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(72) Inventeurs/Inventors:
KANNAN, GUNASEKARAN, US;
LIU, LING, US;
BELOUSKI, EDWARD J., US;
XU, CEN, US

(73) Propriétaire/Owner:
AMGEN INC., US

(74) Agent: GOWLING WLG (CANADA) LLP

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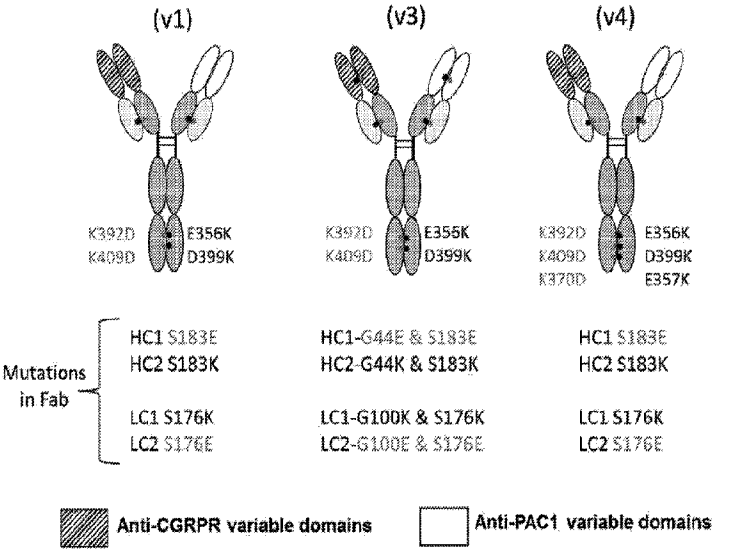
(54) Title: BI-SPECIFIC ANTI-CGRP RECEPTOR/PAC1 RECEPTOR ANTIGEN BINDING PROTEINS AND USES THEREOF



(57) Abrégé/Abstract:
The present invention relates to bispecific antigen binding proteins that are capable of binding to both the human CGRP receptor and the human PAC1 receptor. Pharmaceutical compositions comprising the bispecific antigen binding proteins as well as methods for producing them are also disclosed. Methods of using the bispecific antigen binding proteins to ameliorate or treat conditions associated with the two receptors, such as chronic pain, migraine, and cluster headache, are also described.

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(71) **Applicant**: **AMGEN INC.** [US/US]; One Amgen Center Drive, Thousand Oaks, California 91320-1799 (US).

(72) **Inventors**: **KANNAN, Gunasekaran**; 1056 Amberton Lane, Newbury Park, California 91320 (US). **LIU, Ling**; 1870 Red Robin Place, Thousand Oaks, California 91320 (US). **BELOUSKI, Edward J.**; 761 Camino Las Conchas, Thousand Oaks, California 91360 (US). **XU, Cen**; 5221 Via Jacinto, Newbury Park, California 91320 (US).

(74) **Agent**: **PURCELL, Angela L.**; One Amgen Center Drive, Patent Operations, M/S 28-2-C, Thousand Oaks, California 91320-1799 (US).

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(54) **Title**: BI-SPECIFIC ANTI-CGRP RECEPTOR/PAC1 RECEPTOR ANTIGEN BINDING PROTEINS AND USES THEREOF

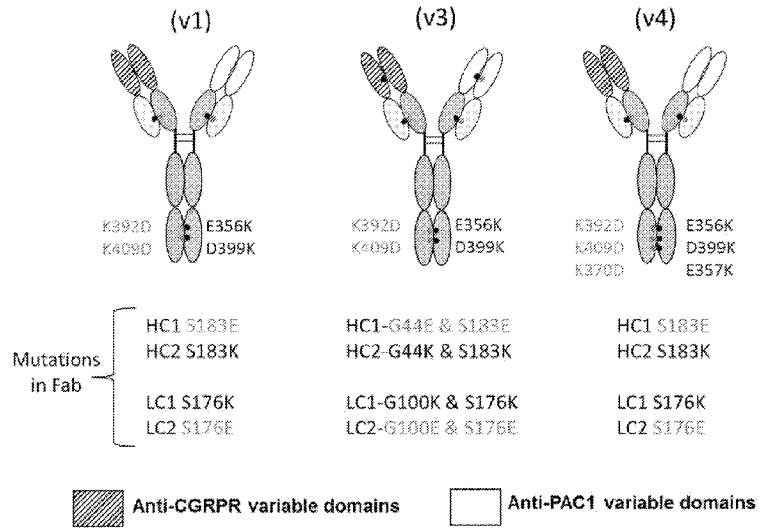

FIG. 1

(57) **Abstract**: The present invention relates to bispecific antigen binding proteins that are capable of binding to both the human CGRP receptor and the human PAC1 receptor. Pharmaceutical compositions comprising the bispecific antigen binding proteins as well as methods for producing them are also disclosed. Methods of using the bispecific antigen binding proteins to ameliorate or treat conditions associated with the two receptors, such as chronic pain, migraine, and cluster headache, are also described.

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BI-SPECIFIC ANTI-CGRP RECEPTOR/PAC1 RECEPTOR ANTIGEN BINDING PROTEINS AND USES THEREOF

FIELD OF THE INVENTION

[0001] The present invention relates to the field of biopharmaceuticals. In particular, the invention relates to bispecific antigen binding proteins that are capable of specifically binding to human calcitonin gene-related peptide (CGRP) receptor and human pituitary adenylate cyclase-activating polypeptide type I (PAC1) receptor, pharmaceutical compositions comprising the bispecific antigen binding proteins, and methods of producing and using such bispecific antigen binding proteins.

BACKGROUND OF THE INVENTION

[0002] Migraine is a complex, common neurological condition that is characterized by severe, episodic attacks of headache and associated features, which may include nausea, vomiting, sensitivity to light, sound or movement.

[0003] In some patients, the headache is preceded or accompanied by sensory warning signs or symptoms (i.e. auras). The headache pain may be severe and may also be unilateral in certain patients.

[0004] Migraine attacks are disruptive to daily life and cost billions of dollars each year in missed work days and impaired performance (Modi and Lowder, Am. Fam. Physician, Vol. 73:72-78, 2006).

[0005] Migraine is a highly prevalent disease worldwide with approximately 15% of the European population and 12% of the United States population suffering from migraine attacks

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(Lipton *et al*, Neurology, Vol. 68:343-349, 2007). Additionally, migraines have been found to be associated with a number of psychiatric and medical comorbidities such as depression and vascular disorders (Buse *et al.*, Neurol. Neurosurg. Psychiatry, Vol. 81:428-432, 2010; Bigal *et al.*, Neurology, Vol. 72:1864-1871, 2009).

[0006] Migraine headache is commonly treated acutely, primarily with analgesics and a class of drugs called triptans (Humphrey *et al.* Ann NY Acad Sci., Vol. 600:587-598, 1990; Houston and Vanhoutte, Drugs, Vol. 31:149-163 1986). The triptans, which are selective serotonin 5-HT1B/1D agonists, are effective drugs for acute migraine and are generally well tolerated, but are contraindicated in the presence of cardiovascular disease due to their potential for coronary vasoconstriction. In addition, many migraine patients do not respond favorably to triptans. In a meta-analysis of 53 trials, up to a third of all people with migraine and 40% of all migraine attacks did not respond to triptans (Ferrari *et al.*, Lancet, Vol. 358:1668-1675, 2001).

[0007] Migraine prophylaxis is an area of large unmet medical need. Approximately 40% of the migraine patient population would benefit from preventive therapy (Lipton *et al.*, Neurology, Vol. 68:343-349, 2007). However, only approximately 12% of patients receive any preventive therapy due in part to limited efficacy and significant tolerability and safety issues with available preventive therapies. Topiramate, an anticonvulsant that blocks voltage-dependent sodium channels and certain glutamate receptors (AMPA-kainate), is the medication most often used for migraine prophylaxis in the United States. Topiramate is the only migraine prophylactic agent with demonstrated efficacy in both episodic and chronic migraine patients through randomized placebo-controlled trials (Diener *et al.*, Cephalalgia, Vol. 27:814-823, 2007; Silberstein *et al.*, Headache, Vol. 47:170-180, 2007). However, approximately 50% of patients fail to respond to topiramate and it is poorly tolerated. Common adverse events associated with topiramate treatment include paresthesia, anorexia, and cognitive adverse events, including psychomotor slowing, somnolence, language difficulties, and difficulties with memory and concentration (Brandes *et al.*, JAMA, Vol. 291:965-973, 2004; Adelman *et al.*, Pain Med., Vol. 9:175–185 2008; Silberstein *et al.*, Arch Neurol., Vol. 61:490-495, 2004). In an open-label, flexible-dose study, 20% of patients withdrew from topiramate because of adverse effects (Nelles *et al.*, Headache, Vol. 49:1454–1465, 2009). Thus, migraine sufferers have an urgent medical need for more effective and/or tolerable treatment options.

[0008] Calcitonin gene-related peptide (CGRP) belongs to the calcitonin family of peptides, which also includes calcitonin, amylin, and adrenomedullin. CGRP is a 37-amino acid peptide expressed in both the central and peripheral nervous systems, and has been implicated as a key mediator in the initiation and progression of migraine pain. In addition to its ability to act as a vasodilator, CGRP also acts as a neurotransmitter in the trigeminal ganglion and the trigeminal nucleus caudalis, facilitating synaptic transmission and pain responses (Durham *et al.*, Curr Opin Investig Drugs, Vol. 5:731-735, 2004; Zimmermann *et al.*, Brain Res., Vol. 724:238-245, 1996; Wang *et al.*, Proc Natl Acad Sci USA., Vol. 92:11480-11484, 1995; Poyner, Pharmacol. Ther.,Vol. 56:23-51, 1992).

