD name	Linker	Inner VD name
45	PR-1563988H	hBDI-9E8.4 VH (PDGF) (SEQ ID NO: 1)	GS-H10	hBDB-4G8.3 VH (VEGF) (SEQ ID NO: 17)
46	PR-1563988L	hBDI-9E8.4 VL (PDGF) (SEQ ID NO: 2)	GS-L10	hBDB-4G8.3 VL (VEGF) (SEQ ID NO: 18)
47	PR-1563990H	hBDI-9E8.4 VH (PDGF) (SEQ ID NO: 1)	HG-short	hBDB-4G8.3 VH (VEGF) (SEQ ID NO: 17)
48	PR-1563990L	hBDI-9E8.4 VL (PDGF) (SEQ ID NO: 2)	LK-short	hBDB-4G8.3 VL (VEGF) (SEQ ID NO: 18)
49	PR-1563998H	hBDI-9E8.4 VH (PDGF) (SEQ ID NO: 1)	HG-short	hBDB-4G8.3 VH (VEGF) (SEQ ID NO: 17)
50	PR-1563998L	hBDI-9E8.4 VL (PDGF) (SEQ ID NO: 2)	LK-long	hBDB-4G8.3 VL (VEGF) (SEQ ID NO: 18)
51	PR-1564009H	hBDI-9E8.4 VH (PDGF) (SEQ ID NO: 1)	HG-long	hBDB-4G8.3 VH (VEGF) (SEQ ID NO: 17)
51	PR-1564009L	hBDI-9E8.4 VL (PDGF) (SEQ ID NO: 2)	LK-short	hBDB-4G8.3 VL (VEGF) (SEQ ID NO: 18)
53	PR-1564010H	hBDB-4G8.3 VH (VEGF) (SEQ ID NO: 17)	GS-H10	hBDI-9E8.4 VH (PDGF) (SEQ ID NO: 1)
54	PR-1564010L	hBDB-4G8.3 VL (VEGF) (SEQ ID NO: 18)	GS-L10	hBDI-9E8.4 VL (PDGF) (SEQ ID NO: 2)
55	PR-1564011H	hBDB-4G8.3 VH (VEGF) (SEQ ID NO: 17)	HG-short	hBDI-9E8.4 VH (PDGF) (SEQ ID NO: 1)

56	PR-1564011L	hBDB-4G8.3 VL (VEGF) (SEQ ID NO: 18)	LK-short	hBDI-9E8.4 VL (PDGF) (SEQ ID NO: 2)
57	PR-1564012H	hBDB-4G8.3 VH (VEGF) (SEQ ID NO: 17)	HG-short	hBDI-9E8.4 VH (PDGF) (SEQ ID NO: 1)
58	PR-1564012L	hBDB-4G8.3 VL (VEGF) (SEQ ID NO: 18)	LK-long	hBDI-9E8.4 VL (PDGF) (SEQ ID NO: 2)
59	PR-1564013H	hBDB-4G8.3 VH (VEGF) (SEQ ID NO: 17)	HG-long	hBDI-9E8.4 VH (PDGF) (SEQ ID NO: 1)
60	PR-1564013L	hBDB-4G8.3 VL (VEGF) (SEQ ID NO: 18)	LK-short	hBDI-9E8.4 VL (PDGF) (SEQ ID NO: 2)
61	PR-1564883H (DVD3896H)a	hBDI-5H1.9 VH (PDGF) (SEQ ID NO: 3)	HG-short	hBDB-4G8.13 VH (VEGF) (SEQ ID NO: 19)
62	PR-1564883L (DVD3896L)a	hBDI-5H1.9 VL (PDGF) (SEQ ID NO: 4)	LK-long	hBDB-4G8.13 VL (VEGF) (SEQ ID NO: 20)
63	PR-1564893H (DVD3897H)a	hBDI-5H1.9 VH (PDGF) (SEQ ID NO: 3)	HG-short	hBDB-4G8.14 VH (VEGF) (SEQ ID NO: 21)
64	PR-1564893L (DVD3897L)a	hBDI-5H1.9 VL (PDGF) (SEQ ID NO: 4)	LK-long	hBDB-4G8.14 VL (VEGF) (SEQ ID NO: 22)
209	PR-1564896H (DVD3898H)a	hBDI-5H1.9 VH (PDGF) (SEQ ID NO: 3)	HG-short	hBDB-4G8.15 VH (VEGF) (SEQ ID NO: 23)
65	PR-1564896L (DVD3898L)a	hBDI-5H1.9 VL (PDGF) (SEQ ID NO: 4)	LK-long	hBDB-4G8.15 VL (VEGF) (SEQ ID NO: 24)
66	PR-1564898H (DVD3899H)a	hBDI-5H1.12 VH (PDGF) (SEQ ID NO: 211)	HG-short	hBDB-4G8.14 VH (VEGF) (SEQ ID NO: 21)
67	PR-1564898L (DVD3899L)a	hBDI-5H1.12 VL (PDGF) (SEQ ID NO: 212)	LK-long	hBDB-4G8.14 VL (VEGF) (SEQ ID NO: 22)
68	PR-1564899H (DVD3900H)a	hBDI-5H1.12 VH (PDGF) (SEQ ID NO: 211)	HG-short	hBDB-4G8.15 VH (VEGF) (SEQ ID NO: 23)
69	PR-1564899L (DVD3900L)a	hBDI-5H1.12 VL (PDGF) (SEQ ID NO: 212)	LK-long	hBDB-4G8.15 VL (VEGF) (SEQ ID NO: 24)
70	PR-1565023H (DVD3901H)a	hBDI-9E8.9 VH (PDGF) (SEQ ID NO: 7)	HG-short	hBDB-4G8.13 VH (VEGF) (SEQ ID NO: 19)
71	PR-1565023L (DVD3901L)a	hBDI-9E8.9 VL (PDGF) (SEQ ID NO: 8)	LK-long	hBDB-4G8.13 VL (VEGF) (SEQ ID NO: 20)
72	PR-1565029H (DVD3902H)a	hBDI-9E8.9 VH (PDGF) (SEQ ID NO: 7)	HG-short	hBDB-4G8.14 VH (VEGF) (SEQ ID NO: 21)
73	PR-1565029L (DVD3902L)a	hBDI-9E8.9 VL (PDGF) (SEQ ID NO: 8)	LK-long	hBDB-4G8.14 VL (VEGF) (SEQ ID NO: 22)
74	PR-1565030H (DVD3903H)a	hBDI-9E8.9 VH (PDGF) (SEQ ID NO: 7)	HG-short	hBDB-4G8.15 VH (VEGF) (SEQ ID NO: 23)
75	PR-1565030L (DVD3903L)a	hBDI-9E8.9 VL (PDGF) (SEQ ID NO: 8)	LK-long	hBDB-4G8.15 VL (VEGF) (SEQ ID NO: 24)
76	PR-1565031H (DVD3904H)a	hBDI-9E8.12 VH (PDGF) (SEQ ID NO: 9)	HG-short	hBDB-4G8.14 VH (VEGF) (SEQ ID NO: 21)
77	PR-1565031L	hBDI-9E8.12 VL	LK-long	hBDB-4G8.14 VL (VEGF)

	(DVD3904L)a	(PDGF) (SEQ ID NO: 10)		(SEQ ID NO: 22)
78	PR-1565032H (DVD3905H)a	hBDI-9E8.12 VH (PDGF) (SEQ ID NO: 5)	HG-short	hBDB-4G8.15 VH (VEGF) (SEQ ID NO: 23)
79	PR-1565032L (DVD3905L)a	hBDI-9E8.12 VL (PDGF) (SEQ ID NO: 6)	LK-long	hBDB-4G8.15 VL (VEGF) (SEQ ID NO: 24)
80	PR-1565035H (DVD3906H)a	hBDI-5H1.10 VH (PDGF) (SEQ ID NO: 9)	HG-short	hBDB-4G8.15 VH (VEGF) (SEQ ID NO: 23)
81	PR-1565035L (DVD3906L)a	hBDI-5H1.10 VL (PDGF) (SEQ ID NO: 10)	LK-long	hBDB-4G8.15 VL (VEGF) (SEQ ID NO: 24)
82	PR-1565033H (DVD3907H)a	hBDI-9E8.10 VH (PDGF) (SEQ ID NO: 9)	HG-short	hBDB-4G8.15 VH (VEGF) (SEQ ID NO: 23)
83	PR-1565033L (DVD3907L)a	hBDI-9E8.10 VL (PDGF) (SEQ ID NO: 10)	LK-long	hBDB-4G8.15 VL (VEGF) (SEQ ID NO: 24)
84	PR-1569574H	hBDI-9E8.4 VH (PDGF) (SEQ ID NO: 1)	GS-H10	hBDB-4G8.3 VH (VEGF) (SEQ ID NO: 17)
85	PR-1569574L	hBDI-9E8.4 VL (PDGF) (SEQ ID NO: 2)	GS-L10	hBDB-4G8.3 VL (VEGF) (SEQ ID NO: 18)
86	PR-1569579H	hBDI-9E8.4 VH (PDGF) (SEQ ID NO: 1)	HG-short	hBDB-4G8.3 VH (VEGF) (SEQ ID NO: 17)
87	PR-1569579L	hBDI-9E8.4 VL (PDGF) (SEQ ID NO: 2)	LK-long	hBDB-4G8.3 VL (VEGF) (SEQ ID NO: 18)
88	PR-1572102H	hBDB-4G8.3 VH (VEGF) (SEQ ID NO: 17)	GS-H10	hBDI-9E8.4 VH (PDGF) (SEQ ID NO: 1)
89	PR-1572102L	hBDB-4G8.3 VL (VEGF) (SEQ ID NO: 18)	GS-L10	hBDI-9E8.4 VL (PDGF) (SEQ ID NO: 2)
90	PR-1572103H	hBDB-4G8.3 VH (VEGF) (SEQ ID NO: 17)	GS-H10	hBDI-9E8.4 VH (PDGF) (SEQ ID NO: 1)
91	PR-1572103L	hBDB-4G8.3 VL (VEGF) (SEQ ID NO: 18)	GS-L11	hBDI-9E8.4 VL (PDGF) (SEQ ID NO: 2)
92	PR-1572104H	hBDB-4G8.3 VH (VEGF) (SEQ ID NO: 17)	GS-H10	hBDI-9E8.4 VH (PDGF) (SEQ ID NO: 1)
93	PR-1572104L	hBDB-4G8.3 VL (VEGF) (SEQ ID NO: 18)	GS-L10(dR)	hBDI-9E8.4 VL (PDGF) (SEQ ID NO: 2)
94	PR-1572105H	hBDB-4G8.3 VH (VEGF) (SEQ ID NO: 17)	HG-short	hBDI-9E8.4 VH (PDGF) (SEQ ID NO: 1)
95	PR-1572105L	hBDB-4G8.3 VL (VEGF) (SEQ ID NO: 18)	LK-long	hBDI-9E8.4 VL (PDGF) (SEQ ID NO: 2)
96	PR-1572106H	hBDB-4G8.3 VH (VEGF) (SEQ ID NO: 17)	HG-long	hBDI-9E8.4 VH (PDGF) (SEQ ID NO: 1)
97	PR-1572106L	hBDB-4G8.3 VL (VEGF) (SEQ ID NO: 18)	LK-short	hBDI-9E8.4 VL (PDGF) (SEQ ID NO: 2)

210	PR-1575573H	hBDI-9E8.4 VH (PDGF) (SEQ ID NO: 1)	HG-long	hBDB-4G8.3 VH (VEGF) (SEQ ID NO: 17)
98	PR-1575573L	hBDI-9E8.4 VL (PDGF) (SEQ ID NO: 2)	LK-short	hBDB-4G8.3 VL (VEGF) (SEQ ID NO: 18)
99	PR-1575832H	hBDB-4G8.3 VH (VEGF) (SEQ ID NO: 17)	GS-H10	hBDI-9E8.4E VH (PDGF) (SEQ ID NO: 11)
100	PR-1575832L	hBDB-4G8.3 VL (VEGF) (SEQ ID NO: 18)	GS-L10	hBDI-9E8.4E VL (PDGF) (SEQ ID NO: 12)
101	PR-1575834H	hBDB-4G8.3 VH (VEGF) (SEQ ID NO: 17)	HG-short	hBDI-9E8.4E VH (PDGF) (SEQ ID NO: 11)
102	PR-1575834L	hBDB-4G8.3 VL (VEGF) (SEQ ID NO: 18)	LK-long	hBDI-9E8.4E VL (PDGF) (SEQ ID NO: 12)
103	PR-1575835H	hBDB-4G8.3 VH (VEGF) (SEQ ID NO: 17)	HG-long	hBDI-9E8.4E VH (PDGF) (SEQ ID NO: 11)
104	PR-1575835L	hBDB-4G8.3 VL (VEGF) (SEQ ID NO: 18)	LK-short	hBDI-9E8.4E VL (PDGF) (SEQ ID NO: 12)
105	PR-1577165H	hBEW-9A8.12 VH (VEGF) (SEQ ID NO: 25)	GS-H10	hBDI-9E8.4E VH (PDGF) (SEQ ID NO: 11)
106	PR-1577165L	hBEW-9A8.12 VL (VEGF) (SEQ ID NO: 26)	GS-L10	hBDI-9E8.4E VL (PDGF) (SEQ ID NO: 12)
107	PR-1577166H	hBEW-9A8.12 VH (VEGF) (SEQ ID NO: 25)	HG-short	hBDI-9E8.4E VH (PDGF) (SEQ ID NO: 11)
108	PR-1577166L	hBEW-9A8.12 VL (VEGF) (SEQ ID NO: 26)	LK-long	hBDI-9E8.4E VL (PDGF) (SEQ ID NO: 12)
109	PR-1577547H	hBEW-9A8.12 VH (VEGF) (SEQ ID NO: 25)	HG-long	hBDI-9E8.4E VH (PDGF) (SEQ ID NO: 11)
110	PR-1577547L	hBEW-9A8.12 VL (VEGF) (SEQ ID NO: 26)	LK-short	hBDI-9E8.4E VL (PDGF) (SEQ ID NO: 12)
111	PR-1577548H	hBDI-9E8.4E VH (PDGF) (SEQ ID NO: 11)	HG-short	hBEW-9A8.12 VH (VEGF) (SEQ ID NO: 25)
112	PR-1577548L	hBDI-9E8.4E VL (PDGF) (SEQ ID NO: 12)	LK-long	hBEW-9A8.12 VL (VEGF) (SEQ ID NO: 26)
113	PR-1577550H	hBDI-9E8.4E VH (PDGF) (SEQ ID NO: 11)	HG-long	hBEW-9A8.12 VH (VEGF) (SEQ ID NO: 25)
114	PR-1577550L	hBDI-9E8.4E VL (PDGF) (SEQ ID NO: 12)	LK-short	hBEW-9A8.12 VL (VEGF) (SEQ ID NO: 26)
115	PR-1578137H	hBDI-9E8.4E VH (PDGF) (SEQ ID NO:	GS-H10	hBEW-9A8.12 VH (VEGF) (SEQ ID NO: 25)

		11)		
116	PR-1578137L	hBDI-9E8.4E VL (PDGF) (SEQ ID NO: 12)	GS-L10	hBEW-9A8.12 VL (VEGF) (SEQ ID NO: 26)
117	PR-1598261H	hBDB-4G8.2 VH (VEGF) (SEQ ID NO: 27)	GS-H10	hBDI-9E8.4 VH (PDGF) (SEQ ID NO: 1)
118	PR-1598261L	hBDB-4G8.2 VL (VEGF) (SEQ ID NO: 28)	GS-L10	hBDI-9E8.4 VL (PDGF) (SEQ ID NO: 2)
119	PR-1598262H	hBDB-4G8.4 VH (VEGF) (SEQ ID NO: 29)	GS-H10	hBDI-9E8.4 VH (PDGF) (SEQ ID NO: 1)
120	PR-1598262L	hBDB-4G8.4 VL (VEGF) (SEQ ID NO: 30)	GS-L10	hBDI-9E8.4 VL (PDGF) (SEQ ID NO: 2)
121	PR-1598263H	hBDB-4G8.5 VH (VEGF) (SEQ ID NO: 31)	GS-H10	hBDI-9E8.4 VH (PDGF) (SEQ ID NO: 1)
122	PR-1598263L	hBDB-4G8.5 VL (VEGF) (SEQ ID NO: 32)	GS-L10	hBDI-9E8.4 VL (PDGF) (SEQ ID NO: 2)
123	PR-1598264H	hBDB-4G8.12 VH (VEGF) (SEQ ID NO: 33)	GS-H10	hBDI-9E8.4 VH (PDGF) (SEQ ID NO: 1)
124	PR-1598264L	hBDB-4G8.12 VL (VEGF) (SEQ ID NO: 34)	GS-L10	hBDI-9E8.4 VL (PDGF) (SEQ ID NO: 2)
125	PR-1598265H	hBDB-4G8.13 VH (VEGF) (SEQ ID NO: 19)	GS-H10	hBDI-9E8.4 VH (PDGF) (SEQ ID NO: 1)
126	PR-1598265L	hBDB-4G8.13 VL (VEGF) (SEQ ID NO: 20)	GS-L10	hBDI-9E8.4 VL (PDGF) (SEQ ID NO: 2)
127	PR-1598266H	hBDB-4G8.14 VH (VEGF) (SEQ ID NO: 21)	GS-H10	hBDI-9E8.4 VH (PDGF) (SEQ ID NO: 1)
128	PR-1598266L	hBDB-4G8.14 VL (VEGF) (SEQ ID NO: 22)	GS-L10	hBDI-9E8.4 VL (PDGF) (SEQ ID NO: 2)
129	PR-1610560H	hBDB-4G8.5 VH (VEGF) (SEQ ID NO: 31)	GS-H10	hBFU-3E2.1 VH (PDGF) (SEQ ID NO: 13)
130	PR-1610560L	hBDB-4G8.5 VL (VEGF) (SEQ ID NO: 32)	GS-L10(dR)	hBFU-3E2.1 VL (PDGF) (SEQ ID NO: 14)
131	PR-1610561H	hBEW-9E10.1 VH (VEGF) (SEQ ID NO: 35)	GS-H10	CL-33675 VH (PDGF) (SEQ ID NO: 15)
132	PR-1610561L	hBEW-9E10.1 VL (VEGF) (SEQ ID NO: 36)	GS-L10(dR)	CL-33675 VL (PDGF) (SEQ ID NO: 16)
133	PR-1610562H	hBEW-9E10.1 VH (VEGF) (SEQ ID NO:	GS-H10	hBFU-3E2.1 VH (PDGF) (SEQ ID NO: 13)

		35)		
134	PR-1610562L	hBEW-9E10.1 VL (VEGF) (SEQ ID NO: 36)	GS-L10(dR)	hBFU-3E2.1 VL (PDGF) (SEQ ID NO: 14)
135	PR-1610563H	hBEW-9E10.6 VH (VEGF) (SEQ ID NO: 37)	GS-H10	hBFU-3E2.1 VH (PDGF) (SEQ ID NO: 13)
136	PR-1610563L	hBEW-9E10.6 VL (VEGF) (SEQ ID NO: 38)	GS-L10(dR)	hBFU-3E2.1 VL (PDGF) (SEQ ID NO: 14)
137	PR-1610564H	hBEW-1B10.1 VH (VEGF) (SEQ ID NO: 39)	GS-H10	hBFU-3E2.1 VH (PDGF) (SEQ ID NO: 13)
138	PR-1610564L	hBEW-1B10.1 VL (VEGF) (SEQ ID NO: 40)	GS-L10(dR)	hBFU-3E2.1 VL (PDGF) (SEQ ID NO: 14)
139	PR-1611291H	hBDB-4G8.5 VH (VEGF) (SEQ ID NO: 31)	GS-H10	CL-33675 VH (PDGF) (SEQ ID NO: 15)
140	PR-1611291L	hBDB-4G8.5 VL (VEGF) (SEQ ID NO: 32)	GS-L10(dR)	CL-33675 VL (PDGF) (SEQ ID NO: 16)
141	PR-1611292H	hBEW-1B10.1 VH (VEGF) (SEQ ID NO: 39)	GS-H10	CL-33675 VH (PDGF) (SEQ ID NO: 15)
142	PR-1611292L	hBEW-1B10.1 VL (VEGF) (SEQ ID NO: 40)	GS-L10(dR)	CL-33675 VL (PDGF) (SEQ ID NO: 16)
143	PR-1611293H	hBEW-1E3.4 VH (VEGF) (SEQ ID NO: 41)	GS-H10	CL-33675 VH (PDGF) (SEQ ID NO: 15)
144	PR-1611293L	hBEW-1E3.4 VL (VEGF) (SEQ ID NO: 42)	GS-L10(dR)	CL-33675 VL (PDGF) (SEQ ID NO: 16)
145	PR-1611294H	hBEW-1E3.4 VH (VEGF) (SEQ ID NO: 41)	GS-H10	hBDI-9E8.4 VH (PDGF) (SEQ ID NO: 1)
146	PR-1611294L	hBEW-1E3.4 VL (VEGF) (SEQ ID NO: 42)	GS-L10(dR)	hBDI-9E8.4 VL (PDGF) (SEQ ID NO: 2)
147	PR-1611295H	CL-33675 VH (PDGF) (SEQ ID NO: 15)	GS-H10	hBEW-9E10.1 VH (VEGF) (SEQ ID NO: 35)
148	PR-1611295L	CL-33675 VL (PDGF) (SEQ ID NO: 16)	GS-L10(dR)	hBEW-9E10.1 VL (VEGF) (SEQ ID NO: 36)
149	PR-1611296H	CL-33675 VH (PDGF) (SEQ ID NO: 15)	GS-H10	hBEW-9E10.6 VH (VEGF) (SEQ ID NO: 37)
150	PR-1611296L	CL-33675 VL (PDGF) (SEQ ID NO: 16)	GS-L10(dR)	hBEW-9E10.6 VL (VEGF) (SEQ ID NO: 38)
151	PR-1611297H	CL-33675 VH (PDGF) (SEQ ID NO: 15)	GS-H10	hBEW-1E3.4 VH (VEGF) (SEQ ID NO: 41)
152	PR-1611297L	CL-33675 VL (PDGF) (SEQ ID NO: 16)	GS-L10(dR)	hBEW-1E3.4 VL (VEGF) (SEQ ID NO: 42)
153	PR-1611298H	hBDI-9E8.4 VH (PDGF) (SEQ ID NO: 1)	GS-H10	hBEW-9E10.1 VH (VEGF) (SEQ ID NO: 35)

154	PR-1611298L	hBDI-9E8.4 VL (PDGF) (SEQ ID NO: 2)	GS-L10(dR)	hBEW-9E10.1 VL (VEGF) (SEQ ID NO: 36)
155	PR-1611299H	hBDI-9E8.4 VH (PDGF) (SEQ ID NO: 1)	GS-H10	hBEW-9E10.6 VH (VEGF) (SEQ ID NO: 37)
156	PR-1611299L	hBDI-9E8.4 VL (PDGF) (SEQ ID NO: 2)	GS-L10(dR)	hBEW-9E10.6 VL (VEGF) (SEQ ID NO: 38)
157	PR-1611300H	hBDI-9E8.4 VH (PDGF) (SEQ ID NO: 1)	GS-H10	hBEW-1B10.1 VH (VEGF) (SEQ ID NO: 39)
158	PR-1611300L	hBDI-9E8.4 VL (PDGF) (SEQ ID NO: 2)	GS-L10(dR)	hBEW-1B10.1 VL (VEGF) (SEQ ID NO: 40)
159	PR-1611301H	hBDI-9E8.4 VH (PDGF) (SEQ ID NO: 1)	GS-H10	hBEW-1E3.4 VH (VEGF) (SEQ ID NO: 41)
160	PR-1611301L	hBDI-9E8.4 VL (PDGF) (SEQ ID NO: 2)	GS-L10(dR)	hBEW-1E3.4 VH (VEGF) (SEQ ID NO: 42)
161	PR-1612489H	hBDB-4G8.5 VH (VEGF) (SEQ ID NO: 31)	GS-H10	hBDI-9E8.4 VH (PDGF) (SEQ ID NO: 1)
162	PR-1612489L	hBDB-4G8.5 VL (VEGF) (SEQ ID NO: 32)	GS-L10(dR)	hBDI-9E8.4 VL (PDGF) (SEQ ID NO: 2)
163	PR-1612491H	hBEW-9E10.1 VH (VEGF) (SEQ ID NO: 35)	GS-H10	hBDI-9E8.4 VH (PDGF) (SEQ ID NO: 1)
164	PR-1612491L	hBEW-9E10.1 VL (VEGF) (SEQ ID NO: 36)	GS-L10(dR)	hBDI-9E8.4 VL (PDGF) (SEQ ID NO: 2)
165	PR-1612492H	hBEW-9E10.6 VH (VEGF) (SEQ ID NO: 37)	GS-H10	CL-33675 VH (PDGF) (SEQ ID NO: 15)
166	PR-1612492L	hBEW-9E10.6 VL (VEGF) (SEQ ID NO: 38)	GS-L10(dR)	CL-33675 VL (PDGF) (SEQ ID NO: 16)
167	PR-1612493H	hBEW-9E10.6 VH (VEGF) (SEQ ID NO: 37)	GS-H10	hBDI-9E8.4 VH (PDGF) (SEQ ID NO: 1)
168	PR-1612493L	hBEW-9E10.6 VL (VEGF) (SEQ ID NO: 38)	GS-L10(dR)	hBDI-9E8.4 VL (PDGF) (SEQ ID NO: 2)
169	PR-1612494H	hBEW-1B10.1 VH (VEGF) (SEQ ID NO: 39)	GS-H10	hBDI-9E8.4 VH (PDGF) (SEQ ID NO: 1)
170	PR-1612494L	BEW-1B10.1 VL (VEGF) (SEQ ID NO: 40)	GS-L10(dR)	hBDI-9E8.4 VL (PDGF) (SEQ ID NO: 2)
171	PR-1612495H	hBEW-1E3.4 VH (VEGF) (SEQ ID NO: 41)	GS-H10	hBFU-3E2.1 VH (PDGF) (SEQ ID NO: 13)
172	PR-1612495L	hBEW-1E3.4 VL (VEGF) (SEQ ID NO: 42)	GS-L10(dR)	hBFU-3E2.1 VL (PDGF) (SEQ ID NO: 14)
173	PR-1612496H	CL-33675 VH (PDGF) (SEQ ID NO: 15)	GS-H10	hBDB-4G8.5 VH (VEGF) (SEQ ID NO: 31)
174	PR-1612496L	CL-33675 VL (PDGF) (SEQ ID NO: 16)	GS-L10(dR)	hBDB-4G8.5 VL (VEGF) (SEQ ID NO: 32)

175	PR-1612498H	CL-33675 VH (PDGF) (SEQ ID NO: 15)	GS-H10	hBEW-1B10.1 VH (VEGF) (SEQ ID NO: 39)
176	PR-1612498L	CL-33675 VL (PDGF) (SEQ ID NO: 16)	GS-L10(dR)	hBEW-1B10.1 VL (VEGF) (SEQ ID NO: 40)
177	PR-1612499H	hBFU-3E2.1 VH (PDGF) (SEQ ID NO: 13)	GS-H10	hBDB-4G8.5 VH (VEGF) (SEQ ID NO: 31)
178	PR-1612499L	hBFU-3E2.1 VL (PDGF) (SEQ ID NO: 14)	GS-L10(dR)	hBDB-4G8.5 VL (VEGF) (SEQ ID NO: 32)
179	PR-1612500H	hBFU-3E2.1 VH (PDGF) (SEQ ID NO: 13)	GS-H10	hBEW-9E10.1 VH (VEGF) (SEQ ID NO: 35)
180	PR-1612500L	hBFU-3E2.1 VL (PDGF) (SEQ ID NO: 14)	GS-L10(dR)	hBEW-9E10.1 VL (VEGF) (SEQ ID NO: 36)
181	PR-1612501H	hBFU-3E2.1 VH (PDGF) (SEQ ID NO: 13)	GS-H10	hBEW-9E10.6 VH (VEGF) (SEQ ID NO: 37)
182	PR-1612501L	hBFU-3E2.1 VL (PDGF) (SEQ ID NO: 14)	GS-L10(dR)	hBEW-9E10.6 VL (VEGF) (SEQ ID NO: 38)
183	PR-1612502H	hBFU-3E2.1 VH (PDGF) (SEQ ID NO: 13)	GS-H10	hBEW-1B10.1 VH (VEGF) (SEQ ID NO: 39)
184	PR-1612502L	hBFU-3E2.1 VL (PDGF) (SEQ ID NO: 14)	GS-L10(dR)	hBEW-1B10.1 VL (VEGF) (SEQ ID NO: 40)
185	PR-1613183H	CL-34565 VH (VEGF) (SEQ ID NO: 43)	GS-H10	CL-33675 VH (PDGF) (SEQ ID NO: 15)
186	PR-1613183L	CL-34565 VL (VEGF) (SEQ ID NO: 44)	GS-L10(dR)	CL-33675 VL (PDGF) (SEQ ID NO: 16)
187	PR-1613184H	CL-34565 VH (VEGF) (SEQ ID NO: 43)	GS-H10	hBDI-9E8.4 VH (PDGF) (SEQ ID NO: 1)
188	PR-1613184L	CL-34565 VL (VEGF) (SEQ ID NO: 44)	GS-L10(dR)	hBDI-9E8.4 VL (PDGF) (SEQ ID NO: 2)
189	PR-1613185H	CL-34565 VH (VEGF) (SEQ ID NO: 43)	GS-H10	hBFU-3E2.1 VH (PDGF) (SEQ ID NO: 13)
190	PR-1613185L	CL-34565 VL (VEGF) (SEQ ID NO: 44)	GS-L10(dR)	hBFU-3E2.1 VL (PDGF) (SEQ ID NO: 14)
191	PR-1613186H	CL-33675 VH (PDGF) (SEQ ID NO: 15)	GS-H10	CL-34565 VH (VEGF) (SEQ ID NO: 43)
192	PR-1613186L	CL-33675 VL (PDGF) (SEQ ID NO: 16)	GS-L10(dR)	CL-34565 VL (VEGF) (SEQ ID NO: 44)
193	PR-1613187H	hBDI-9E8.4 VH (PDGF) (SEQ ID NO: 1)	GS-H10	CL-34565 VH (VEGF) (SEQ ID NO: 43)
194	PR-1613187L	hBDI-9E8.4 VL (PDGF) (SEQ ID NO: 2)	GS-L10(dR)	CL-34565 VL (VEGF) (SEQ ID NO: 44)
195	PR-1613188H	hBDI-9E8.4 VH (PDGF) (SEQ ID NO: 1)	GS-H10	hBDB-4G8.5 VH (VEGF) (SEQ ID NO: 31)
196	PR-1613188L	hBDI-9E8.4 VL (PDGF) (SEQ ID NO: 2)	GS-L10(dR)	hBDB-4G8.5 VL (VEGF) (SEQ ID NO: 32)
197	PR-1613189H	hBFU-3E2.1 VH (PDGF) (SEQ ID NO:	GS-H10	CL-34565 VH (VEGF) (SEQ ID NO: 43)

		13)		
198	PR-1613189L	hBFU-3E2.1 VL (PDGF) (SEQ ID NO: 14)	GS-L10(dR)	CL-34565 VL (VEGF) (SEQ ID NO: 44)
199	PR-1613190H	hBFU-3E2.1 VH (PDGF) (SEQ ID NO: 13)	GS-H10	hBEW-1E3.4 VH (VEGF) (SEQ ID NO: 41)
200	PR-1613190L	hBFU-3E2.1 VL (PDGF) (SEQ ID NO: 14)	GS-L10(dR)	hBEW-1E3.4 VL (VEGF) (SEQ ID NO: 42)
201	PR-1629646H	hBEW-9E10.1 VH (VEGF) (SEQ ID NO: 35)	HG-short	CL-33675 VH (PDGF) (SEQ ID NO: 15)
202	PR-1629646L	hBEW-9E10.1 VL (VEGF) (SEQ ID NO: 36)	LK-long	CL-33675 VL (PDGF) (SEQ ID NO: 16)
203	PR-1629647H	hBEW-1B10.1 VH (VEGF) (SEQ ID NO: 39)	HG-short	CL-33675 VH (PDGF) (SEQ ID NO: 15)
204	PR-1629647L	hBEW-1B10.1 VL (VEGF) (SEQ ID NO: 40)	LK-long	CL-33675 VL (PDGF) (SEQ ID NO: 16)
205	PR-1629648H	hBEW-9E10.1 VH (VEGF) (SEQ ID NO: 35)	HG-long	CL-33675 VH (PDGF) (SEQ ID NO: 15)
206	PR-1629648L	hBEW-9E10.1 VL (VEGF) (SEQ ID NO: 36)	LK-short	CL-33675 VL (PDGF) (SEQ ID NO: 16)
207	PR-1629649H	hBEW-1B10.1 VH (VEGF) (SEQ ID NO: 39)	HG-long	CL-33675 VH (PDGF) (SEQ ID NO: 15)
208	PR-1629649L	hBEW-1B10.1 VL (VEGF) (SEQ ID NO: 40)	LK-short	CL-33675 VL (PDGF) (SEQ ID NO: 16)

Table 96. Sequences of Exemplary DVD-Ig Binding Proteins

SEQ ID NO	DVD-Ig	Sequence
45	PR-1563988H	EVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMGVGWIRQPPGKALEWLANIWWD DDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPVDTATYYCARIESIGTTYSFDYW GQGTMVTVSSGGGGSGGGGSEVQLVQSGSELKKPGASVKVSCKASGYTFTNYGMY WVRQAPGQGLEWMGWINTETGKPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDT AVYYCARTNYYYRSYIFYFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPGK
46	PR-1563988L	EFVLTQSPGTLSLSPGERATLSCERSSGDIGDSYVSWYQQKPGQAPRLVIYADDQRPS GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKGGGSGGG GSGDTVLTQSPATLSLSPGERATLSCRASESVSTHMHWYQQKPGQAPRLLIYGASNL ESGVPARFSGSGSGTDFTLTISSLEPEDFAVYFCQQSWNDPFTFGQGTKLEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD

		STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
47	PR-1563990H	EVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMGVGWIRQPPGKALEWLANIWWD DDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPVDTATYYCARIESIGTTYSFDYW GQGTMVTVSSASTKGPEVQLVQSGSELKKPGASVKVSCKASGYTFTNYGMYWVRQ APGQGLEWMGWINTETGKPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYY CARTNYYYRSYIFYFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGK
48	PR-1563990L	EFVLTQSPGTLSLSPGERATLSCERSSGDIGDSYVSWYQQKPGQAPRLVIYADDQRPS GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKGTVAAPDT VLTQSPATLSLSPGERATLSCRASESVSTHMHWYQQKPGQAPRLLIYGASNLESGVP ARFSGSGSGTDFTLTISSLEPEDFAVYFCQQSWNDPFTFGQGTKLEIKRTVAAPSVFIF PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
49	PR-1563998H	EVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMGVGWIRQPPGKALEWLANIWWD DDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPVDTATYYCARIESIGTTYSFDYW GQGTMVTVSSASTKGPEVQLVQSGSELKKPGASVKVSCKASGYTFTNYGMYWVRQ APGQGLEWMGWINTETGKPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYY CARTNYYYRSYIFYFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGK
50	PR-1563998L	EFVLTQSPGTLSLSPGERATLSCERSSGDIGDSYVSWYQQKPGQAPRLVIYADDQRPS GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKGTVAAPSV FIFPPDTVLTQSPATLSLSPGERATLSCRASESVSTHMHWYQQKPGQAPRLLIYGASN LESGVPARFSGSGSGTDFTLTISSLEPEDFAVYFCQQSWNDPFTFGQGTKLEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
51	PR-1564009H	EVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMGVGWIRQPPGKALEWLANIWWD DDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPVDTATYYCARIESIGTTYSFDYW GQGTMVTVSSASTKGPSVFPLAPEVQLVQSGSELKKPGASVKVSCKASGYTFTNYG MYWVRQAPGQGLEWMGWINTETGKPTYADDFKGRFVFSLDTSVSTAYLQISSLKAE DTAVYYCARTNYYYRSYIFYFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK
51	PR-1564009L	EFVLTQSPGTLSLSPGERATLSCERSSGDIGDSYVSWYQQKPGQAPRLVIYADDQRPS GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKGTVAAPDT VLTQSPATLSLSPGERATLSCRASESVSTHMHWYQQKPGQAPRLLIYGASNLESGVP ARFSGSGSGTDFTLTISSLEPEDFAVYFCQQSWNDPFTFGQGTKLEIKRTVAAPSVFIF PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
53	PR-1564010H	EVQLVQSGSELKKPGASVKVSCKASGYTFTNYGMYWVRQAPGQGLEWMGWINTE TGKPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARTNYYYRSYIFYFD YWGQGTMVTVSSGGGGSGGGGSEVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGM GVGWIRQPPGKALEWLANIWWDDDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDP VDTATYYCARIESIGTTYSFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD

		WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPGK
54	PR-1564010L	DTVLTQSPATLSLSPGERATLSCRASESVSTHMHWYQQKPGQAPRLLIYGASNLESG VPARFSGSGSGTDFTLTISSLEPEDFAVYFCQQSWNDPFTFGQGTKLEIKRGGSGGGG SGEFVLTQSPGTLSLSPGERATLSCERSSGDIGDSYVSWYQQKPGQAPRLVIYADDQR PSGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKGTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
55	PR-1564011H	EVQLVQSGSELKKPGASVKVSCKASGYTFTNYGMYWVRQAPGQGLEWMGWINTE TGKPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARTNYYYRSYIFYFD YWGQGTMVTVSSASTKGPEVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMGVGWI RQPPGKALEWLANIWWDDDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPVDTAT YYCARIESIGTTYSFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
56	PR-1564011L	DTVLTQSPATLSLSPGERATLSCRASESVSTHMHWYQQKPGQAPRLLIYGASNLESG VPARFSGSGSGTDFTLTISSLEPEDFAVYFCQQSWNDPFTFGQGTKLEIKRTVAAPEFV LTQSPGTLSLSPGERATLSCERSSGDIGDSYVSWYQQKPGQAPRLVIYADDQRPSGIP DRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKGTVAAPSVFIF PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
57	PR-1564012H	EVQLVQSGSELKKPGASVKVSCKASGYTFTNYGMYWVRQAPGQGLEWMGWINTE TGKPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARTNYYYRSYIFYFD YWGQGTMVTVSSASTKGPEVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMGVGWI RQPPGKALEWLANIWWDDDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPVDTAT YYCARIESIGTTYSFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
58	PR-1564012L	DTVLTQSPATLSLSPGERATLSCRASESVSTHMHWYQQKPGQAPRLLIYGASNLESG VPARFSGSGSGTDFTLTISSLEPEDFAVYFCQQSWNDPFTFGQGTKLEIKRTVAAPSVF IFPPEFVLTQSPGTLSLSPGERATLSCERSSGDIGDSYVSWYQQKPGQAPRLVIYADDQ RPSGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKGTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
59	PR-1564013H	EVQLVQSGSELKKPGASVKVSCKASGYTFTNYGMYWVRQAPGQGLEWMGWINTE TGKPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARTNYYYRSYIFYFD YWGQGTMVTVSSASTKGPSVFPLAPEVTLRESGPALVKPTQTLTLTCTFSGFSLSTYG MGVGWIRQPPGKALEWLANIWWDDDKYYNPSLKNRLTISKDTSKNQVVLTMTNM DPVDTATYYCARIESIGTTYSFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK
60	PR-1564013L	DTVLTQSPATLSLSPGERATLSCRASESVSTHMHWYQQKPGQAPRLLIYGASNLESG VPARFSGSGSGTDFTLTISSLEPEDFAVYFCQQSWNDPFTFGQGTKLEIKRTVAAPEFV LTQSPGTLSLSPGERATLSCERSSGDIGDSYVSWYQQKPGQAPRLVIYADDQRPSGIP DRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKGTVAAPSVFIF PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

61	PR-1564883H (DVD3896H)a	EVTLRESGPALVKPTQTLTLTCTFSGFSLSTFGMGVGWIRQPPGKALEWLANIWWDD DKYYNPSLKNRLTISKDTSKNQAVLTITNMDPVDTATYYCARISTGISSYYVMDAWG QGTTVTVSSASTKGPEIQLVQSGTEVKKPGESLKISCKASGYTFTNYGMYWVKQMP GKGLEYMGWINTETGKPTYADDFKGRFTFSLDKSFNTAFLQWSSLKASDTAMYFCA RTNYYYRSYIFYFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKP SNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK
62	PR-1564883L (DVD3896L)a	DFVLTQSPDSLAVSLGERATINCERSSGDIGDTYVSWYQQKPGQPPKNVIYGNDQRP SGVPDRFSGSGSGNSATLTISSLQAEDVAVYFCQSYDSDIDIVFGGGTKVEIKGTVAA PSVFIFPPETVLTQSPATLSVSPGERATLSCRASESVSTHMHWYQQKPGQAPRLLIYG ASNLESGVPARFSGSGSGTDFTLTISSLQSEDFAVYFCQQSWNDPFTFGQGTRLEIKRT VAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQ DSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
63	PR-1564893H (DVD3897H)a	EVTLRESGPALVKPTQTLTLTCTFSGFSLSTFGMGVGWIRQPPGKALEWLANIWWDD DKYYNPSLKNRLTISKDTSKNQAVLTITNMDPVDTATYYCARISTGISSYYVMDAWG QGTTVTVSSASTKGPEIQLVQSGGGVVQPGGSLRLSCAASGYTFTNYGMYWVKQAP GKGLEYMGWINTETGKPTYADDFKGRFTFSLDTSKSTAYLQLNSLRAEDTAVYFCA RTNYYYRSYIFYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKP SNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK
64	PR-1564893L (DVD3897L)a	DFVLTQSPDSLAVSLGERATINCERSSGDIGDTYVSWYQQKPGQPPKNVIYGNDQRP SGVPDRFSGSGSGNSATLTISSLQAEDVAVYFCQSYDSDIDIVFGGGTKVEIKGTVAA PSVFIFPPDTVLTQSPSTLSASPGERATISCRASESVSTHMHWYQQKPGQAPKLLIYGA SNLESGVPSRFSGSRSGTDFTLTISSLQPEDFAVYFCQQSWNDPFTFGQGTKVEIKRTV AAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD SKDSTYSLSSTLTLSKADYEK
209	PR-1564896H (DVD3898H)a	EVTLRESGPALVKPTQTLTLTCTFSGFSLSTFGMGVGWIRQPPGKALEWLANIWWDD DKYYNPSLKNRLTISKDTSKNQAVLTITNMDPVDTATYYCARISTGISSYYVMDAWG QGTTVTVSSASTKGPEVQLVESGGGLVQPGGSLRLSCAASGYTFTNYGMYWVKQAP GKGLEYMGWINTETGKPTYADDFKGRFTFSLDTSKSTAYLQMNSLRAEDTAVYFCA RTNYYYRSYIFYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKP SNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK
65	PR-1564896L (DVD3898L)a	DFVLTQSPDSLAVSLGERATINCERSSGDIGDTYVSWYQQKPGQPPKNVIYGNDQRP SGVPDRFSGSGSGNSATLTISSLQAEDVAVYFCQSYDSDIDIVFGGGTKVEIKGTVAA PSVFIFPPDTQLTQSPSSLSASVGDRVTISCRASESVSTHMHWYQQKPGKAPKLLIYG ASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCQQSWNDPFTFGQGTKVEIKRT VAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQ DSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
66	PR-1564898H (DVD3899H)a	EVQLVESGGGLVQPGGSLRLSCAFSGFSLSTFGMGVGWIRQAPGKGLEWLANIWWD DDKYYNPSLKNRLTISKDTSKNQAYLQINSLRAEDTAVYYCARISTGISSYYVMDAW GQGTLVTVSSASTKGPEIQLVQSGGGVVQPGGSLRLSCAASGYTFTNYGMYWVKQA PGKGLEYMGWINTETGKPTYADDFKGRFTFSLDTSKSTAYLQLNSLRAEDTAVYFC ARTNYYYRSYIFYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS

		DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
67	PR-1564898L (DVD3899L)a	DFQLTQSPSSLSASVGDRVTITCERSSGDIGDTYVSWYQQKPGKAPKNVIYGNDQRPS GVPSRFSGSGSGNSATLTISSLQPEDFATYFCQSYDSDIDIVFGQGTKVEIKGTVAAPS VFIFPPDTVLTQSPSTLSASPGERATISCRASESVSTHMHWYQQKPGQAPKLLIYGASN LESGVPSRFSGSRSGTDFTLTISSLQPEDFAVYFCQQSWNDPFTFGQGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
68	PR-1564899H (DVD3900H)a	EVQLVESGGGLVQPGGSLRLSCAFSGFSLSTFGMGVGWIRQAPGKGLEWLANIWWD DDKYYNPSLKNRLTISKDTSKNQAYLQINSLRAEDTAVYYCARISTGISSYYVMDAW GQGTLVTVSSASTKGPEVQLVESGGGLVQPGGSLRLSCAASGYTFTNYGMYWVKQ APGKGLEYMGWINTETGKPTYADDFKGRFTFSLDTSKSTAYLQMNSLRAEDTAVYF CARTNYYYRSYIFYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGK
69	PR-1564899L (DVD3900L)a	DFQLTQSPSSLSASVGDRVTITCERSSGDIGDTYVSWYQQKPGKAPKNVIYGNDQRPS GVPSRFSGSGSGNSATLTISSLQPEDFATYFCQSYDSDIDIVFGQGTKVEIKGTVAAPS VFIFPPDTQLTQSPSSLSASVGDRVTISCRASESVSTHMHWYQQKPGKAPKLLIYGAS NLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCQQSWNDPFTFGQGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
70	PR-1565023H (DVD3901H)a	EVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMGVGWIRQPPGKALEWLANIWWD DDKYYNPSLKNRLTISKDTSKNQAVLTITNMDPVDTATYYCARIESIGTTYSFDYWG QGTTVTVSSASTKGPEIQLVQSGTEVKKPGESLKISCKASGYTFTNYGMYWVKQMP GKGLEYMGWINTETGKPTYADDFKGRFTFSLDKSFNTAFLQWSSLKASDTAMYFCA RTNYYYRSYIFYFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKP SNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK
71	PR-1565023L (DVD3901L)a	DFVLTQSPDSLAVSLGERATINCERSSGDIGDSYVSWYQQKPGQPPKNVIYADDQRPS GVPDRFSGSGSGNSASLTISSLQAEDVAVYFCQSYDINIDIVFGGGTKVEIKGTVAAPS VFIFPPETVLTQSPATLSVSPGERATLSCRASESVSTHMHWYQQKPGQAPRLLIYGAS NLESGVPARFSGSGSGTDFTLTISSLQSEDFAVYFCQQSWNDPFTFGQGTRLEIKRTV AAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
72	PR-1565029H (DVD3902H)a	EVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMGVGWIRQPPGKALEWLANIWWD DDKYYNPSLKNRLTISKDTSKNQAVLTITNMDPVDTATYYCARIESIGTTYSFDYWG QGTTVTVSSASTKGPEIQLVQSGGGVVQPGGSLRLSCAASGYTFTNYGMYWVKQAP GKGLEYMGWINTETGKPTYADDFKGRFTFSLDTSKSTAYLQLNSLRAEDTAVYFCA RTNYYYRSYIFYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKP SNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK
73	PR-1565029L (DVD3902L)a	DFVLTQSPDSLAVSLGERATINCERSSGDIGDSYVSWYQQKPGQPPKNVIYADDQRPS GVPDRFSGSGSGNSASLTISSLQAEDVAVYFCQSYDINIDIVFGGGTKVEIKGTVAAPS VFIFPPDTVLTQSPSTLSASPGERATISCRASESVSTHMHWYQQKPGQAPKLLIYGASN LESGVPSRFSGSRSGTDFTLTISSLQPEDFAVYFCQQSWNDPFTFGQGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

74	PR-1565030H (DVD3903H)a	EVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMGVGWIRQPPGKALEWLANIWWD DDKYYNPSLKNRLTISKDTSKNQAVLTITNMDPVDTATYYCARIESIGTTYSFDYWG QGTTVTVSSASTKGPEVQLVESGGGLVQPGGSLRLSCAASGYTFTNYGMYWVKQAP GKGLEYMGWINTETGKPTYADDFKGRFTFSLDTSKSTAYLQMNSLRAEDTAVYFCA RTNYYYRSYIFYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKP SNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK
75	PR-1565030L (DVD3903L)a	DFVLTQSPDSLAVSLGERATINCERSSGDIGDSYVSWYQQKPGQPPKNVIYADDQRPS GVPDRFSGSGSGNSASLTISSLQAEDVAVYFCQSYDINIDIVFGGGTKVEIKGTVAAPS VFIFPPDTQLTQSPSSLSASVGDRVTISCRASESVSTHMHWYQQKPGKAPKLLIYGAS NLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCQQSWNDPFTFGQGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
76	PR-1565031H (DVD3904H)a	EVQLVESGGGLVQPGGSLRLSCAFSGFSLSTYGMGVGWIRQAPGKGLEWLANIWW DDDKYYNPSLKNRLTISKDTSKNQAYLQINSLRAEDTAVYYCARIESIGTTYSFDYW GQGTLVTVSSASTKGPEIQLVQSGGGVVQPGGSLRLSCAASGYTFTNYGMYWVKQA PGKGLEYMGWINTETGKPTYADDFKGRFTFSLDTSKSTAYLQLNSLRAEDTAVYFC ARTNYYYRSYIFYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
77	PR-1565031L (DVD3904L)a	DFQLTQSPSSLSASVGDRVTITCERSSGDIGDSYVSWYQQKPGKAPKNVIYADDQRPS GVPSRFSGSGSGNSASLTISSLQPEDFATYFCQSYDINIDIVFGQGTKVEIKGTVAAPSV FIFPPDTVLTQSPSTLSASPGERATISCRASESVSTHMHWYQQKPGQAPKLLIYGASNL ESGVPSRFSGSRSGTDFTLTISSLQPEDFAVYFCQQSWNDPFTFGQGTKVEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
78	PR-1565032H (DVD3905H)a	EVQLVESGGGLVQPGGSLRLSCAFSGFSLSTYGMGVGWIRQAPGKGLEWLANIWW DDDKYYNPSLKNRLTISKDTSKNQAYLQINSLRAEDTAVYYCARIESIGTTYSFDYW GQGTLVTVSSASTKGPEVQLVESGGGLVQPGGSLRLSCAASGYTFTNYGMYWVKQ APGKGLEYMGWINTETGKPTYADDFKGRFTFSLDTSKSTAYLQMNSLRAEDTAVYF CARTNYYYRSYIFYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGK
79	PR-1565032L (DVD3905L)a	DFQLTQSPSSLSASVGDRVTITCERSSGDIGDSYVSWYQQKPGKAPKNVIYADDQRPS GVPSRFSGSGSGNSASLTISSLQPEDFATYFCQSYDINIDIVFGQGTKVEIKGTVAAPSV FIFPPDTQLTQSPSSLSASVGDRVTISCRASESVSTHMHWYQQKPGKAPKLLIYGASN LESGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCQQSWNDPFTFGQGTKVEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
80	PR-1565035H (DVD3906H)a	EVTLRESGPALVKPTQTLTLTCTFSGFSLSTFGMGVGWIRQPPGKALEWLANIWWDD DKYYNPSLKNRLTISKDTSKNQAVLTITNMDPVDTATYYCARISTGISSYYVMDAWG QGTTVTVSSASTKGPEVQLVESGGGLVQPGGSLRLSCAASGYTFTNYGMYWVKQAP GKGLEYMGWINTETGKPTYADDFKGRFTFSLDTSKSTAYLQMNSLRAEDTAVYFCA RTNYYYRSYIFYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKP SNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD

		IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK
81	PR-1565035L (DVD3906L)a	DFQLTQSPSSLSASVGDRVTITCERSSGDIGDTYVSWYQQKPGKAPKNVIYGNDQRPS GVPSRFSGSGSGNSATLTISSLQPEDFATYFCQSYDSDIDIVFGQGTKVEIKGTVAAPS VFIFPPDTQLTQSPSSLSASVGDRVTISCRASESVSTHMHWYQQKPGKAPKLLIYGAS NLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCQQSWNDPFTFGQGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
82	PR-1565033H (DVD3907H)a	EVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMGVGWIRQPPGKALEWLANIWWD DDKYYNPSLKNRLTISKDTSKNQAVLTITNMDPVDTATYYCARIESIGTTYSFDYWG QGTTVTVSSASTKGPEVQLVESGGGLVQPGGSLRLSCAASGYTFTNYGMYWVKQAP GKGLEYMGWINTETGKPTYADDFKGRFTFSLDTSKSTAYLQMNSLRAEDTAVYFCA RTNYYYRSYIFYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKP SNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK
83	PR-1565033L (DVD3907L)a	DFQLTQSPSSLSASVGDRVTITCERSSGDIGDSYVSWYQQKPGKAPKNVIYADDQRPS GVPSRFSGSGSGNSASLTISSLQPEDFATYFCQSYDINIDIVFGQGTKVEIKGTVAAPSV FIFPPDTVLTQSPSTLSASPGERATISCRASESVSTHMHWYQQKPGQAPKLLIYGASNL ESGVPSRFSGSRSGTDFTLTISSLQPEDFAVYFCQQSWNDPFTFGQGTKVEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
84	PR-1569574H	EVQLVQSGSELKKPGASVKVSCKASGYTFTNYGMYWVRQAPGQGLEWMGWINTE TGKPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARTNYYYRSYIFYFD YWGQGTMVTVSSGGGGSGGGGSEVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGM GVGWIRQPPGKALEWLANIWWDDDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDP VDTATYYCARIESIGTTYSFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNAYTQKSLSLSPGK
85	PR-1569574L	DTVLTQSPATLSLSPGERATLSCRASESVSTHMHWYQQKPGQAPRLLIYGASNLESG VPARFSGSGSGTDFTLTISSLEPEDFAVYFCQQSWNDPFTFGQGTKLEIKRGGSGGGG SGEFVLTQSPGTLSLSPGERATLSCERSSGDIGDSYVSWYQQKPGQAPRLVIYADDQR PSGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKGTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
86	PR-1569579H	EVQLVQSGSELKKPGASVKVSCKASGYTFTNYGMYWVRQAPGQGLEWMGWINTE TGKPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARTNYYYRSYIFYFD YWGQGTMVTVSSASTKGPEVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMGVGWI RQPPGKALEWLANIWWDDDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPVDTAT YYCARIESIGTTYSFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNAYTQKSLSLSPGK
87	PR-1569579L	DTVLTQSPATLSLSPGERATLSCRASESVSTHMHWYQQKPGQAPRLLIYGASNLESG VPARFSGSGSGTDFTLTISSLEPEDFAVYFCQQSWNDPFTFGQGTKLEIKRTVAAPSVF IFPPEFVLTQSPGTLSLSPGERATLSCERSSGDIGDSYVSWYQQKPGQAPRLVIYADDQ RPSGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKGTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

88	PR-1572102H	EVQLVQSGSELKKPGASVKVSCKASGYTFTNYGMYWVRQAPGQGLEWMGWINTE TGKPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARTNYYYRSYIFYFD YWGQGTMVTVSSGGGGSGGGGSEVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGM GVGWIRQPPGKALEWLANIWWDDDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDP VDTATYYCARIESIGTTYSFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNAYTQKSLSLSPGK
89	PR-1572102L	DTVLTQSPATLSLSPGERATLSCRASESVSTHMHWYQQKPGQAPRLLIYGASNLESG VPARFSGSGSGTDFTLTISSLEPEDFAVYFCQQSWNDPFTFGQGTKLEIKRGGSGGGG SGEFVLTQSPGTLSLSPGERATLSCERSSGDIGDSYVSWYQQKPGQAPRLVIYADDQR PSGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
90	PR-1572103H	EVQLVQSGSELKKPGASVKVSCKASGYTFTNYGMYWVRQAPGQGLEWMGWINTE TGKPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARTNYYYRSYIFYFD YWGQGTMVTVSSGGGGSGGGGSEVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGM GVGWIRQPPGKALEWLANIWWDDDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDP VDTATYYCARIESIGTTYSFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNAYTQKSLSLSPGK
91	PR-1572103L	DTVLTQSPATLSLSPGERATLSCRASESVSTHMHWYQQKPGQAPRLLIYGASNLESG VPARFSGSGSGTDFTLTISSLEPEDFAVYFCQQSWNDPFTFGQGTKLEIKRGGSGGGG SGGEFVLTQSPGTLSLSPGERATLSCERSSGDIGDSYVSWYQQKPGQAPRLVIYADDQ RPSGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
92	PR-1572104H	EVQLVQSGSELKKPGASVKVSCKASGYTFTNYGMYWVRQAPGQGLEWMGWINTE TGKPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARTNYYYRSYIFYFD YWGQGTMVTVSSGGGGSGGGGSEVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGM GVGWIRQPPGKALEWLANIWWDDDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDP VDTATYYCARIESIGTTYSFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNAYTQKSLSLSPGK
93	PR-1572104L	DTVLTQSPATLSLSPGERATLSCRASESVSTHMHWYQQKPGQAPRLLIYGASNLESG VPARFSGSGSGTDFTLTISSLEPEDFAVYFCQQSWNDPFTFGQGTKLEIKGGSGGGGS GGEFVLTQSPGTLSLSPGERATLSCERSSGDIGDSYVSWYQQKPGQAPRLVIYADDQ RPSGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
94	PR-1572105H	EVQLVQSGSELKKPGASVKVSCKASGYTFTNYGMYWVRQAPGQGLEWMGWINTE TGKPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARTNYYYRSYIFYFD YWGQGTMVTVSSASTKGPEVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMGVGWI RQPPGKALEWLANIWWDDDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPVDTAT YYCARIESIGTTYSFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS

		DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNAYTQKSLSLSPGK
95	PR-1572105L	DTVLTQSPATLSLSPGERATLSCRASESVSTHMHWYQQKPGQAPRLLIYGASNLESG VPARFSGSGSGTDFTLTISSLEPEDFAVYFCQQSWNDPFTFGQGTKLEIKRTVAAPSVF IFPPEFVLTQSPGTLSLSPGERATLSCERSSGDIGDSYVSWYQQKPGQAPRLVIYADDQ RPSGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
96	PR-1572106H	EVQLVQSGSELKKPGASVKVSCKASGYTFTNYGMYWVRQAPGQGLEWMGWINTE TGKPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARTNYYYRSYIFYFD YWGQGTMVTVSSASTKGPSVFPLAPEVTLRESGPALVKPTQTLTLTCTFSGFSLSTYG MGVGWIRQPPGKALEWLANIWWDDDKYYNPSLKNRLTISKDTSKNQVVLTMTNM DPVDTATYYCARIESIGTTYSFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNAYTQKSLSLSPGK
97	PR-1572106L	DTVLTQSPATLSLSPGERATLSCRASESVSTHMHWYQQKPGQAPRLLIYGASNLESG VPARFSGSGSGTDFTLTISSLEPEDFAVYFCQQSWNDPFTFGQGTKLEIKRTVAAPEFV LTQSPGTLSLSPGERATLSCERSSGDIGDSYVSWYQQKPGQAPRLVIYADDQRPSGIP DRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKRTVAAPSVFIF PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
210	PR-1575573H	EVQLVQSGSELKKPGASVKVSCKASGYTFTNYGMYWVRQAPGQGLEWMGWINTE TGKPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARTNYYYRSYIFYFD YWGQGTMVTVSSASTKGPSVFPLAPEVTLRESGPALVKPTQTLTLTCTFSGFSLSTYG MGVGWIRQPPGKALEWLANIWWDDDKYYNPSLKNRLTISKDTSKNQVVLTMTNM DPVDTATYYCARIESIGTTYSFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNAYTQKSLSLSPGK
98	PR-1575573L	DTVLTQSPATLSLSPGERATLSCRASESVSTHMHWYQQKPGQAPRLLIYGASNLESG VPARFSGSGSGTDFTLTISSLEPEDFAVYFCQQSWNDPFTFGQGTKLEIKRTVAAPEFV LTQSPGTLSLSPGERATLSCERSSGDIGDSYVSWYQQKPGQAPRLVIYADDQRPSGIP DRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKGTVAAPSVFIF PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
99	PR-1575832H	EVQLVQSGSELKKPGASVKVSCKASGYTFTNYGMYWVRQAPGQGLEWMGWINTE TGKPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARTNYYYRSYIFYFD YWGQGTMVTVSSGGGGSGGGGSEVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGM GVGWIRQPPGKALEWLANIWWDDDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDP VDTATYYCARIESIGTTYSFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNAYTQKSLSLSPGK
100	PR-1575832L	DTVLTQSPATLSLSPGERATLSCRASESVSTHMHWYQQKPGQAPRLLIYGASNLESG VPARFSGSGSGTDFTLTISSLEPEDFAVYFCQQSWNDPFTFGQGTKLEIKRGGSGGGG SGEFVLTQSPGTLSLSPGERATLSCERSSGDIGESYVSWYQQKPGQAPRLVIYADDQR PSGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

101	PR-1575834H	EVQLVQSGSELKKPGASVKVSCKASGYTFTNYGMYWVRQAPGQGLEWMGWINTE TGKPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARTNYYYRSYIFYFD YWGQGTMVTVSSASTKGPEVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMGVGWI RQPPGKALEWLANIWWDDDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPVDTAT YYCARIESIGTTYSFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNAYTQKSLSLSPGK
102	PR-1575834L	DTVLTQSPATLSLSPGERATLSCRASESVSTHMHWYQQKPGQAPRLLIYGASNLESG VPARFSGSGSGTDFTLTISSLEPEDFAVYFCQQSWNDPFTFGQGTKLEIKRTVAAPSVF IFPPEFVLTQSPGTLSLSPGERATLSCERSSGDIGESYVSWYQQKPGQAPRLVIYADDQ RPSGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
103	PR-1575835H	EVQLVQSGSELKKPGASVKVSCKASGYTFTNYGMYWVRQAPGQGLEWMGWINTE TGKPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARTNYYYRSYIFYFD YWGQGTMVTVSSASTKGPSVFPLAPEVTLRESGPALVKPTQTLTLTCTFSGFSLSTYG MGVGWIRQPPGKALEWLANIWWDDDKYYNPSLKNRLTISKDTSKNQVVLTMTNM DPVDTATYYCARIESIGTTYSFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNAYTQKSLSLSPGK
104	PR-1575835L	DTVLTQSPATLSLSPGERATLSCRASESVSTHMHWYQQKPGQAPRLLIYGASNLESG VPARFSGSGSGTDFTLTISSLEPEDFAVYFCQQSWNDPFTFGQGTKLEIKRTVAAPEFV LTQSPGTLSLSPGERATLSCERSSGDIGESYVSWYQQKPGQAPRLVIYADDQRPSGIP DRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKRTVAAPSVFIF PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
105	PR-1577165H	EVQLVQSGAEVKKPGASVKVSCKASGYTFTNYGMYWVRQAPGQGLEWMGWINTE TGKPIYADDFKGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARVDYDGSFWFAY WGQGTLVTVSSGGGGSGGGGSEVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMGV GWIRQPPGKALEWLANIWWDDDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPVD TATYYCARIESIGTTYSFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNAYTQKSLSLSPGK
106	PR-1577165L	DTQLTQSPSSLSASVGDRVTITCRASESVSTVIHWYQQKPGKQPKLLIHGASNLESGV PSRFSGSGSGTDFTLTISSLQPEDFATYFCQQHWNDPPTFGQGTKLEIKRGGSGGGGS GEFVLTQSPGTLSLSPGERATLSCERSSGDIGESYVSWYQQKPGQAPRLVIYADDQRP SGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
107	PR-1577166H	EVQLVQSGAEVKKPGASVKVSCKASGYTFTNYGMYWVRQAPGQGLEWMGWINTE TGKPIYADDFKGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARVDYDGSFWFAY WGQGTLVTVSSASTKGPEVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMGVGWIR QPPGKALEWLANIWWDDDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPVDTATY YCARIESIGTTYSFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKP SNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD

		IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNAYTQKSLSLSPGK
108	PR-1577166L	DTQLTQSPSSLSASVGDRVTITCRASESVSTVIHWYQQKPGKQPKLLIHGASNLESGV PSRFSGSGSGTDFTLTISSLQPEDFATYFCQQHWNDPPTFGQGTKLEIKRTVAAPSVFI FPPEFVLTQSPGTLSLSPGERATLSCERSSGDIGESYVSWYQQKPGQAPRLVIYADDQ RPSGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
109	PR-1577547H	EVQLVQSGAEVKKPGASVKVSCKASGYTFTNYGMYWVRQAPGQGLEWMGWINTE TGKPIYADDFKGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARVDYDGSFWFAY WGQGTLVTVSSASTKGPSVFPLAPEVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGM GVGWIRQPPGKALEWLANIWWDDDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDP VDTATYYCARIESIGTTYSFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNAYTQKSLSLSPGK
110	PR-1577547L	DTQLTQSPSSLSASVGDRVTITCRASESVSTVIHWYQQKPGKQPKLLIHGASNLESGV PSRFSGSGSGTDFTLTISSLQPEDFATYFCQQHWNDPPTFGQGTKLEIKRTVAAPEFVL TQSPGTLSLSPGERATLSCERSSGDIGESYVSWYQQKPGQAPRLVIYADDQRPSGIPD RFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKRTVAAPSVFIFP PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
111	PR-1577548H	EVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMGVGWIRQPPGKALEWLANIWWD DDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPVDTATYYCARIESIGTTYSFDYW GQGTMVTVSSASTKGPEVQLVQSGAEVKKPGASVKVSCKASGYTFTNYGMYWVRQ APGQGLEWMGWINTETGKPIYADDFKGRVTMTTDTSTSTAYMELRSLRSDDTAVYY CARVDYDGSFWFAYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKP SNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNAYTQKSLSLSPGK
112	PR-1577548L	EFVLTQSPGTLSLSPGERATLSCERSSGDIGESYVSWYQQKPGQAPRLVIYADDQRPS GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKRTVAAPSV FIFPPDTQLTQSPSSLSASVGDRVTITCRASESVSTVIHWYQQKPGKQPKLLIHGASNL ESGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCQQHWNDPPTFGQGTKLEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
113	PR-1577550H	EVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMGVGWIRQPPGKALEWLANIWWD DDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPVDTATYYCARIESIGTTYSFDYW GQGTMVTVSSASTKGPSVFPLAPEVQLVQSGAEVKKPGASVKVSCKASGYTFTNYG MYWVRQAPGQGLEWMGWINTETGKPIYADDFKGRVTMTTDTSTSTAYMELRSLRS DDTAVYYCARVDYDGSFWFAYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNAYTQKSLSLSPGK
114	PR-1577550L	EFVLTQSPGTLSLSPGERATLSCERSSGDIGESYVSWYQQKPGQAPRLVIYADDQRPS GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKRTVAAPDT QLTQSPSSLSASVGDRVTITCRASESVSTVIHWYQQKPGKQPKLLIHGASNLESGVPS RFSGSGSGTDFTLTISSLQPEDFATYFCQQHWNDPPTFGQGTKLEIKRTVAAPSVFIFP PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

115	PR-1578137H	EVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMGVGWIRQPPGKALEWLANIWWD DDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPVDTATYYCARIESIGTTYSFDYW GQGTMVTVSSGGGGSGGGGSEVQLVQSGAEVKKPGASVKVSCKASGYTFTNYGMY WVRQAPGQGLEWMGWINTETGKPIYADDFKGRVTMTTDTSTSTAYMELRSLRSDD TAVYYCARVDYDGSFWFAYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNAYTQKSLSLSPGK
116	PR-1578137L	EFVLTQSPGTLSLSPGERATLSCERSSGDIGESYVSWYQQKPGQAPRLVIYADDQRPS GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKRGGSGGG GSGDTQLTQSPSSLSASVGDRVTITCRASESVSTVIHWYQQKPGKQPKLLIHGASNLE SGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCQQHWNDPPTFGQGTKLEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
117	PR-1598261H	EVQLVQSGSELKKPGASVKVSCKASGYTFTNYGMYWVRQAPGQGLEWMGWINTE TGKPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARTNYYYRSYIFYFD YWGQGTMVTVSSGGGGSGGGGSEVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGM GVGWIRQPPGKALEWLANIWWDDDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDP VDTATYYCARIESIGTTYSFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPGK
118	PR-1598261L	ATQLTQSPSLSASVGDRVTITCRASESVSTHMHWYQQKPGKQPKLLIYGASNLESGV PSRFSGSGSGTDFTLTISSLQPEDFATYFCQQSWNDPFTFGQGTKLEIKRGGSGGGGS GEFVLTQSPGTLSLSPGERATLSCERSSGDIGDSYVSWYQQKPGQAPRLVIYADDQRP SGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
119	PR-1598262H	EIQLVQSGSELKKPGASVKVSCKASGYTFTNYGMYWVRQAPGQGLEYMGWINTET GKPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYFCARTNYYYRSYIFYFDY WGQGTMVTVSSGGGGSGGGGSEVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMG VGWIRQPPGKALEWLANIWWDDDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPV DTATYYCARIESIGTTYSFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK
120	PR-1598262L	AIQLTQSPSSLSASVGDRVTITCRASESVSTHMHWYQQKPGKAPKLLIYGASNLESGV PSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSWNDPFTFGQGTKLEIKRGGSGGGGS GEFVLTQSPGTLSLSPGERATLSCERSSGDIGDSYVSWYQQKPGQAPRLVIYADDQRP SGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
121	PR-1598263H	EIQLVQSGSELKKPGASVKVSCKASGYTFTNYGMYWVRQAPGQGLEYMGWINTET GKPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYFCARTNYYYRSYIFYFDY WGQGTMVTVSSGGGGSGGGGSEVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMG VGWIRQPPGKALEWLANIWWDDDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPV DTATYYCARIESIGTTYSFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK

		GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK
122	PR-1598263L	ATQLTQSPSLSASVGDRVTITCRASESVSTHMHWYQQKPGKQPKLLIYGASNLESGV PSRFSGSGSGTDFTLTISSLQPEDFATYFCQQSWNDPFTFGQGTKLEIKRGGSGGGGS GEFVLTQSPGTLSLSPGERATLSCERSSGDIGDSYVSWYQQKPGQAPRLVIYADDQRP SGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
123	PR-1598264H	EIQLVQSGAEVKKPGASVKVSCKASGYTFTNYGMYWVRQAPGQGLEYMGWINTET GKPTYADDFKGRFTFTLDTSTSTAYMELRSLRSDDTAVYFCARTNYYYRSYIFYFDY WGQGTMVTVSSGGGGSGGGGSEVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMG VGWIRQPPGKALEWLANIWWDDDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPV DTATYYCARIESIGTTYSFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK
124	PR-1598264L	DTVLTQSPATLSLSPGERATLSCRASESVSTHMHWYQQKPGQAPRLLIYGASNLESG VPARFSGSGSGTDFTLTISSLEPEDFAVYFCQQSWNDPFTFGQGTKLEIKRGGSGGGG SGEFVLTQSPGTLSLSPGERATLSCERSSGDIGDSYVSWYQQKPGQAPRLVIYADDQR PSGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
125	PR-1598265H	EIQLVQSGTEVKKPGESLKISCKASGYTFTNYGMYWVKQMPGKGLEYMGWINTETG KPTYADDFKGRFTFSLDKSFNTAFLQWSSLKASDTAMYFCARTNYYYRSYIFYFDY WGQGTMVTVSSGGGGSGGGGSEVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMG VGWIRQPPGKALEWLANIWWDDDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPV DTATYYCARIESIGTTYSFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK
126	PR-1598265L	ETVLTQSPATLSVSPGERATLSCRASESVSTHMHWYQQKPGQAPRLLIYGASNLESG VPARFSGSGSGTDFTLTISSLQSEDFAVYFCQQSWNDPFTFGQGTRLEIKRGGSGGGG SGEFVLTQSPGTLSLSPGERATLSCERSSGDIGDSYVSWYQQKPGQAPRLVIYADDQR PSGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
127	PR-1598266H	EIQLVQSGGGVVQPGGSLRLSCAASGYTFTNYGMYWVKQAPGKGLEYMGWINTET GKPTYADDFKGRFTFSLDTSKSTAYLQLNSLRAEDTAVYFCARTNYYYRSYIFYFDY WGQGTLVTVSSGGGGSGGGGSEVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMGV GWIRQPPGKALEWLANIWWDDDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPVD TATYYCARIESIGTTYSFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPGK
128	PR-1598266L	DTVLTQSPSTLSASPGERATISCRASESVSTHMHWYQQKPGQAPKLLIYGASNLESGV PSRFSGSRSGTDFTLTISSLQPEDFAVYFCQQSWNDPFTFGQGTKVEIKRGGSGGGGS GEFVLTQSPGTLSLSPGERATLSCERSSGDIGDSYVSWYQQKPGQAPRLVIYADDQRP SGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

129	PR-1610560H	EIQLVQSGSELKKPGASVKVSCKASGYTFTNYGMYWVRQAPGQGLEYMGWINTET GKPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYFCARTNYYYRSYIFYFDY WGQGTMVTVSSGGGGSGGGGSEVQLVQSGAEVKKPGSSVKVSCKASGYTFTESYM YWVKQAPGQGLELIGRIDPEDGSTDYVEKFKNKATLTADKSTSTAYMELSSLRSEDT AVYFCARFGARSYFYPMDAWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNAYTQKSLSLSPGK
130	PR-1610560L	ATQLTQSPSLSASVGDRVTITCRASESVSTHMHWYQQKPGKQPKLLIYGASNLESGV PSRFSGSGSGTDFTLTISSLQPEDFATYFCQQSWNDPFTFGQGTKLEIKGGSGGGGSG GETVLTQSPATLSLSPGERATLSCRASESVSTLMHWYQQKPGQQPRLLIYGASNLESG VPARFSGSGSGTDFTLTISSLEPEDFAVYFCQQSWNDPWTFGGGTKVEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST YSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
131	PR-1610561H	EIQLVQSGSELKKPGASVKVSCKASGYTFTNYGMYWVKQAPGQGLEYMGWIDTET GRPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYFCARWSGDTTGIRGPWFA YWGQGTLVTVSSGGGGSGGGGSEVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMG VGWIRQPPGKALEWLANIWWDDDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPV DTATYYCARIESSGPKYSFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNAYTQKSLSLSPGK
132	PR-1610561L	DIRMTQSPSSLSASVGDRVTIECLASEDIYSDLAWYQQKPGKSPKLLIYNANGLQNGV PSRFSGSGSGTDYSLTISSLQPEDVATYFCQQYNYFPGTFGQGTKLEIKGGSGGGGSG GEIVLTQSPGTLSLSPGERATLSCRASSGSIWYSFVSWYQQKPGQAPRLLIYADDQRA SGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYGINIDVVFGGGTKVEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
133	PR-1610562H	EIQLVQSGSELKKPGASVKVSCKASGYTFTNYGMYWVKQAPGQGLEYMGWIDTET GRPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYFCARWSGDTTGIRGPWFA YWGQGTLVTVSSGGGGSGGGGSEVQLVQSGAEVKKPGSSVKVSCKASGYTFTESY MYWVKQAPGQGLELIGRIDPEDGSTDYVEKFKNKATLTADKSTSTAYMELSSLRSE DTAVYFCARFGARSYFYPMDAWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNAYTQKSLSLSPGK
134	PR-1610562L	DIRMTQSPSSLSASVGDRVTIECLASEDIYSDLAWYQQKPGKSPKLLIYNANGLQNGV PSRFSGSGSGTDYSLTISSLQPEDVATYFCQQYNYFPGTFGQGTKLEIKGGSGGGGSG GETVLTQSPATLSLSPGERATLSCRASESVSTLMHWYQQKPGQQPRLLIYGASNLESG VPARFSGSGSGTDFTLTISSLEPEDFAVYFCQQSWNDPWTFGGGTKVEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST YSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
135	PR-1610563H	EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYGMYWVRQAPGQGLEWMGWIDTE TGRPTYADDFKGRFTFTADKSTSTAYMELSSLRSEDTAVYYCARWSGDTTGIRGPWF AYWGQGTLVTVSSGGGGSGGGGSEVQLVQSGAEVKKPGSSVKVSCKASGYTFTESY MYWVKQAPGQGLELIGRIDPEDGSTDYVEKFKNKATLTADKSTSTAYMELSSLRSE DTAVYFCARFGARSYFYPMDAWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV

		KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNAYTQKSLSLSPGK
136	PR-1610563L	DIRMTQSPSSLSASVGDRVTITCLASEDIYSDLAWYQQKPGKSPKLLIYNANGLQNGV PSRFSGSGSGTDYTLTISSLQPEDVATYFCQQYNYFPGTFGQGTKLEIKGGSGGGGSG GETVLTQSPATLSLSPGERATLSCRASESVSTLMHWYQQKPGQQPRLLIYGASNLESG VPARFSGSGSGTDFTLTISSLEPEDFAVYFCQQSWNDPWTFGGGTKVEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST YSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
137	PR-1610564H	EVQLVESGGGLVQPGGSLRLSCAASGFSFSKYDMAWFRQAPGKGLEWVASITTSGV GTYYRDSVKGRFTVSRDNAKSTLYLQMNSLRAEDTAVYYCARGYGAMDAWGQGT TVTVSSGGGGSGGGGSEVQLVQSGAEVKKPGSSVKVSCKASGYTFTESYMYWVKQ APGQGLELIGRIDPEDGSTDYVEKFKNKATLTADKSTSTAYMELSSLRSEDTAVYFC ARFGARSYFYPMDAWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKP SNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNAYTQKSLSLSPGK
138	PR-1610564L	DIQMTQSPSSLSASVGDRVTITCKASQDIDDYLSWYQQKPGKSPKLVIYAATRLADG VPSRFSGSGSGTDYTLTISSLQPEDFATYYCLQSSSTPWTFGGGTKVEIKGGSGGGGS GGETVLTQSPATLSLSPGERATLSCRASESVSTLMHWYQQKPGQQPRLLIYGASNLES GVPARFSGSGSGTDFTLTISSLEPEDFAVYFCQQSWNDPWTFGGGTKVEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
139	PR-1611291H	EIQLVQSGSELKKPGASVKVSCKASGYTFTNYGMYWVRQAPGQGLEYMGWINTET GKPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYFCARTNYYYRSYIFYFDY WGQGTMVTVSSGGGGSGGGGSEVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMG VGWIRQPPGKALEWLANIWWDDDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPV DTATYYCARIESSGPKYSFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNAYTQKSLSLSPGK
140	PR-1611291L	ATQLTQSPSLSASVGDRVTITCRASESVSTHMHWYQQKPGKQPKLLIYGASNLESGV PSRFSGSGSGTDFTLTISSLQPEDFATYFCQQSWNDPFTFGQGTKLEIKGGSGGGGSG GEIVLTQSPGTLSLSPGERATLSCRASSGSIWYSFVSWYQQKPGQAPRLLIYADDQRA SGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYGINIDVVFGGGTKVEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
141	PR-1611292H	EVQLVESGGGLVQPGGSLRLSCAASGFSFSKYDMAWFRQAPGKGLEWVASITTSGV GTYYRDSVKGRFTVSRDNAKSTLYLQMNSLRAEDTAVYYCARGYGAMDAWGQGT TVTVSSGGGGSGGGGSEVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMGVGWIRQ PPGKALEWLANIWWDDDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPVDTATYY CARIESSGPKYSFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKP SNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNAYTQKSLSLSPGK
142	PR-1611292L	DIQMTQSPSSLSASVGDRVTITCKASQDIDDYLSWYQQKPGKSPKLVIYAATRLADG VPSRFSGSGSGTDYTLTISSLQPEDFATYYCLQSSSTPWTFGGGTKVEIKGGSGGGGS GGEIVLTQSPGTLSLSPGERATLSCRASSGSIWYSFVSWYQQKPGQAPRLLIYADDQR ASGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYGINIDVVFGGGTKVEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

143	PR-1611293H	EIQLVQSGSELKKPGASVKVSCKASGYPFTNSGMYWVKQAPGQGLEYMGWINTEA GKPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYFCARWGYISDNSYGWFDY WGQGTLVTVSSGGGGSGGGGSEVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMGV GWIRQPPGKALEWLANIWWDDDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPVD TATYYCARIESSGPKYSFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNAYTQKSLSLSPGK
144	PR-1611293L	ATQLTQSPSSLSASVGDRVTISCRASEGVYSYMHWYQQKPGKQPKLLIYKASNLASG VPSRFSGSGSGTDFTLTISSLQPEDFATYFCHQNWNDPLTFGQGTKLEIKGGSGGGGS GGEIVLTQSPGTLSLSPGERATLSCRASSGSIWYSFVSWYQQKPGQAPRLLIYADDQR ASGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYGINIDVVFGGGTKVEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
145	PR-1611294H	EIQLVQSGSELKKPGASVKVSCKASGYPFTNSGMYWVKQAPGQGLEYMGWINTEA GKPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYFCARWGYISDNSYGWFDY WGQGTLVTVSSGGGGSGGGGSEVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMGV GWIRQPPGKALEWLANIWWDDDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPVD TATYYCARIESIGTTYSFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNAYTQKSLSLSPGK
146	PR-1611294L	ATQLTQSPSSLSASVGDRVTISCRASEGVYSYMHWYQQKPGKQPKLLIYKASNLASG VPSRFSGSGSGTDFTLTISSLQPEDFATYFCHQNWNDPLTFGQGTKLEIKGGSGGGGS GGEFVLTQSPGTLSLSPGERATLSCERSSGDIGDSYVSWYQQKPGQAPRLVIYADDQ RPSGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
147	PR-1611295H	EVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMGVGWIRQPPGKALEWLANIWWD DDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPVDTATYYCARIESSGPKYSFDYW GQGTMVTVSSGGGGSGGGGSEIQLVQSGSELKKPGASVKVSCKASGYTFTNYGMY WVKQAPGQGLEYMGWIDTETGRPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDT AVYFCARWSGDTTGIRGPWFAYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNAYTQKSLSLSPGK
148	PR-1611295L	EIVLTQSPGTLSLSPGERATLSCRASSGSIWYSFVSWYQQKPGQAPRLLIYADDQRAS GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYGINIDVVFGGGTKVEIKGGSGGGG SGGDIRMTQSPSSLSASVGDRVTIECLASEDIYSDLAWYQQKPGKSPKLLIYNANGLQ NGVPSRFSGSGSGTDYSLTISSLQPEDVATYFCQQYNYFPGTFGQGTKLEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
149	PR-1611296H	EVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMGVGWIRQPPGKALEWLANIWWD DDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPVDTATYYCARIESSGPKYSFDYW GQGTMVTVSSGGGGSGGGGSEVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYGMY WVRQAPGQGLEWMGWIDTETGRPTYADDFKGRFTFTADKSTSTAYMELSSLRSEDT AVYYCARWSGDTTGIRGPWFAYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTC

		LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNAYTQKSLSLSPGK
150	PR-1611296L	EIVLTQSPGTLSLSPGERATLSCRASSGSIWYSFVSWYQQKPGQAPRLLIYADDQRAS GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYGINIDVVFGGGTKVEIKGGSGGGG SGGDIRMTQSPSSLSASVGDRVTITCLASEDIYSDLAWYQQKPGKSPKLLIYNANGLQ NGVPSRFSGSGSGTDYTLTISSLQPEDVATYFCQQYNYFPGTFGQGTKLEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
151	PR-1611297H	EVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMGVGWIRQPPGKALEWLANIWWD DDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPVDTATYYCARIESSGPKYSFDYW GQGTMVTVSSGGGGSGGGGSEIQLVQSGSELKKPGASVKVSCKASGYPFTNSGMYW VKQAPGQGLEYMGWINTEAGKPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTA VYFCARWGYISDNSYGWFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNAYTQKSLSLSPGK
152	PR-1611297L	EIVLTQSPGTLSLSPGERATLSCRASSGSIWYSFVSWYQQKPGQAPRLLIYADDQRAS GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYGINIDVVFGGGTKVEIKGGSGGGG SGGATQLTQSPSSLSASVGDRVTISCRASEGVYSYMHWYQQKPGKQPKLLIYKASNL ASGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCHQNWNDPLTFGQGTKLEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
153	PR-1611298H	EVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMGVGWIRQPPGKALEWLANIWWD DDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPVDTATYYCARIESIGTTYSFDYW GQGTMVTVSSGGGGSGGGGSEIQLVQSGSELKKPGASVKVSCKASGYTFTNYGMY WVKQAPGQGLEYMGWIDTETGRPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDT AVYFCARWSGDTTGIRGPWFAYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNAYTQKSLSLSPGK
154	PR-1611298L	EFVLTQSPGTLSLSPGERATLSCERSSGDIGDSYVSWYQQKPGQAPRLVIYADDQRPS GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKGGSGGGG SGGDIRMTQSPSSLSASVGDRVTIECLASEDIYSDLAWYQQKPGKSPKLLIYNANGLQ NGVPSRFSGSGSGTDYSLTISSLQPEDVATYFCQQYNYFPGTFGQGTKLEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
155	PR-1611299H	EVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMGVGWIRQPPGKALEWLANIWWD DDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPVDTATYYCARIESIGTTYSFDYW GQGTMVTVSSGGGGSGGGGSEVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYGMY WVRQAPGQGLEWMGWIDTETGRPTYADDFKGRFTFTADKSTSTAYMELSSLRSEDT AVYYCARWSGDTTGIRGPWFAYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNAYTQKSLSLSPGK
156	PR-1611299L	EFVLTQSPGTLSLSPGERATLSCERSSGDIGDSYVSWYQQKPGQAPRLVIYADDQRPS GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKGGSGGGG SGGDIRMTQSPSSLSASVGDRVTITCLASEDIYSDLAWYQQKPGKSPKLLIYNANGLQ NGVPSRFSGSGSGTDYTLTISSLQPEDVATYFCQQYNYFPGTFGQGTKLEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

157	PR-1611300H	EVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMGVGWIRQPPGKALEWLANIWWD DDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPVDTATYYCARIESIGTTYSFDYW GQGTMVTVSSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFSFSKYDMA WFRQAPGKGLEWVASITTSGVGTYYRDSVKGRFTVSRDNAKSTLYLQMNSLRAEDT AVYYCARGYGAMDAWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNAYTQKSLSLSPGK
158	PR-1611300L	EFVLTQSPGTLSLSPGERATLSCERSSGDIGDSYVSWYQQKPGQAPRLVIYADDQRPS GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKGGSGGGG SGGDIQMTQSPSSLSASVGDRVTITCKASQDIDDYLSWYQQKPGKSPKLVIYAATRL ADGVPSRFSGSGSGTDYTLTISSLQPEDFATYYCLQSSSTPWTFGGGTKVEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
159	PR-1611301H	EVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMGVGWIRQPPGKALEWLANIWWD DDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPVDTATYYCARIESIGTTYSFDYW GQGTMVTVSSGGGGSGGGGSEIQLVQSGSELKKPGASVKVSCKASGYPFTNSGMYW VKQAPGQGLEYMGWINTEAGKPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTA VYFCARWGYISDNSYGWFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNAYTQKSLSLSPGK
160	PR-1611301L	EFVLTQSPGTLSLSPGERATLSCERSSGDIGDSYVSWYQQKPGQAPRLVIYADDQRPS GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKGGSGGGG SGGATQLTQSPSSLSASVGDRVTISCRASEGVYSYMHWYQQKPGKQPKLLIYKASNL ASGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCHQNWNDPLTFGQGTKLEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
161	PR-1612489H	EIQLVQSGSELKKPGASVKVSCKASGYTFTNYGMYWVRQAPGQGLEYMGWINTET GKPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYFCARTNYYYRSYIFYFDY WGQGTMVTVSSGGGGSGGGGSEVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMG VGWIRQPPGKALEWLANIWWDDDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPV DTATYYCARIESIGTTYSFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNAYTQKSLSLSPGK
162	PR-1612489L	ATQLTQSPSLSASVGDRVTITCRASESVSTHMHWYQQKPGKQPKLLIYGASNLESGV PSRFSGSGSGTDFTLTISSLQPEDFATYFCQQSWNDPFTFGQGTKLEIKGGSGGGGSG GEFVLTQSPGTLSLSPGERATLSCERSSGDIGDSYVSWYQQKPGQAPRLVIYADDQRP SGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
163	PR-1612491H	EIQLVQSGSELKKPGASVKVSCKASGYTFTNYGMYWVKQAPGQGLEYMGWIDTET GRPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYFCARWSGDTTGIRGPWFA YWGQGTLVTVSSGGGGSGGGGSEVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMG VGWIRQPPGKALEWLANIWWDDDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPV DTATYYCARIESIGTTYSFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK

		GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNAYTQKSLSLSPGK
164	PR-1612491L	DIRMTQSPSSLSASVGDRVTIECLASEDIYSDLAWYQQKPGKSPKLLIYNANGLQNGV PSRFSGSGSGTDYSLTISSLQPEDVATYFCQQYNYFPGTFGQGTKLEIKGGSGGGGSG GEFVLTQSPGTLSLSPGERATLSCERSSGDIGDSYVSWYQQKPGQAPRLVIYADDQRP SGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
165	PR-1612492H	EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYGMYWVRQAPGQGLEWMGWIDTE TGRPTYADDFKGRFTFTADKSTSTAYMELSSLRSEDTAVYYCARWSGDTTGIRGPWF AYWGQGTLVTVSSGGGGSGGGGSEVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGM GVGWIRQPPGKALEWLANIWWDDDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDP VDTATYYCARIESSGPKYSFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNAYTQKSLSLSPGK
166	PR-1612492L	DIRMTQSPSSLSASVGDRVTITCLASEDIYSDLAWYQQKPGKSPKLLIYNANGLQNGV PSRFSGSGSGTDYTLTISSLQPEDVATYFCQQYNYFPGTFGQGTKLEIKGGSGGGGSG GEIVLTQSPGTLSLSPGERATLSCRASSGSIWYSFVSWYQQKPGQAPRLLIYADDQRA SGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYGINIDVVFGGGTKVEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
167	PR-1612493H	EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYGMYWVRQAPGQGLEWMGWIDTE TGRPTYADDFKGRFTFTADKSTSTAYMELSSLRSEDTAVYYCARWSGDTTGIRGPWF AYWGQGTLVTVSSGGGGSGGGGSEVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGM GVGWIRQPPGKALEWLANIWWDDDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDP VDTATYYCARIESIGTTYSFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNAYTQKSLSLSPGK
168	PR-1612493L	DIRMTQSPSSLSASVGDRVTITCLASEDIYSDLAWYQQKPGKSPKLLIYNANGLQNGV PSRFSGSGSGTDYTLTISSLQPEDVATYFCQQYNYFPGTFGQGTKLEIKGGSGGGGSG GEFVLTQSPGTLSLSPGERATLSCERSSGDIGDSYVSWYQQKPGQAPRLVIYADDQRP SGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
169	PR-1612494H	EVQLVESGGGLVQPGGSLRLSCAASGFSFSKYDMAWFRQAPGKGLEWVASITTSGV GTYYRDSVKGRFTVSRDNAKSTLYLQMNSLRAEDTAVYYCARGYGAMDAWGQGT TVTVSSGGGGSGGGGSEVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMGVGWIRQ PPGKALEWLANIWWDDDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPVDTATYY CARIESIGTTYSFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNAYTQKSLSLSPGK
170	PR-1612494L	DIQMTQSPSSLSASVGDRVTITCKASQDIDDYLSWYQQKPGKSPKLVIYAATRLADG VPSRFSGSGSGTDYTLTISSLQPEDFATYYCLQSSSTPWTFGGGTKVEIKGGSGGGGS GGEFVLTQSPGTLSLSPGERATLSCERSSGDIGDSYVSWYQQKPGQAPRLVIYADDQ RPSGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

171	PR-1612495H	EIQLVQSGSELKKPGASVKVSCKASGYPFTNSGMYWVKQAPGQGLEYMGWINTEA GKPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYFCARWGYISDNSYGWFDY WGQGTLVTVSSGGGGSGGGGSEVQLVQSGAEVKKPGSSVKVSCKASGYTFTESYM YWVKQAPGQGLELIGRIDPEDGSTDYVEKFKNKATLTADKSTSTAYMELSSLRSEDT AVYFCARFGARSYFYPMDAWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNAYTQKSLSLSPGK
172	PR-1612495L	ATQLTQSPSSLSASVGDRVTISCRASEGVYSYMHWYQQKPGKQPKLLIYKASNLASG VPSRFSGSGSGTDFTLTISSLQPEDFATYFCHQNWNDPLTFGQGTKLEIKGGSGGGGS GGETVLTQSPATLSLSPGERATLSCRASESVSTLMHWYQQKPGQQPRLLIYGASNLES GVPARFSGSGSGTDFTLTISSLEPEDFAVYFCQQSWNDPWTFGGGTKVEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
173	PR-1612496H	EVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMGVGWIRQPPGKALEWLANIWWD DDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPVDTATYYCARIESSGPKYSFDYW GQGTMVTVSSGGGGSGGGGSEIQLVQSGSELKKPGASVKVSCKASGYTFTNYGMY WVRQAPGQGLEYMGWINTETGKPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDT AVYFCARTNYYYRSYIFYFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNAYTQKSLSLSPGK
174	PR-1612496L	EIVLTQSPGTLSLSPGERATLSCRASSGSIWYSFVSWYQQKPGQAPRLLIYADDQRAS GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYGINIDVVFGGGTKVEIKGGSGGGG SGGATQLTQSPSLSASVGDRVTITCRASESVSTHMHWYQQKPGKQPKLLIYGASNLE SGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCQQSWNDPFTFGQGTKLEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
175	PR-1612498H	EVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMGVGWIRQPPGKALEWLANIWWD DDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPVDTATYYCARIESSGPKYSFDYW GQGTMVTVSSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFSFSKYDMA WFRQAPGKGLEWVASITTSGVGTYYRDSVKGRFTVSRDNAKSTLYLQMNSLRAEDT AVYYCARGYGAMDAWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNAYTQKSLSLSPGK
176	PR-1612498L	EIVLTQSPGTLSLSPGERATLSCRASSGSIWYSFVSWYQQKPGQAPRLLIYADDQRAS GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYGINIDVVFGGGTKVEIKGGSGGGG SGGDIQMTQSPSSLSASVGDRVTITCKASQDIDDYLSWYQQKPGKSPKLVIYAATRL ADGVPSRFSGSGSGTDYTLTISSLQPEDFATYYCLQSSSTPWTFGGGTKVEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
177	PR-1612499H	EVQLVQSGAEVKKPGSSVKVSCKASGYTFTESYMYWVKQAPGQGLELIGRIDPEDG STDYVEKFKNKATLTADKSTSTAYMELSSLRSEDTAVYFCARFGARSYFYPMDAWG QGTTVTVSSGGGGSGGGGSEIQLVQSGSELKKPGASVKVSCKASGYTFTNYGMYWV RQAPGQGLEYMGWINTETGKPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVY FCARTNYYYRSYIFYFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF

		YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNAYTQKSLSLSPGK
178	PR-1612499L	ETVLTQSPATLSLSPGERATLSCRASESVSTLMHWYQQKPGQQPRLLIYGASNLESGV PARFSGSGSGTDFTLTISSLEPEDFAVYFCQQSWNDPWTFGGGTKVEIKGGSGGGGS GGATQLTQSPSLSASVGDRVTITCRASESVSTHMHWYQQKPGKQPKLLIYGASNLES GVPSRFSGSGSGTDFTLTISSLQPEDFATYFCQQSWNDPFTFGQGTKLEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST YSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
179	PR-1612500H	EVQLVQSGAEVKKPGSSVKVSCKASGYTFTESYMYWVKQAPGQGLELIGRIDPEDG STDYVEKFKNKATLTADKSTSTAYMELSSLRSEDTAVYFCARFGARSYFYPMDAWG QGTTVTVSSGGGGSGGGGSEIQLVQSGSELKKPGASVKVSCKASGYTFTNYGMYWV KQAPGQGLEYMGWIDTETGRPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVY FCARWSGDTTGIRGPWFAYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNAYTQKSLSLSPGK
180	PR-1612500L	ETVLTQSPATLSLSPGERATLSCRASESVSTLMHWYQQKPGQQPRLLIYGASNLESGV PARFSGSGSGTDFTLTISSLEPEDFAVYFCQQSWNDPWTFGGGTKVEIKGGSGGGGS GGDIRMTQSPSSLSASVGDRVTIECLASEDIYSDLAWYQQKPGKSPKLLIYNANGLQN GVPSRFSGSGSGTDYSLTISSLQPEDVATYFCQQYNYFPGTFGQGTKLEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
181	PR-1612501H	EVQLVQSGAEVKKPGSSVKVSCKASGYTFTESYMYWVKQAPGQGLELIGRIDPEDG STDYVEKFKNKATLTADKSTSTAYMELSSLRSEDTAVYFCARFGARSYFYPMDAWG QGTTVTVSSGGGGSGGGGSEVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYGMYW VRQAPGQGLEWMGWIDTETGRPTYADDFKGRFTFTADKSTSTAYMELSSLRSEDTA VYYCARWSGDTTGIRGPWFAYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNAYTQKSLSLSPGK
182	PR-1612501L	ETVLTQSPATLSLSPGERATLSCRASESVSTLMHWYQQKPGQQPRLLIYGASNLESGV PARFSGSGSGTDFTLTISSLEPEDFAVYFCQQSWNDPWTFGGGTKVEIKGGSGGGGS GGDIRMTQSPSSLSASVGDRVTITCLASEDIYSDLAWYQQKPGKSPKLLIYNANGLQN GVPSRFSGSGSGTDYTLTISSLQPEDVATYFCQQYNYFPGTFGQGTKLEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
183	PR-1612502H	EVQLVQSGAEVKKPGSSVKVSCKASGYTFTESYMYWVKQAPGQGLELIGRIDPEDG STDYVEKFKNKATLTADKSTSTAYMELSSLRSEDTAVYFCARFGARSYFYPMDAWG QGTTVTVSSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFSFSKYDMAWF RQAPGKGLEWVASITTSGVGTYYRDSVKGRFTVSRDNAKSTLYLQMNSLRAEDTAV YYCARGYGAMDAWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH NAYTQKSLSLSPGK
184	PR-1612502L	ETVLTQSPATLSLSPGERATLSCRASESVSTLMHWYQQKPGQQPRLLIYGASNLESGV PARFSGSGSGTDFTLTISSLEPEDFAVYFCQQSWNDPWTFGGGTKVEIKGGSGGGGS GGDIQMTQSPSSLSASVGDRVTITCKASQDIDDYLSWYQQKPGKSPKLVIYAATRLA DGVPSRFSGSGSGTDYTLTISSLQPEDFATYYCLQSSSTPWTFGGGTKVEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

185	PR-1613183H	EVQLVQSGSELKKPGASVKVSCKASGYTFTDYGMYWVRQAPGQGLEWMGWIDTE TGDPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARTNYYYRNYMFYF DYWGQGTMVTVSSGGGGSGGGGSEVTLRESGPALVKPTQTLTLTCTFSGFSLSTYG MGVGWIRQPPGKALEWLANIWWDDDKYYNPSLKNRLTISKDTSKNQVVLTMTNM DPVDTATYYCARIESSGPKYSFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQ TYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNAYTQKSLSLSPGK
186	PR-1613183L	EIVLTQSPATLSLSPGERATLFCRASQSVSNHMHWYQQKPGQAPRLLIYGASILESGV PARFSGSGSGTDFTLTISSLEPEDFAVYYCQQSWYDPITFGQGTKLEIKGGSGGGGSG GEIVLTQSPGTLSLSPGERATLSCRASSGSIWYSFVSWYQQKPGQAPRLLIYADDQRA SGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYGINIDVVFGGGTKVEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
187	PR-1613184H	EVQLVQSGSELKKPGASVKVSCKASGYTFTDYGMYWVRQAPGQGLEWMGWIDTE TGDPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARTNYYYRNYMFYF DYWGQGTMVTVSSGGGGSGGGGSEVTLRESGPALVKPTQTLTLTCTFSGFSLSTYG MGVGWIRQPPGKALEWLANIWWDDDKYYNPSLKNRLTISKDTSKNQVVLTMTNM DPVDTATYYCARIESIGTTYSFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNAYTQKSLSLSPGK
188	PR-1613184L	EIVLTQSPATLSLSPGERATLFCRASQSVSNHMHWYQQKPGQAPRLLIYGASILESGV PARFSGSGSGTDFTLTISSLEPEDFAVYYCQQSWYDPITFGQGTKLEIKGGSGGGGSG GEFVLTQSPGTLSLSPGERATLSCERSSGDIGDSYVSWYQQKPGQAPRLVIYADDQRP SGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
189	PR-1613185H	EVQLVQSGSELKKPGASVKVSCKASGYTFTDYGMYWVRQAPGQGLEWMGWIDTE TGDPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARTNYYYRNYMFYF DYWGQGTMVTVSSGGGGSGGGGSEVQLVQSGAEVKKPGSSVKVSCKASGYTFTES YMYWVKQAPGQGLELIGRIDPEDGSTDYVEKFKNKATLTADKSTSTAYMELSSLRS EDTAVYFCARFGARSYFYPMDAWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNAYTQKSLSLSPGK
190	PR-1613185L	EIVLTQSPATLSLSPGERATLFCRASQSVSNHMHWYQQKPGQAPRLLIYGASILESGV PARFSGSGSGTDFTLTISSLEPEDFAVYYCQQSWYDPITFGQGTKLEIKGGSGGGGSG GETVLTQSPATLSLSPGERATLSCRASESVSTLMHWYQQKPGQQPRLLIYGASNLESG VPARFSGSGSGTDFTLTISSLEPEDFAVYFCQQSWNDPWTFGGGTKVEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST YSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
191	PR-1613186H	EVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMGVGWIRQPPGKALEWLANIWWD DDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPVDTATYYCARIESSGPKYSFDYW GQGTMVTVSSGGGGSGGGGSEVQLVQSGSELKKPGASVKVSCKASGYTFTDYGMY WVRQAPGQGLEWMGWIDTETGDPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDT AVYYCARTNYYYRNYMFYFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTC

		LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNAYTQKSLSLSPGK
192	PR-1613186L	EIVLTQSPGTLSLSPGERATLSCRASSGSIWYSFVSWYQQKPGQAPRLLIYADDQRAS GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYGINIDVVFGGGTKVEIKGGSGGGG SGGEIVLTQSPATLSLSPGERATLFCRASQSVSNHMHWYQQKPGQAPRLLIYGASILE SGVPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQSWYDPITFGQGTKLEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
193	PR-1613187H	EVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMGVGWIRQPPGKALEWLANIWWD DDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPVDTATYYCARIESIGTTYSFDYW GQGTMVTVSSGGGGSGGGGSEVQLVQSGSELKKPGASVKVSCKASGYTFTDYGMY WVRQAPGQGLEWMGWIDTETGDPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDT AVYYCARTNYYYRNYMFYFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNAYTQKSLSLSPGK
194	PR-1613187L	EFVLTQSPGTLSLSPGERATLSCERSSGDIGDSYVSWYQQKPGQAPRLVIYADDQRPS GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKGGSGGGG SGGEIVLTQSPATLSLSPGERATLFCRASQSVSNHMHWYQQKPGQAPRLLIYGASILE SGVPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQSWYDPITFGQGTKLEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
195	PR-1613188H	EVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMGVGWIRQPPGKALEWLANIWWD DDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPVDTATYYCARIESIGTTYSFDYW GQGTMVTVSSGGGGSGGGGSEIQLVQSGSELKKPGASVKVSCKASGYTFTNYGMY WVRQAPGQGLEYMGWINTETGKPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDT AVYFCARTNYYYRSYIFYFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNAYTQKSLSLSPGK
196	PR-1613188L	EFVLTQSPGTLSLSPGERATLSCERSSGDIGDSYVSWYQQKPGQAPRLVIYADDQRPS GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYDINIDIVFGGGTKVEIKGGSGGGG SGGATQLTQSPSLSASVGDRVTITCRASESVSTHMHWYQQKPGKQPKLLIYGASNLE SGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCQQSWNDPFTFGQGTKLEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
197	PR-1613189H	EVQLVQSGAEVKKPGSSVKVSCKASGYTFTESYMYWVKQAPGQGLELIGRIDPEDG STDYVEKFKNKATLTADKSTSTAYMELSSLRSEDTAVYFCARFGARSYFYPMDAWG QGTTVTVSSGGGGSGGGGSEVQLVQSGSELKKPGASVKVSCKASGYTFTDYGMYW VRQAPGQGLEWMGWIDTETGDPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTA VYYCARTNYYYRNYMFYFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNAYTQKSLSLSPGK
198	PR-1613189L	ETVLTQSPATLSLSPGERATLSCRASESVSTLMHWYQQKPGQQPRLLIYGASNLESGV PARFSGSGSGTDFTLTISSLEPEDFAVYFCQQSWNDPWTFGGGTKVEIKGGSGGGGS GGEIVLTQSPATLSLSPGERATLFCRASQSVSNHMHWYQQKPGQAPRLLIYGASILES GVPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQSWYDPITFGQGTKLEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

199	PR-1613190H	EVQLVQSGAEVKKPGSSVKVSCKASGYTFTESYMYWVKQAPGQGLELIGRIDPEDG STDYVEKFKNKATLTADKSTSTAYMELSSLRSEDTAVYFCARFGARSYFYPMDAWG QGTTVTVSSGGGGSGGGGSEIQLVQSGSELKKPGASVKVSCKASGYPFTNSGMYWV KQAPGQGLEYMGWINTEAGKPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAV YFCARWGYISDNSYGWFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNAYTQKSLSLSPGK
200	PR-1613190L	ETVLTQSPATLSLSPGERATLSCRASESVSTLMHWYQQKPGQQPRLLIYGASNLESGV PARFSGSGSGTDFTLTISSLEPEDFAVYFCQQSWNDPWTFGGGTKVEIKGGSGGGGS GGATQLTQSPSSLSASVGDRVTISCRASEGVYSYMHWYQQKPGKQPKLLIYKASNLA SGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCHQNWNDPLTFGQGTKLEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
201	PR-1629646H	EIQLVQSGSELKKPGASVKVSCKASGYTFTNYGMYWVKQAPGQGLEYMGWIDTET GRPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYFCARWSGDTTGIRGPWFA YWGQGTLVTVSSASTKGPEVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMGVGWI RQPPGKALEWLANIWWDDDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPVDTAT YYCARIESSGPKYSFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE ALHNAYTQKSLSLSPGK
202	PR-1629646L	DIRMTQSPSSLSASVGDRVTIECLASEDIYSDLAWYQQKPGKSPKLLIYNANGLQNGV PSRFSGSGSGTDYSLTISSLQPEDVATYFCQQYNYFPGTFGQGTKLEIKRTVAAPSVFI FPPEIVLTQSPGTLSLSPGERATLSCRASSGSIWYSFVSWYQQKPGQAPRLLIYADDQR ASGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYGINIDVVFGGGTKVEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
203	PR-1629647H	EVQLVESGGGLVQPGGSLRLSCAASGFSFSKYDMAWFRQAPGKGLEWVASITTSGV GTYYRDSVKGRFTVSRDNAKSTLYLQMNSLRAEDTAVYYCARGYGAMDAWGQGT TVTVSSASTKGPEVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMGVGWIRQPPGKA LEWLANIWWDDDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPVDTATYYCARIE SSGPKYSFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK VDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNA YTQKSLSLSPGK
204	PR-1629647L	DIQMTQSPSSLSASVGDRVTITCKASQDIDDYLSWYQQKPGKSPKLVIYAATRLADG VPSRFSGSGSGTDYTLTISSLQPEDFATYYCLQSSSTPWTFGGGTKVEIKRTVAAPSVF IFPPEIVLTQSPGTLSLSPGERATLSCRASSGSIWYSFVSWYQQKPGQAPRLLIYADDQ RASGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYGINIDVVFGGGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
205	PR-1629648H	EIQLVQSGSELKKPGASVKVSCKASGYTFTNYGMYWVKQAPGQGLEYMGWIDTET GRPTYADDFKGRFVFSLDTSVSTAYLQISSLKAEDTAVYFCARWSGDTTGIRGPWFA YWGQGTLVTVSSASTKGPSVFPLAPEVTLRESGPALVKPTQTLTLTCTFSGFSLSTYG MGVGWIRQPPGKALEWLANIWWDDDKYYNPSLKNRLTISKDTSKNQVVLTMTNM DPVDTATYYCARIESSGPKYSFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQ TYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT

		CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNAYTQKSLSLSPGK
206	PR-1629648L	DIRMTQSPSSLSASVGDRVTIECLASEDIYSDLAWYQQKPGKSPKLLIYNANGLQNGV PSRFSGSGSGTDYSLTISSLQPEDVATYFCQQYNYFPGTFGQGTKLEIKRTVAAPEIVL TQSPGTLSLSPGERATLSCRASSGSIWYSFVSWYQQKPGQAPRLLIYADDQRASGIPD RFSGSGSGTDFTLTISRLEPEDFAVYYCQSYGINIDVVFGGGTKVEIKRTVAAPSVFIFP PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
207	PR-1629649H	EVQLVESGGGLVQPGGSLRLSCAASGFSFSKYDMAWFRQAPGKGLEWVASITTSGV GTYYRDSVKGRFTVSRDNAKSTLYLQMNSLRAEDTAVYYCARGYGAMDAWGQGT TVTVSSASTKGPSVFPLAPEVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGMGVGWI RQPPGKALEWLANIWWDDDKYYNPSLKNRLTISKDTSKNQVVLTMTNMDPVDTAT YYCARIESSGPKYSFDYWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE ALHNAYTQKSLSLSPGK
208	PR-1629649L	DIQMTQSPSSLSASVGDRVTITCKASQDIDDYLSWYQQKPGKSPKLVIYAATRLADG VPSRFSGSGSGTDYTLTISSLQPEDFATYYCLQSSSTPWTFGGGTKVEIKRTVAAPEIV LTQSPGTLSLSPGERATLSCRASSGSIWYSFVSWYQQKPGQAPRLLIYADDQRASGIP DRFSGSGSGTDFTLTISRLEPEDFAVYYCQSYGINIDVVFGGGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTY SLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Example 18: PR-1610561 Cell Lines

[0470] Chimeric, humanized, and affinity matured antibodies, and DVD-Ig binding proteins were expressed using pHybE vectors. Transient expression of PR-1610561 in HEK cells was also achieved using a vector similar to pHybE-hCg1,z,non-a,mut(234,235) V2. See US Patent No. 8,187,836.

[0471] CHO cell lines producing PR-1610561 have been generated. The growth and productivity of the CHO cell lines were similar to those of other DVD-Ig molecules. All cell lines passed a screening for acceptable product quality by MS, SEC, and CIEX. CHO cell lines were produced using pBJ and pCD plasmid vectors encoding the amino acid sequences of PR-1610561. See US 2014/0295497.

Example 19: Epitope Binning

[0472] Antibodies and binding proteins disclosed herein are tested in a label-free cell-based competition assay in order to determine which antibodies and binding proteins are capable of binding to the same antigen (e.g., VEGF, PDGF, or one of their receptors) simultaneously. If antibodies or binding proteins are not able to bind simultaneously (therefore possibly competing for the same or similar epitope), those antibodies or binding proteins are assigned to the same "epitope bin." If antibodies or binding proteins are capable of binding simultaneously and therefore do not compete for antigen binding, those antibodies or binding proteins are assigned to different epitope bins.

Incorporation by Reference

[0473] The contents of all cited references (including literature references, patents, patent applications, and websites) that maybe cited throughout this application are hereby expressly incorporated by reference in their entirety for any purpose, as are the references cited therein. To the extent those references contradict or are inconsistent with any statements in this application, the text of the application will control. The disclosure will employ, unless otherwise indicated, conventional techniques of immunology, molecular biology and cell biology, and pathology, which are well known in the art.

Equivalents

[0474] The invention may be embodied in other specific forms without departing from the spirit or essential characteristics thereof. The foregoing embodiments are therefore to be considered in all respects illustrative rather than limiting of the inventions described herein. Scope of the invention is thus indicated by the appended claims rather than by the foregoing description, and all changes that come within the meaning and range of equivalency of the claims are therefore intended to be embraced herein.

We claim:

1. A binding protein comprising first and second polypeptide chains, each independently comprising VD1-(X1)n-VD2-C-X2, wherein

VD1 is a first variable domain;

VD2 is a second variable domain;

C is a constant domain;

X1 is a linker;

X2 is an Fc region; and

n is 0 or 1,

wherein the VD1 domains on the first and second polypeptide chains form a first functional target binding site and the VD2 domains on the first and second polypeptide chains form a second functional target binding site,

wherein the binding protein is capable of binding VEGF, wherein the variable domains that form a functional target binding site for VEGF comprise:

(i) a CDR-H1 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10} (SEQ ID NO: >>), wherein

X_1 is G;

X_2 is Y;

X_3 is T;

X_4 is F;

X_5 is T, Q, D, E, N, A, G, H, K, M, L, R, I, Y, or V;

X_6 is N, S, K, Y, T, M, G, A, I, L, E, P, Q, or F;

X_7 is Y;

X_8 is G, S, D, K, C, V, E, L, W, P, Y, M, N, or T;

X_9 is M; and

X_{10} is Y;

(ii) a CDR-H2 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-X_{15}-X_{16}-X_{17} (SEQ ID NO: >>), wherein

X_1 is W;

X_2 is I;

X_3 is N;

X_4 is T;

X_5 is E, Y, L, V, W, A, Q, H, G, K, N, M, T, or P;

X_6 is T;

X_7 is G;

X_8 is K, N, D, T, P, W, Y, V, S, M, A, I, G, R, or L;

X_9 is P;

X_{10} is T, I, M, K, A, N, P, L, V, W, D, Y, G, or E;

X_{11} is Y;

X_{12} is A;

X_{13} is D, Y, or H;

X_{14} is D;

X_{15} is F;

X_{16} is K or N; and

X_{17} is G;

(iii) a CDR-H3 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14} (SEQ ID NO: >>), wherein

X_1 is T, Y, G, I, S, K, N, P, L, W, M, F, R, or Q;

X_2 is N, H, I, T, D, F, L, E, V, Y, A, G, W, Q, or R;

X_3 is Y;

X_4 is Y;

X_5 is Y;

X_6 is R, S, N, E, M, L, T, W, Q, G, I, A, C, or V;

X_7 is S, N, T, K, M, Y, C, I, F, L, D, W, X, or V;

X_8 is Y;

X_9 is I, L, N, T, V, A, R, F, D, or S;

X_{10} is F;

X_{11} is Y;

X_{12} is F;

X_{13} is D; and

X_{14} is Y;

(iv) a CDR-L1 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11} (SEQ ID NO: >>), wherein

X_1 is R;

X_2 is A;

X_3 is S;

X_4 is E;

X_5 is S;

X_6 is V;

X_7 is S, N, D, T, R, H, E, I, L, Q, C, M, Y, K, or V;

X_8 is T, S, R, A, E, D, M, P, Y, I, W, or F;

X_9 is H, A, D, C, P, R, Y, L, Q, or K;

X_{10} is M; and

X_{11} is H, A, or P;

(v) a CDR-L2 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7 (SEQ ID NO: >>), wherein;

X_1 is G, W, V, I, E, S, or D;

X_2 is A;

X_3 is S;

X_4 is N, H, Y, M, T, F, V, R, Q, A, S, E, G, C, D, or P;

X_5 is L;

X_6 is E; and

X_7 is S or Y;

and

(vi) a CDR-L3 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9 (SEQ ID NO: >>), wherein

X_1 is Q;

X_2 is Q;

X_3 is S, C, G, I, W, R, N, A, Y, K, Q, or F;

X_4 is W, C, L, G, E, or S;

X_5 is N, I, T, D, G, M, S, H, A, R, V, L, F, K, or Q;

X_6 is D, N, Y, A, L, M, P, G, H, F, or K;

X_7 is P;

X_8 is F, M, G, Y, A, W, S, V, C, or P; and

X_9 is T.

2. The binding protein of claim 1, wherein the binding protein is also capable of binding PDGF.

3. The binding protein of claim 2, wherein the variable domains that form a functional target binding site for PDGF comprise:

(i) a CDR-H1 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12} (SEQ ID NO: >>), wherein

X_1 is G;

X_2 is F;

X_3 is S, I, or R;

X_4 is L;

X_5 is S, Y, A, D, T, M, R, L, C, F, W, or P;

X_6 is T;

X_7 is Y or S;

X_8 is G or E;

X_9 is M or V;

X_{10} is G, S, or R;

X_{11} is V or I; and

X_{12} is G, D, L, A, C, V, Y, R, T, E, or S;

(ii) a CDR-H2 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-X_{15}-X_{16} (SEQ ID NO: >>), wherein

X_1 is N or L;

X_2 is I;

X_3 is W, D, C, or G;

X_4 is W or C;

X_5 is D, Y, N, H, V, E, I, P, A, C, or G;

X_6 is D, G, N, or H;

X_7 is D, E, G, V, A, H, Y, N, Q, S, or L;

X_8 is K, E, T, I, Q, V, N, R, Y, L, M or C;

X_9 is Y, H, C, D, N, S, A, F, or G;

X_{10} is Y;

X_{11} is N or S;

X_{12} is P, L, or T;

X_{13} is S;

X_{14} is L;

X_{15} is K or N; and

X_{16} is N, S, or T;

(iii) a CDR-H3 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12} (SEQ ID NO: >>), wherein

X_1 is I, Y, N, L, M, V, R, K, F, C, T, or E;

X_2 is E, Q, V, K, Y, L, D, G, A, M, R, or S;

X_3 is S, T, A, Y, W, P, L, V, E, K, F, or C;

X_4 is I, G, S, M, V, L, F, N, D, H, Y, T, R, Q, K, E, or P;

X_5 is G, W, P, F, C, Y, A, E, L, V, S, D, or R;

X_6 is T, P, W, R, I, F, A, M, Y, S, L, G, D, K, V, N, or E;

X_7 is T, N, S, K, R, M, A, E, I, V, L, W, P, or Q;

X_8 is Y;

X_9 is S, E, D, Y, A, C, N, M, W, T, Q, G, I, L, or P;

X_{10} is F;

X_{11} is D or Y; and

X_{12} is Y;

(iv) a CDR CDR-L1 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13} (SEQ ID NO: >>), wherein

X_1 is E, R, or K;

X_2 is R, A, or E;

X_3 is S or Y;

X_4 is S;

X_5 is G, C, V, or S;

X_6 is D, S, or Y;

X_7 is I, N, T, or M;

X_8 is G, W, Y, S, M, H, D, R, E, N, C, A, L, V, F, T, Q, or K;

X_9 is D, Y, Q, N, H, G, E, S, K, F, R, L, C, A, or P;

X_{10} is S, T, Y, M, K, A, C, F, L, E, W, D, P, or G;

X_{11} is Y, F, L, R, H, N, C, A, D, S, or T;

X_{12} is V, F, or S; and

X_{13} is S or P;

(v) a CDR-L2 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7 (SEQ ID NO: >>), wherein

X_1 is A, G, S, W, T, L, V, F, N, P, E, or D;

X_2 is D, Y, A, or V;

X_3 is D or G;

X_4 is Q, L, R, H, W, Y, M, K, D, A, E, N, V, S, F, or P;

X_5 is R, Q, or P;

X_6 is P or A; and

X_7 is S, I, T, R, or G;

and

(vi) a CDR-L3 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10} (SEQ ID NO: >>), wherein

X_1 is Q or K;

X_2 is S, P, Q, or H;

X_3 is Y;

X_4 is D or G;

X_5 is I, L, V, E, T, S, Q, R, N, K, G, A, C, or F;

X_6 is N, F, D, E, T, I, Y, C, V, S, R, A, L, G, H, or K;

X_7 is I, T, S, V, D, R, E, M, L, P, F, N, or K;

X_8 is D, N, P, A, Y, G, H, E, V, L, Q, or T;

X_9 is I, V, L, G, T, S, N, F, A, H, R, or Q; and

X_{10} is V or T.

4. The binding protein of any one of claims 1-3, further comprising human framework sequences.

5. A binding protein comprising first and second polypeptide chains, each independently comprising VD1-(X1)n-VD2-C-X2, wherein

VD1 is a first variable domain;

VD2 is a second variable domain;

C is a constant domain;

X1 is a linker;

X2 is an Fc region; and

n is 0 or 1,

wherein the VD1 domains on the first and second polypeptide chains form a first functional target binding site and the VD2 domains on the first and second polypeptide chains form a second functional target binding site,

wherein the binding protein is capable of binding PDGF, wherein the variable domains that form a functional target binding site for PDGF comprise:

(i) a CDR-H1 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12} (SEQ ID NO: >>), wherein

X_1 is G;

X_2 is F;

X_3 is S, I, or R;

X_4 is L;

X_5 is S, Y, A, D, T, M, R, L, C, F, W, or P;

X_6 is T;

X_7 is Y or S;

X_8 is G or E;

X_9 is M or V;

X_{10} is G, S, or R;

X_{11} is V or I; and

X_{12} is G, D, L, A, C, V, Y, R, T, E, or S;

(ii) a CDR-H2 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-X_{15}-X_{16} (SEQ ID NO: >>), wherein

X_1 is N or L;

X_2 is I;

X_3 is W, D, C, or G;

X_4 is W or C;

X_5 is D, Y, N, H, V, E, I, P, A, C, or G;

X_6 is D, G, N, or H;

X_7 is D, E, G, V, A, H, Y, N, Q, S, or L;

X_8 is K, E, T, I, Q, V, N, R, Y, L, M or C;

X_9 is Y, H, C, D, N, S, A, F, or G;

X_{10} is Y;

X_{11} is N or S;

X_{12} is P, L, or T;

X_{13} is S;

X_{14} is L;

X_{15} is K or N; and

X_{16} is N, S, or T;

(iii) a CDR-H3 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12} (SEQ ID NO: >>), wherein

X_1 is I, Y, N, L, M, V, R, K, F, C, T, or E;

X_2 is E, Q, V, K, Y, L, D, G, A, M, R, or S;

X_3 is S, T, A, Y, W, P, L, V, E, K, F, or C;

X_4 is I, G, S, M, V, L, F, N, D, H, Y, T, R, Q, K, E, or P;

X_5 is G, W, P, F, C, Y, A, E, L, V, S, D, or R;

X_6 is T, P, W, R, I, F, A, M, Y, S, L, G, D, K, V, N, or E;

X_7 is T, N, S, K, R, M, A, E, I, V, L, W, P, or Q;

X_8 is Y;

X_9 is S, E, D, Y, A, C, N, M, W, T, Q, G, I, L, or P;

X_{10} is F;

X_{11} is D or Y; and

X_{12} is Y;

(iv) a CDR CDR-L1 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13} (SEQ ID NO: >>), wherein

X_1 is E, R, or K;

X_2 is R, A, or E;

X_3 is S or Y;

X_4 is S;

X_5 is G, C, V, or S;

X_6 is D, S, or Y;

X_7 is I, N, T, or M;

X_8 is G, W, Y, S, M, H, D, R, E, N, C, A, L, V, F, T, Q, or K;

X_9 is D, Y, Q, N, H, G, E, S, K, F, R, L, C, A, or P;

X_{10} is S, T, Y, M, K, A, C, F, L, E, W, D, P, or G;

X_{11} is Y, F, L, R, H, N, C, A, D, S, or T;

X_{12} is V, F, or S; and

X_{13} is S or P;

(v) a CDR-L2 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7 (SEQ ID NO: >>), wherein

X_1 is A, G, S, W, T, L, V, F, N, P, E, or D;

X_2 is D, Y, A, or V;

X_3 is D or G;

X_4 is Q, L, R, H, W, Y, M, K, D, A, E, N, V, S, F, or P;

X_5 is R, Q, or P;

X_6 is P or A; and

X_7 is S, I, T, R, or G;

and

(vi) a CDR-L3 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10} (SEQ ID NO: >>), wherein

X_1 is Q or K;

X_2 is S, P, Q, or H;

X_3 is Y;

X_4 is D or G;

X_5 is I, L, V, E, T, S, Q, R, N, K, G, A, C, or F;

X_6 is N, F, D, E, T, I, Y, C, V, S, R, A, L, G, H, or K;

X_7 is I, T, S, V, D, R, E, M, L, P, F, N, or K;

X_8 is D, N, P, A, Y, G, H, E, V, L, Q, or T;

X_9 is I, V, L, G, T, S, N, F, A, H, R, or Q; and

X_{10} is V or T.

6. The binding protein of claim 5, wherein the binding protein is also capable of binding VEGF.

7. The binding protein of claim 6, wherein the variable domains that form a functional target binding site for VEGF comprise:

(i) a CDR-H1 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10} (SEQ ID NO: >>), wherein

X_1 is G;

X_2 is Y;

X_3 is T;

X_4 is F;

X_5 is T, Q, D, E, N, A, G, H, K, M, L, R, I, Y, or V;

X_6 is N, S, K, Y, T, M, G, A, I, L, E, P, Q, or F;

X_7 is Y;

X_8 is G, S, D, K, C, V, E, L, W, P, Y, M, N, or T;

X_9 is M; and

X_{10} is Y;

(ii) a CDR-H2 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-X_{15}-X_{16}-X_{17} (SEQ ID NO: >>), wherein

X_1 is W;

X_2 is I;

X_3 is N;

X_4 is T;

X_5 is E, Y, L, V, W, A, Q, H, G, K, N, M, T, or P;

X_6 is T;

X_7 is G;

X_8 is K, N, D, T, P, W, Y, V, S, M, A, I, G, R, or L;

X_9 is P;

X_{10} is T, I, M, K, A, N, P, L, V, W, D, Y, G, or E;

X_{11} is Y;

X_{12} is A;

X_{13} is D, Y, or H;

X_{14} is D;

X_{15} is F;

X_{16} is K or N; and

X_{17} is G;

(iii) a CDR-H3 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14} (SEQ ID NO: >>), wherein

X_1 is T, Y, G, I, S, K, N, P, L, W, M, F, R, or Q;

X_2 is N, H, I, T, D, F, L, E, V, Y, A, G, W, Q, or R;

X_3 is Y;

X_4 is Y;

X_5 is Y;

X_6 is R, S, N, E, M, L, T, W, Q, G, I, A, C, or V;

X_7 is S, N, T, K, M, Y, C, I, F, L, D, W, X, or V;

X_8 is Y;

X_9 is I, L, N, T, V, A, R, F, D, or S;

X_{10} is F;

X_{11} is Y;

X_{12} is F;

X_{13} is D; and

X_{14} is Y;

(iv) a CDR-L1 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11} (SEQ ID NO: >>), wherein

X_1 is R;

X_2 is A;

X_3 is S;

X_4 is E;

X_5 is S;

X_6 is V;

X_7 is S, N, D, T, R, H, E, I, L, Q, C, M, Y, K, or V;

X_8 is T, S, R, A, E, D, M, P, Y, I, W, or F;

X_9 is H, A, D, C, P, R, Y, L, Q, or K;

X_{10} is M; and

X_{11} is H, A, or P;

(v) a CDR-L2 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7 (SEQ ID NO: >>), wherein;

X_1 is G, W, V, I, E, S, or D;

X_2 is A;

X_3 is S;

X_4 is N, H, Y, M, T, F, V, R, Q, A, S, E, G, C, D, or P;

X_5 is L;

X_6 is E; and

X_7 is S or Y;

and

(vi) a CDR-L3 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9 (SEQ ID NO: >>), wherein

X_1 is Q;

X_2 is Q;

X_3 is S, C, G, I, W, R, N, A, Y, K, Q, or F;

X_4 is W, C, L, G, E, or S;

X_5 is N, I, T, D, G, M, S, H, A, R, V, L, F, K, or Q;

X_6 is D, N, Y, A, L, M, P, G, H, F, or K;

X_7 is P;

X_8 is F, M, G, Y, A, W, S, V, C, or P; and

X_9 is T.

8. The binding protein of any one of claims 5-7, further comprising human framework sequences.

9. A binding protein comprising first and second polypeptide chains, each independently comprising VD1-(X1)n-VD2-C-X2, wherein

VD1 is a first variable domain;

VD2 is a second variable domain;

C is a constant domain;

X1 is a linker;

X2 is an Fc region; and

n is 0 or 1,

wherein the VD1 domains on the first and second polypeptide chains form a first functional target binding site and the VD2 domains on the first and second polypeptide chains form a second functional target binding site,

wherein the binding protein is capable of binding VEGF, wherein the variable domains that form a functional target binding site for VEGF comprise a CDR set of heavy chain CDRs 1-3 and paired light chain CDRs 1-3 selected from any of the CDR sets listed in Tables A, 27 or 38-42.

10. The binding protein of claim 9, wherein the variable domains that form a functional target binding site for VEGF comprise a heavy chain and paired light chain selected from any of those listed in Tables A, 27 or 38-42.
11. The binding protein of claim 9 or 10, wherein the binding protein is also capable of binding PDGF.
12. The binding protein of claim 9, wherein the variable domains that form a functional target binding site for PDGF comprise a CDR set of heavy chain CDRs 1-3 and paired light chain CDRs 1-3 selected from any of the CDR sets listed in Tables A, 28 or 46-50.
13. The binding protein of claim 9 or 10, wherein the variable domains that form a functional target binding site for PDGF comprise a heavy chain and paired light chain selected from any of those listed in Tables A, 28 or 46-50.
14. A binding protein comprising first and second polypeptide chains, each independently comprising VD1-(X1)n-VD2-C-X2, wherein

VD1 is a first variable domain;

VD2 is a second variable domain;

C is a constant domain;

X1 is a linker;

X2 is an Fc region; and

n is 0 or 1,

wherein the VD1 domains on the first and second polypeptide chains form a first functional target binding site and the VD2 domains on the first and second polypeptide chains form a second functional target binding site,

wherein the binding protein is capable of binding PDGF, wherein the variable domains that form a functional target binding site for PDGF comprise a CDR set of heavy chain CDRs 1-3 and paired light chain CDRs 1-3 selected from any of the CDR sets listed in Tables A, 28 or 46-50.

15. The binding protein of claim 14, wherein the variable domains that form a functional target binding site for PDGF comprise a heavy chain and paired light chain selected from any of those listed in Tables A, 28 or 46-50.
16. The binding protein of claim 14 or 15, wherein the binding protein is also capable of binding VEGF.
17. The binding protein of claim 14, wherein the variable domains that form a functional target binding site for VEGF comprise a CDR set of heavy chain CDRs 1-3 and paired light chain CDRs 1-3 selected from any of the CDR sets listed in Tables A, 27 or 38-42.
18. The binding protein of claim 14 or 15, wherein the variable domains that form a functional target binding site for VEGF comprise a heavy chain and paired light chain selected from any of those listed in Tables A, 27 or 38-42.
19. A binding protein comprising first and second polypeptide chains, each independently comprising VD1-(X1)n-VD2-C-X2, wherein

VD1 is a first variable domain;

VD2 is a second variable domain;

C is a constant domain;

X1 is a linker;

X2 is an Fc region; and

n is 0 or 1,

wherein the VD1 domains on the first and second polypeptide chains form a first functional target binding site and the VD2 domains on the first and second polypeptide chains form a second functional target binding site,

wherein the binding protein is capable of binding VEGF and PDGF, wherein

a. the variable domains that form a functional target binding site for VEGF comprise:
CDRs 1-3 from SEQ ID NO: 17 and CDRs-1-3 from SEQ ID NO: 18,
CDRs 1-3 from SEQ ID NO: 19 and CDRs-1-3 from SEQ ID NO: 20,
CDRs 1-3 from SEQ ID NO: 21 and CDRs-1-3 from SEQ ID NO: 22,
CDRs 1-3 from SEQ ID NO: 23 and CDRs-1-3 from SEQ ID NO: 24,
CDRs 1-3 from SEQ ID NO: 25 and CDRs-1-3 from SEQ ID NO: 26,
CDRs 1-3 from SEQ ID NO: 27 and CDRs-1-3 from SEQ ID NO: 28,
CDRs 1-3 from SEQ ID NO: 29 and CDRs-1-3 from SEQ ID NO: 30,
CDRs 1-3 from SEQ ID NO: 31 and CDRs-1-3 from SEQ ID NO: 32,
CDRs 1-3 from SEQ ID NO: 33 and CDRs-1-3 from SEQ ID NO: 34,
CDRs 1-3 from SEQ ID NO: 35 and CDRs-1-3 from SEQ ID NO: 36,

CDRs 1-3 from SEQ ID NO: 37 and CDRs-1-3 from SEQ ID NO: 38,
CDRs 1-3 from SEQ ID NO: 39 and CDRs-1-3 from SEQ ID NO: 40,
CDRs 1-3 from SEQ ID NO: 41 and CDRs-1-3 from SEQ ID NO: 42, or
CDRs 1-3 from SEQ ID NO: 43 and CDRs-1-3 from SEQ ID NO: 44, and

b. the variable domains that form a functional target binding site for PDGF comprise:
CDRs 1-3 from SEQ ID NO: 1 and CDRs-1-3 from SEQ ID NO: 2,
CDRs 1-3 from SEQ ID NO: 3 and CDRs-1-3 from SEQ ID NO: 4,
CDRs 1-3 from SEQ ID NO: 5 and CDRs-1-3 from SEQ ID NO: 6,
CDRs 1-3 from SEQ ID NO: 7 and CDRs-1-3 from SEQ ID NO: 8,
CDRs 1-3 from SEQ ID NO: 9 and CDRs-1-3 from SEQ ID NO: 10,
CDRs 1-3 from SEQ ID NO: 11 and CDRs-1-3 from SEQ ID NO: 12,
CDRs 1-3 from SEQ ID NO: 13 and CDRs-1-3 from SEQ ID NO: 14,
CDRs 1-3 from SEQ ID NO: 15 and CDRs-1-3 from SEQ ID NO: 16, or
CDRs 1-3 from SEQ ID NO: 211 and CDRs-1-3 from SEQ ID NO: 212.

20. A binding protein comprising first and second polypeptide chains, each independently comprising VD1-(X1)n-VD2-C-X2, wherein

VD1 is a first variable domain;
VD2 is a second variable domain;
C is a constant domain;
X1 is a linker;
X2 is an Fc region; and
n is 0 or 1,

wherein the VD1 domains on the first and second polypeptide chains form a first functional target binding site and the VD2 domains on the first and second polypeptide chains form a second functional target binding site, and wherein the binding protein is capable of binding VEGF and PDGF, wherein

a. the variable domains that form a functional target binding site for VEGF comprise a sequence selected from the group consisting of SEQ ID NO: 17-44 and
b. the variable domains that form a functional target binding site for PDGF comprise a sequence selected from the group consisting of SEQ ID NO: 1-16, 211, and 212.

21. The binding protein of any one of claims 19-20, wherein:

a. the variable domains that form a functional target binding site for VEGF comprise:
SEQ ID NO: 17 and SEQ ID NO: 18,
SEQ ID NO: 19 and SEQ ID NO: 20,
SEQ ID NO: 21 and SEQ ID NO: 22,

SEQ ID NO: 23 and SEQ ID NO: 24,
SEQ ID NO: 25 and SEQ ID NO: 26,
SEQ ID NO: 27 and SEQ ID NO: 28,
SEQ ID NO: 29 and SEQ ID NO: 30,
SEQ ID NO: 31 and SEQ ID NO: 32,
SEQ ID NO: 33 and SEQ ID NO: 34,
SEQ ID NO: 35 and SEQ ID NO: 36,
SEQ ID NO: 37 and SEQ ID NO: 38,
SEQ ID NO: 39 and SEQ ID NO: 40,
SEQ ID NO: 41 and SEQ ID NO: 42, or
SEQ ID NO: 43 and SEQ ID NO: 44, and

b. the variable domains that form a functional target binding site for PDGF comprise:

SEQ ID NO: 1 and SEQ ID NO: 2,
SEQ ID NO: 3 and SEQ ID NO: 4,
SEQ ID NO: 5 and SEQ ID NO: 6,
SEQ ID NO: 7 and SEQ ID NO: 8,
SEQ ID NO: 9 and SEQ ID NO: 10,
SEQ ID NO: 11 and SEQ ID NO: 12,
SEQ ID NO: 13 and SEQ ID NO: 14,
SEQ ID NO: 15 and SEQ ID NO: 16, or
SEQ ID NO: 211 and SEQ ID NO: 212.

22. The binding protein of any one of claims 1-21, wherein the first polypeptide chain comprises a first VD1-(X1)n-VD2-C-X2, wherein

VD1 is a first heavy chain variable domain;
VD2 is a second heavy chain variable domain;
C is a heavy chain constant domain;
X1 is a linker;
X2 is an Fc;
n is 0 or 1, and

wherein the second polypeptide chain comprises a second VD1-(X1)n-VD2-C, wherein

VD1 is a first light chain variable domain;
VD2 is a second light chain variable domain;
C is a light chain constant domain;
X1 is a linker;
n is 0 or 1; and
the second polypeptide chain does not comprise an Fc,

wherein the VD1 domains on the first and second polypeptide chains form a first functional target binding site and the VD2 domains on the first and second polypeptide chains form a second functional target binding site.

23. The binding protein of any one of claims 1-22, wherein the X1 linkers on the first and second polypeptide chains independently comprise any one or more of the sequences listed in Table 55.