[0009] The CGRP receptor is a complex composed of the G-protein coupled calcitonin-like receptor (CLR) and a single transmembrane domain protein receptor activity modifying protein (RAMP1). The CGRP receptor complex is located at sites that are relevant to migraine including the cerebrovasculature, the trigeminocervical complex in the brainstem, and the trigeminal ganglion (Zhang *et al.*, J. Neurosci., Vol. 27: 2693-2703, 2007; Storer *et al.*, Br J Pharmacol., Vol. 142:1171-1181, 2004; Oliver *et al.*, J Cereb Blood Flow Metab., Vol. 22:620-629, 2002). Several lines of evidence indicate that CGRP is a potent vasodilator and nociceptive modulator that has been associated with migraine pathophysiology: (1) it is expressed in the trigeminal system, which is implicated in the pathophysiology of migraines; (2) CGRP levels are elevated in migraineurs during an attack (Bellamy *et al.*, Headache, Vol. 46:24-33, 2006; Ashina *et al.*, Pain, Vol. 86:133-138, 2000; Gallai *et al.*, Cephalalgia, Vol.15:384-390, 1995; Goadsby *et al.*, Ann Neurol., Vol. 28:183-187, 1990; Goadsby *et al.*, Ann Neurol., Vol. 23:193-196, 1988); (3) acute migraine therapies such as triptans restore CGRP levels to normal after treatment (Juhasz *et al.*, Cephalalgia, Vol. 25:179-183, 2005); (4) CGRP infusion triggers the onset of migraine headaches in migraine sufferers (Petersen *et al.*, Br J Pharmacol., Vol. 143:1074-1075, 2004; Lassen *et al.*, Cephalalgia, Vol. 22:54-61, 2002); and (5) CGRP antagonists have demonstrated efficacy in acute migraine reversal (Connor *et al.*, Neurology, Vol. 73:970-977, 2009; Hewitt *et al.*, Abstract for the 14th Congress of the International Headache Society, 2009; LBOR3; Ho *et al.*, Lancet, Vol. 372:2115-2123, 2008a; Ho *et al.*, Neurology, Vol. 70:1304-1312, 2008b). Additionally, small-molecule CGRP receptor antagonists and antibody CGRP ligand antagonists have demonstrated clinical efficacy in episodic migraine prevention (Dodick *et al.*, Lancet Neurol., Vol. 13:1100-1107, 2014a; Dodick *et al.*, Lancet Neurol., Vol. 13:885-892 2014b; Ho *et*

al., Neurology, Vol. 83:958-966, 2014). Taken together, these data suggest a role for the CGRP neuropeptide and its receptor in the pathogenesis of migraine.

[0010] Pituitary adenylate cyclase-activating polypeptide (PACAP) belongs to the VIP/secretin/glucagon superfamily. The sequence of PACAP 27 corresponds to the 27 N-terminal amino acids of PACAP 38 and shares 68% identity with vasoactive intestinal polypeptide (VIP) (Pantaloni *et al.*, J. Biol. Chem., Vol. 271: 22146-22151, 1996; Pisegna and Wank, Proc. Natl. Acad. Sci. USA, Vol. 90: 6345-49, 1993; Campbell and Scanes, Growth Regul., Vol. 2:175–191, 1992). The major form of PACAP peptide in the human body is PACAP 38 and the pharmacology of PACAP 38 and PACAP 27 has not been shown to be different from each other. Three PACAP receptors have been reported: one receptor that binds PACAP with high affinity and has a much lower affinity for VIP (PAC1 receptor), and the other two receptors that recognize PACAP and VIP equally well (VPAC1 and VPAC2 receptors) (Vaudry *et al.*, Pharmacol Rev., Vol. 61:283-357, 2009). PACAP is capable of binding all three receptors with similar potency and is thus not particularly selective. VIP, on the other hand, binds with significantly higher affinity to VPAC1 and VPAC2, as compared with PAC1. In addition to endogenous agonists PACAP and VIP, maxadilan, a 65 amino acid peptide originally isolated from the sand-fly, is exquisitely selective for PAC1 compared with VPAC1 or VPAC2.

[0011] Human experimental migraine models using PACAP as a challenge agent to induce migraine-like headaches support the role of PAC1 receptor antagonism as a potential treatment for migraine prophylaxis. Infusion of PACAP 38 causes headaches in healthy subjects and migraine-like headaches in migraine patients (Schytz *et al.*, Brain, Vol. 132:16-25, 2009). In addition, in the same model, VIP does not cause migraine-like headaches in migraine patients (Rahmann *et al.*, Cephalalgia, Vol. 28:226-236, 2008). The lack of migraine-like headache induction from VIP infusion suggests that PAC1 receptor, but not VPAC1 or VPAC2 receptors, is involved in migraine because VIP has a much higher affinity at the latter two receptors. These data suggest that a selective PAC1 antagonist has the potential to treat migraine.

[0012] There is a need in the art to develop migraine-specific prophylactic therapies having novel mechanisms of action that are directed to targets that underlie migraine pathophysiology. In particular, therapeutic molecules having a dual function in antagonizing both the CGRP/CGRP receptor and PACAP/PAC1 receptor pathways would be particularly beneficial.

SUMMARY OF THE INVENTION

[0013] The present invention is based, in part, on the design and generation of bispecific antigen binding proteins capable of blocking both the human CGRP receptor and the human PAC1 receptor. Such bispecific antigen binding proteins comprise a first binding domain that specifically binds to human CGRP receptor and a second binding domain that specifically binds to human PAC1 receptor. In some embodiments, each of the binding domains comprises variable regions from immunoglobulin light and heavy chains. The binding domains may be prepared from anti-CGRP receptor and anti-PAC1 receptor antibodies.

[0014] In certain embodiments, one of the binding domains is a Fab fragment and the other binding domain is a single-chain variable fragment (scFv). In other embodiments, both binding domains are Fab fragments. The bispecific antigen binding proteins may also comprise an immunoglobulin constant region or Fc region, which, in some embodiments, is derived from a human immunoglobulin IgG1 or IgG2. In certain embodiments, the constant region comprises one or more amino acid substitutions that reduce glycosylation and/or effector function of the bispecific antigen binding protein.

[0015] In some embodiments, the bispecific antigen binding proteins are monovalent for each target. In such embodiments, the bispecific antigen binding protein can be an antibody where one antigen binding domain or arm binds to the CGRP receptor and the other antigen binding domain or arm binds to the PAC1 receptor. In other embodiments, the bispecific antigen binding proteins are bivalent for each target. In such embodiments, one binding domain is positioned at the amino terminus of an immunoglobulin Fc region and the other binding domain is positioned at the carboxyl terminus of the Fc region such that, when dimerized, the antigen binding protein comprises two antigen binding domains that bind to the CGRP receptor and two antigen binding domains that bind to the PAC1 receptor.

[0016] In some embodiments, the bispecific antigen binding protein is an antibody, such as a heterodimeric antibody. The heterodimeric antibody may comprise a first light chain and a first heavy chain from a first antibody that specifically binds to human CGRP receptor and a second light chain and second heavy chain from a second antibody that specifically binds to human PAC1 receptor. In certain embodiments, the first and second heavy chains comprise one or more charge pair mutations in the constant region (e.g. CH3 domain) to promote heterodimer formation. In related embodiments, the first light chain and first heavy chain (or second light

chain and second heavy chain) comprise one or more charge pair mutations to facilitate correct light-heavy chain pairing. In some such embodiments, the first heavy chain comprises an amino acid substitution introducing a charged amino acid (e.g. glutamic acid) that has the opposite charge of the amino acid introduced into the first light chain (e.g. lysine) so that the first light chain and first heavy chain are attracted to each other. The charged amino acid introduced into the second light chain (e.g. glutamic acid) would preferably have the same charge as the amino acid introduced into the first heavy chain (e.g. glutamic acid), but the opposite charge of the amino acid introduced into the second heavy chain (e.g. lysine) so that the second light chain would be attracted to the second heavy chain, but repelled from the first heavy chain.

[0017] In certain embodiments of the invention, the bispecific antigen binding protein is comprised of an antibody against a first target (e.g. CGRP receptor or PAC1 receptor) and a scFv derived from an antibody against a second target (e.g. PAC1 receptor or CGRP receptor). In this IgG-scFv format, the bispecific, multivalent antigen binding protein comprises (i) a light chain and a heavy chain from a first antibody and (ii) a scFv comprising a light chain variable region (VL) and a heavy chain variable region (VH) from a second antibody, wherein the scFv is fused at its amino terminus to the carboxyl terminus of the heavy chain optionally through a peptide linker to form a modified heavy chain, and wherein the first or second antibody specifically binds to human CGRP receptor and the other antibody specifically binds to human PAC1 receptor. In some embodiments, the scFv comprises, from N-terminus to C-terminus, a VH region, a peptide linker, and a VL region. In other embodiments, the scFv comprises, from N-terminus to C-terminus, a VL region, a peptide linker, and a VH region.