24. The binding protein of any one of claims 19-22, wherein the binding protein is capable of binding VEGF and PDGF, and wherein the binding protein comprises any one of:

PR-1563988 (comprising SEQ ID NOs: 45 and 46),
PR-1563990 (comprising SEQ ID NOs: 47 and 48),
PR-1563998 (comprising SEQ ID NOs: 49 and 50),
PR-1564009 (comprising SEQ ID NOs: 51 and 52),
PR-1564010 (comprising SEQ ID NOs: 53 and 54),
PR-1564011 (comprising SEQ ID NOs: 55 and 56),
PR-1564012 (comprising SEQ ID NOs: 57 and 58),
PR-1564013 (comprising SEQ ID NOs: 59 and 60),
PR-1564896 (comprising SEQ ID NOs: 209 and 65),
PR-1565031 (comprising SEQ ID NOs: 76 and 77),
PR-1565032 (comprising SEQ ID NOs: 78 and 79),
PR-1565035 (comprising SEQ ID NOs: 80 and 81),
PR-1572102 (comprising SEQ ID NOs: 88 and 89),
PR-1572103 (comprising SEQ ID NOs: 90 and 91),
PR-1572104 (comprising SEQ ID NOs: 92 and 93),
PR-1572105 (comprising SEQ ID NOs: 94 and 95),
PR-1572106 (comprising SEQ ID NOs: 96 and 97),
PR-1575573 (comprising SEQ ID NOs: 210 and 98),
PR-1575832 (comprising SEQ ID NOs: 99 and 100),
PR-1575834 (comprising SEQ ID NOs: 101 and 102),
PR-1575835 (comprising SEQ ID NOs: 103 and 104),
PR-1577165 (comprising SEQ ID NOs: 105 and 106),
PR-1577166 (comprising SEQ ID NOs: 107 and 108),
PR-1577547 (comprising SEQ ID NOs: 109 and 110),
PR-1577548 (comprising SEQ ID NOs: 111 and 112),
PR-1577550 (comprising SEQ ID NOs: 113 and 114),
PR-1578137 (comprising SEQ ID NOs: 116 and 117),
PR-1610560 (comprising SEQ ID NOs: 129 and 130),

PR-1610561 (comprising SEQ ID NOs: 131 and 132),
PR-1610562 (comprising SEQ ID NOs: 133 and 134),
PR-1610563 (comprising SEQ ID NOs: 135 and 136),
PR-1611291 (comprising SEQ ID NOs: 139 and 140),
PR-1611292 (comprising SEQ ID NOs: 141 and 142),
PR-1612489 (comprising SEQ ID NOs: 161 and 162),
PR-1612491 (comprising SEQ ID NOs: 163 and 164),
PR-1612492 (comprising SEQ ID NOs: 165 and 166),
PR-1612495 (comprising SEQ ID NOs: 171 and 172),
PR-1612496 (comprising SEQ ID NOs: 173 and 174),
PR-1612499 (comprising SEQ ID NOs: 177 and 178),
PR-1612500 (comprising SEQ ID NOs: 179 and 180),
PR-1612501 (comprising SEQ ID NOs: 181 and 182),
PR-1612502 (comprising SEQ ID NOs: 183 and 184),
PR-1613183 (comprising SEQ ID NOs: 185 and 186),
PR-1613184 (comprising SEQ ID NOs: 187 and 188),
PR-1613185 (comprising SEQ ID NOs: 189 and 190),
PR-1613190 (comprising SEQ ID NOs: 199 and 200),
PR-1565040 (comprising SEQ ID NOs: 209 and 210),
PR-1565042 (comprising SEQ ID NOs: XX and YY),
PR-1565044 (comprising SEQ ID NOs: 213 and 214),
PR-1565051 (comprising SEQ ID NOs: 215 and 216),
PR-1565083 (comprising SEQ ID NOs: 217 and 218),
PR-1565084 (comprising SEQ ID NOs: 219 and 220),
PR-1565085 (comprising SEQ ID NOs: 221 and 222),
PR-1565086 (comprising SEQ ID NOs: 223 and 224),
PR-1571821 (comprising SEQ ID NOs: 225 and 226),
PR-1571823 (comprising SEQ ID NOs: 227 and 228),
PR-1575521 (comprising SEQ ID NOs: 229 and 230),
PR-1571824 (comprising SEQ ID NOs: 231 and 232),
PR-1571825 (comprising SEQ ID NOs: 233 and 234),
PR-1571826 (comprising SEQ ID NOs: 235 and 236),
PR-1571827 (comprising SEQ ID NOs: 237 and 238),
PR-1571828 (comprising SEQ ID NOs: 239 and 240),
PR-1571830 (comprising SEQ ID NOs: 241 and 242),
PR-1571831 (comprising SEQ ID NOs: 243 and 244),
PR-1571832 (comprising SEQ ID NOs: 245 and 246),

PR-1571836 (comprising SEQ ID NOs: 247 and 248),
PR-1577053 (comprising SEQ ID NOs: 249 and 250), or
PR-1577056 (comprising SEQ ID NOs: 251 and 252).

25. The binding protein of any one of claims 19-24, wherein:

(i) the binding protein is capable of binding VEGF with a K_D of at most about 1.5×10^{-11} M, as measured by surface plasmon resonance, or capable of inhibiting human VEGF with an IC50 of at most about 0.213 nM, as measured in a VEGF neutralization assay, and/or

(ii) the binding protein is capable of binding PDGF with a K_D of at most about 2.1×10^{-10} M, as measured by surface plasmon resonance, or capable of inhibiting PDGF with an IC50 of at most about 0.035 nM, as measured in a PDGF neutralization assay.

26. The binding protein of any one of claims 1-25, wherein the Fc region is a variant sequence Fc region.

27. The binding protein of any one of claims 1-26, wherein the binding protein comprises:

a) a heavy chain constant region on the first polypeptide chain comprising a human IgG1 heavy chain sequence modified by one or more amino acid changes, wherein the changes comprise substitution of leucines at positions 234 and 235 with alanines, and optionally also comprise a substitution of histidine at position 435 with alanine, wherein the amino acid positions are numbered using EU index numbering; and

(b) a light chain constant region on the second polypeptide chain comprising a human kappa light chain constant region sequence.

28. The binding protein of claim 19 wherein the binding protein is capable of binding VEGF and PDGF, wherein

a. the variable domains that form a functional target binding site for VEGF comprise: CDRs 1-3 from SEQ ID NO: 35 and CDRs-1-3 from SEQ ID NO: 36, and
b. the variable domains that form a functional target binding site for PDGF comprise: CDRs 1-3 from SEQ ID NO: 15 and CDRs-1-3 from SEQ ID NO: 16.

29. The binding protein of claim 28, wherein the binding protein is capable of binding VEGF and PDGF, wherein

a. the variable domains that form a functional target binding site for VEGF comprise: SEQ ID NO: 35 and SEQ ID NO: 36, and
b. the variable domains that form a functional target binding site for PDGF comprise: SEQ ID NO: 15 and SEQ ID NO: 16.

30. The binding protein of claim 28 or 29, wherein the binding protein is capable of binding VEGF and PDGF, and wherein the binding protein comprises PR-1610561 (comprising SEQ ID NOs: 131 and 132).

31. The binding protein of any one of claims 28-30, wherein the binding protein comprises:

a) a heavy chain constant region on the first polypeptide chain comprising a human IgG1 heavy chain sequence modified by one or more amino acid changes, wherein the changes comprise substitution of leucines at positions 234 and 235 with alanines, and optionally also comprising a substitution of histidine at position 435 with alanine, wherein the amino acid positions are numbered using EU index numbering; and

(b) a light chain constant region on the second polypeptide chain comprising a human kappa light chain constant region sequence.

32. The binding protein of any one of claims 28-31, wherein the binding protein is capable of binding:

(i) VEGF with a K_D of at most about 1.8×10^{-12} M, as measured by surface plasmon resonance, or capable of inhibiting human VEGF with an IC50 of at most about 0.097 nM measured in a VEGF neutralization assay, and/or

(ii) PDGF with a K_D of at most about 4.5×10^{-13} M, as measured by surface plasmon resonance, or capable of inhibiting PDGF with an IC50 of at most about 0.032 nM, as measured in a PDGF neutralization assay.

33. The binding protein of claim 19, wherein the binding protein is capable of binding VEGF and PDGF, wherein

a. the variable domains that form a functional target binding site for VEGF comprise: CDRs 1-3 from SEQ ID NO: 17 and CDRs-1-3 from SEQ ID NO: 18, and
b. the variable domains that form a functional target binding site for PDGF comprise: CDRs 1-3 from SEQ ID NO: 1 and CDRs-1-3 from SEQ ID NO: 2.

34. The binding protein of claim 33, wherein the binding protein is capable of binding VEGF and PDGF, wherein

a. the variable domains that form a functional target binding site for VEGF comprise: SEQ ID NO: 17 and SEQ ID NO: 18,and
b. the variable domains that form a functional target binding site for PDGF comprise: SEQ ID NO: 1 and SEQ ID NO: 2.

35. The binding protein of claim 33 or 34, wherein the binding protein is capable of binding VEGF and PDGF, and wherein the binding protein comprises PR-1572102 (comprising SEQ ID NOs: 88 and 89).

36. The binding protein of any one of claims 33-35, wherein the binding protein comprises:

a) a heavy chain constant region on the first polypeptide chain comprising a human IgG1 heavy chain sequence modified by one or more amino acid changes, wherein the changes comprise substitution of leucines at positions 234 and 235 with alanines, and optionally also comprising a substitution of histidine at position 435 with alanine, wherein the amino acid positions are numbered using EU index numbering; and

(b) a light chain constant region on the second polypeptide chain comprising a human kappa light chain constant region sequence.

37. The binding protein of any one of claims 33-36, wherein the binding protein is capable of binding:

(i) VEGF with a K_D of at most about 1.3 x 10^{-11} M, as measured by surface plasmon resonance, or capable of inhibiting human VEGF with an IC50 of at most about 0.182 nM measured in a VEGF neutralization assay, and/or

(ii) PDGF with a K_D of at most about 1.3 x 10^{-11} M, as measured by surface plasmon resonance, or capable of inhibiting PDGF with an IC50 of at most about 0.139 nM, as measured in a PDGF neutralization assay.

38. The binding protein of claim 33 or 34, wherein the binding protein is capable of binding VEGF and PDGF, and wherein the binding protein comprises PR-1572105 (comprising SEQ ID NOs: 94 and 95).

39. The binding protein of claim 38, wherein the binding protein comprises:

a) a heavy chain constant region on the first polypeptide chain comprising a human IgG1 heavy chain sequence modified by one or more amino acid changes, wherein the changes comprise substitution of leucines at positions 234 and 235 with alanines, and optionally also comprising a substitution of histidine at position 435 with alanine, wherein the amino acid positions are numbered using EU index numbering; and

(b) a light chain constant region on the second polypeptide chain comprising a human kappa light chain constant region sequence.

40. The binding protein of any one of claims 33-34 or 38-39, wherein the binding protein is capable of binding:

(i) VEGF with a K_D of at most about 1.1 x 10^{-11} M, as measured by surface plasmon resonance, or capable of inhibiting human VEGF with an IC50 of at most about 0.139 nM measured in a VEGF neutralization assay, and/or

(ii) PDGF with a K_D of at most about 1.3 x 10^{-11} M, as measured by surface plasmon resonance, or capable of inhibiting PDGF with an IC50 of at most about 0.096 nM, as measured in a PDGF neutralization assay.

41. The binding protein of any one of claims 1-40, comprising two first polypeptide chains and two second polypeptide chains, and four functional target binding sites.

42. The binding protein of any one of claims 1-41, wherein X1 is not CH1 or CL.

43. The binding protein of any one of claims 1-42, wherein the Fc region is an Fc region from an IgG1, IgG2, IgG3, IgG4, IgA, IgM, IgE, or IgD, or a variant thereof.

44. The binding protein of any one of claims 1-43, wherein the binding protein is a crystallized binding protein.

45. A binding protein conjugate comprising a binding protein according to any one of claims 1-44, the binding protein conjugate further comprising an immunoadhesion molecule, an imaging agent, a therapeutic agent, or a cytotoxic agent.

46. The binding protein conjugate of claim 45, wherein the imaging agent is a radiolabel, an enzyme, a fluorescent label, a luminescent label, a bioluminescent label, a magnetic label, or biotin.

47. The binding protein conjugate of claim 46, wherein the radiolabel is ^{3}H, ^{14}C, ^{35}S, ^{90}Y, ^{99}Tc, ^{111}In, ^{125}I, ^{131}I, ^{177}Lu, ^{166}Ho, or ^{153}Sm.

48. The binding protein conjugate of claim 45, wherein the therapeutic or cytotoxic agent is an anti-metabolite, an alkylating agent, an antibiotic, a growth factor, a cytokine, an anti-angiogenic agent, an anti-mitotic agent, an anthracycline, toxin, or an apoptotic agent.

49. An isolated nucleic acid encoding the binding protein amino acid sequence of any one of claims 1-44.

50. A vector comprising the isolated nucleic acid according to claim 49.

51. The vector of claim 50, wherein the vector comprises pcDNA, pTT, pTT3, pEFBOS, pBV, pJV, pcDNA3.1 TOPO, pEF6, pHybE, TOPO, or pBJ.

52. A host cell comprising the vector of claim 50 or 51.

53. The host cell of claim 52, wherein the host cell is a prokaryotic cell, *Escherichia coli*, a eukaryotic cell, a protist cell, an animal cell, a plant cell, a fungal cell, a yeast cell, an Sf9 cell, a mammalian cell, an avian cell, an insect cell, a CHO cell or a COS cell.

54. A method of producing a binding protein, comprising culturing the host cell of claim 52 or 53 in culture medium under conditions sufficient to produce the binding protein.

55. A pharmaceutical composition comprising the binding protein according to any one of claims 1-44, and a pharmaceutically acceptable carrier.

56. The pharmaceutical composition of claim 55, further comprising at least one additional therapeutic agent.

57. The pharmaceutical composition according to claim 56, wherein the additional therapeutic agent is an imaging agent, a cytotoxic agent, an angiogenesis inhibitor, a kinase inhibitor, a co-stimulation molecule blocker, an adhesion molecule blocker, an anti-cytokine antibody or functional fragment thereof, methotrexate, cyclosporin, rapamycin, FK506, a detectable label or reporter, a TNF antagonist, an antirheumatic, a muscle relaxant, a narcotic, a non-steroid anti-inflammatory drug (NSAID), an analgesic, an anesthetic, a sedative, a local anesthetic, a neuromuscular blocker, an antimicrobial, an antipsoriatic, a corticosteriod, an anabolic steroid, an erythropoietin, an immunization, an immunoglobulin, an immunosuppressive, a growth hormone, a hormone replacement drug, a radiopharmaceutical, an antidepressant, an antipsychotic, a stimulant, an asthma medication, a beta agonist, an inhaled steroid, an epinephrine or analog, a cytokine, or a cytokine antagonist.

58. A method of treating a subject for a disease or a disorder by administering the binding protein of any one of claims 1-44 to the subject.

59. The method of claim 58, wherein the disorder is arthritis, osteoarthritis, juvenile chronic arthritis, septic arthritis, Lyme arthritis, psoriatic arthritis, reactive arthritis, spondyloarthropathy, systemic lupus erythematosus, Crohn's disease, ulcerative colitis, inflammatory bowel disease, insulin dependent diabetes mellitus, thyroiditis, asthma, allergic diseases, psoriasis, dermatitis scleroderma, graft versus host disease, organ transplant rejection, acute or chronic immune disease associated with organ transplantation, sarcoidosis, atherosclerosis, disseminated intravascular coagulation, Kawasaki's disease, Grave's disease, nephrotic syndrome, chronic fatigue syndrome, Wegener's granulomatosis, Henoch-Schoenlein purpurea, microscopic vasculitis of the kidneys, chronic active hepatitis, uveitis, septic shock, toxic shock syndrome, sepsis syndrome, cachexia, infectious diseases, parasitic diseases, acute transverse myelitis, Huntington's chorea, Parkinson's disease, Alzheimer's

disease, stroke, primary biliary cirrhosis, hemolytic anemia, malignancies, heart failure, myocardial infarction, Addison's disease, sporadic polyglandular deficiency type I and polyglandular deficiency type II, Schmidt's syndrome, adult (acute) respiratory distress syndrome, alopecia, alopecia areata, seronegative arthopathy, arthropathy, Reiter's disease, psoriatic arthropathy, ulcerative colitic arthropathy, enteropathic synovitis, chlamydia, yersinia and salmonella associated arthropathy, spondyloarthopathy, atheromatous disease/arteriosclerosis, atopic allergy, autoimmune bullous disease, pemphigus vulgaris, pemphigus foliaceus, pemphigoid, linear IgA disease, autoimmune haemolytic anaemia, Coombs positive haemolytic anaemia, acquired pernicious anaemia, juvenile pernicious anaemia, myalgic encephalitis/Royal Free Disease, chronic mucocutaneous candidiasis, giant cell arteritis, primary sclerosing hepatitis, cryptogenic autoimmune hepatitis, Acquired Immunodeficiency Syndrome, Acquired Immunodeficiency Related Diseases, Hepatitis B, Hepatitis C, common varied immunodeficiency (common variable hypogammaglobulinaemia), dilated cardiomyopathy, female infertility, ovarian failure, premature ovarian failure, fibrotic lung disease, cryptogenic fibrosing alveolitis, post-inflammatory interstitial lung disease, interstitial pneumonitis, connective tissue disease associated interstitial lung disease, mixed connective tissue disease associated lung disease, systemic sclerosis associated interstitial lung disease, rheumatoid arthritis associated interstitial lung disease, systemic lupus erythematosus associated lung disease, dermatomyositis/polymyositis associated lung disease, Sjögren's disease associated lung disease, ankylosing spondylitis associated lung disease, vasculitic diffuse lung disease, haemosiderosis associated lung disease, drug-induced interstitial lung disease, fibrosis, radiation fibrosis, bronchiolitis obliterans, chronic eosinophilic pneumonia, lymphocytic infiltrative lung disease, postinfectious interstitial lung disease, gouty arthritis, autoimmune hepatitis, type-1 autoimmune hepatitis (classical autoimmune or lupoid hepatitis), type-2 autoimmune hepatitis (anti-LKM antibody hepatitis), autoimmune mediated hypoglycaemia, type B insulin resistance with acanthosis nigricans, hypoparathyroidism, acute immune disease associated with organ transplantation, chronic immune disease associated with organ transplantation, osteoarthrosis, primary sclerosing cholangitis, psoriasis type 1, psoriasis type 2, idiopathic leucopaenia, autoimmune neutropaenia, renal disease NOS, glomerulonephritides, microscopic vasulitis of the kidneys, lyme disease, discoid lupus erythematosus, male infertility idiopathic or NOS, sperm autoimmunity, multiple sclerosis (all subtypes), sympathetic ophthalmia, pulmonary hypertension secondary to connective tissue disease, Goodpasture's syndrome, pulmonary manifestation of polyarteritis nodosa, acute rheumatic fever, rheumatoid spondylitis, Still's disease, systemic sclerosis, Sjörgren's syndrome, Takayasu's disease/arteritis, autoimmune thrombocytopaenia, idiopathic thrombocytopaenia, autoimmune thyroid disease, hyperthyroidism, goitrous autoimmune

hypothyroidism (Hashimoto's disease), atrophic autoimmune hypothyroidism, primary myxoedema, phacogenic uveitis, primary vasculitis, vitiligo acute liver disease, chronic liver diseases, alcoholic cirrhosis, alcohol-induced liver injury, cholestasis, idiosyncratic liver disease, Drug-Induced hepatitis, Non-alcoholic Steatohepatitis, allergy and asthma, group B streptococci (GBS) infection, mental disorders (*e.g.*, depression and schizophrenia), Th2 Type and Th1 Type mediated diseases, acute and chronic pain (different forms of pain), and cancers such as lung, breast, stomach, bladder, colon, pancreas, ovarian, prostate and rectal cancer and hematopoietic malignancies (leukemia and lymphoma) abetalipoproteinemia, Acrocyanosis, acute and chronic parasitic or infectious processes, acute leukemia, acute lymphoblastic leukemia (ALL), acute myeloid leukemia (AML), acute or chronic bacterial infection, acute pancreatitis, acute renal failure, adenocarcinomas, aerial ectopic beats, AIDS dementia complex, alcohol-induced hepatitis, allergic conjunctivitis, allergic contact dermatitis, allergic rhinitis, allograft rejection, alpha-l- antitrypsin deficiency, amyotrophic lateral sclerosis, anemia, angina pectoris, anterior horn cell degeneration, anti cd3 therapy, antiphospholipid syndrome, anti-receptor hypersensitivity reactions, aordic and peripheral aneuryisms, aortic dissection, arterial hypertension, arteriosclerosis, arteriovenous fistula, ataxia, atrial fibrillation (sustained or paroxysmal), atrial flutter, atrioventricular block, B cell lymphoma, bone graft rejection, bone marrow transplant (BMT) rejection, bundle branch block, Burkitt's lymphoma, burns, cardiac arrhythmias, cardiac stun syndrome, cardiac tumors, cardiomyopathy, cardiopulmonary bypass inflammation response, cartilage transplant rejection, cerebellar cortical degenerations, cerebellar disorders, chaotic or multifocal atrial tachycardia, chemotherapy associated disorders, chronic myelocytic leukemia (CML), chronic alcoholism, chronic inflammatory pathologies, chronic lymphocytic leukemia (CLL), chronic obstructive pulmonary disease (COPD), chronic salicylate intoxication, colorectal carcinoma, congestive heart failure, conjunctivitis, contact dermatitis, cor pulmonale, coronary artery disease, Creutzfeldt-Jakob disease, culture negative sepsis, cystic fibrosis, cytokine therapy associated disorders, Dementia pugilistica, demyelinating diseases, dengue hemorrhagic fever, dermatitis, dermatologic conditions, diabetes, diabetes mellitus, diabetic ateriosclerotic disease, Diffuse Lewy body disease, dilated congestive cardiomyopathy, disorders of the basal ganglia, Down's Syndrome in middle age, drug- induced movement disorders induced by drugs which block CNS dopamine receptors, drug sensitivity, eczema, encephalomyelitis, endocarditis, endocrinopathy, epiglottitis, epstein-barr virus infection, erythromelalgia, extrapyramidal and cerebellar disorders, familial hematophagocytic lymphohistiocytosis, fetal thymus implant rejection, Friedreich's ataxia, functional peripheral arterial disorders, fungal sepsis, gas gangrene, gastric ulcer, graft rejection of any organ or tissue, gram negative sepsis, gram positive sepsis, granulomas due to intracellular organisms, hairy cell leukemia, Hallerrorden-Spatz disease, hashimoto's thyroiditis, hay fever, heart transplant rejection,

hemachromatosis, hemodialysis, hemolytic uremic syndrome/thrombolytic thrombocytopenic purpura, hemorrhage, hepatitis A, His bundle arryhthmias, HIV infection/HIV neuropathy, Hodgkin's disease, hyperkinetic movement disorders, hypersensitity reactions, hypersensitivity pneumonitis, hypertension, hypokinetic movement disorders, hypothalamic-pituitary-adrenal axis evaluation, idiopathic Addison's disease, idiopathic pulmonary fibrosis, antibody mediated cytotoxicity, Asthenia, infantile spinal muscular atrophy, inflammation of the aorta, influenza a, ionizing radiation exposure, iridocyclitis/uveitis/optic neuritis, ischemia- reperfusion injury, ischemic stroke, juvenile rheumatoid arthritis, juvenile spinal muscular atrophy, Kaposi's sarcoma, kidney transplant rejection, legionella, leishmaniasis, leprosy, lesions of the corticospinal system, lipedema, liver transplant rejection, lymphederma, malaria, malignamt Lymphoma, malignant histiocytosis, malignant melanoma, meningitis, meningococcemia, metabolic/idiopathic, migraine headache, mitochondrial multi.system disorder, mixed connective tissue disease, monoclonal gammopathy, multiple myeloma, multiple systems degenerations (Mencel Dejerine- Thomas Shy-Drager and Machado-Joseph), myasthenia gravis, mycobacterium avium intracellulare, mycobacterium tuberculosis, myelodyplastic syndrome, myocardial ischemic disorders, nasopharyngeal carcinoma, neonatal chronic lung disease, nephritis, nephrosis, neurodegenerative diseases, neurogenic I muscular atrophies , neutropenic fever, non- hodgkins lymphoma, occlusion of the abdominal aorta and its branches, occulsive arterial disorders, okt3 therapy, orchitis/epidydimitis, orchitis/vasectomy reversal procedures, organomegaly, osteoporosis, pancreas transplant rejection, pancreatic carcinoma, paraneoplastic syndrome/hypercalcemia of malignancy, parathyroid transplant rejection, pelvic inflammatory disease, perennial rhinitis, pericardial disease, peripheral atherlosclerotic disease, peripheral vascular disorders, peritonitis, pernicious anemia, pneumocystis carinii pneumonia, pneumonia, POEMS syndrome (polyneuropathy, organomegaly, endocrinopathy, monoclonal gammopathy, and skin changes syndrome), post perfusion syndrome, post pump syndrome, post-MI cardiotomy syndrome, preeclampsia, Progressive supranucleo Palsy, primary pulmonary hypertension, radiation therapy, Raynaud's phenomenon and disease, Raynoud's disease, Refsum's disease, regular narrow QRS tachycardia, renovascular hypertension, reperfusion injury, restrictive cardiomyopathy, sarcomas, scleroderma, senile chorea, Senile Dementia of Lewy body type, seronegative arthropathies, shock, sickle cell anemia, skin allograft rejection, skin changes syndrome, small bowel transplant rejection, solid tumors, specific arrythmias, spinal ataxia, spinocerebellar degenerations, streptococcal myositis, structural lesions of the cerebellum, Subacute sclerosing panencephalitis, Syncope, syphilis of the cardiovascular system, systemic anaphalaxis, systemic inflammatory response syndrome, systemic onset juvenile rheumatoid arthritis, T-cell or FAB ALL, Telangiectasia, thromboangitis obliterans, thrombocytopenia, toxicity, transplants, trauma/hemorrhage, type III hypersensitivity reactions, type IV

hypersensitivity, unstable angina, uremia, urosepsis, urticaria, valvular heart diseases, varicose veins, ,vasculitis, venous diseases, venous thrombosis, ventricular fibrillation, viral and fungal infections, vital encephalitis/aseptic meningitis, vital-associated hemaphagocytic syndrome, Wernicke- Korsakoff syndrome, Wilson's disease, xenograft rejection of any organ or tissue, acute coronary syndromes, acute idiopathic polyneuritis, acute inflammatory demyelinating polyradiculoneuropathy, acute ischemia, adult Still's disease, anaphylaxis, anti-phospholipid antibody syndrome, aplastic anemia, atopic eczema, atopic dermatitis, autoimmune dermatitis, autoimmune disorder associated with streptococcus infection, autoimmune enteropathy, autoimmune hearing loss, autoimmune lymphoproliferative syndrome (ALPS), autoimmune myocarditis, autoimmune premature ovarian failure, blepharitis, bronchiectasis, bullous pemphigoid, cardiovascular disease, catastrophic antiphospholipid syndrome, celiac disease, cervical spondylosis, chronic ischemia, cicatricial pemphigoid, clinically isolated syndrome (cis) with risk for multiple sclerosis, childhood onset psychiatric disorder, dacryocystitis, dermatomyositis, diabetic retinopathy, disk herniation, disk prolaps, drug induced immune hemolytic anemia, endometriosis, endophthalmitis, episcleritis, erythema multiforme, erythema multiforme major, gestational pemphigoid, Guillain-Barré syndrome (GBS), hay fever, Hughes syndrome, idiopathic Parkinson's disease, idiopathic interstitial pneumonia, IgE-mediated allergy, immune hemolytic anemia, inclusion body myositis, infectious ocular inflammatory disease, inflammatory demyelinating disease, inflammatory heart disease, inflammatory kidney disease, IPF/UIP, iritis, keratitis, keratoconjunctivitis sicca, Kussmaul disease or Kussmaul-Meier disease, Landry's paralysis, Langerhan's cell histiocytosis, livedo reticularis, macular degeneration, microscopic polyangiitis, morbus bechterev, motor neuron disorders, mucous membrane pemphigoid, multiple organ failure, myelodysplastic syndrome, myocarditis, nerve root disorders, neuropathy, non-A non-B hepatitis, optic neuritis, osteolysis, ovarian cancer, pauciarticular JRA, peripheral artery occlusive disease (PAOD), peripheral vascular disease (PVD), peripheral artery, disease (PAD), phlebitis, polyarteritis nodosa (or periarteritis nodosa), polychondritis, polymyalgia rheumatica, poliosis, polyarticular JRA, polyendocrine deficiency syndrome, polymyositis, post-pump syndrome, primary Parkinsonism, prostate and rectal cancer and hematopoietic malignancies (leukemia and lymphoma), prostatitis, pure red cell aplasia, primary adrenal insufficiency, recurrent neuromyelitis optica, restenosis, rheumatic heart disease, sapho (synovitis, acne, pustulosis, hyperostosis, and osteitis), scleroderma, secondary amyloidosis, shock lung, scleritis, sciatica, secondary adrenal insufficiency, silicone associated connective tissue disease, sneddon-wilkinson dermatosis, spondilitis ankylosans, Stevens-Johnson syndrome (SJS), systemic inflammatory response syndrome, temporal arteritis, toxoplasmic retinitis, toxic epidermal necrolysis, transverse myelitis, TRAPS (tumor necrosis factor receptor, type 1 allergic reaction, type II diabetes,

usual interstitial pneumonia (UIP), vernal conjunctivitis, viral retinitis, Vogt-Koyanagi-Harada syndrome (VKH syndrome), wet macular degeneration, wound healing, age related macular degeneration (AMD), diabetic retinopathy, diabetic macular edema, central retinal vein occlusion, corneal neovascularization, exudative AMD, iris neovascularization, neovascular glaucoma, post-surgical fibrosis in glaucoma, proliferative vitreoretinopathy (PVR), choroidal neovascularization, optic disc neovascularization, retinal neovascularization, vitreal neovascularization, pannus, pterygium, macular edema, diabetic macular edema (DME), vascular retinopathy, retinal degeneration, uveitis, or an inflammatory disease of the eye.

60. The method of claim 58 or 59, wherein the disorder is
    a. an autoimmune disorder, asthma, macular degeneration, keratoconjunctivitis sicca, blepharitis, keratitis, ocular inflammation, age-related macular degeneration, Crohn's disease, ulcerative colitis, inflammatory bowel disease (IBD), insulin dependent diabetes mellitus, rheumatoid arthritis, osteoarthritis, systemic lupus erythematosus (SLE), multiple sclerosis, sepsis, a neurodegenerative disease, wet macular degeneration, dry macular degeneration, or an oncological disorder,
    b. age related macular degeneration (AMD), wet AMD, dry AMD, vascular retinopathy, diabetic retinopathy, diabetic macular edema, central retinal vein occlusion, corneal neovascularization, exudative AMD, iris neovascularization, neovascular glaucoma, post-surgical fibrosis in glaucoma, proliferative vitreoretinopathy (PVR), choroidal neovascularization, optic disc neovascularization, retinal neovascularization, vitreal neovascularization, pannus, pterygium, macular edema, diabetic macular edema (DME), vascular retinopathy, retinal degeneration, uveitis, or inflammatory diseases of the eye, and/or
    c. ocular inflammation, age related macular degeneration (AMD), wet ADM, dry AMD, diabetic macular edema (DME), vascular retinopathy, retinal degeneration, uveitis, cancer, colitis, or rheumatoid arthritis.

61. The method of any one of claims 58-60, wherein the binding protein is formulated for parenteral, intravitreous, subcutaneous, intramuscular, intravenous, intrarticular, intrabronchial, intraabdominal, intracapsular, intracartilaginous, intracavitary, intracelial, intracerebellar, intracerebroventricular, intracolic, intracervical, intragastric, intrahepatic, intramyocardial, intraosteal, intrapelvic, intrapericardiac, intraperitoneal, intrapleural, intraprostatic, intrapulmonary, intrarectal, intrarenal, intraretinal, intraspinal, intrasynovial, intrathoracic, intrauterine, intravesical, bolus, vaginal, rectal, buccal, sublingual, intranasal, or transdermal administration,

and optionally wherein the binding protein is formulated for intravitreous administration, and optionally wherein the binding is administered intravitreously at a dose of about 0.1-5, or about 0.1-1, or about 0.1-0.3, or about 0.25 mg, and optionally wherein the administered binding protein has an ocular half-life of about 4.6 days.

62. Use of the binding protein of any one of claims 1-44 in the manufacture of a medicament for treating a subject for a disease or a disorder.

63. The use according to claim 62, wherein the disorder is arthritis, osteoarthritis, juvenile chronic arthritis, septic arthritis, Lyme arthritis, psoriatic arthritis, reactive arthritis, spondyloarthropathy, systemic lupus erythematosus, Crohn's disease, ulcerative colitis, inflammatory bowel disease, insulin dependent diabetes mellitus, thyroiditis, asthma, allergic diseases, psoriasis, dermatitis scleroderma, graft versus host disease, organ transplant rejection, acute or chronic immune disease associated with organ transplantation, sarcoidosis, atherosclerosis, disseminated intravascular coagulation, Kawasaki's disease, Grave's disease, nephrotic syndrome, chronic fatigue syndrome, Wegener's granulomatosis, Henoch-Schoenlein purpurea, microscopic vasculitis of the kidneys, chronic active hepatitis, uveitis, septic shock, toxic shock syndrome, sepsis syndrome, cachexia, infectious diseases, parasitic diseases, acute transverse myelitis, Huntington's chorea, Parkinson's disease, Alzheimer's disease, stroke, primary biliary cirrhosis, hemolytic anemia, malignancies, heart failure, myocardial infarction, Addison's disease, sporadic polyglandular deficiency type I and polyglandular deficiency type II, Schmidt's syndrome, adult (acute) respiratory distress syndrome, alopecia, alopecia areata, seronegative arthopathy, arthropathy, Reiter's disease, psoriatic arthropathy, ulcerative colitic arthropathy, enteropathic synovitis, chlamydia, yersinia and salmonella associated arthropathy, spondyloarthopathy, atheromatous disease/arteriosclerosis, atopic allergy, autoimmune bullous disease, pemphigus vulgaris, pemphigus foliaceus, pemphigoid, linear IgA disease, autoimmune haemolytic anaemia, Coombs positive haemolytic anaemia, acquired pernicious anaemia, juvenile pernicious anaemia, myalgic encephalitis/Royal Free Disease, chronic mucocutaneous candidiasis, giant cell arteritis, primary sclerosing hepatitis, cryptogenic autoimmune hepatitis, Acquired Immunodeficiency Syndrome, Acquired Immunodeficiency Related Diseases, Hepatitis B, Hepatitis C, common varied immunodeficiency (common variable hypogammaglobulinaemia), dilated cardiomyopathy, female infertility, ovarian failure, premature ovarian failure, fibrotic lung disease, cryptogenic fibrosing alveolitis, post-inflammatory interstitial lung disease, interstitial pneumonitis, connective tissue disease associated interstitial lung disease, mixed connective tissue disease associated lung disease, systemic sclerosis associated interstitial lung disease, rheumatoid arthritis associated

interstitial lung disease, systemic lupus erythematosus associated lung disease, dermatomyositis/polymyositis associated lung disease, Sjögren's disease associated lung disease, ankylosing spondylitis associated lung disease, vasculitic diffuse lung disease, haemosiderosis associated lung disease, drug-induced interstitial lung disease, fibrosis, radiation fibrosis, bronchiolitis obliterans, chronic eosinophilic pneumonia, lymphocytic infiltrative lung disease, postinfectious interstitial lung disease, gouty arthritis, autoimmune hepatitis, type-1 autoimmune hepatitis (classical autoimmune or lupoid hepatitis), type-2 autoimmune hepatitis (anti-LKM antibody hepatitis), autoimmune mediated hypoglycaemia, type B insulin resistance with acanthosis nigricans, hypoparathyroidism, acute immune disease associated with organ transplantation, chronic immune disease associated with organ transplantation, osteoarthrosis, primary sclerosing cholangitis, psoriasis type 1, psoriasis type 2, idiopathic leucopaenia, autoimmune neutropaenia, renal disease NOS, glomerulonephritides, microscopic vasulitis of the kidneys, lyme disease, discoid lupus erythematosus, male infertility idiopathic or NOS, sperm autoimmunity, multiple sclerosis (all subtypes), sympathetic ophthalmia, pulmonary hypertension secondary to connective tissue disease, Goodpasture's syndrome, pulmonary manifestation of polyarteritis nodosa, acute rheumatic fever, rheumatoid spondylitis, Still's disease, systemic sclerosis, Sjörgren's syndrome, Takayasu's disease/arteritis, autoimmune thrombocytopaenia, idiopathic thrombocytopaenia, autoimmune thyroid disease, hyperthyroidism, goitrous autoimmune hypothyroidism (Hashimoto's disease), atrophic autoimmune hypothyroidism, primary myxoedema, phacogenic uveitis, primary vasculitis, vitiligo acute liver disease, chronic liver diseases, alcoholic cirrhosis, alcohol-induced liver injury, cholestasis, idiosyncratic liver disease, Drug-Induced hepatitis, Non-alcoholic Steatohepatitis, allergy and asthma, group B streptococci (GBS) infection, mental disorders (*e.g.*, depression and schizophrenia), Th2 Type and Th1 Type mediated diseases, acute and chronic pain (different forms of pain), and cancers such as lung, breast, stomach, bladder, colon, pancreas, ovarian, prostate and rectal cancer and hematopoietic malignancies (leukemia and lymphoma) abetalipoproteinemia, Acrocyanosis, acute and chronic parasitic or infectious processes, acute leukemia, acute lymphoblastic leukemia (ALL), acute myeloid leukemia (AML), acute or chronic bacterial infection, acute pancreatitis, acute renal failure, adenocarcinomas, aerial ectopic beats, AIDS dementia complex, alcohol-induced hepatitis, allergic conjunctivitis, allergic contact dermatitis, allergic rhinitis, allograft rejection, alpha-l- antitrypsin deficiency, amyotrophic lateral sclerosis, anemia, angina pectoris, anterior horn cell degeneration, anti cd3 therapy, antiphospholipid syndrome, anti-receptor hypersensitivity reactions, aordic and peripheral aneuryisms, aortic dissection, arterial hypertension, arteriosclerosis, arteriovenous fistula, ataxia, atrial fibrillation (sustained or paroxysmal), atrial flutter, atrioventricular block, B cell lymphoma, bone graft rejection, bone marrow transplant (BMT) rejection, bundle branch block, Burkitt's

lymphoma, burns, cardiac arrhythmias, cardiac stun syndrome, cardiac tumors, cardiomyopathy, cardiopulmonary bypass inflammation response, cartilage transplant rejection, cerebellar cortical degenerations, cerebellar disorders, chaotic or multifocal atrial tachycardia, chemotherapy associated disorders, chronic myelocytic leukemia (CML), chronic alcoholism, chronic inflammatory pathologies, chronic lymphocytic leukemia (CLL), chronic obstructive pulmonary disease (COPD), chronic salicylate intoxication, colorectal carcinoma, congestive heart failure, conjunctivitis, contact dermatitis, cor pulmonale, coronary artery disease, Creutzfeldt-Jakob disease, culture negative sepsis, cystic fibrosis, cytokine therapy associated disorders, Dementia pugilistica, demyelinating diseases, dengue hemorrhagic fever, dermatitis, dermatologic conditions, diabetes, diabetes mellitus, diabetic ateriosclerotic disease, Diffuse Lewy body disease, dilated congestive cardiomyopathy, disorders of the basal ganglia, Down's Syndrome in middle age, drug- induced movement disorders induced by drugs which block CNS dopamine receptors, drug sensitivity, eczema, encephalomyelitis, endocarditis, endocrinopathy, epiglottitis, epstein-barr virus infection, erythromelalgia, extrapyramidal and cerebellar disorders, familial hematophagocytic lymphohistiocytosis, fetal thymus implant rejection, Friedreich's ataxia, functional peripheral arterial disorders, fungal sepsis, gas gangrene, gastric ulcer, graft rejection of any organ or tissue, gram negative sepsis, gram positive sepsis, granulomas due to intracellular organisms, hairy cell leukemia, Hallerrorden-Spatz disease, hashimoto's thyroiditis, hay fever, heart transplant rejection, hemachromatosis, hemodialysis, hemolytic uremic syndrome/thrombolytic thrombocytopenic purpura, hemorrhage, hepatitis A, His bundle arryhthmias, HIV infection/HIV neuropathy, Hodgkin's disease, hyperkinetic movement disorders, hypersensitity reactions, hypersensitivity pneumonitis, hypertension, hypokinetic movement disorders, hypothalamic-pituitary-adrenal axis evaluation, idiopathic Addison's disease, idiopathic pulmonary fibrosis, antibody mediated cytotoxicity, Asthenia, infantile spinal muscular atrophy, inflammation of the aorta, influenza a, ionizing radiation exposure, iridocyclitis/uveitis/optic neuritis, ischemia- reperfusion injury, ischemic stroke, juvenile rheumatoid arthritis, juvenile spinal muscular atrophy, Kaposi's sarcoma, kidney transplant rejection, legionella, leishmaniasis, leprosy, lesions of the corticospinal system, lipedema, liver transplant rejection, lymphederma, malaria, malignamt Lymphoma, malignant histiocytosis, malignant melanoma, meningitis, meningococcemia, metabolic/idiopathic, migraine headache, mitochondrial multi.system disorder, mixed connective tissue disease, monoclonal gammopathy, multiple myeloma, multiple systems degenerations (Mencel Dejerine- Thomas Shy-Drager and Machado-Joseph), myasthenia gravis, mycobacterium avium intracellulare, mycobacterium tuberculosis, myelodyplastic syndrome, myocardial ischemic disorders, nasopharyngeal carcinoma, neonatal chronic lung disease, nephritis, nephrosis, neurodegenerative diseases, neurogenic I muscular atrophies , neutropenic fever, non- hodgkins lymphoma, occlusion of

the abdominal aorta and its branches, occulsive arterial disorders, okt3 therapy, orchitis/epidydimitis, orchitis/vasectomy reversal procedures, organomegaly, osteoporosis, pancreas transplant rejection, pancreatic carcinoma, paraneoplastic syndrome/hypercalcemia of malignancy, parathyroid transplant rejection, pelvic inflammatory disease, perennial rhinitis, pericardial disease, peripheral atherlosclerotic disease, peripheral vascular disorders, peritonitis, pernicious anemia, pneumocystis carinii pneumonia, pneumonia, POEMS syndrome (polyneuropathy, organomegaly, endocrinopathy, monoclonal gammopathy, and skin changes syndrome), post perfusion syndrome, post pump syndrome, post-MI cardiotomy syndrome, preeclampsia, Progressive supranucleo Palsy, primary pulmonary hypertension, radiation therapy, Raynaud's phenomenon and disease, Raynoud's disease, Refsum's disease, regular narrow QRS tachycardia, renovascular hypertension, reperfusion injury, restrictive cardiomyopathy, sarcomas, scleroderma, senile chorea, Senile Dementia of Lewy body type, seronegative arthropathies, shock, sickle cell anemia, skin allograft rejection, skin changes syndrome, small bowel transplant rejection, solid tumors, specific arrythmias, spinal ataxia, spinocerebellar degenerations, streptococcal myositis, structural lesions of the cerebellum, Subacute sclerosing panencephalitis, Syncope, syphilis of the cardiovascular system, systemic anaphalaxis, systemic inflammatory response syndrome, systemic onset juvenile rheumatoid arthritis, T-cell or FAB ALL, Telangiectasia, thromboangitis obliterans, thrombocytopenia, toxicity, transplants, trauma/hemorrhage, type III hypersensitivity reactions, type IV hypersensitivity, unstable angina, uremia, urosepsis, urticaria, valvular heart diseases, varicose veins, ,vasculitis, venous diseases, venous thrombosis, ventricular fibrillation, viral and fungal infections, vital encephalitis/aseptic meningitis, vital-associated hemaphagocytic syndrome, Wernicke- Korsakoff syndrome, Wilson's disease, xenograft rejection of any organ or tissue, acute coronary syndromes, acute idiopathic polyneuritis, acute inflammatory demyelinating polyradiculoneuropathy, acute ischemia, adult Still's disease, anaphylaxis, anti-phospholipid antibody syndrome, aplastic anemia, atopic eczema, atopic dermatitis, autoimmune dermatitis, autoimmune disorder associated with streptococcus infection, autoimmune enteropathy, autoimmune hearing loss, autoimmune lymphoproliferative syndrome (ALPS), autoimmune myocarditis, autoimmune premature ovarian failure, blepharitis, bronchiectasis, bullous pemphigoid, cardiovascular disease, catastrophic antiphospholipid syndrome, celiac disease, cervical spondylosis, chronic ischemia, cicatricial pemphigoid, clinically isolated syndrome (cis) with risk for multiple sclerosis, childhood onset psychiatric disorder, dacryocystitis, dermatomyositis, diabetic retinopathy, disk herniation, disk prolaps, drug induced immune hemolytic anemia, endometriosis, endophthalmitis, episcleritis, erythema multiforme, erythema multiforme major, gestational pemphigoid, Guillain-Barré syndrome (GBS), hay fever, Hughes syndrome, idiopathic Parkinson's disease, idiopathic interstitial pneumonia, IgE-mediated allergy, immune

hemolytic anemia, inclusion body myositis, infectious ocular inflammatory disease, inflammatory demyelinating disease, inflammatory heart disease, inflammatory kidney disease, IPF/UIP, iritis, keratitis, keratoconjunctivitis sicca, Kussmaul disease or Kussmaul-Meier disease, Landry's paralysis, Langerhan's cell histiocytosis, livedo reticularis, macular degeneration, microscopic polyangiitis, morbus bechterev, motor neuron disorders, mucous membrane pemphigoid, multiple organ failure, myelodysplastic syndrome, myocarditis, nerve root disorders, neuropathy, non-A non-B hepatitis, optic neuritis, osteolysis, ovarian cancer, pauciarticular JRA, peripheral artery occlusive disease (PAOD), peripheral vascular disease (PVD), peripheral artery, disease (PAD), phlebitis, polyarteritis nodosa (or periarteritis nodosa), polychondritis, polymyalgia rheumatica, poliosis, polyarticular JRA, polyendocrine deficiency syndrome, polymyositis, post-pump syndrome, primary Parkinsonism, prostate and rectal cancer and hematopoietic malignancies (leukemia and lymphoma), prostatitis, pure red cell aplasia, primary adrenal insufficiency, recurrent neuromyelitis optica, restenosis, rheumatic heart disease, sapho (synovitis, acne, pustulosis, hyperostosis, and osteitis), scleroderma, secondary amyloidosis, shock lung, scleritis, sciatica, secondary adrenal insufficiency, silicone associated connective tissue disease, sneddon-wilkinson dermatosis, spondilitis ankylosans, Stevens-Johnson syndrome (SJS), systemic inflammatory response syndrome, temporal arteritis, toxoplasmic retinitis, toxic epidermal necrolysis, transverse myelitis, TRAPS (tumor necrosis factor receptor, type 1 allergic reaction, type II diabetes, usual interstitial pneumonia (UIP), vernal conjunctivitis, viral retinitis, Vogt-Koyanagi-Harada syndrome (VKH syndrome), wet macular degeneration, wound healing, age related macular degeneration (AMD), diabetic retinopathy, diabetic macular edema, central retinal vein occlusion, corneal neovascularization, exudative AMD, iris neovascularization, neovascular glaucoma, post-surgical fibrosis in glaucoma, proliferative vitreoretinopathy (PVR), choroidal neovascularization, optic disc neovascularization, retinal neovascularization, vitreal neovascularization, pannus, pterygium, macular edema, diabetic macular edema (DME), vascular retinopathy, retinal degeneration, uveitis, or an inflammatory disease of the eye.

64. The use according to claim 62 or 63 wherein the disorder is

    a. an autoimmune disorder, asthma, macular degeneration, keratoconjunctivitis sicca, blepharitis, keratitis, ocular inflammation, Crohn's disease, ulcerative colitis, inflammatory bowel disease (IBD), insulin dependent diabetes mellitus, rheumatoid arthritis, osteoarthritis, systemic lupus erythematosus (SLE), multiple sclerosis, sepsis, a neurodegenerative disease, wet macular degeneration, dry macular degeneration, or an oncological disorder, and/or

b. age related macular degeneration (AMD), diabetic retinopathy, diabetic macular edema, central retinal vein occlusion, corneal neovascularization, exudative AMD, iris neovascularization, neovascular glaucoma, post-surgical fibrosis in glaucoma, proliferative vitreoretinopathy (PVR), choroidal neovascularization, optic disc neovascularization, retinal neovascularization, vitreal neovascularization, pannus, pterygium, macular edema, diabetic macular edema (DME), vascular retinopathy, retinal degeneration, uveitis, or an inflammatory disease of the eye.

65. The use according to any one of claims 62-64, wherein the binding protein is formulated for intravitreous, parenteral, subcutaneous, intravitreous, intramuscular, intravenous, intrarticular, intrabronchial, intraabdominal, intracapsular, intracartilaginous, intracavitary, intracelial, intracerebellar, intracerebroventricular, intracolic, intracervical, intragastric, intrahepatic, intramyocardial, intraosteal, intrapelvic, intrapericardiac, intraperitoneal, intrapleural, intraprostatic, intrapulmonary, intrarectal, intrarenal, intraretinal, intraspinal, intrasynovial, intrathoracic, intrauterine, intravesical, bolus, vaginal, rectal, buccal, sublingual, intranasal, or transdermal administration,

and optionally wherein the binding protein is formulated for intravitreous administration, and optionally wherein the binding is administered intravitreously at a dose of about 0.1-5, or about 0.1-1, or about 0.1-0.3, or about 0.25 mg, and optionally wherein the administered binding protein has an ocular half-life of about 4.6 days.

66. A method of detecting the presence, amount, or concentration of at least one target or fragment thereof in a test sample by an immunoassay,

wherein the immunoassay comprises contacting the test sample with at least one binding protein and at least one detectable label, and

wherein the at least one binding protein comprises the binding protein of any one of claims 1-44.

67. The method of claim 66, further comprising:

(i) contacting the test sample with the at least one binding protein, wherein the binding protein binds to an epitope on the target or fragment thereof so as to form a first complex;

(ii) contacting the complex with the at least one detectable label, wherein the detectable label binds to the binding protein or an epitope on the target or fragment thereof that is not bound by the binding protein to form a second complex; and

(iii) detecting the presence, amount, or concentration of the target or fragment thereof in the test sample based on the signal generated by the detectable label in the second complex,

wherein the presence, amount, or concentration of the target or fragment thereof is directly correlated with the signal generated by the detectable label.

68. The method of claim 66, further comprising:

(i) contacting the test sample with the at least one binding protein, wherein the binding protein binds to an epitope on the target or fragment thereof so as to form a first complex;

(ii) contacting the complex with the at least one detectable label, wherein the detectable label competes with the target or fragment thereof for binding to the binding protein so as to form a second complex; and

(iii) detecting the presence, amount, or concentration of the target or fragment thereof in the test sample based on the signal generated by the detectable label in the second complex, wherein the presence, amount, or concentration of the target or fragment thereof is indirectly correlated with the signal generated by the detectable label.

69. A kit for assaying a test sample for the presence, amount, or concentration of a target or fragment thereof in the sample, the kit comprising (a) instructions for assaying the test sample for the target or fragment thereof and (b) at least one binding protein comprising the binding protein of any one of claims 1-44.

70. A method of quantitating the conformational stability of a variable domain from any one of the binding proteins in claims 1-44 using differential scanning calorimetry (DSC), wherein

the highest peak in a DSC thermogram is the midpoint of the unfolding transition or process of an antibody's binding region (VH-VL) due to increasing temperature; and

the corresponding temperature of that highest peak is a quantitation of the stability of that region.

71. The method of claim 70, wherein the thermal stability of the VH-VL region of a parental antibody corresponds to the thermal stability of the binding domains incorporated into the DVD-Ig format.

72. The method of claim 70, wherein the temperature predicts the conformation stability of the DVD-Ig outer variable domain (OVD) when the VH-VL region of the parental antibody is incorporated into the DVD-Ig molecule as the outer variable domain.

73. The method of any one of claims 70-72, wherein the VH-VL region of the parental antibody is ranked for incorporation into the DVD-Ig format so as to maximize the stability of the DVD-Ig molecule.

74. The method of any one of claims 70-73, wherein the conformational stability of a DVD-Ig binding protein correlates with storage stability (shelf-life) of the binding protein.

75. The method of claim 70, wherein the conformational stability of the DVD-Ig binding protein predicts other DVD-Ig binding proteins in terms of storage stability (shelf-life).

76. An antibody or antigen binding fragment thereof capable of binding VEGF, wherein the antibody or antigen binding fragment comprises

(i) a CDR-H1 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10} (SEQ ID NO: >>), wherein

X_1 is G;

X_2 is Y;

X_3 is T;

X_4 is F;

X_5 is T, Q, D, E, N, A, G, H, K, M, L, R, I, Y, or V;

X_6 is N, S, K, Y, T, M, G, A, I, L, E, P, Q, or F;

X_7 is Y;

X_8 is G, S, D, K, C, V, E, L, W, P, Y, M, N, or T;

X_9 is M; and

X_{10} is Y;

(ii) a CDR-H2 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-X_{15}-X_{16}-X_{17} (SEQ ID NO: >>), wherein

X_1 is W;

X_2 is I;

X_3 is N;

X_4 is T;

X_5 is E, Y, L, V, W, A, Q, H, G, K, N, M, T, or P;

X_6 is T;

X_7 is G;

X_8 is K, N, D, T, P, W, Y, V, S, M, A, I, G, R, or L;

X_9 is P;

X_{10} is T, I, M, K, A, N, P, L, V, W, D, Y, G, or E;

X_{11} is Y;

X_{12} is A;

X_{13} is D, Y, or H;

X_{14} is D;

X_{15} is F;

X_{16} is K or N; and

X_{17} is G;

(iii) a CDR-H3 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14} (SEQ ID NO: >>), wherein

X_1 is T, Y, G, I, S, K, N, P, L, W, M, F, R, or Q;

X_2 is N, H, I, T, D, F, L, E, V, Y, A, G, W, Q, or R;

X_3 is Y;

X_4 is Y;

X_5 is Y;

X_6 is R, S, N, E, M, L, T, W, Q, G, I, A, C, or V;

X_7 is S, N, T, K, M, Y, C, I, F, L, D, W, X, or V;

X_8 is Y;

X_9 is I, L, N, T, V, A, R, F, D, or S;

X_{10} is F;

X_{11} is Y;

X_{12} is F;

X_{13} is D; and

X_{14} is Y;

(iv) a CDR-L1 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11} (SEQ ID NO: >>), wherein

X_1 is R;

X_2 is A;

X_3 is S;

X_4 is E;

X_5 is S;

X_6 is V;

X_7 is S, N, D, T, R, H, E, I, L, Q, C, M, Y, K, or V;

X_8 is T, S, R, A, E, D, M, P, Y, I, W, or F;

X_9 is H, A, D, C, P, R, Y, L, Q, or K;

X_{10} is M; and

X_{11} is H, A, or P;

(v) a CDR-L2 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7 (SEQ ID NO: >>), wherein;

X_1 is G, W, V, I, E, S, or D;

X_2 is A;

X_3 is S;

X_4 is N, H, Y, M, T, F, V, R, Q, A, S, E, G, C, D, or P;

X_5 is L;

X_6 is E; and

X_7 is S or Y;

and

(vi) a CDR-L3 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9 (SEQ ID NO: >>), wherein

X_1 is Q;

X_2 is Q;

X_3 is S, C, G, I, W, R, N, A, Y, K, Q, or F;

X_4 is W, C, L, G, E, or S;

X_5 is N, I, T, D, G, M, S, H, A, R, V, L, F, K, or Q;

X_6 is D, N, Y, A, L, M, P, G, H, F, or K;

X_7 is P;

X_8 is F, M, G, Y, A, W, S, V, C, or P; and

X_9 is T.

77. The antibody or antigen binding fragment of claim 76, further comprising human framework sequences.
78. The antibody or antigen fragment of claim 76 or 77, wherein the antibody or antigen binding fragment comprises heavy chain CDRs 1-3 and light chain chain CDRs 1-3 having at least about 80%, 90%, 95%, or 99% homology to GYTFTNYGMY (CDR-H1), WINTETGKPTYADDFKG (CDR-H2), TNYYYRSYIFYFDY (CDR-H3), RASESVSTHMH (CDR-L1), GASNLES (CDR-L2), and QQSWNDPFT (CDR-L3).
79. The antibody or antigen fragment of any one of claims 76-78, wherein the antibody or antigen binding fragment comprises GYTFTNYGMY (CDR-H1), WINTETGKPTYADDFKG (CDR-H2), TNYYYRSYIFYFDY (CDR-H3), RASESVSTHMH (CDR-L1), GASNLES (CDR-L2), and QQSWNDPFT (CDR-L3).
80. An antibody or antigen binding fragment thereof capable of binding VEGF, wherein the antibody or antigen binding fragment comprises a CDR set comprising heavy chain CDRs 1-3 and light chain CDRs 1-3 having at least about 80%, 90%, 95%, or 99% homology to a CDR set selected from any of those in Tables A, 27 or 38-42.
81. The antibody or antigen binding fragment of claim 80, wherein the antibody or antigen binding fragment comprises a CDR set comprising heavy chain CDRs 1-3 and light chain CDRs 1-3 selected from any of those in Tables A, 27 or 38-42.
82. The antibody or antigen binding fragment of claim 80 or 81, further comprising human framework sequences.
83. The antibody or antigen binding fragment of claim 80, wherein the antibody or antigen binding fragment comprises a heavy chain variable domain and paired light chain variable domain having at least about 80%, 90%, 95%, or 99% homology to any of the paired variable domains in Tables A, 27 or 38-42.

84. The antibody or antigen binding fragment of claim 80, wherein the antibody or antigen binding fragment comprises a heavy chain variable domain and paired light chain variable domain selected from any of the paired variable domains in Tables A, 27 or 38-42.

85. An antibody or antigen binding fragment thereof capable of binding PDGF, wherein the antibody or antigen binding fragment comprises

(i) a CDR-H1 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12} (SEQ ID NO: >>), wherein

X_1 is G;

X_2 is F;

X_3 is S, I, or R;

X_4 is L;

X_5 is S, Y, A, D, T, M, R, L, C, F, W, or P;

X_6 is T;

X_7 is Y or S;

X_8 is G or E;

X_9 is M or V;

X_{10} is G, S, or R;

X_{11} is V or I; and

X_{12} is G, D, L, A, C, V, Y, R, T, E, or S;

(ii) a CDR-H2 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-X_{15}-X_{16} (SEQ ID NO: >>), wherein

X_1 is N or L;

X_2 is I;

X_3 is W, D, C, or G;

X_4 is W or C;

X_5 is D, Y, N, H, V, E, I, P, A, C, or G;

X_6 is D, G, N, or H;

X_7 is D, E, G, V, A, H, Y, N, Q, S, or L;

X_8 is K, E, T, I, Q, V, N, R, Y, L, M, or C;

X_9 is Y, H, C, D, N, S, A, F, or G;

X_{10} is Y;

X_{11} is N or S;

X_{12} is P, L, or T;

X_{13} is S;

X_{14} is L;

X_{15} is K or N; and

X_{16} is N, S, or T;

(iii) a CDR-H3 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12} (SEQ ID NO: >>), wherein

X_1 is I, Y, N, L, M, V, R, K, F, C, T, or E;

X_2 is E, Q, V, K, Y, L, D, G, A, M, R, or S;

X_3 is S, T, A, Y, W, P, L, V, E, K, F, or C;

X_4 is I, G, S, M, V, L, F, N, D, H, Y, T, R, Q, K, E, or P;

X_5 is G, W, P, F, C, Y, A, E, L, V, S, D, or R;

X_6 is T, P, W, R, I, F, A, M, Y, S, L, G, D, K, V, N, or E;

X_7 is T, N, S, K, R, M, A, E, I, V, L, W, P, or Q;

X_8 is Y;

X_9 is S, E, D, Y, A, C, N, M, W, T, Q, G, I, L, or P;

X_{10} is F;

X_{11} is D or Y; and

X_{12} is Y;

(iv) a CDR CDR-L1 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13} (SEQ ID NO: >>), wherein

X_1 is E, R, or K;

X_2 is R, A, or E;

X_3 is S or Y;

X_4 is S;

X_5 is G, C, V, or S;

X_6 is D, S, or Y;

X_7 is I, N, T, or M;

X_8 is G, W, Y, S, M, H, D, R, E, N, C, A, L, V, F, T, Q, or K;

X_9 is D, Y, Q, N, H, G, E, S, K, F, R, L, C, A, or P;

X_{10} is S, T, Y, M, K, A, C, F, L, E, W, D, P, or G;

X_{11} is Y, F, L, R, H, N, C, A, D, S, or T;

X_{12} is V, F, or S; and

X_{13} is S or P;

(v) a CDR-L2 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7 (SEQ ID NO: >>), wherein

X_1 is A, G, S, W, T, L, V, F, N, P, E, or D;

X_2 is D, Y, A, or V;

X_3 is D or G;

X_4 is Q, L, R, H, W, Y, M, K, D, A, E, N, V, S, F, or P;

X_5 is R, Q, or P;

X_6 is P or A; and

X_7 is S, I, T, R, or G;

and

(vi) a CDR-L3 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10} (SEQ ID NO: >>), wherein

X_1 is Q or K;

X_2 is S, P, Q, or H;

X_3 is Y;

X_4 is D or G;

X_5 is I, L, V, E, T, S, Q, R, N, K, G, A, C, or F;

X_6 is N, F, D, E, T, I, Y, C, V, S, R, A, L, G, H, or K;

X_7 is I, T, S, V, D, R, E, M, L, P, F, N, or K;

X_8 is D, N, P, A, Y, G, H, E, V, L, Q, or T;

X_9 is I, V, L, G, T, S, N, F, A, H, R, or Q; and

X_{10} is V or T.

86. The antibody or antigen binding fragment of claim 85, further comprising human framework sequences.
87. The antibody or antigen fragment of claim 85 or 86, wherein the antibody or antigen binding fragment comprises heavy chain CDRs 1-3 and light chain CDRs 1-3 having at least about 80%, 90%, 95%, or 99% homology to GFSLSTYGMGVG (CDR-H1), NIWWDDDKYYNPSLKN (CDR-H2), IESIGTTYSFDY (CDR-H3), ERSSGDIGDSYVS (CDR-L1), ADDQRPS (CDR-L2), and QSYDINIDIV (CDR-L3).
88. The antibody or antigen fragment of any one of claims 85-87, wherein the antibody or antigen binding fragment comprises GFSLSTYGMGVG (CDR-H1), NIWWDDDKYYNPSLKN (CDR-H2), IESIGTTYSFDY (CDR-H3), ERSSGDIGDSYVS (CDR-L1), ADDQRPS (CDR-L2), and QSYDINIDIV (CDR-L3).
89. An antibody or antigen binding fragment thereof capable of binding PDGF, wherein the antibody or antigen binding fragment comprises a CDR set comprising heavy chain CDRs 1-3 and light chain CDRs 1-3 having at least about 80%, 90%, 95%, or 99% homology to a CDR set selected from any of those in Tables A, 28 or 46-50.
90. The antibody or antigen binding fragment of claim 89, wherein the antibody or antigen binding fragment comprises a CDR set comprising heavy chain CDRs 1-3 and light chain CDRs 1-3 selected from any of those in Tables A, 28 or 46-50.
91. The antibody or antigen binding fragment of claim 89 or 90, further comprising human framework sequences.
92. The antibody or antigen binding fragment of claim 89, wherein the antibody or antigen binding fragment comprises a heavy chain variable domain and paired light chain variable domain having at least about 80%, 90%, 95%, or 99% homology to any of the paired variable domains in Tables A, 28 or 46-50.

93. The antibody or antigen binding fragment of claim 89, wherein the antibody or antigen binding fragment comprises a heavy chain variable domain and paired light chain variable domain selected from any of the paired variable domains in Tables A, 28 or 46-50.

94. The antibody or antigen binding fragment of any one of claims 76-93, comprising an Fc region from an IgG1, IgG2, IgG3, IgG4, IgA, IgM, IgE, or IgD, or a variant thereof.

95. The antibody or antigen binding fragment of any one of claims 76-94, wherein the Fc region is a variant sequence Fc region.

96. The antibody or antigen binding fragment of any one of claims 76-95, wherein the antibody or antigen binding fragment comprises:

a) a heavy chain constant region comprising a human IgG1 heavy chain sequence modified by one or more amino acid changes, wherein the changes comprise substitution of leucines at positions 234 and 235 with alanines, and optionally also comprise a substitution of histidine at position 435 with alanine, wherein the amino acid positions are numbered using EU index numbering; and

(b) a light chain constant region comprising a human kappa light chain constant region sequence.

97. A binding protein comprising heavy and light chain variable domains forming a functional binding site for VEGF, wherein the variable domains that form a functional binding site for VEGF comprise:

(i) a CDR-H1 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10} (SEQ ID NO: >>), wherein

X_1 is G;

X_2 is Y;

X_3 is T;

X_4 is F;

X_5 is T, Q, D, E, N, A, G, H, K, M, L, R, I, Y, or V;

X_6 is N, S, K, Y, T, M, G, A, I, L, E, P, Q, or F;

X_7 is Y;

X_8 is G, S, D, K, C, V, E, L, W, P, Y, M, N, or T;

X_9 is M; and

X_{10} is Y;

(ii) a CDR-H2 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-X_{15}-X_{16}-X_{17} (SEQ ID NO: >>), wherein

X_1 is W;

X_2 is I;

X_3 is N;

X_4 is T;

X_5 is E, Y, L, V, W, A, Q, H, G, K, N, M, T, or P;

X_6 is T;

X_7 is G;

X_8 is K, N, D, T, P, W, Y, V, S, M, A, I, G, R, or L;

X_9 is P;

X_{10} is T, I, M, K, A, N, P, L, V, W, D, Y, G, or E;

X_{11} is Y;

X_{12} is A;

X_{13} is D, Y, or H;

X_{14} is D;

X_{15} is F;

X_{16} is K or N; and

X_{17} is G;

(iii) a CDR-H3 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14} (SEQ ID NO: >>), wherein

X_1 is T, Y, G, I, S, K, N, P, L, W, M, F, R, or Q;

X_2 is N, H, I, T, D, F, L, E, V, Y, A, G, W, Q, or R;

X_3 is Y;

X_4 is Y;

X_5 is Y;

X_6 is R, S, N, E, M, L, T, W, Q, G, I, A, C, or V;

X_7 is S, N, T, K, M, Y, C, I, F, L, D, W, X, or V;

X_8 is Y;

X_9 is I, L, N, T, V, A, R, F, D, or S;

X_{10} is F;

X_{11} is Y;

X_{12} is F;

X_{13} is D; and

X_{14} is Y;

(iv) a CDR-L1 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11} (SEQ ID NO: >>), wherein

X_1 is R;

X_2 is A;

X_3 is S;

X_4 is E;

X_5 is S;

X_6 is V;

X_7 is S, N, D, T, R, H, E, I, L, Q, C, M, Y, K, or V;

X_8 is T, S, R, A, E, D, M, P, Y, I, W, or F;

X_9 is H, A, D, C, P, R, Y, L, Q, or K;

X_{10} is M; and

X_{11} is H, A, or P;

(v) a CDR-L2 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7 (SEQ ID NO: >>), wherein;

X_1 is G, W, V, I, E, S, or D;

X_2 is A;

X_3 is S;

X_4 is N, H, Y, M, T, F, V, R, Q, A, S, E, G, C, D, or P;

X_5 is L;

X_6 is E; and

X_7 is S or Y;

and

(vi) a CDR-L3 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9 (SEQ ID NO: >>), wherein

X_1 is Q;

X_2 is Q;

X_3 is S, C, G, I, W, R, N, A, Y, K, Q, or F;

X_4 is W, C, L, G, E, or S;

X_5 is N, I, T, D, G, M, S, H, A, R, V, L, F, K, or Q;

X_6 is D, N, Y, A, L, M, P, G, H, F, or K;

X_7 is P;

X_8 is F, M, G, Y, A, W, S, V, C, or P; and

X_9 is T.