[0018] In other embodiments of the invention, the bispecific antigen binding protein is comprised of an antibody against a first target (e.g. CGRP receptor or PAC1 receptor) and a Fab fragment derived from an antibody against a second target (e.g. PAC1 receptor or CGRP receptor). In this IgG-Fab format, the bispecific, multivalent antigen binding protein comprises (i) a light chain from a first antibody, (ii) a heavy chain from the first antibody, wherein the heavy chain is fused at its carboxyl terminus optionally through a peptide linker to a first polypeptide comprising VL-CL domains or VH-CH1 domains of a second antibody to form a modified heavy chain, and (iii) a second polypeptide comprising VH-CH1 domains or VL-CL domains of the second antibody, wherein the first or second antibody specifically binds to human CGRP receptor and the other antibody specifically binds to human PAC1 receptor. In particular

embodiments, the first polypeptide, which is fused to the carboxyl terminus of the heavy chain, comprises VL and CL domains (i.e. a light chain) from the second antibody, and the second polypeptide comprises VH and CH1 domains (i.e. a Fd fragment) from the second antibody. In other particular embodiments, the first polypeptide, which is fused to the carboxyl terminus of the heavy chain, comprises VH and CH1 domains (i.e. a Fd fragment) from the second antibody, and the second polypeptide comprises VL and CL domains (i.e. a light chain) from the second antibody. The CL and CH1 domains may be switched in some embodiments between the first and second polypeptide. Thus, in some embodiments, the first polypeptide, which is fused to the carboxyl terminus of the heavy chain, comprises VL and CH1 domains from the second antibody, and the second polypeptide comprises VH and CL domains from the second antibody. In other embodiments, the first polypeptide, which is fused to the carboxyl terminus of the heavy chain, comprises VH and CL domains from the second antibody, and the second polypeptide comprises VL and CH1 domains from the second antibody.

[0019] The present invention includes one or more nucleic acids encoding any of the bispecific antigen binding proteins described herein or components thereof, as well as vectors comprising the nucleic acids. Also encompassed within the invention is a recombinant host cell, such as a CHO cell, that expresses any of the bispecific antigen binding proteins.

[0020] The bispecific antigen binding proteins described herein can be used in the manufacture of a pharmaceutical composition or medicament for the treatment of conditions associated with CGRP receptor and/or PAC1 receptor, such as headache, migraine, and chronic pain. Thus, the present invention also provides a pharmaceutical composition comprising a bispecific antigen binding protein and a pharmaceutically acceptable diluent, excipient or carrier.

[0021] In some embodiments, the present invention provides a method for treating or preventing headache in a patient in need thereof comprising administering to the patient an effective amount of a bispecific antigen binding protein described herein. In some embodiments, the headache is migraine headache. The migraine can be episodic migraine or chronic migraine. In other embodiments, the headache is cluster headache. In particular embodiments, the methods provide prophylactic treatment for these conditions.

[0022] In another embodiment, the present invention provides a method for treating chronic pain in a patient in need thereof comprising administering to the patient an effective amount of a bispecific antigen binding protein described herein. The chronic pain syndromes to be treated

according to the methods of the invention can include arthritic pain, such as pain associated with osteoarthritis or rheumatoid arthritis.

[0023] The use of the bispecific antigen binding proteins in any of the methods disclosed herein or for preparation of medicaments for administration according to any of the methods disclosed herein is specifically contemplated. For instance, the present invention includes a bispecific antigen binding protein for use in a method for treating or preventing a condition associated with CGRP receptor and/or PAC1 receptor in a patient in need thereof. The condition can include headache (e.g. migraine headache or cluster headache) and chronic pain.

[0024] The present invention also includes the use of a bispecific antigen binding protein in the preparation of a medicament for treating or preventing a condition associated with CGRP receptor and/or PAC1 receptor in a patient in need thereof. The condition can include headache (e.g. migraine headache or cluster headache) and chronic pain.

BRIEF DESCRIPTION OF THE DRAWINGS

[0025] Figure 1 shows a schematic representation of three bispecific hetero immunoglobulin formats used to generate anti-CGRP receptor/PAC1 receptor bispecific antibodies. The Kabat-EU numbering scheme is used to denote the positions of charge pair mutations within each of the chains. This IgG-like bispecific antibody format is a heterotetramer comprising two different light chains and two different heavy chains. HC1 and LC1 refer to the heavy chain and light chain, respectively, of one Fab binding arm and HC2 and LC2 refers to the heavy chain and light chain, respectively, of the second Fab binding arm. For example, in the schematic, HC1 and LC1 correspond to the anti-CGRP receptor binding arm and HC2 and LC2 correspond to the anti-PAC1 binding arm. However, the two binding arms can be switched such that HC1 and LC1 correspond to the anti-PAC1 binding arm and HC2 and LC2 correspond to the anti-CGRP receptor binding arm.

[0026] Figure 2 depicts a schematic representation of an IgG-scFv format used to generate anti-CGRP receptor/PAC1 receptor bispecific antigen binding proteins. In this format, a single-chain variable fragment (scFv), which comprises variable domains from a second antibody linked together by a glycine-serine linker, is fused to the carboxyl terminus of the heavy chain of a first antibody through a peptide linker to produce a modified heavy chain. Although the VH-VL orientation of the variable domains within the scFv is shown, the variable domains may also be

organized in a VL-VH orientation. The complete molecule is a homotetramer comprising two modified heavy chains and two light chains from the first antibody.

[0027] Figure 3 depicts a schematic representation of an IgG-Fab format used to generate anti-CGRP receptor/PAC1 receptor bispecific antigen binding proteins. In this format, one polypeptide chain of a Fab fragment from a second antibody (e.g. the light chain (VL2-CL)) is fused to the carboxyl terminus of the heavy chain of a first antibody through a peptide linker to produce a modified heavy chain. The complete molecule is homohexamer comprising two modified heavy chains, two light chains from the first antibody, and two polypeptide chains containing the other half of the Fab fragment from the second antibody (e.g. the Fd chain (VH2-CH1)). Charge pair mutations (represented by the circles) can be introduced into the Fab regions of the first antibody (Fab 1) or second antibody (Fab 2) to promote correct heavy chain-light chain pairs. Although the light chain of the second antibody is shown as the fusion partner for the heavy chain of the first antibody in the schematic, the Fd region (VH-CH1) of the second antibody can be fused to the carboxyl terminus of the heavy chain with the light chain of the second antibody completing the Fab domain at the carboxyl terminus of the Fc region.

DETAILED DESCRIPTION

[0028] The present invention is directed to bispecific antigen binding proteins that specifically bind to both the human CGRP receptor and the human PAC1 receptor. As both CGRP receptor and PAC1 receptor signaling are implicated in the control of cerebral vascular tone, the bispecific binding proteins of the invention provide a means to simultaneously modulate both signaling cascades to ameliorate conditions associated with dysregulation of the cranial vasculature, such as cluster headache and migraine. Accordingly, in one embodiment, the present invention provides a bispecific antigen binding protein comprising a first binding domain that specifically binds to human CGRP receptor and a second binding domain that specifically binds to human PAC1 receptor.

[0029] As used herein, the term "antigen binding protein" refers to a protein that specifically binds to one or more target antigens. An antigen binding protein can include an antibody and functional fragments thereof. A "functional antibody fragment" is a portion of an antibody that lacks at least some of the amino acids present in a full-length heavy chain and/or light chain, but which is still capable of specifically binding to an antigen. A functional antibody fragment

includes, but is not limited to, a single-chain variable fragment (scFv), a nanobody (*e.g.* VH domain of camelid heavy chain antibodies; VHH fragment, *see* Cortez-Retamozo *et al.*, Cancer Research, Vol. 64:2853-57, 2004), a Fab fragment, a Fab' fragment, a $F(ab')_2$ fragment, a Fv fragment, a Fd fragment, and a complementarity determining region (CDR) fragment, and can be derived from any mammalian source, such as human, mouse, rat, rabbit, or camelid. Functional antibody fragments may compete for binding of a target antigen with an intact antibody and the fragments may be produced by the modification of intact antibodies (e.g. enzymatic or chemical cleavage) or synthesized *de novo* using recombinant DNA technologies or peptide synthesis.

[0030] An antigen binding protein can also include a protein comprising one or more functional antibody fragments incorporated into a single polypeptide chain or into multiple polypeptide chains. For instance, antigen binding proteins can include, but are not limited to, a diabody (*see, e.g.*, EP 404,097; WO 93/11161; and Hollinger *et al.*, Proc. Natl. Acad. Sci. USA, Vol. 90:6444-6448, 1993); an intrabody; a domain antibody (single VL or VH domain or two or more VH domains joined by a peptide linker; *see Ward et al.*, Nature, Vol. 341:544-546, 1989); a maxibody (2 scFvs fused to Fc region, *see* Fredericks *et al.*, Protein Engineering, Design & Selection, Vol. 17:95-106, 2004 and Powers *et al.*, Journal of Immunological Methods, Vol. 251:123-135, 2001); a triabody; a tetrabody; a minibody (scFv fused to CH3 domain; *see* Olafsen *et al.*, Protein Eng Des Sel. , Vol.17:315-23, 2004); a peptibody (one or more peptides attached to an Fc region, *see* WO 00/24782); a linear antibody (a pair of tandem Fd segments (VH-CH1-VH-CH1) which, together with complementary light chain polypeptides, form a pair of antigen binding regions, *see* Zapata *et al.*, Protein Eng., Vol. 8:1057-1062, 1995); a small modular immunopharmaceutical (*see* U.S. Patent Publication No. 20030133939); and immunoglobulin fusion proteins (e.g. IgG-scFv, IgG-Fab, 2scFv-IgG, 4scFv-IgG, VH-IgG, IgG-VH, and Fab-scFv-Fc).