98. The binding protein of claim 97, wherein the binding protein is also capable of binding PDGF.

99. The binding protein of claim 98, wherein the binding protein comprises heavy and light chain variable domains that form a functional binding site for PDGF, comprising:

(i) a CDR-H1 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12} (SEQ ID NO: >>), wherein

X_1 is G;

X_2 is F;

X_3 is S, I, or R;

X_4 is L;

X_5 is S, Y, A, D, T, M, R, L, C, F, W, or P;

X_6 is T;

X_7 is Y or S;

X_8 is G or E;

X_9 is M or V;

X_{10} is G, S, or R;

X_{11} is V or I; and

X_{12} is G, D, L, A, C, V, Y, R, T, E, or S;

(ii) a CDR-H2 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-X_{15}-X_{16} (SEQ ID NO: >>), wherein

X_1 is N or L;

X_2 is I;

X_3 is W, D, C, or G;

X_4 is W or C;

X_5 is D, Y, N, H, V, E, I, P, A, C, or G;

X_6 is D, G, N, or H;

X_7 is D, E, G, V, A, H, Y, N, Q, S, or L;

X_8 is K, E, T, I, Q, V, N, R, Y, L, M or C;

X_9 is Y, H, C, D, N, S, A, F, or G;

X_{10} is Y;

X_{11} is N or S;

X_{12} is P, L, or T;

X_{13} is S;

X_{14} is L;

X_{15} is K or N; and

X_{16} is N, S, or T;

(iii) a CDR-H3 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12} (SEQ ID NO: >>), wherein

X_1 is I, Y, N, L, M, V, R, K, F, C, T, or E;

X_2 is E, Q, V, K, Y, L, D, G, A, M, R, or S;

X_3 is S, T, A, Y, W, P, L, V, E, K, F, or C;

X_4 is I, G, S, M, V, L, F, N, D, H, Y, T, R, Q, K, E, or P;

X_5 is G, W, P, F, C, Y, A, E, L, V, S, D, or R;

X_6 is T, P, W, R, I, F, A, M, Y, S, L, G, D, K, V, N, or E;

X_7 is T, N, S, K, R, M, A, E, I, V, L, W, P, or Q;

X_8 is Y;

X_9 is S, E, D, Y, A, C, N, M, W, T, Q, G, I, L, or P;

X_{10} is F;

X_{11} is D or Y; and

X_{12} is Y;

(iv) a CDR CDR-L1 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13} (SEQ ID NO: >>), wherein

X_1 is E, R, or K;

X_2 is R, A, or E;

X_3 is S or Y;

X_4 is S;

X_5 is G, C, V, or S;

X_6 is D, S, or Y;

X_7 is I, N, T, or M;

X_8 is G, W, Y, S, M, H, D, R, E, N, C, A, L, V, F, T, Q, or K;

X_9 is D, Y, Q, N, H, G, E, S, K, F, R, L, C, A, or P;

X_{10} is S, T, Y, M, K, A, C, F, L, E, W, D, P, or G;

X_{11} is Y, F, L, R, H, N, C, A, D, S, or T;

X_{12} is V, F, or S; and

X_{13} is S or P;

(v) a CDR-L2 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7 (SEQ ID NO: >>), wherein

X_1 is A, G, S, W, T, L, V, F, N, P, E, or D;

X_2 is D, Y, A, or V;

X_3 is D or G;

X_4 is Q, L, R, H, W, Y, M, K, D, A, E, N, V, S, F, or P;

X_5 is R, Q, or P;

X_6 is P or A; and

X_7 is S, I, T, R, or G;

and

(vi) a CDR-L3 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10} (SEQ ID NO: >>), wherein

X_1 is Q or K;

X_2 is S, P, Q, or H;

X_3 is Y;

X_4 is D or G;

X_5 is I, L, V, E, T, S, Q, R, N, K, G, A, C, or F;

X_6 is N, F, D, E, T, I, Y, C, V, S, R, A, L, G, H, or K;

X_7 is I, T, S, V, D, R, E, M, L, P, F, N, or K;

X_8 is D, N, P, A, Y, G, H, E, V, L, Q, or T;

X_9 is I, V, L, G, T, S, N, F, A, H, R, or Q; and

X_{10} is V or T.

100. The binding protein of any one of claims 97-99, further comprising human framework sequences.

101. A binding protein comprising heavy and light chain variable domains forming a functional binding site for PDGF, wherein the variable domains that form a functional binding site for PDGF comprise:

(i) a CDR-H1 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12} (SEQ ID NO: >>), wherein

X_1 is G;

X_2 is F;

X_3 is S, I, or R;

X_4 is L;

X_5 is S, Y, A, D, T, M, R, L, C, F, W, or P;

X_6 is T;

X_7 is Y or S;

X_8 is G or E;

X_9 is M or V;

X_{10} is G, S, or R;

X_{11} is V or I; and

X_{12} is G, D, L, A, C, V, Y, R, T, E, or S;

(ii) a CDR-H2 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-X_{15}-X_{16} (SEQ ID NO: >>), wherein

X_1 is N or L;

X_2 is I;

X_3 is W, D, C, or G;

X_4 is W or C;

X_5 is D, Y, N, H, V, E, I, P, A, C, or G;

X_6 is D, G, N, or H;

X_7 is D, E, G, V, A, H, Y, N, Q, S, or L;

X_8 is K, E, T, I, Q, V, N, R, Y, L, M or C;

X_9 is Y, H, C, D, N, S, A, F, or G;

X_{10} is Y;

X_{11} is N or S;

X_{12} is P, L, or T;

X_{13} is S;

X_{14} is L;

X_{15} is K or N; and

X_{16} is N, S, or T;

(iii) a CDR-H3 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12} (SEQ ID NO: >>), wherein

X_1 is I, Y, N, L, M, V, R, K, F, C, T, or E;

X_2 is E, Q, V, K, Y, L, D, G, A, M, R, or S;

X_3 is S, T, A, Y, W, P, L, V, E, K, F, or C;

X_4 is I, G, S, M, V, L, F, N, D, H, Y, T, R, Q, K, E, or P;

X_5 is G, W, P, F, C, Y, A, E, L, V, S, D, or R;

X_6 is T, P, W, R, I, F, A, M, Y, S, L, G, D, K, V, N, or E;

X_7 is T, N, S, K, R, M, A, E, I, V, L, W, P, or Q;

X_8 is Y;

X_9 is S, E, D, Y, A, C, N, M, W, T, Q, G, I, L, or P;

X_{10} is F;

X_{11} is D or Y; and

X_{12} is Y;

(iv) a CDR CDR-L1 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13} (SEQ ID NO: >>), wherein

X_1 is E, R, or K;

X_2 is R, A, or E;

X_3 is S or Y;

X_4 is S;

X_5 is G, C, V, or S;

X_6 is D, S, or Y;

X_7 is I, N, T, or M;

X_8 is G, W, Y, S, M, H, D, R, E, N, C, A, L, V, F, T, Q, or K;

X_9 is D, Y, Q, N, H, G, E, S, K, F, R, L, C, A, or P;

X_{10} is S, T, Y, M, K, A, C, F, L, E, W, D, P, or G;

X_{11} is Y, F, L, R, H, N, C, A, D, S, or T;

X_{12} is V, F, or S; and

X_{13} is S or P;

(v) a CDR-L2 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7 (SEQ ID NO: >>), wherein

X_1 is A, G, S, W, T, L, V, F, N, P, E, or D;

X_2 is D, Y, A, or V;

X_3 is D or G;

X_4 is Q, L, R, H, W, Y, M, K, D, A, E, N, V, S, F, or P;

X_5 is R, Q, or P;

X_6 is P or A; and

X_7 is S, I, T, R, or G;

and

(vi) a CDR-L3 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10} (SEQ ID NO: >>), wherein

X_1 is Q or K;

X_2 is S, P, Q, or H;

X_3 is Y;

X_4 is D or G;

X_5 is I, L, V, E, T, S, Q, R, N, K, G, A, C, or F;

X_6 is N, F, D, E, T, I, Y, C, V, S, R, A, L, G, H, or K;

X_7 is I, T, S, V, D, R, E, M, L, P, F, N, or K;

X_8 is D, N, P, A, Y, G, H, E, V, L, Q, or T;

X_9 is I, V, L, G, T, S, N, F, A, H, R, or Q; and

X_{10} is V or T.

102. The binding protein of claim 101, wherein the binding protein is also capable of binding VEGF.

103. The binding protein of claim 102, wherein the binding protein comprises heavy and light chain variable domains that form a functional binding site for VEGF, comprising:

(i) a CDR-H1 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10} (SEQ ID NO: >>), wherein

X_1 is G;

X_2 is Y;

X_3 is T;

X_4 is F;

X_5 is T, Q, D, E, N, A, G, H, K, M, L, R, I, Y, or V;

X_6 is N, S, K, Y, T, M, G, A, I, L, E, P, Q, or F;

X_7 is Y;

X_8 is G, S, D, K, C, V, E, L, W, P, Y, M, N, or T;

X_9 is M; and

X_{10} is Y;

(ii) a CDR-H2 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-X_{15}-X_{16}-X_{17} (SEQ ID NO: >>), wherein

X_1 is W;

X_2 is I;

X_3 is N;

X_4 is T;

X_5 is E, Y, L, V, W, A, Q, H, G, K, N, M, T, or P;

X_6 is T;

X_7 is G;

X_8 is K, N, D, T, P, W, Y, V, S, M, A, I, G, R, or L;

X_9 is P;

X_{10} is T, I, M, K, A, N, P, L, V, W, D, Y, G, or E;

X_{11} is Y;

X_{12} is A;

X_{13} is D, Y, or H;

X_{14} is D;

X_{15} is F;

X_{16} is K or N; and

X_{17} is G;

(iii) a CDR-H3 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14} (SEQ ID NO: >>), wherein

X_1 is T, Y, G, I, S, K, N, P, L, W, M, F, R, or Q;

X_2 is N, H, I, T, D, F, L, E, V, Y, A, G, W, Q, or R;

X_3 is Y;

X_4 is Y;

X_5 is Y;

X_6 is R, S, N, E, M, L, T, W, Q, G, I, A, C, or V;

X_7 is S, N, T, K, M, Y, C, I, F, L, D, W, X, or V;

X_8 is Y;

X_9 is I, L, N, T, V, A, R, F, D, or S;

X_{10} is F;

X_{11} is Y;

X_{12} is F;

X_{13} is D; and

X_{14} is Y;

(iv) a CDR-L1 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11} (SEQ ID NO: >>), wherein

X_1 is R;

X_2 is A;

X_3 is S;

X_4 is E;

X_5 is S;

X_6 is V;

X_7 is S, N, D, T, R, H, E, I, L, Q, C, M, Y, K, or V;

X_8 is T, S, R, A, E, D, M, P, Y, I, W, or F;

X_9 is H, A, D, C, P, R, Y, L, Q, or K;

X_{10} is M; and

X_{11} is H, A, or P;

(v) a CDR-L2 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7 (SEQ ID NO: >>), wherein;

X_1 is G, W, V, I, E, S, or D;

X_2 is A;

X_3 is S;

X_4 is N, H, Y, M, T, F, V, R, Q, A, S, E, G, C, D, or P;

X_5 is L;

X_6 is E; and

X_7 is S or Y;

and

(vi) a CDR-L3 comprising X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9 (SEQ ID NO: >>), wherein

X_1 is Q;

X_2 is Q;

X_3 is S, C, G, I, W, R, N, A, Y, K, Q, or F;

X_4 is W, C, L, G, E, or S;

X_5 is N, I, T, D, G, M, S, H, A, R, V, L, F, K, or Q;

X_6 is D, N, Y, A, L, M, P, G, H, F, or K;

X_7 is P;

X_8 is F, M, G, Y, A, W, S, V, C, or P; and

X_9 is T.

104. The binding protein of any one of claims 101-103, further comprising human framework sequences.

105. A binding protein comprising heavy and light chain variable domains forming a functional binding site for VEGF, wherein the variable domains that form a functional binding site for VEGF comprise a set of heavy chain CDRs 1-3 and paired light chain CDRs 1-3 selected from any of the CDR sets listed in Tables A, 27 or 38-42.

106. The binding protein of claim 105, wherein the variable domains that form a functional binding site for VEGF comprise a heavy chain and paired light chain selected from any of those listed in Tables A, 27 or 38-42.

107. The binding protein of claim 105 or 106, wherein the binding protein is also capable of binding PDGF.

108. The binding protein of claim 107, wherein the binding protein comprises heavy and light chain variable domains forming a functional binding site for PDGF, and the variable domains that form the functional binding site for PDGF comprise a set of heavy chain CDRs 1-3 and

paired light chain CDRs 1-3 selected from any of the CDR sets listed in Tables A, 28 or 46-50.

109. The binding protein of claim 108, wherein the variable domains that form a functional target binding site for PDGF comprise a heavy chain and paired light chain selected from any of those listed in Tables A, 28 or 46-50.

110. A binding protein comprising heavy and light chain variable domains forming a functional binding site for PDGF, wherein the variable domains that form a functional binding site for PDGF comprise a set of heavy chain CDRs 1-3 and paired light chain CDRs 1-3 selected from any of the CDR sets listed in Tables A, 28 or 46-50.

111. The binding protein of claim 110, wherein the variable domains that form a functional binding site for PDGF comprise a heavy chain and paired light chain selected from any of those listed in Tables A, 28 or 46-50.

112. The binding protein of claim 110 or 111, wherein the binding protein is also capable of binding VEGF.

113. The binding protein of claim 112, wherein the binding protein comprises heavy and light chain variable domains forming a functional binding site for VEGF, and the variable domains that form the functional binding site for VEGF comprise a set of heavy chain CDRs 1-3 and paired light chain CDRs 1-3 selected from any of the CDR sets listed in Tables A, 27 or 38-42.

114. The binding protein of claim 112 or 113, wherein the variable domains that form a functional binding site for VEGF comprise a heavy chain and paired light chain selected from any of those listed in Tables A, 27 or 38-42.

115. A binding protein comprising heavy and light chain variable domains forming a functional binding site for VEGF and heavy and light chain variable domains forming a functional binding site for PDGF, wherein

a. the variable domains that form a functional binding site for VEGF comprise:
CDRs 1-3 from SEQ ID NO: 17 and CDRs-1-3 from SEQ ID NO: 18,
CDRs 1-3 from SEQ ID NO: 19 and CDRs-1-3 from SEQ ID NO: 20,
CDRs 1-3 from SEQ ID NO: 21 and CDRs-1-3 from SEQ ID NO: 22,
CDRs 1-3 from SEQ ID NO: 23 and CDRs-1-3 from SEQ ID NO: 24,
CDRs 1-3 from SEQ ID NO: 25 and CDRs-1-3 from SEQ ID NO: 26,
CDRs 1-3 from SEQ ID NO: 27 and CDRs-1-3 from SEQ ID NO: 28,
CDRs 1-3 from SEQ ID NO: 29 and CDRs-1-3 from SEQ ID NO: 30,
CDRs 1-3 from SEQ ID NO: 31 and CDRs-1-3 from SEQ ID NO: 32,
CDRs 1-3 from SEQ ID NO: 33 and CDRs-1-3 from SEQ ID NO: 34,
CDRs 1-3 from SEQ ID NO: 35 and CDRs-1-3 from SEQ ID NO: 36,

CDRs 1-3 from SEQ ID NO: 37 and CDRs-1-3 from SEQ ID NO: 38,
CDRs 1-3 from SEQ ID NO: 39 and CDRs-1-3 from SEQ ID NO: 40,
CDRs 1-3 from SEQ ID NO: 41 and CDRs-1-3 from SEQ ID NO: 42, or
CDRs 1-3 from SEQ ID NO: 43 and CDRs-1-3 from SEQ ID NO: 44, and

b. the variable domains that form a functional binding site for PDGF comprise:
CDRs 1-3 from SEQ ID NO: 1 and CDRs-1-3 from SEQ ID NO: 2,
CDRs 1-3 from SEQ ID NO: 3 and CDRs-1-3 from SEQ ID NO: 4,
CDRs 1-3 from SEQ ID NO: 5 and CDRs-1-3 from SEQ ID NO: 6,
CDRs 1-3 from SEQ ID NO: 7 and CDRs-1-3 from SEQ ID NO: 8,
CDRs 1-3 from SEQ ID NO: 9 and CDRs-1-3 from SEQ ID NO: 10,
CDRs 1-3 from SEQ ID NO: 11 and CDRs-1-3 from SEQ ID NO: 12,
CDRs 1-3 from SEQ ID NO: 13 and CDRs-1-3 from SEQ ID NO: 14,
CDRs 1-3 from SEQ ID NO: 15 and CDRs-1-3 from SEQ ID NO: 16, or
CDRs 1-3 from SEQ ID NO: 211 and CDRs-1-3 from SEQ ID NO: 212.

116. A binding protein comprising heavy and light chain variable domains forming a functional binding site for VEGF and heavy and light chain variable domains forming a functional binding site for PDGF, wherein

a. the variable domains that form a functional binding site for VEGF comprise a sequence selected from the group consisting of SEQ ID NO: 17-44 and

b. the variable domains that form a functional binding site for PDGF comprise a sequence selected from the group consisting of SEQ ID NO: 1-16, 211, and 212.

117. The binding protein of any one of claims 115-116, wherein:

a. the variable domains that form a functional binding site for VEGF comprise:
SEQ ID NO: 17 and SEQ ID NO: 18,
SEQ ID NO: 19 and SEQ ID NO: 20,
SEQ ID NO: 21 and SEQ ID NO: 22,
SEQ ID NO: 23 and SEQ ID NO: 24,
SEQ ID NO: 25 and SEQ ID NO: 26,
SEQ ID NO: 27 and SEQ ID NO: 28,
SEQ ID NO: 29 and SEQ ID NO: 30,
SEQ ID NO: 31 and SEQ ID NO: 32,
SEQ ID NO: 33 and SEQ ID NO: 34,
SEQ ID NO: 35 and SEQ ID NO: 36,
SEQ ID NO: 37 and SEQ ID NO: 38,
SEQ ID NO: 39 and SEQ ID NO: 40,

SEQ ID NO: 41 and SEQ ID NO: 42, or

SEQ ID NO: 43 and SEQ ID NO: 44, and

b. the variable domains that form a functional binding site for PDGF comprise:

SEQ ID NO: 1 and SEQ ID NO: 2,

SEQ ID NO: 3 and SEQ ID NO: 4,

SEQ ID NO: 5 and SEQ ID NO: 6,

SEQ ID NO: 7 and SEQ ID NO: 8,

SEQ ID NO: 9 and SEQ ID NO: 10,

SEQ ID NO: 11 and SEQ ID NO: 12,

SEQ ID NO: 13 and SEQ ID NO: 14,

SEQ ID NO: 15 and SEQ ID NO: 16, or

SEQ ID NO: 211 and SEQ ID NO: 212.

118. The binding protein of any one of claims 97-117, wherein the binding protein is an antibody or an antigen binding fragment thereof, a monoclonal antibody, a humanized antibody, a human antibody, a bispecific antibody, a bispecific binding protein, a multispecific binding protein, a DVD-Ig binding protein, a CrossMab binding protein, a diabody, a tandem single-chain Fv molecule, a bispecific diabody, a single-chain diabody molecule, or a di-diabody.

119. The binding protein of claim 118, wherein the binding protein comprises PR-1610561 (comprising SEQ ID NOs: 131 and 132) or PR-1572102 (comprising SEQ ID NOs: 88 and 89) or PR-1572105 (comprising SEQ ID NOs: 94 and 95) or PR1611292 (comprising SEQ ID NOs: 141 and 142).

120. A binding protein that competes with a binding protein of any one of claims 1-44 for binding to one or more of VEGF, PDGF, a VEGF receptor, and a PDGF receptor.

121. A binding protein that competes with an antibody or antigen binding fragment of any one of claims 76-96 for binding to one or more of VEGF, PDGF, a VEGF receptor, and a PDGF receptor.

122. A binding protein that competes with a binding protein of any one of claims 97-119 for binding to one or more of VEGF, PDGF, a VEGF receptor, and a PDGF receptor.

123. A binding protein that binds to the same epitope of VEGF, PDGF, a VEGF receptor, and/or a PDGF receptor as a binding protein of any one of claims 1-44.

124. A binding protein that binds to the same epitope of VEGF, PDGF, a VEGF receptor, and/or a PDGF receptor as an antibody or antigen binding fragment of any one of claims 76-96.

125. A binding protein that binds to the same epitope of VEGF, PDGF, a VEGF receptor, and/or a PDGF receptor as a binding protein of any one of claims 97-119.

126. The binding protein of any one of claims 120-125, wherein the binding is an antibody or an antigen binding fragment thereof, a monoclonal antibody, a humanized antibody, a human antibody, a bispecific antibody, a bispecific binding protein, a multispecific binding protein, a DVD-Ig binding protein, a CrossMab binding protein, a diabody, a tandem single-chain Fv molecule, a bispecific diabody, a single-chain diabody molecule, or a di-diabody.

127. An antibody or antigen binding fragment thereof comprising heavy and light chain variable domains forming a functional binding site for VEGF, wherein the variable domains that form a functional binding site for VEGF comprise CDRs 1-3 from SEQ ID NO: 35 and CDRs 1-3 from SEQ ID NO: 36, or comprise SEQ ID NO: 35 and SEQ ID NO: 36.

128. An antibody or antigen binding fragment thereof comprising heavy and light chain variable domains forming a functional binding site for VEGF, wherein the variable domains that form a functional binding site for VEGF comprise CDRs 1-3 from SEQ ID NO: 17 and CDRs 1-3 from SEQ ID NO: 18, or comprise SEQ ID NO: 17 and SEQ ID NO: 18.

129. An antibody or antigen binding fragment thereof comprising heavy and light chain variable domains forming a functional binding site for VEGF, wherein the variable domains that form a functional binding site for VEGF comprise CDRs 1-3 from SEQ ID NO: 39 and CDRs 1-3 from SEQ ID NO: 40, or comprise SEQ ID NO: 39 and SEQ ID NO: 40.

130. An antibody or antigen binding fragment thereof comprising heavy and light chain variable domains forming a functional binding site for PDGF, wherein the variable domains that form a functional binding site for PDGF comprise CDRs 1-3 from SEQ ID NO: 1 and CDRs 1-3 from SEQ ID NO: 2, or comprise SEQ ID NO: 1 and SEQ ID NO: 2.

131. An antibody or antigen binding fragment thereof comprising heavy and light chain variable domains forming a functional binding site for PDGF, wherein the variable domains that form a functional binding site for PDGF comprise CDRs 1-3 from SEQ ID NO: 15 and CDRs 1-3 from SEQ ID NO: 16, or comprise SEQ ID NO: 15 and SEQ ID NO: 16.

132. A binding protein comprising heavy and light chain variable domains forming a functional binding site for VEGF, wherein the variable domains that form a functional binding site for VEGF comprise CDRs 1-3 from SEQ ID NO: 35 and CDRs 1-3 from SEQ ID NO: 36.

133. The binding protein of claim 132, wherein the binding protein also comprises heavy and light chain variable domains forming a functional binding site for PDGF, and wherein the variable domains that form a functional binding site for PDGF comprise a CDR set of heavy chain CDRs 1-3 and paired light chain CDRs 1-3 selected from any of Tables A, 1.4.1-1.4.7, 28, and 46-50.

134. A binding protein comprising heavy and light chain variable domains forming a functional binding site for VEGF, wherein the variable domains that form a functional

binding site for VEGF comprise CDRs 1-3 from SEQ ID NO: 17 and CDRs 1-3 from SEQ ID NO: 18.

135. The binding protein of claim 134, wherein the binding protein also comprises heavy and light chain variable domains forming a functional binding site for PDGF, and wherein the variable domains that form a functional binding site for PDGF comprise a CDR set of heavy chain CDRs 1-3 and paired light chain CDRs 1-3 selected from any of Tables A, 1.4.1-1.4.7, 28, and 46-50.

136. A binding protein comprising heavy and light chain variable domains forming a functional binding site for VEGF, wherein the variable domains that form a functional binding site for VEGF comprise CDRs 1-3 from SEQ ID NO: 39 and CDRs 1-3 from SEQ ID NO: 40.

137. The binding protein of claim 136, wherein the binding protein also comprises heavy and light chain variable domains forming a functional binding site for PDGF, and wherein the variable domains that form a functional binding site for PDGF comprise a CDR set of heavy chain CDRs 1-3 and paired light chain CDRs 1-3 selected from any of Tables A, 1.4.1-1.4.7, 28, and 46-50.

138. A binding protein comprising heavy and light chain variable domains forming a functional binding site for PDGF, wherein the variable domains that form a functional binding site for PDGF comprise CDRs 1-3 from SEQ ID NO: 1 and CDRs 1-3 from SEQ ID NO: 2.

139. The binding protein of claim 138, wherein the binding protein also comprises heavy and light chain variable domains forming a functional binding site for VEGF, and wherein the variable domains that form a functional binding site for VEGF comprise a CDR set of heavy chain CDRs 1-3 and paired light chain CDRs 1-3 selected from any of Tables A, 2.4.1-2.4.9, 27, and 38-42.

140. A binding protein comprising heavy and light chain variable domains forming a functional binding site for PDGF, wherein the variable domains that form a functional binding site for PDGF comprise CDRs 1-3 from SEQ ID NO: 15 and CDRs 1-3 from SEQ ID NO: 16.

141. The binding protein of claim 140, wherein the binding protein also comprises heavy and light chain variable domains forming a functional binding site for VEGF, and wherein the variable domains that form a functional binding site for VEGF comprise a CDR set of heavy chain CDRs 1-3 and paired light chain CDRs 1-3 selected from any of Tables A, 2.4.1-2.4.9, 27, and 38-42.

142. A binding protein comprising heavy and light chain variable domains forming a functional binding site for VEGF and heavy and light chain variable domains forming a functional binding site for PDGF, wherein:

(a) the variable domains that form a functional binding site for VEGF comprise CDRs 1-3 from SEQ ID NO: 35 and CDRs 1-3 from SEQ ID NO: 36; and

(b) the variable domains that form a functional binding site for PDGF comprise CDRs 1-3 from SEQ ID NO: 15 and CDRs 1-3 from SEQ ID NO: 16.

143. A binding protein comprising heavy and light chain variable domains forming a functional binding site for VEGF and heavy and light chain variable domains forming a functional binding site for PDGF, wherein:

(a) the variable domains that form a functional binding site for VEGF comprise CDRs 1-3 from SEQ ID NO: 17 and CDRs 1-3 from SEQ ID NO: 18; and

(b) the variable domains that form a functional binding site for PDGF comprise CDRs 1-3 from SEQ ID NO: 1 and CDRs 1-3 from SEQ ID NO: 2.

144. A binding protein comprising heavy and light chain variable domains forming a functional binding site for VEGF and heavy and light chain variable domains forming a functional binding site for PDGF, wherein:

(a) the variable domains that form a functional binding site for VEGF comprise CDRs 1-3 from SEQ ID NO: 39 and CDRs 1-3 from SEQ ID NO: 40; and

(b) the variable domains that form a functional binding site for PDGF comprise CDRs 1-3 from SEQ ID NO: 15 and CDRs 1-3 from SEQ ID NO: 16.

145. A binding protein comprising heavy and light chain variable domains forming a functional binding site for VEGF and heavy and light chain variable domains forming a functional binding site for PDGF, wherein:

(a) the variable domains that form a functional binding site for VEGF comprise SEQ ID NO: 35 and SEQ ID NO: 36; and

(b) the variable domains that form a functional binding site for PDGF comprise SEQ ID NO: 15 and SEQ ID NO: 16.

146. A binding protein comprising heavy and light chain variable domains forming a functional binding site for VEGF and heavy and light chain variable domains forming a functional binding site for PDGF, wherein:

(a) the variable domains that form a functional binding site for VEGF comprise SEQ ID NO: 17 and SEQ ID NO: 18; and

(b) the variable domains that form a functional binding site for PDGF comprise SEQ ID NO: 1 and SEQ ID NO: 2.

147. A binding protein comprising heavy and light chain variable domains forming a functional binding site for VEGF and heavy and light chain variable domains forming a functional binding site for PDGF, wherein:

(a) the variable domains that form a functional binding site for VEGF comprise SEQ ID NO: 39 and SEQ ID NO: 40; and

(b) the variable domains that form a functional binding site for PDGF comprise SEQ ID NO: 15 and SEQ ID NO: 16.

148. A binding protein capable of binding VEGF and PDGF, wherein the binding protein comprises a DVD-Ig heavy chain variable domain of SEQ ID NO: 131 and a DVD-Ig light chain variable domain of SEQ ID NO: 132.

149. A binding protein capable of binding VEGF and PDGF, wherein the binding protein comprises a DVD-Ig heavy chain variable domain of SEQ ID NO: 88 and a DVD-Ig light chain variable domain of SEQ ID NO: 89.

150. A binding protein capable of binding VEGF and PDGF, wherein the binding protein comprises a DVD-Ig heavy chain variable domain of SEQ ID NO: 94 and a DVD-Ig light chain variable domain of SEQ ID NO: 95.

151. A binding protein capable of binding VEGF and PDGF, wherein the binding protein comprises a DVD-Ig heavy chain variable domain of SEQ ID NO: 141 and a DVD-Ig light chain variable domain of SEQ ID NO: 142.

152. A binding protein capable of binding VEGF and PDGF, comprising SEQ ID NO: 131 and SEQ ID NO: 132.

153. A binding protein capable of binding VEGF and PDGF, comprising SEQ ID NO: 88 and SEQ ID NO: 89.

154. A binding protein capable of binding VEGF and PDGF, comprising SEQ ID NO: 94 and SEQ ID NO: 95.

155. A binding protein capable of binding VEGF and PDGF, comprising SEQ ID NO: 141 and SEQ ID NO: 142.

FIG. 1A

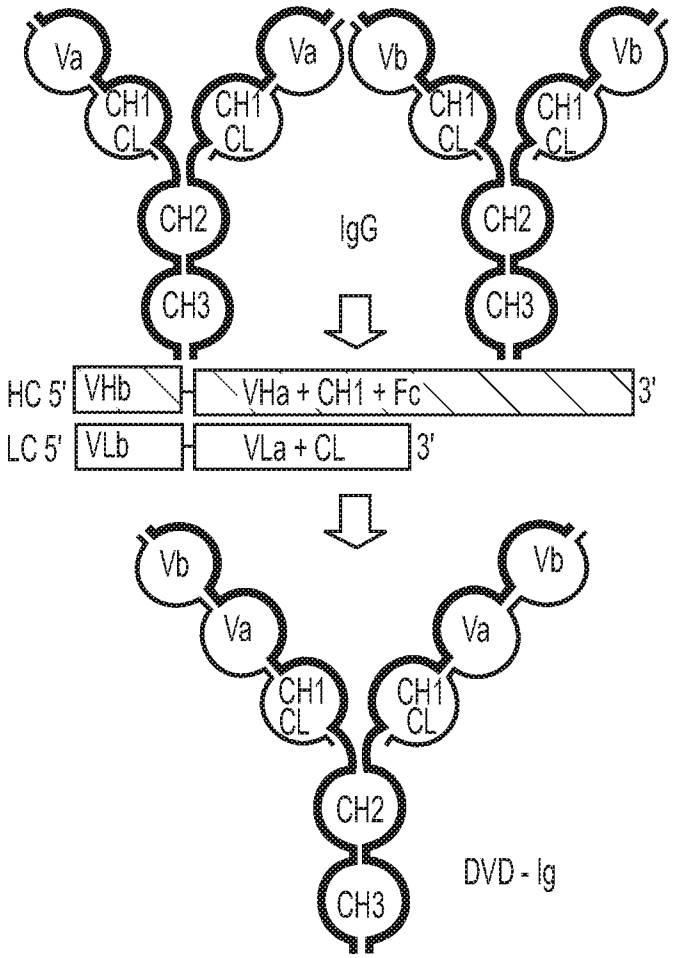
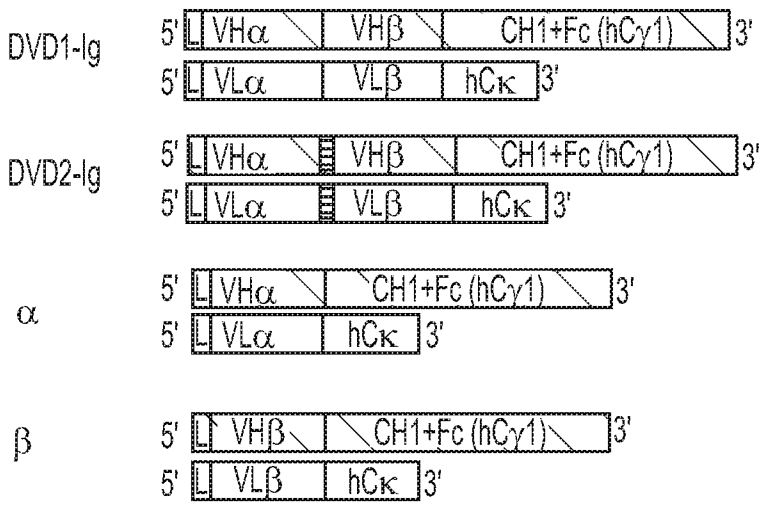

Va
Vb
CH1
CL
CH2
CH3
IgG
HC 5'
VHb
VHa + CH1 + Fc
3'
LC 5'
VLb
VLa + CL
3'
DVD - Ig

FIG. 1B


DVD1-Ig
5'
L
VHα
VHβ
CH1+Fc (hCγ1)
3'
VLα
VLβ
hCκ
DVD2-Ig
α
β

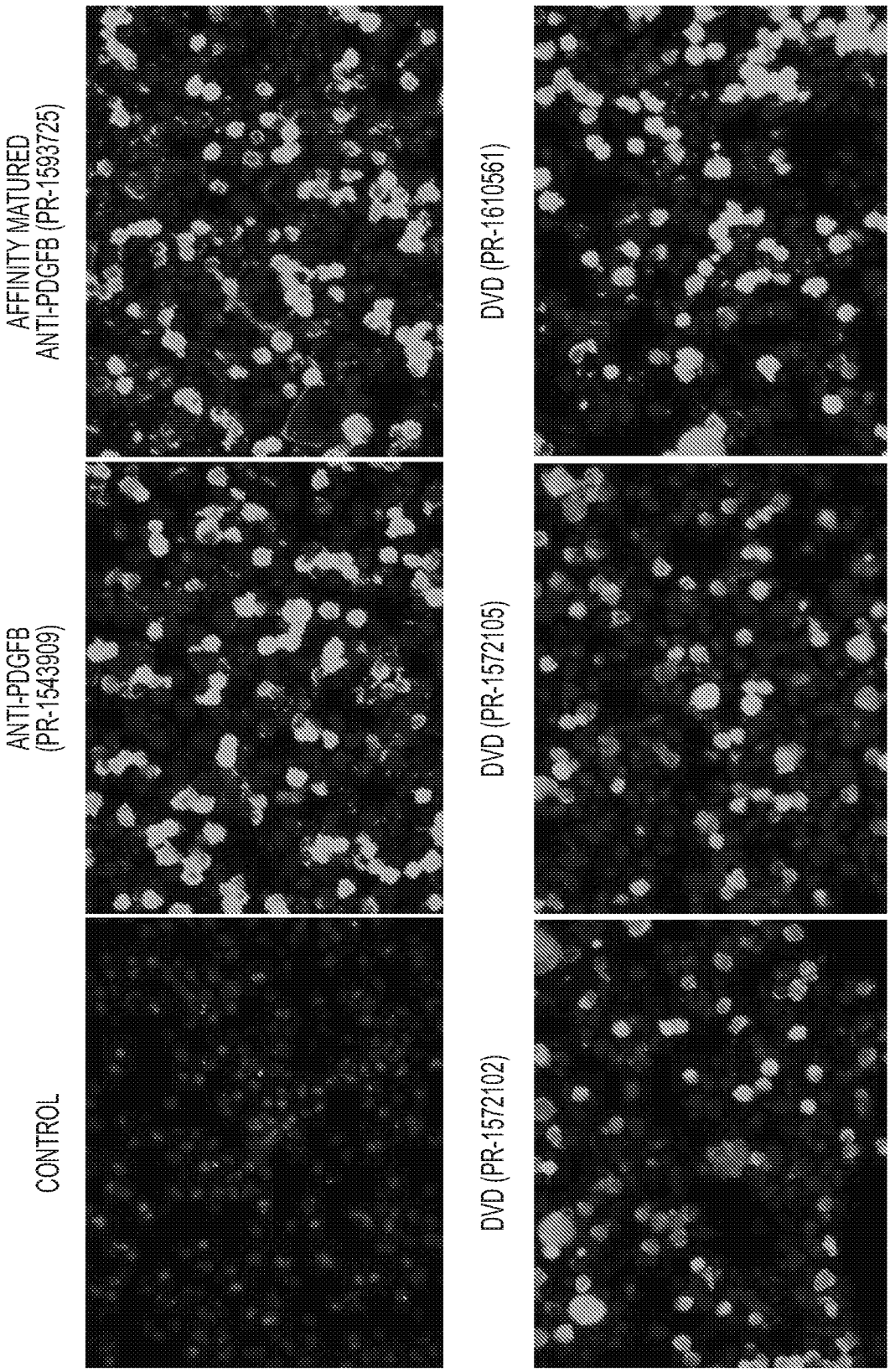

CONTROL
ANTI-PDGFB (PR-1543909)
AFFINITY MATURED ANTI-PDGFB (PR-1593725)
DVD (PR-1572102)
DVD (PR-1572105)
DVD (PR-1610561)