[0031] The antigen binding proteins of the present invention are "bispecific" meaning that they are capable of specifically binding to two different antigens, human CGRP receptor and human PAC1 receptor. As used herein, an antigen binding protein "specifically binds" to a target antigen when it has a significantly higher binding affinity for, and consequently is capable of distinguishing, that antigen, compared to its affinity for other unrelated proteins, under similar binding assay conditions. Antigen binding proteins that specifically bind an antigen may have an equilibrium dissociation constant (K_D) $\leq 1 \times 10^{-6}$ M. The antigen binding protein specifically

binds antigen with "high affinity" when the K_D is $\leq 1 \times 10^{-8}$ M. In one embodiment, the antigen binding proteins of the invention bind to human CGRP receptor and/or human PAC1 receptor with a K_D of $\leq 5 \times 10^{-7}$ M. In another embodiment, the antigen binding proteins of the invention bind to human CGRP receptor and/or human PAC1 receptor with a K_D of $\leq 1 \times 10^{-7}$ M. In yet another embodiment, the antigen binding proteins of the invention bind to human CGRP receptor and/or human PAC1 receptor with a K_D of $\leq 5 \times 10^{-8}$ M. In another embodiment, the antigen binding proteins of the invention bind to human CGRP receptor and/or human PAC1 receptor with a K_D of $\leq 1 \times 10^{-8}$ M. In certain embodiments, the antigen binding proteins of the invention bind to human CGRP receptor and/or human PAC1 receptor with a K_D of $\leq 5 \times 10^{-9}$ M. In other embodiments, the antigen binding proteins of the invention bind to human CGRP receptor and/or human PAC1 receptor with a K_D of $\leq 1 \times 10^{-9}$ M. In one particular embodiment, the antigen binding proteins of the invention bind to human CGRP receptor and/or human PAC1 receptor with a K_D of $\leq 5 \times 10^{-10}$ M. In another particular embodiment, the antigen binding proteins of the invention bind to human CGRP receptor and/or human PAC1 receptor with a K_D of $\leq 1 \times 10^{-10}$ M.

[0032] Affinity is determined using a variety of techniques, an example of which is an affinity ELISA assay. In various embodiments, affinity is determined by a surface plasmon resonance assay (e.g., BIAcore®-based assay). Using this methodology, the association rate constant (k_a in $M^{-1}s^{-1}$) and the dissociation rate constant (k_d in s^{-1}) can be measured. The equilibrium dissociation constant (K_D in M) can then be calculated from the ratio of the kinetic rate constants (k_d/k_a). In some embodiments, affinity is determined by a kinetic method, such as a Kinetic Exclusion Assay (KinExA) as described in Rathanaswami *et al.* Analytical Biochemistry, Vol. 373:52-60, 2008. Using a KinExA assay, the equilibrium dissociation constant (K_D in M) and the association rate constant (k_a in $M^{-1}s^{-1}$) can be measured. The dissociation rate constant (k_d in s^{-1}) can be calculated from these values ($K_D \times k_a$). In other embodiments, affinity is determined by an equilibrium/solution method. In certain embodiments, affinity is determined by a FACS binding assay. WO 2010/075238 and WO 2014/144632 describe suitable affinity assays for determining the affinity of a binding protein for human CGRP receptor and human PAC1 receptor. In certain embodiments of the invention, the antigen binding protein specifically binds to human CGRP receptor and/or human PAC1 receptor expressed by a mammalian cell (e.g., CHO, HEK 293, Jurkat), with a K_D of 20 nM (2.0×10^{-8} M) or less, K_D of 10 nM (1.0×10^{-8} M)

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or less, K_D of 1 nM (1.0×10^{-9} M) or less, K_D of 500 pM (5.0×10^{-10} M) or less, K_D of 200 pM (2.0×10^{-10} M) or less, K_D of 150 pM (1.50×10^{-10} M) or less, K_D of 125 pM (1.25×10^{-10} M) or less, K_D of 105 pM (1.05×10^{-10} M) or less, K_D of 50 pM (5.0×10^{-11} M) or less, or K_D of 20 pM (2.0×10^{-11} M) or less, as determined by a Kinetic Exclusion Assay, conducted by the method described in Rathanaswami *et al*. Analytical Biochemistry, Vol. 373:52-60, 2008. In some embodiments, the bispecific antigen binding proteins described herein exhibit desirable characteristics such as binding avidity as measured by k_d (dissociation rate constant) for human CGRP receptor or human PAC1 receptor of about 10^{-2}, 10^{-3}, 10^{-4}, 10^{-5}, 10^{-6}, 10^{-7}, 10^{-8}, 10^{-9}, 10^{-10} s^{-1} or lower (lower values indicating higher binding avidity), and/or binding affinity as measured by K_D (equilibrium dissociation constant) for human CGRP receptor or human PAC1 of about 10^{-9}, 10^{-10}, 10^{-11}, 10^{-12}, 10^{-13}, 10^{-14}, 10^{-15}, 10^{-16} M or lower (lower values indicating higher binding affinity).

[0033] In some embodiments of the invention, the antigen binding proteins are multivalent. The valency of the binding protein denotes the number of individual antigen binding domains within the binding protein. For example, the terms "monovalent," "bivalent," and "tetravalent" with reference to the antigen binding proteins of the invention refer to binding proteins with one, two, and four antigen binding domains, respectively. Thus, a multivalent antigen binding protein comprises two or more antigen binding domains. In some embodiments, the bispecific antigen binding proteins of the invention are bivalent. Thus, such bispecific, bivalent antigen binding proteins contain two antigen binding domains: one antigen-binding domain binding to human CGRP receptor and one antigen-binding domain binding to human PAC1 receptor. In other embodiments, the bispecific antigen binding proteins are multivalent. For instance, in certain embodiments, the bispecific antigen binding proteins are tetravalent comprising four antigen-binding domains: two antigen-binding domains binding to human CGRP receptor and two antigen-binding domains binding to human PAC1 receptor.

[0034] As used herein, the term "antigen binding domain," which is used interchangeably with "binding domain," refers to the region of the antigen binding protein that contains the amino acid residues that interact with the antigen and confer on the antigen binding protein its specificity and affinity for the antigen. In some embodiments, the binding domain may be derived from the natural ligands of the human CGRP receptor and the human PAC1 receptor. For example, the binding domain that specifically binds to human CGRP receptor may be derived from human α-

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binds antigen with "high affinity" when the K_D is $\leq 1 \times 10^{-8}$ M. In one embodiment, the antigen binding proteins of the invention bind to human CGRP receptor and/or human PAC1 receptor with a K_D of $\leq 5 \times 10^{-7}$ M. In another embodiment, the antigen binding proteins of the invention bind to human CGRP receptor and/or human PAC1 receptor with a K_D of $\leq 1 \times 10^{-7}$ M. In yet another embodiment, the antigen binding proteins of the invention bind to human CGRP receptor and/or human PAC1 receptor with a K_D of $\leq 5 \times 10^{-8}$ M. In another embodiment, the antigen binding proteins of the invention bind to human CGRP receptor and/or human PAC1 receptor with a K_D of $\leq 1 \times 10^{-8}$ M. In certain embodiments, the antigen binding proteins of the invention bind to human CGRP receptor and/or human PAC1 receptor with a K_D of $\leq 5 \times 10^{-9}$ M. In other embodiments, the antigen binding proteins of the invention bind to human CGRP receptor and/or human PAC1 receptor with a K_D of $\leq 1 \times 10^{-9}$ M. In one particular embodiment, the antigen binding proteins of the invention bind to human CGRP receptor and/or human PAC1 receptor with a K_D of $\leq 5 \times 10^{-10}$ M. In another particular embodiment, the antigen binding proteins of the invention bind to human CGRP receptor and/or human PAC1 receptor with a K_D of $\leq 1 \times 10^{-10}$ M.

[0032] Affinity is determined using a variety of techniques, an example of which is an affinity ELISA assay. In various embodiments, affinity is determined by a surface plasmon resonance assay (e.g., BIAcore®-based assay). Using this methodology, the association rate constant (k_a in $M^{-1}s^{-1}$) and the dissociation rate constant (k_d in s^{-1}) can be measured. The equilibrium dissociation constant (K_D in M) can then be calculated from the ratio of the kinetic rate constants (k_d/k_a). In some embodiments, affinity is determined by a kinetic method, such as a Kinetic Exclusion Assay (KinExA) as described in Rathanaswami *et al.* Analytical Biochemistry, Vol. 373:52-60, 2008. Using a KinExA assay, the equilibrium dissociation constant (K_D in M) and the association rate constant (k_a in $M^{-1}s^{-1}$) can be measured. The dissociation rate constant (k_d in s^{-1}) can be calculated from these values ($K_D \times k_a$). In other embodiments, affinity is determined by an equilibrium/solution method. In certain embodiments, affinity is determined by a FACS binding assay. WO 2010/075238 and WO 2014/144632 describe suitable affinity assays for determining the affinity of a binding protein for human CGRP receptor and human PAC1 receptor. In certain embodiments of the invention, the antigen binding protein specifically binds to human CGRP receptor and/or human PAC1 receptor expressed by a mammalian cell (e.g., CHO, HEK 293, Jurkat), with a K_D of 20 nM (2.0×10^{-8} M) or less, K_D of 10 nM (1.0×10^{-8} M)

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or less, K_D of 1 nM (1.0×10^{-9} M) or less, K_D of 500 pM (5.0×10^{-10} M) or less, K_D of 200 pM (2.0×10^{-10} M) or less, K_D of 150 pM (1.50×10^{-10} M) or less, K_D of 125 pM (1.25×10^{-10} M) or less, K_D of 105 pM (1.05×10^{-10} M) or less, K_D of 50 pM (5.0×10^{-11} M) or less, or K_D of 20 pM (2.0×10^{-11} M) or less, as determined by a Kinetic Exclusion Assay, conducted by the method described in Rathanaswami *et al*. Analytical Biochemistry, Vol. 373:52-60, 2008. In some embodiments, the bispecific antigen binding proteins described herein exhibit desirable characteristics such as binding avidity as measured by k_d (dissociation rate constant) for human CGRP receptor or human PAC1 receptor of about 10^{-2}, 10^{-3}, 10^{-4}, 10^{-5}, 10^{-6}, 10^{-7}, 10^{-8}, 10^{-9}, 10^{-10} s^{-1} or lower (lower values indicating higher binding avidity), and/or binding affinity as measured by K_D (equilibrium dissociation constant) for human CGRP receptor or human PAC1 of about 10^{-9}, 10^{-10}, 10^{-11}, 10^{-12}, 10^{-13}, 10^{-14}, 10^{-15}, 10^{-16} M or lower (lower values indicating higher binding affinity).

[0033] In some embodiments of the invention, the antigen binding proteins are multivalent. The valency of the binding protein denotes the number of individual antigen binding domains within the binding protein. For example, the terms "monovalent," "bivalent," and "tetravalent" with reference to the antigen binding proteins of the invention refer to binding proteins with one, two, and four antigen binding domains, respectively. Thus, a multivalent antigen binding protein comprises two or more antigen binding domains. In some embodiments, the bispecific antigen binding proteins of the invention are bivalent. Thus, such bispecific, bivalent antigen binding proteins contain two antigen binding domains: one antigen-binding domain binding to human CGRP receptor and one antigen-binding domain binding to human PAC1 receptor. In other embodiments, the bispecific antigen binding proteins are multivalent. For instance, in certain embodiments, the bispecific antigen binding proteins are tetravalent comprising four antigen-binding domains: two antigen-binding domains binding to human CGRP receptor and two antigen-binding domains binding to human PAC1 receptor.

[0034] As used herein, the term "antigen binding domain," which is used interchangeably with "binding domain," refers to the region of the antigen binding protein that contains the amino acid residues that interact with the antigen and confer on the antigen binding protein its specificity and affinity for the antigen. In some embodiments, the binding domain may be derived from the natural ligands of the human CGRP receptor and the human PAC1 receptor. For example, the binding domain that specifically binds to human CGRP receptor may be derived from human α-

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CGRP and comprise peptide antagonists, such as the CGRP8-37 antagonist peptide and variants thereof described in Chiba *et al.*, Am. J. Physiol., Vol. 256: E331-E335, 1989 and Taylor *et al.*, J. Pharmacol. Exp. Ther., Vol. 319: 749-757, 2006. Similarly, the binding domain that specifically binds to human PAC1 receptor may be derived from PACAP38 or PACAP27 and may comprise peptide antagonists such as those described in Bourgault *et al.*, J. Med. Chem., Vol. 52: 3308-3316, 2009 and U.S. Patent No. 6,017,533.

[0035] In certain embodiments of the bispecific antigen binding proteins of the invention, the binding domain may be derived from an antibody or functional fragment thereof. For instance, the binding domains of the bispecific antigen binding proteins of the invention may comprise one or more complementarity determining regions (CDR) from the light and heavy chain variable regions of antibodies that specifically bind to human CGRP receptor or human PAC1 receptor. As used herein, the term "CDR" refers to the complementarity determining region (also termed "minimal recognition units" or "hypervariable region") within antibody variable sequences. There are three heavy chain variable region CDRs (CDRH1, CDRH2 and CDRH3) and three light chain variable region CDRs (CDRL1, CDRL2 and CDRL3). The term "CDR region" as used herein refers to a group of three CDRs that occur in a single variable region (i.e. the three light chain CDRs or the three heavy chain CDRs). The CDRs in each of the two chains typically are aligned by the framework regions to form a structure that binds specifically with a specific epitope or domain on the target protein (*e.g.*, human CGRP receptor or human PAC1 receptor). From N-terminus to C-terminus, naturally-occurring light and heavy chain variable regions both typically conform with the following order of these elements: FR1, CDR1, FR2, CDR2, FR3, CDR3 and FR4. A numbering system has been devised for assigning numbers to amino acids that occupy positions in each of these domains. This numbering system is defined in Kabat Sequences of Proteins of Immunological Interest (1987 and 1991, NIH, Bethesda, MD), or Chothia & Lesk, 1987, *J. Mol. Biol.* 196:901-917; Chothia *et al.*, 1989, Nature 342:878-883. Complementarity determining regions (CDRs) and framework regions (FR) of a given antibody may be identified using this system. In some embodiments, the anti-CGRP receptor binding domain of the bispecific antigen binding proteins of the invention comprise all six CDRs of the heavy and light chain variable regions of an anti-CGRP receptor antibody and the anti-PAC1 receptor binding domain of the bispecific antigen binding proteins of the invention comprise all six CDRs of the heavy and light chain variable regions of an anti-PAC1 receptor antibody.

[0036] In some embodiments of the bispecific antigen binding proteins of the invention, the binding domains (the anti-CGRP receptor binding domain, the anti-PAC1 receptor binding domain or both) comprise a Fab, a Fab', a $F(ab')_2$, a Fv, a single-chain variable fragment (scFv), or a nanobody. In one embodiment, both binding domains are Fab fragments. In another embodiment, one binding domain is a Fab fragment and the other binding domain is a scFv.

[0037] Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments, each with a single antigen-binding site, and a residual "Fc" fragment which contains the immunoglobulin constant region. The Fab fragment contains all of the variable domain, as well as the constant domain of the light chain and the first constant domain (CH1) of the heavy chain. Thus, a "Fab fragment" is comprised of one immunoglobulin light chain (light chain variable region (VL) and constant region (CL)) and the CH1 region and variable region (VH) of one immunoglobulin heavy chain. The heavy chain of a Fab molecule cannot form a disulfide bond with another heavy chain molecule. The Fc fragment displays carbohydrates and is responsible for many antibody effector functions (such as binding complement and cell receptors), that distinguish one class of antibody from another. The "Fd fragment" comprises the VH and CH1 domains from an immunoglobulin heavy chain. The Fd fragment represents the heavy chain component of the Fab fragment.

[0038] A "Fab' fragment" is a Fab fragment having at the C-terminus of the CH1 domain one or more cysteine residues from the antibody hinge region.

[0039] A "$F(ab')_2$ fragment" is a bivalent fragment including two Fab' fragments linked by a disulfide bridge between the heavy chains at the hinge region.

[0040] The "Fv" fragment is the minimum fragment that contains a complete antigen recognition and binding site from an antibody. This fragment consists of a dimer of one immunoglobulin heavy chain variable region (VH) and one immunoglobulin light chain variable region (VL) in tight, non-covalent association. It is in this configuration that the three CDRs of each variable region interact to define an antigen binding site on the surface of the VH-VL dimer. A single light chain or heavy chain variable region (or half of an Fv fragment comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site comprising both VH and VL.

[0041] A "single-chain variable antibody fragment" or "scFv fragment" comprises the VH and VL regions of an antibody, wherein these regions are present in a single polypeptide chain, and

optionally comprising a peptide linker between the VH and VL regions that enables the Fv to form the desired structure for antigen binding (*see e.g.*, Bird *et al.*, Science, Vol. 242:423-426, 1988; and Huston *et al.*, Proc. Natl. Acad. Sci. USA, Vol. 85:5879-5883, 1988).

[0042] A "nanobody" is the heavy chain variable region of a heavy-chain antibody. Such variable domains are the smallest fully functional antigen-binding fragment of such heavy-chain antibodies with a molecular mass of only 15 kDa. *See* Cortez-Retamozo *et al.*, *Cancer Research* 64:2853-57, 2004. Functional heavy-chain antibodies devoid of light chains are naturally occurring in certain species of animals, such as nurse sharks, wobbegong sharks and *Camelidae*, such as camels, dromedaries, alpacas and llamas. The antigen-binding site is reduced to a single domain, the VHH domain, in these animals. These antibodies form antigen-binding regions using only heavy chain variable region, i.e., these functional antibodies are homodimers of heavy chains only having the structure H_2L_2 (referred to as "heavy-chain antibodies" or "HCAbs"). Camelized VHH reportedly recombines with IgG2 and IgG3 constant regions that contain hinge, CH2, and CH3 domains and lack a CH1 domain. Camelized VHH domains have been found to bind to antigen with high affinity (Desmyter *et al.*, J. Biol. Chem., Vol. 276:26285-90, 2001) and possess high stability in solution (Ewert *et al.*, Biochemistry, Vol. 41:3628-36, 2002). Methods for generating antibodies having camelized heavy chains are described in, for example, U.S. Patent Publication Nos. 2005/0136049 and 2005/0037421. Alternative scaffolds can be made from human variable-like domains that more closely match the shark V-NAR scaffold and may provide a framework for a long penetrating loop structure.

[0043] In particular embodiments of the bispecific antigen binding proteins of the invention, the binding domains comprise an immunoglobulin heavy chain variable region (VH) and an immunoglobulin light chain variable region (VL) of an antibody or antibody fragment which specifically binds to the desired antigen. For instance, the anti-CGRP receptor binding domain of the bispecific antigen binding proteins of the invention comprises a VH region and VL region from an anti-CGRP receptor antibody and the anti-PAC1 receptor binding domain comprises a VH region and VL region from an anti-PAC1 receptor antibody.