FIG. 2A

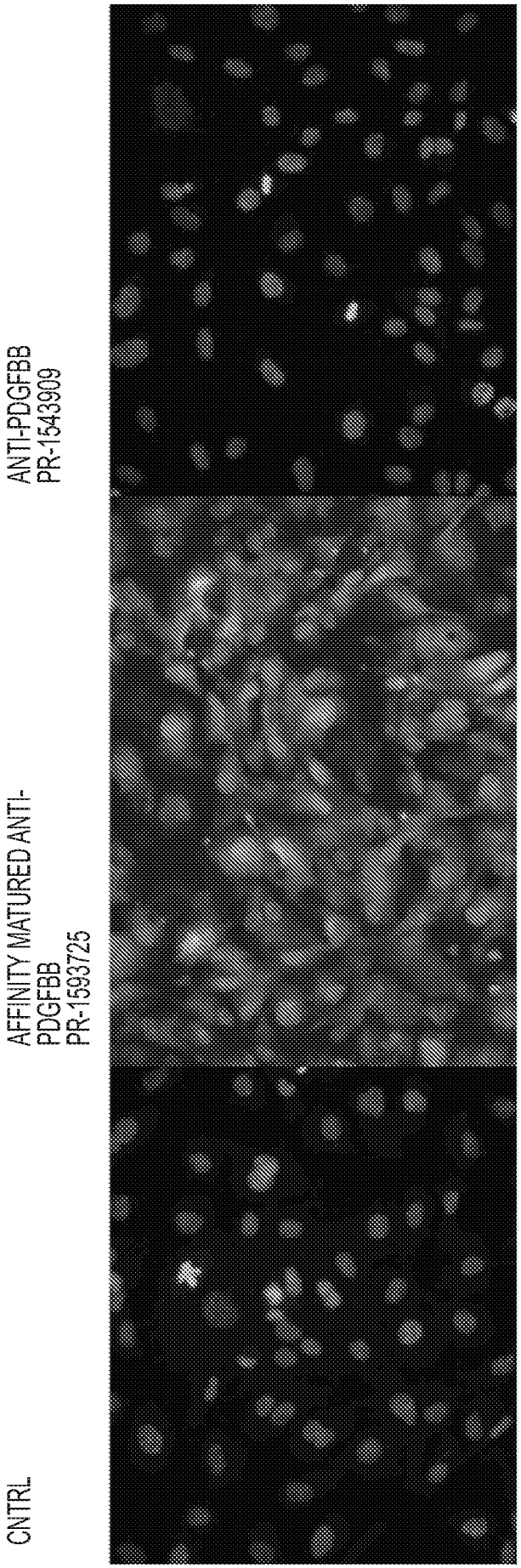

CNTRL
AFFINITY MATURED ANTI-PDGFBB PR-1593725
ANTI-PDGFBB PR-1543909

FIG. 2B

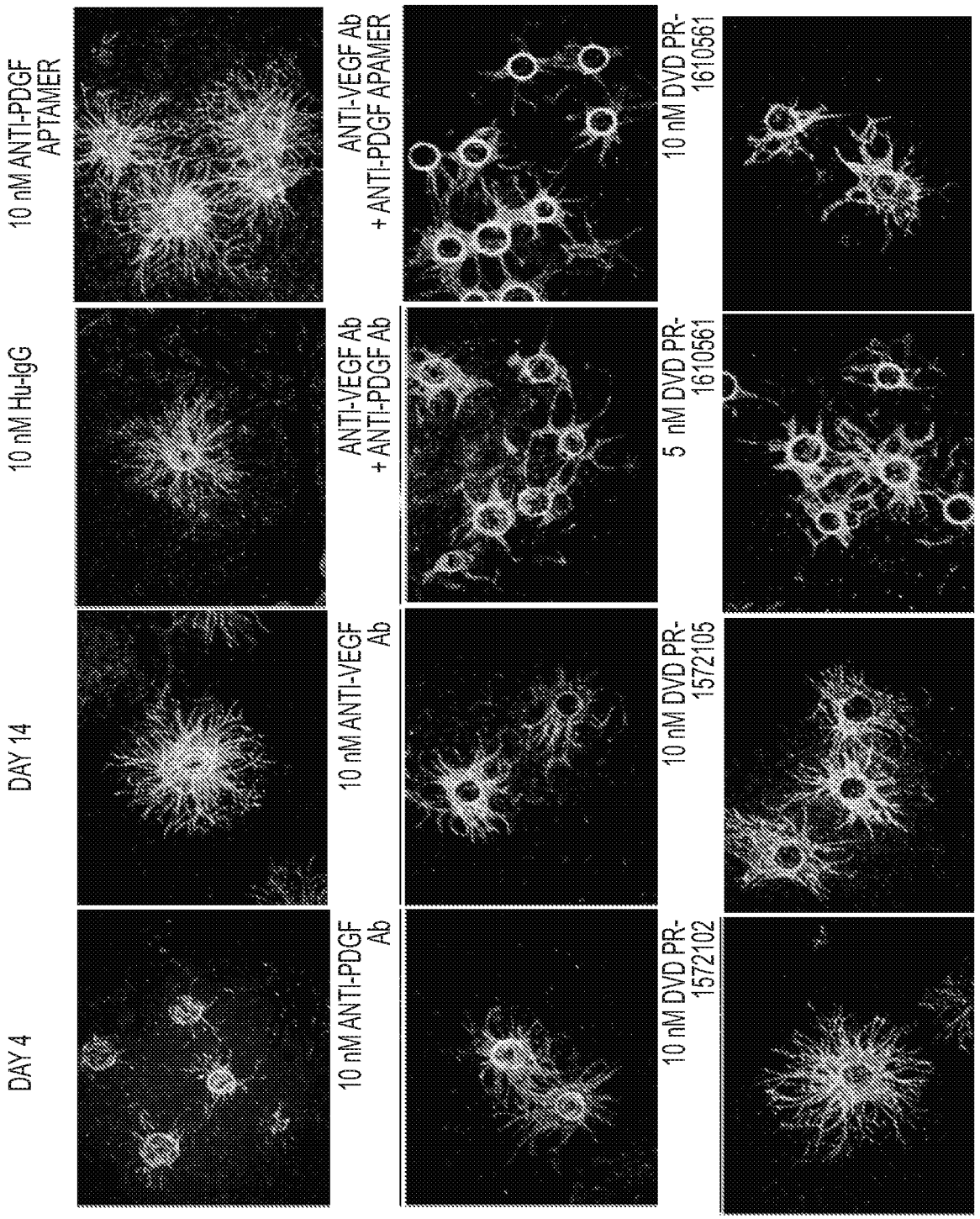

DAY 4
DAY 14
10 nM Hu-IgG
10 nM ANTI-PDGF APTAMER
10 nM ANTI-PDGF Ab
10 nM ANTI-VEGF Ab
ANTI-VEGF Ab + ANTI-PDGF Ab
ANTI-VEGF Ab + ANTI-PDGF APAMER
10 nM DVD PR-1572102
10 nM DVD PR-1572105
5 nM DVD PR-1610561
10 nM DVD PR-1610561

FIG. 3

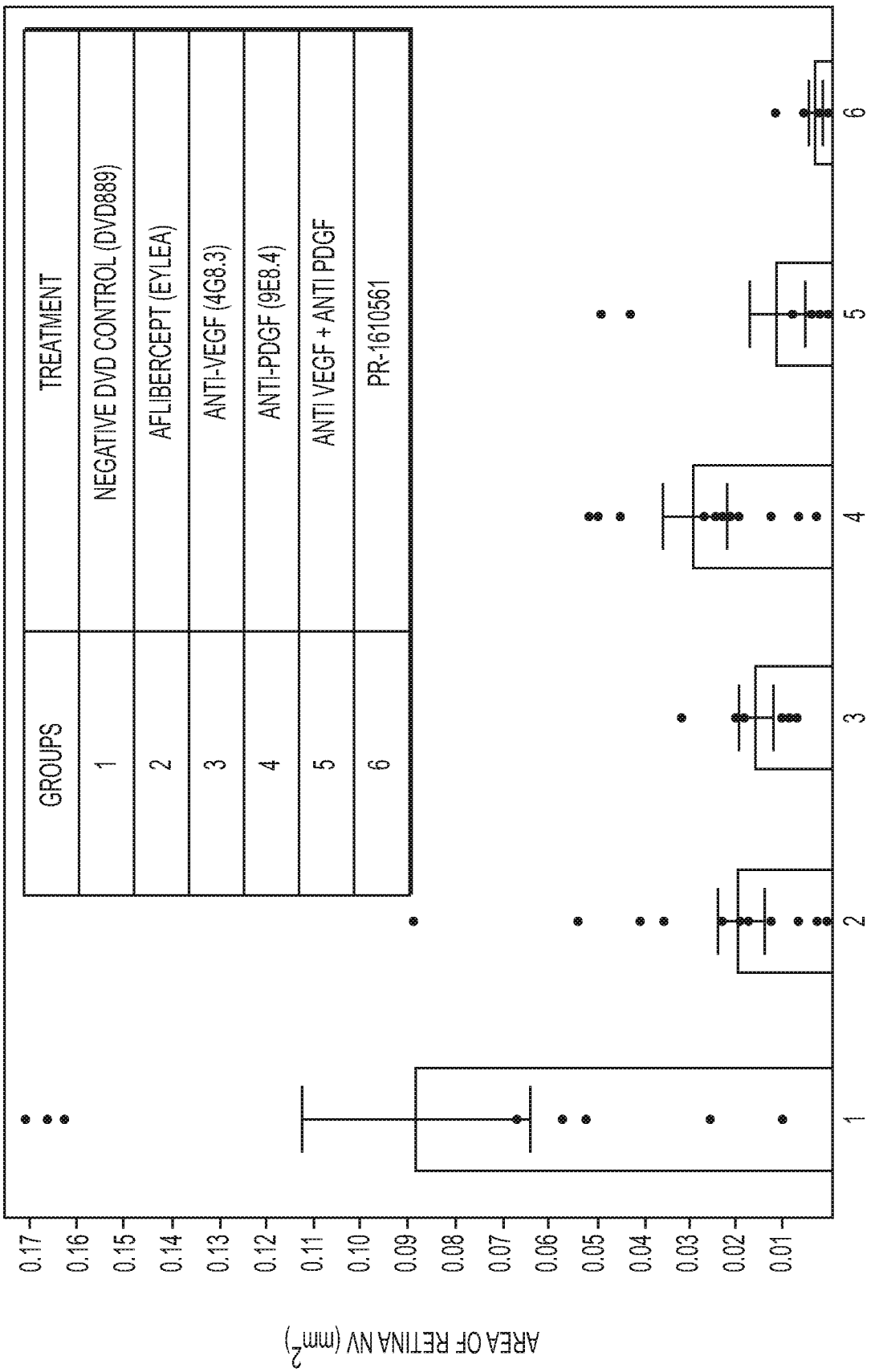

GROUPS
TREATMENT
1
NEGATIVE DVD CONTROL (DVD889)
2
AFLIBERCEPT (EYLEA)
3
ANTI-VEGF (4G8.3)
4
ANTI-PDGF (9E8.4)
5
ANTI VEGF + ANTI PDGF
6
PR-1610561
AREA OF RETINA NV (mm²)
0.17
0.16
0.15
0.14
0.13
0.12
0.11
0.10
0.09
0.08
0.07
0.06
0.05
0.04
0.03
0.02
0.01
1
2
3
4
5
6

FIG. 4

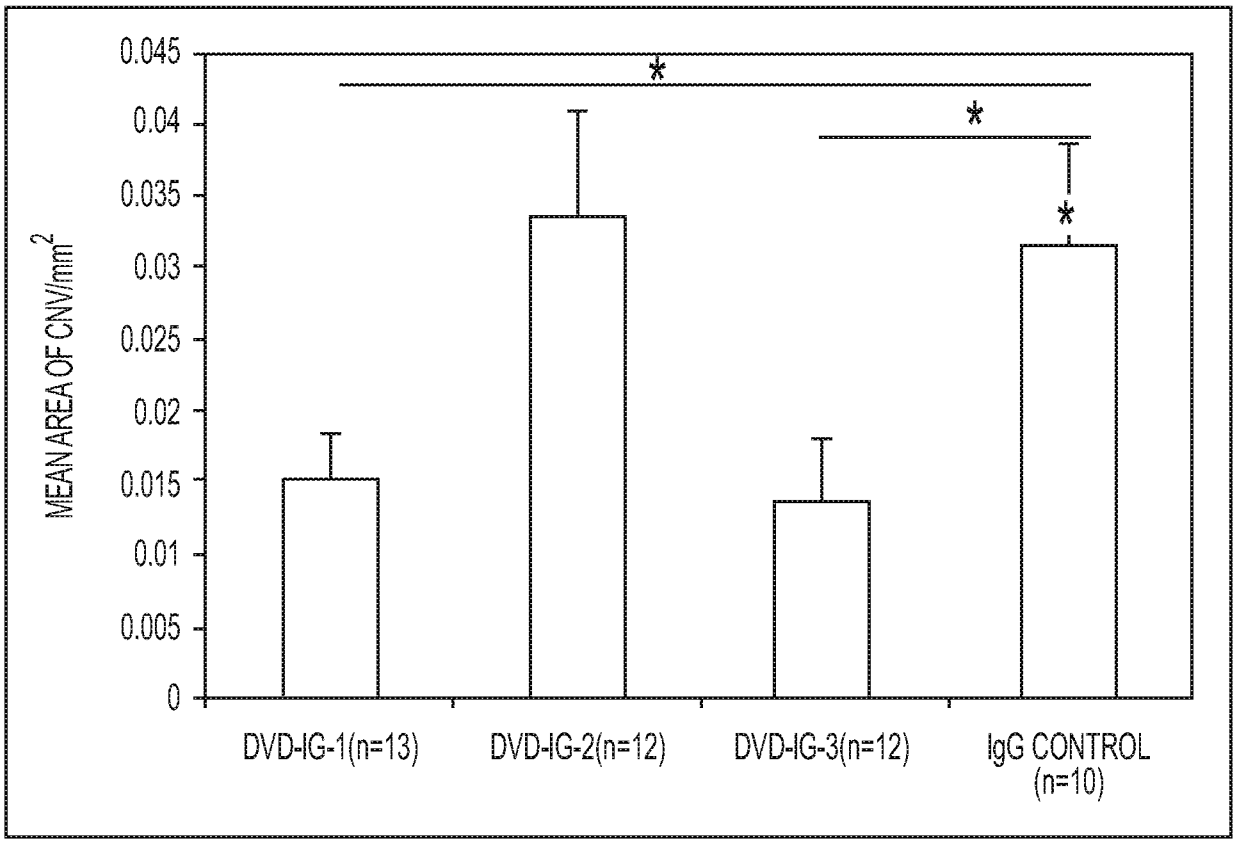

MEAN AREA OF CNV/mm2
0.045
0.04
0.035
0.03
0.025
0.02
0.015
0.01
0.005
0
*
*
*
DVD-IG-1(n=13)
DVD-IG-2(n=12)
DVD-IG-3(n=12)
IgG CONTROL (n=10)

FIG. 5A

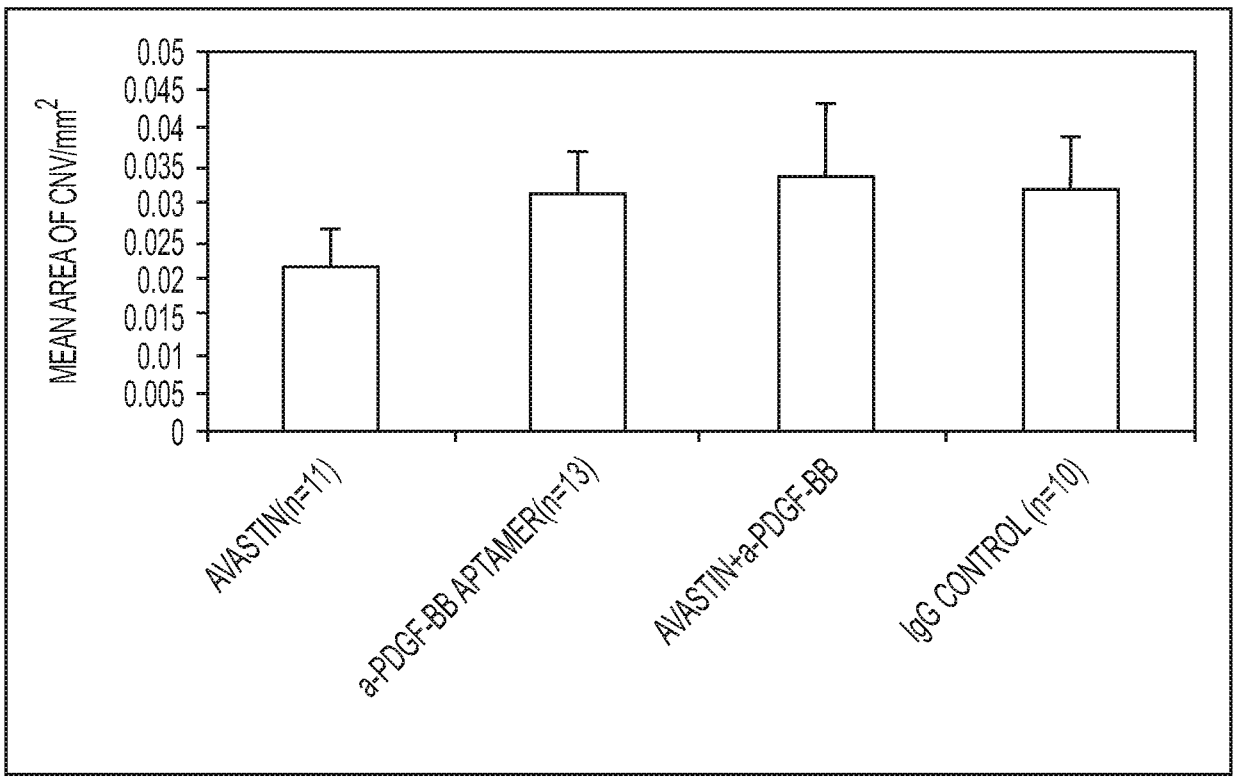

MEAN AREA OF CNV/mm2
0.05
0.045
0.04
0.035
0.03
0.025
0.02
0.015
0.01
0.005
0
AVASTIN(n=11)
a-PDGF-BB APTAMER(n=13)
AVASTIN+a-PDGF-BB
IgG CONTROL (n=10)

FIG. 5B

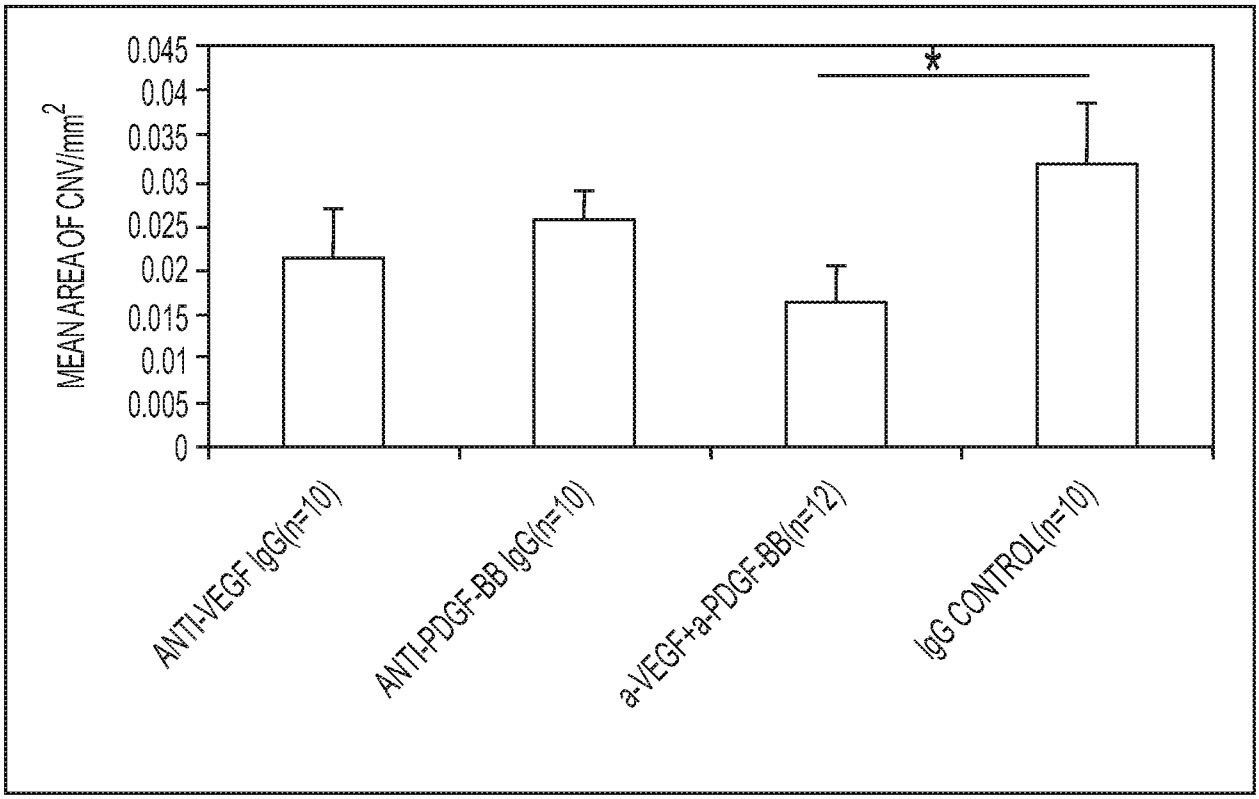

MEAN AREA OF CNV/mm2
0.045
0.04
0.035
0.03
0.025
0.02
0.015
0.01
0.005
0
*
ANTI-VEGF IgG(n=10)
ANTI-PDGF-BB IgG(n=10)
a-VEGF+a-PDGF-BB(n=12)
IgG CONTROL(n=10)

FIG. 5C

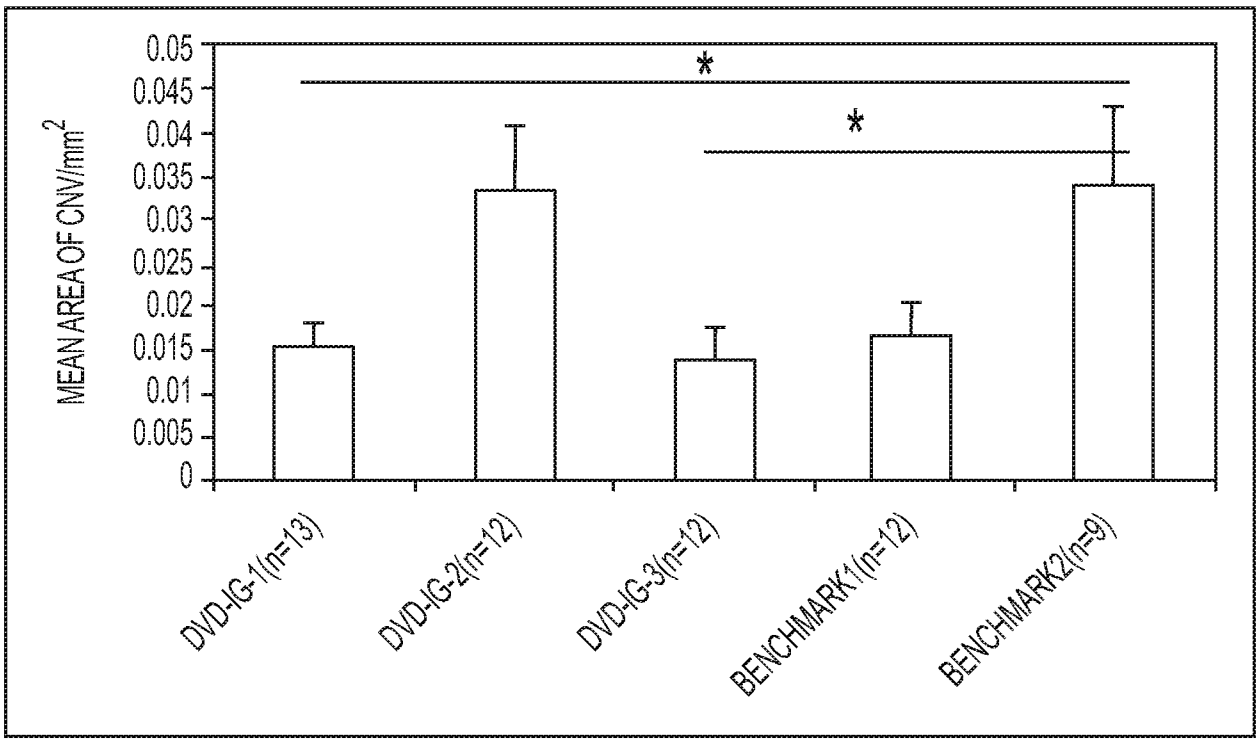

MEAN AREA OF CNV/mm2
0.05
0.045
0.04
0.035
0.03
0.025
0.02
0.015
0.01
0.005
0
*
*
DVD-IG-1(n=13)
DVD-IG-2(n=12)
DVD-IG-3(n=12)
BENCHMARK1(n=12)
BENCHMARK2(n=9)

FIG. 5D

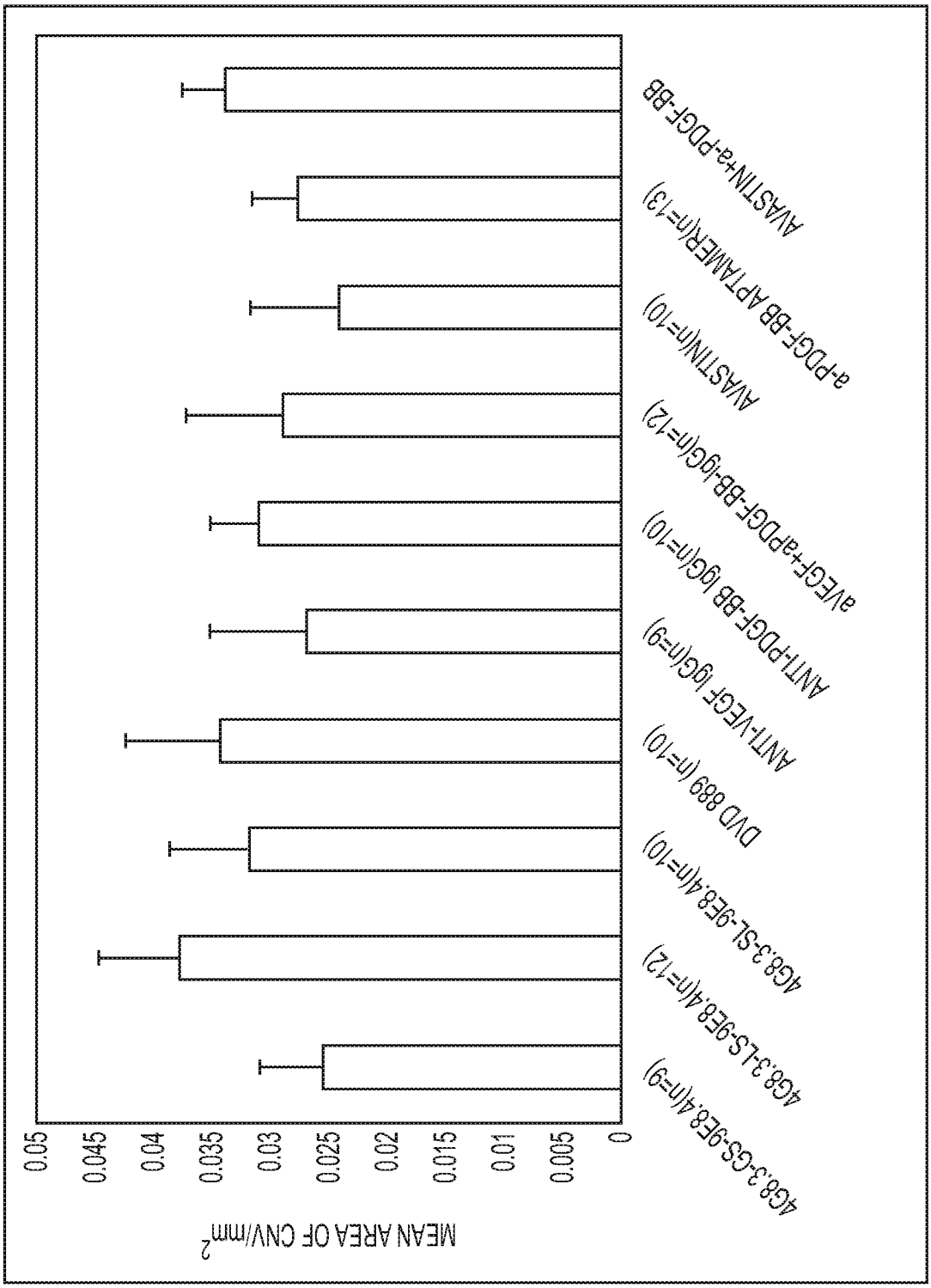

MEAN AREA OF CNV/mm2
0.05
0.045
0.04
0.035
0.03
0.025
0.02
0.015
0.01
0.005
0
4G8.3-GS-9E8.4(n=9)
4G8.3-LS-9E8.4(n=12)
4G8.3-SL-9E8.4(n=10)
DVD 889 (n=10)
ANTI-VEGF IgG(n=9)
ANTI-PDGF-BB IgG(n=10)
aVEGF+aPDGF-BB-IgG(n=12)
AV/ASTIN(n=10)
a-PDGF-BB APTAMER(n=13)
AV/ASTIN+a-PDGF-BB

FIG. 6

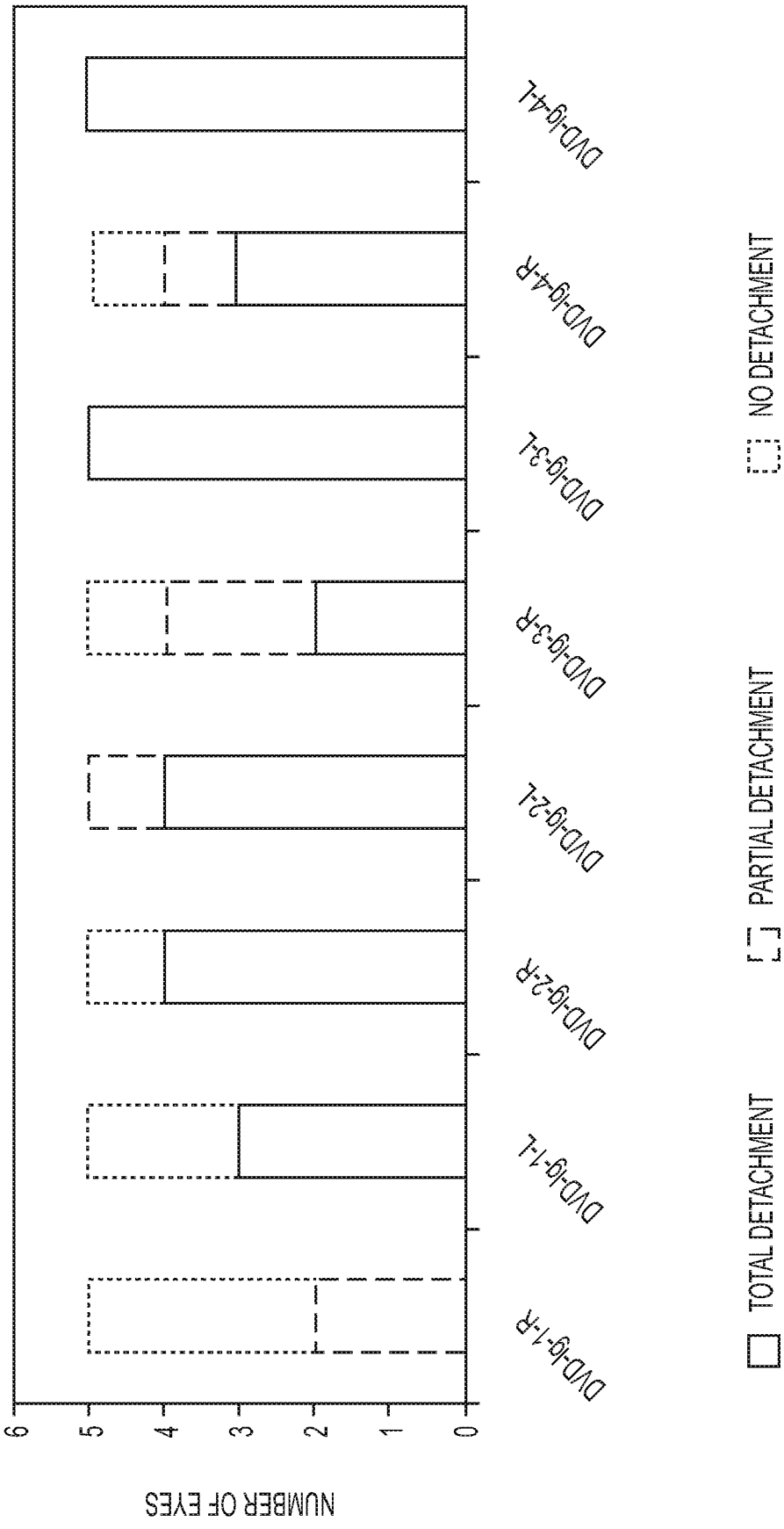

NUMBER OF EYES
0
1
2
3
4
5
6
DVD-ig-1-R
DVD-ig-1-L
DVD-ig-2-R
DVD-ig-2-L
DVD-ig-3-R
DVD-ig-3-L
DVD-ig-4-R
DVD-ig-4-L
TOTAL DETACHMENT
PARTIAL DETACHMENT
NO DETACHMENT

FIG. 7