[0044] The "variable region," used interchangeably herein with "variable domain" (variable region of a light chain (VL), variable region of a heavy chain (VH)) refers to the region in each of the light and heavy immunoglobulin chains which is involved directly in binding the antibody to the antigen. As discussed above, the regions of variable light and heavy chains have the same

general structure and each region comprises four framework (FR) regions whose sequences are widely conserved, connected by three CDRs. The framework regions adopt a beta-sheet conformation and the CDRs may form loops connecting the beta-sheet structure. The CDRs in each chain are held in their three-dimensional structure by the framework regions and form, together with the CDRs from the other chain, the antigen binding site.

[0045] The binding domains that specifically bind to human CGRP receptor or human PAC1 receptor can be derived a) from known antibodies to these antigens or b) from new antibodies or antibody fragments obtained by *de novo* immunization methods using the antigen proteins or fragments thereof, by phage display, or other routine methods. The antibodies from which the binding domains for the bispecific antigen binding proteins are derived can be monoclonal antibodies, polyclonal antibodies, recombinant antibodies, human antibodies, or humanized antibodies. In certain embodiments, the antibodies from which the binding domains are derived are monoclonal antibodies. In these and other embodiments, the antibodies are human antibodies or humanized antibodies and can be of the IgG1-, IgG2-, IgG3-, or IgG4-type.

[0046] The term "monoclonal antibody" (or "mAb") as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally occurring mutations that may be present in minor amounts. Monoclonal antibodies are highly specific, being directed against an individual antigenic site or epitope, in contrast to polyclonal antibody preparations that typically include different antibodies directed against different epitopes. Monoclonal antibodies may be produced using any technique known in the art, e.g., by immortalizing spleen cells harvested from the transgenic animal after completion of the immunization schedule. The spleen cells can be immortalized using any technique known in the art, e.g., by fusing them with myeloma cells to produce hybridomas. Myeloma cells for use in hybridoma-producing fusion procedures preferably are non-antibody-producing, have high fusion efficiency, and enzyme deficiencies that render them incapable of growing in certain selective media which support the growth of only the desired fused cells (hybridomas). Examples of suitable cell lines for use in mouse fusions include Sp-20, P3-X63/Ag8, P3-X63-Ag8.653, NS1/1.Ag 4 1, Sp210-Ag14, FO, NSO/U, MPC-11, MPC11-X45-GTG 1.7 and S194/5XXO Bul; examples of cell lines used in rat fusions include R210.RCY3, Y3-Ag 1.2.3,

IR983F and 4B210. Other cell lines useful for cell fusions are U-266, GM1500-GRG2, LICR-LON-HMy2 and UC729-6.

[0047] In some instances, a hybridoma cell line is produced by immunizing an animal (e.g., a transgenic animal having human immunoglobulin sequences) with a CGRP receptor or PAC1 receptor immunogen; harvesting spleen cells from the immunized animal; fusing the harvested spleen cells to a myeloma cell line, thereby generating hybridoma cells; establishing hybridoma cell lines from the hybridoma cells, and identifying a hybridoma cell line that produces an antibody that binds CGRP receptor or PAC1 receptor.

[0048] Monoclonal antibodies secreted by a hybridoma cell line can be purified using any technique known in the art, such as protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography. Hybridomas or mAbs may be further screened to identify mAbs with particular properties, such as the ability to bind cells expressing CGRP receptor or PAC1 receptor, ability to block or interfere with the binding of the CGRP ligand or PACAP ligand to their respective receptors, or the ability to functionally block either of the receptors, e.g., using a cAMP assay, e.g., as described herein.

[0049] In some embodiments, the anti-PAC1 receptor and anti-CGRP receptor binding domains of the bispecific antigen binding proteins of the invention may be derived from humanized antibodies against the PAC1 receptor and CGRP receptor, respectively. A "humanized antibody" refers to an antibody in which regions (e.g. framework regions) have been modified to comprise corresponding regions from a human immunoglobulin. Generally, a humanized antibody can be produced from a monoclonal antibody raised initially in a non-human animal. Certain amino acid residues in this monoclonal antibody, typically from non-antigen recognizing portions of the antibody, are modified to be homologous to corresponding residues in a human antibody of corresponding isotype. Humanization can be performed, for example, using various methods by substituting at least a portion of a rodent variable region for the corresponding regions of a human antibody (see, e.g., United States Patent Nos. 5,585,089 and 5,693,762; Jones *et al.*, Nature, Vol. 321:522-525, 1986; Riechmann *et al.*, Nature, Vol. 332:323-27, 1988; Verhoeyen *et al.*, Science, Vol. 239:1534-1536, 1988). The CDRs of light and heavy chain variable regions of antibodies generated in another species can be grafted to consensus human FRs. To create consensus human FRs, FRs from several human heavy chain or light chain amino acid sequences may be aligned to identify a consensus amino acid sequence.

[0050] New antibodies generated against the human CGRP receptor or the human PAC1 receptor from which binding domains for the bispecific antigen binding proteins of the invention can be derived can be fully human antibodies. A "fully human antibody" is an antibody that comprises variable and constant regions derived from or indicative of human germ line immunoglobulin sequences. One specific means provided for implementing the production of fully human antibodies is the "humanization" of the mouse humoral immune system. Introduction of human immunoglobulin (Ig) loci into mice in which the endogenous Ig genes have been inactivated is one means of producing fully human monoclonal antibodies (mAbs) in mouse, an animal that can be immunized with any desirable antigen. Using fully human antibodies can minimize the immunogenic and allergic responses that can sometimes be caused by administering mouse or mouse-derived mAbs to humans as therapeutic agents.

[0051] Fully human antibodies can be produced by immunizing transgenic animals (usually mice) that are capable of producing a repertoire of human antibodies in the absence of endogenous immunoglobulin production. Antigens for this purpose typically have six or more contiguous amino acids, and optionally are conjugated to a carrier, such as a hapten. *See, e.g.,* Jakobovits *et al.*, 1993, *Proc. Natl. Acad. Sci. USA* 90:2551-2555; Jakobovits *et al.*, 1993, Nature 362:255-258; and Bruggermann *et al.*, 1993, Year in Immunol. 7:33. In one example of such a method, transgenic animals are produced by incapacitating the endogenous mouse immunoglobulin loci encoding the mouse heavy and light immunoglobulin chains therein, and inserting into the mouse genome large fragments of human genome DNA containing loci that encode human heavy and light chain proteins. Partially modified animals, which have less than the full complement of human immunoglobulin loci, are then cross-bred to obtain an animal having all of the desired immune system modifications. When administered an immunogen, these transgenic animals produce antibodies that are immunospecific for the immunogen but have human rather than murine amino acid sequences, including the variable regions. For further details of such methods, *see*, for example, WO96/33735 and WO94/02602. Additional methods relating to transgenic mice for making human antibodies are described in United States Patent No. 5,545,807; No. 6,713,610; No. 6,673,986; No. 6,162,963; No. 5,939,598; No. 5,545,807; No. 6,300,129; No. 6,255,458; No. 5,877,397; No. 5,874,299 and No. 5,545,806; in PCT publications WO91/10741, WO90/04036, WO 94/02602, WO 96/30498, WO 98/24893 and in EP 546073B1 and EP 546073A1.

[0052] The transgenic mice described above, referred to herein as "HuMab" mice, contain a human immunoglobulin gene minilocus that encodes unrearranged human heavy (mu and gamma) and kappa light chain immunoglobulin sequences, together with targeted mutations that inactivate the endogenous mu and kappa chain loci (Lonberg *et al.*, 1994, Nature 368:856-859). Accordingly, the mice exhibit reduced expression of mouse IgM or kappa and in response to immunization, and the introduced human heavy and light chain transgenes undergo class switching and somatic mutation to generate high affinity human IgG kappa monoclonal antibodies (Lonberg *et al.*, *supra.*; Lonberg and Huszar, 1995, Intern. Rev. Immunol. 13: 65-93; Harding and Lonberg, 1995, Ann. N.Y Acad. Sci. 764:536-546). The preparation of HuMab mice is described in detail in Taylor *et al.*, 1992, Nucleic Acids Research 20:6287-6295; Chen *et al.*, 1993, International Immunology 5:647-656; Tuaillon *et al.*, 1994, J. Immunol. 152:2912-2920; Lonberg *et al.*, 1994, Nature 368:856-859; Lonberg, 1994, Handbook of Exp. Pharmacology 113:49-101; Taylor *et al.*, 1994, International Immunology 6:579-591; Lonberg and Huszar, 1995, Intern. Rev. Immunol. 13:65-93; Harding and Lonberg, 1995, Ann. N.Y Acad. Sci. 764:536-546; Fishwild *et al.*, 1996, Nature Biotechnology 14:845-851. *See*, further United States Patent No. 5,545,806; No. 5,569,825; No. 5,625,126; No. 5,633,425; No. 5,789,650; No. 5,877,397; No. 5,661,016; No. 5,814,318; No. 5,874,299; and No. 5,770,429; as well as United States Patent No. 5,545,807; International Publication Nos. WO 93/1227; WO 92/22646; and WO 92/03918. Technologies utilized for producing human antibodies in these transgenic mice are disclosed also in WO 98/24893, and Mendez *et al.*, 1997, Nature Genetics 15:146-156. For example, the HCo7 and HCo12 transgenic mice strains can be used to generate additional fully human anti-CGRP receptor and anti-PAC1 receptor antibodies.

[0053] Human-derived antibodies can also be generated using phage display techniques. Phage display is described in e.g., Dower *et al.*, WO 91/17271, McCafferty *et al.*, WO 92/01047, and Caton and Koprowski, Proc. Natl. Acad. Sci. USA, 87:6450-6454 (1990). The antibodies produced by phage technology are usually produced as antigen binding fragments, e.g. Fv or Fab fragments, in bacteria and thus lack effector functions. Effector functions can be introduced by one of two strategies: The

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fragments can be engineered either into complete antibodies for expression in mammalian cells, or into bispecific antibody fragments with a second binding site capable of triggering an effector function, if desired. Typically, the Fd fragment (VH-CH1) and light chain (VL-CL) of antibodies are separately cloned by PCR and recombined randomly in combinatorial phage display libraries, which can then be selected for binding to a particular antigen. The antibody fragments are expressed on the phage surface, and selection of Fv or Fab (and therefore the phage containing the DNA encoding the antibody fragment) by antigen binding is accomplished through several rounds of antigen binding and re-amplification, a procedure termed panning. Antibody fragments specific for the antigen are enriched and finally isolated. Phage display techniques can also be used in an approach for the humanization of rodent monoclonal antibodies, called "guided selection" (*see* Jespers, L. S., et al., Bio/Technology 12, 899-903 (1994)). For this, the Fd fragment of the mouse monoclonal antibody can be displayed in combination with a human light chain library, and the resulting hybrid Fab library may then be selected with antigen. The mouse Fd fragment thereby provides a template to guide the selection. Subsequently, the selected human light chains are combined with a human Fd fragment library. Selection of the resulting library yields entirely human Fab.

[0054] The bispecific antigen binding proteins of the invention comprise a binding domain that specifically binds to the human PAC1 receptor. The human PAC1 receptor (also referred to herein as "human PAC1," "hPAC1," and "hPAC1 receptor") is a 468 amino acid protein designated as P41586 (PACR_HUMAN) in the UniProtKB/Swiss-Prot database and is encoded by the *ADCYAP1R1* gene. PACAP-27 and PACAP-38 are the principal endogenous agonists of PAC1. The amino acid sequence of the human PAC1 receptor is set forth below:

MAGVVHVSLA ALLLLPMAPA MHSDCIFKKE QAMCLEKIQR ANELMGFNDS
SPGCPGMWDN ITCWKPAHVG EMVLVSCPEL FRIFNPDQVW ETETIGESDF
GDSNSLDLSD MGVVSRNCTE DGWSEPFPHY FDACGFDEYE SETGDQDYYY
LSVKALYTVG YSTSLVTLTT AMVILCRFRK LHCTRNFIHM NLFVSFMLRA
ISVFIKDWIL YAEQDSNHCF ISTVECKAVM VFFHYCVVSN YFWLFIEGLY
LFTLLVETFF PERRYFYWYT IIGWGTPTVC VTVWATLRLY FDDTGCWDMN
DSTALWWVIK GPVVGSIMVN FVLFIGIIVI LVQKLQSPDM GGNESSIYLR
LARSTLLLIP LFGIHYTVFA FSPENVSKRE RLVFELGLGS FQGFVVAVLY
CFLNGEVQAE IKRKWRSWKV NRYFAVDFKH RHPSLASSGV NGGTQLSILS

KSSSQIRMSG LPADNLAT (SEQ ID NO: 339)

[0055] In certain embodiments, the anti-PAC1 binding domain of the bispecific antigen binding proteins of the invention comprises the VH region and/or the VL region or CDR regions from an anti-PAC1 receptor antibody or functional fragment thereof. Preferably, the anti-PAC1 receptor antibody or functional fragment thereof specifically binds to human PAC1 receptor and prevents or reduces binding of the receptor to PACAP-38 and/or PACAP-27. In some embodiments, the anti-PAC1 receptor antibody or functional fragment thereof specifically binds to an extracellular region of the human PAC1 receptor. In one particular embodiment, the anti-PAC1 receptor antibody or functional fragment thereof specifically binds to the amino-terminal extracellular domain of the PAC1 receptor (i.e. amino acids 21-155 of SEQ ID NO: 339).

[0056] In some embodiments, the anti-PAC1 antibody or functional fragment thereof from which the anti-PAC1 binding domain of the bispecific antigen binding proteins of the invention is derived selectively inhibits the human PAC1 receptor relative to the human VPAC1 and human VPAC2 receptors. An antibody or functional fragment thereof "selectively inhibits" a specific receptor relative to other receptors when the IC50 of the antibody in an inhibition assay of the specific receptor is at least 50-fold lower than the IC50 in an inhibition assay of another "reference" receptor, e.g., a hVPAC1 or hVPAC2 receptor. An "IC50" is the dose/concentration required to achieve 50% inhibition of a biological or biochemical function. With radioactive ligands, IC50 is the concentration of a competing ligand that displaces 50% of the specific binding of the radioligand. The IC50 of any particular substance or antagonist can be determined by constructing a dose-response curve and examining the effect of different concentrations of the drug or antagonist on reversing agonist activity in a particular functional assay. IC50 values can be calculated for a given antagonist or drug by determining the concentration needed to inhibit half of the maximum biological response of the agonist. Thus, the IC50 value for any anti-PAC1 antibody or functional fragment thereof can be calculated by determining the concentration of the antibody or fragment needed to inhibit half of the maximum biological response of the PACAP ligand (PACAP-27 or PACAP-38) in activating the human PAC1 receptor in any functional assay, such as the cAMP assay described in the Examples. An antibody or functional fragment thereof that selectively inhibits a specific receptor is understood to be a neutralizing antibody or neutralizing fragment with respect to that receptor. Thus, in some embodiments, the anti-PAC1 receptor antibody or functional fragment thereof from which the anti-PAC1 binding

domain of the bispecific antigen binding proteins of the invention is derived is a neutralizing antibody or fragment of the human PAC1 receptor.

[0057] The variable regions or CDR regions of any anti-PAC1 receptor antibody or functional fragment thereof can be used to construct the anti-PAC1 binding domain of any of the bispecific antigen binding proteins described herein. For instance, the anti-PAC1 binding domain of the bispecific antigen binding proteins of the invention may comprise VH and/or VL regions or one or more CDRs from any of the anti-human PAC1 receptor antibodies described in WO 2014/144632. In certain embodiments, the anti-PAC1 antibody from which the anti-PAC1 binding domain is derived competes for binding of the human PAC1 receptor with one or more of the human anti-PAC1 antibodies described in WO 2014/144632 or one or more of the anti-PAC1 antibodies described below. The term "compete" refers to the ability of an antibody or other antigen binding protein to interfere with the binding of other antibodies or binding fragments to a target (e.g. the human PAC1 receptor or the human CGRP receptor). The extent to which an antibody or binding fragment is able to interfere with the binding of another antibody or binding fragment to a target (e.g. the human PAC1 receptor or the human CGRP receptor), and therefore whether it can be said to compete, can be determined using competition binding assays. Numerous types of competitive binding assays can be used, including for example: solid phase direct or indirect radioimmunoassay (RIA), solid phase direct or indirect enzyme immunoassay (EIA), sandwich competition assay (*see, e.g.*, Stahli *et al.*, 1983, Methods in Enzymology 9:242-253); solid phase direct biotin-avidin EIA (*see, e.g.*, Kirkland *et al.*, 1986, J. Immunol. 137:3614-3619); solid phase direct-labeled assay, solid phase direct-labeled sandwich assay (*see, e.g.*, Harlow and Lane, 1988, Antibodies, A Laboratory Manual, Cold Spring Harbor Press); solid phase direct label RIA using I-125 label (*see, e.g.*, Morel *et al.*, 1988, Molec. Immunol. 25:7-15); solid phase direct biotin-avidin EIA (*see, e.g.*, Cheung, *et al.*, 1990, Virology 176:546-552); and direct labeled RIA (Moldenhauer *et al.*, 1990, Scand. J. Immunol. 32:77-82). Typically, a competitive binding assay involves the use of purified antigen bound to a solid surface or cells bearing the antigen, an unlabeled test antibody or other antigen binding protein, and a labeled reference antibody or other antigen binding protein. Competitive inhibition is measured by determining the amount of label bound to the solid surface or cells in the presence of the test antibody or other antigen binding protein. Usually the test antibody or other antigen binding protein is

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present in excess. Antibodies or other antigen binding proteins identified by competition assay (i.e. competing antibodies and antigen binding proteins) include antibodies and antigen binding proteins binding to the same epitope as the reference antibody or antigen binding protein. Usually, when a competing antibody or other antigen binding protein is present in excess, it will inhibit specific binding of a reference antibody or other antigen binding protein to a target antigen by at least 40%, 45%, 50%, 55%, 60%, 65%, 70% or 75%. In some instances, binding of the reference antibody or other antigen binding protein is inhibited by at least 80%, 85%, 90%, 95%, or 97% or more. In some embodiments, a competing antibody or binding fragment thereof reduces human PAC1 receptor binding of a reference antibody between about 40% and 100%, such as about 60% and about 100%, specifically between about 70% and 100%, and more specifically between about 80% and 100%.

[0058] A particularly suitable quantitative assay for detecting competitive binding uses a Biacore machine which measures the extent of interactions using surface plasmon resonance technology. An exemplary Biacore-based competitive binding assay involves the immobilization of a reference antibody to a sensor chip. The target antigen is then contacted with the sensor chip where the target antigen is captured by the immobilized reference antibody. Test antibodies are then injected over the captured target antigen. If the injected test antibody recognizes a distinct epitope from that recognized by the immobilized antibody, then a second binding event is observed and the test antibody would be considered not to compete for binding to the target antigen with the reference antibody. Another suitable quantitative competition binding assay uses a FACS-based approach to measure competition between antibodies in terms of their binding to the human PAC1 receptor.

[0059] Light chain and heavy chain variable regions and associated CDRs of exemplary human anti-PAC1 receptor antibodies from which the anti-PAC1 binding domain of the bispecific antigen binding proteins of the invention can be derived or constructed are set forth below in Tables 1A and 1B, respectively.

Table 1A. Exemplary Anti-PAC1 Receptor Light Chain Variable Region Amino Acid Sequences

Antibody ID.	VL Group	VL Amino Acid Sequence	CDRL1	CDRL2	CDRL3
01A, 01C, 01D	LV-01	DIQMTQSPSSLSASVGDRITITCRA SQSISRYLNWYQQKPGKAPKLLIY AASSLQSGIPSRFSGSGSGTDFTLT INSLQPEDFATYFCQQSYSPPFTFG PGTKVDIKR (SEQ ID NO: 28)	RASQSISRYLN (SEQ ID NO: 1)	AASSLQS (SEQ ID NO: 14)	QQSYSPPFT (SEQ ID NO: 20)
01B	LV-02	DIQMTQSPSSLSASVGDRITITCRA SQSISRYLNWYQQKPGKAPKLLIY AASSLQSGIPSRFSGSGSGTDFTLT INSLQPEDFATYFCQQSYSPPFTFG EGTKVDIKR (SEQ ID NO: 29)	RASQSISRYLN (SEQ ID NO: 1)	AASSLQS (SEQ ID NO: 14)	QQSYSPPFT (SEQ ID NO: 20)
02A, 02C	LV-03	DIQMTQSPSSLSASVGDRITITCRA SQSISRYLNWYQQKPGKAPKLLIY AASSLQSGIPSRFSGSGSGTDFTLT INSLQPEDFATYFCQQSYSPPFTFG QGTKVDIKR (SEQ ID NO: 30)	RASQSISRYLN (SEQ ID NO: 1)	AASSLQS (SEQ ID NO: 14)	QQSYSPPFT (SEQ ID NO: 20)
03A, 03C, 03D	LV-04	DIQLTQSPSFLSASVGDRVTITCRA SQSIGRSLHWYQQKPGKAPKLLIK YASQSLSGVPSRFSGSGSGTEFTL TISSLQPEDFATYYCHQSSRLPFTF GPGTKVDIKR (SEQ ID NO: 31)	RASQSIGRSLH (SEQ ID NO: 2)	YASQSLS (SEQ ID NO: 15)	HQSSRLPFT (SEQ ID NO: 21)
03B	LV-05	DIQLTQSPSFLSASVGDRVTITCRA SQSIGRSLHWYQQKPGKAPKLLIK YASQSLSGVPSRFSGSGSGTEFTL TISSLQPEDFATYYCHQSSRLPFTF GEGTKVDIKR (SEQ ID NO: 32)	RASQSIGRSLH (SEQ ID NO: 2)	YASQSLS (SEQ ID NO: 15)	HQSSRLPFT (SEQ ID NO: 21)
04A, 04C, 04D	LV-06	EIVLTQSPATLSLSPGERATLSCRA SQSVGRSLHWYQQKPGQAPRLLI KYASQSLSGIPARFSGSGSGTDFT LTISSLEPEDFAVYYCHQSSRLPFT FGPGTKVDIKR (SEQ ID NO: 33)	RASQSVGRSLH (SEQ ID NO: 3)	YASQSLS (SEQ ID NO: 15)	HQSSRLPFT (SEQ ID NO: 21)
04B	LV-07	EIVLTQSPATLSLSPGERATLSCRA SQSVGRSLHWYQQKPGQAPRLLI KYASQSLSGIPARFSGSGSGTDFT LTISSLEPEDFAVYYCHQSSRLPFT FGEGTKVDIKR (SEQ ID NO: 34)	RASQSVGRSLH (SEQ ID NO: 3)	YASQSLS (SEQ ID NO: 15)	HQSSRLPFT (SEQ ID NO: 21)
05A, 05C, 05D	LV-08	DIVMTQSPDSLAVSLGERATIHCK SSQSVLYSSNNKNFLTWYQQKPG QPPKLLIYRASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVYFCQ QYYSAPFTFGPGTRVDIKR (SEQ ID NO: 35)	KSSQSVLYSSN NKNFLT (SEQ ID NO: 4)	RASTRES (SEQ ID NO: 16)	QQYYSAPF T (SEQ ID NO: 22)
05B	LV-09	DIVMTQSPDSLAVSLGERATIHCK SSQSVLYSSNNKNFLTWYQQKPG QPPKLLIYRASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVYFCQ QYYSAPFTFGEGTRVDIKR (SEQ ID NO: 36)	KSSQSVLYSSN NKNFLT (SEQ ID NO: 4)	RASTRES (SEQ ID NO: 16)	QQYYSAPF T (SEQ ID NO: 22)
06A, 06C	LV-10	DIVMTQSPDSLAVSLGERATINCK SSQSVLYSSNNKNFLTWYQQKPG QPPKLLIYRASTRESGVPDRFSGS	KSSQSVLYSSN NKNFLT	RASTRES (SEQ ID NO:	QQYYSAPF T

Antibody ID.	VL Group	VL Amino Acid Sequence	CDRL1	CDRL2	CDRL3
		GSGTDFTLTISSLQAEDVAVYFCQ QYYSAPFTFGPGTRVDIKR (SEQ ID NO: 37)	(SEQ ID NO: 4)	16)	(SEQ ID NO: 22)
06B	LV-11	DIVMTQSPDSLAVSLGERATINCK SSQSVLYSSNNKNFLTWYQQKPG QPPKLLIYRASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVYFCQ QYYSAPFTFGEGTRVDIKR (SEQ ID NO: 38)	KSSQSVLYSSN NKNFLT (SEQ ID NO: 4)	RASTRES (SEQ ID NO: 16)	QQYYSAPF T (SEQ ID NO: 22)
07	LV-12	EIVLTQSPDFQSVTPKEKVTITCRA SQSIGSSLHWYQQKPDQSPKLLIK YASQSLSGIPSRFSGSGSGTHFTLT INSLEAEDAATYYCHQSSRLPFTF GPGTKVDIKR (SEQ ID NO: 39)	RASQSIGSSLH (SEQ ID NO: 5)	YASQSLS (SEQ ID NO: 15)	HQSSRLPFT (SEQ ID NO: 21)
08, 09, 10	LV-13	EIVLTQSPDFQSVTPKEKVTITCRA SQSVGRSLHWYHQKPDQSPKLLI KYASQSLSGVPSRFSGSGSGTDFT LIINSLEAEDAATYYCHQSSRLPFT FGPGTKVDIKR (SEQ ID NO: 40)	RASQSVGRSLH (SEQ ID NO: 3)	YASQSLS (SEQ ID NO: 15)	HQSSRLPFT (SEQ ID NO: 21)
11	LV-14	DIQLTQSPSFLSASVGDRVTITCRA SQSIGRSLHWYHQKPGKAPKLLIK YASQSLSGVPSRFSGSGSGTEFTLI ISSLQPEDFATYYCHQSSRLPFTFG PGTKVDIKR (SEQ ID NO: 41)	RASQSIGRSLH (SEQ ID NO: 2)	YASQSLS (SEQ ID NO: 15)	HQSSRLPFT (SEQ ID NO: 21)
12, 13, 14	LV-15	EIVLTQSPDFQSVTPKEKVTITCRA SQSVGRSLHWYQQKPDQSPKLLI KYASQSLSGVPSRFSGSGSGTDFT LTINSLEAEDAATYYCHQSSRLPF TFGPGTKVDIKR (SEQ ID NO: 42)	RASQSVGRSLH (SEQ ID NO: 3)	YASQSLS (SEQ ID NO: 15)	HQSSRLPFT (SEQ ID NO: 21)
15, 16, 17, 18	LV-16	EIVLTQSPGTLSLSPGERATLSCRA SQSVGRSLHWYQQKPGQAPRLLI KYASQSLSGIPDRFSGSGSGTDFT LTISRLEPEDFATYYCHQSSRLPFT FGQGTKVEIKR (SEQ ID NO: 43)	RASQSVGRSLH (SEQ ID NO: 3)	YASQSLS (SEQ ID NO: 15)	HQSSRLPFT (SEQ ID NO: 21)
19	LV-17	EIVLTQSPDFQSVTPKEKVTITCRA SQSIGRSLHWYQQKPDQSPKLLF KYASQSLSGVPSRFSGSGSGTDFT LTINSLEAEDAATYYCHQSSRLPF TFGPGTKVDIKR (SEQ ID NO: 44)	RASQSIGRSLH (SEQ ID NO: 2)	YASQSLS (SEQ ID NO: 15)	HQSSRLPFT (SEQ ID NO: 21)
20	LV-18	DIQLTQSPSFLSASVGDRVTITCRA SQSIGRSLHWYQQKPGKAPKLLF KYASQSLSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCHQSSRLPFT FGPGTKVDIKR (SEQ ID NO: 45)	RASQSIGRSLH (SEQ ID NO: 2)	YASQSLS (SEQ ID NO: 15)	HQSSRLPFT (SEQ ID NO: 21)
21	LV-19	EIVLTQSPGTLSLSPGERATLSCRA SQSVSSSYLAWYQQKPGQAPRLL	RASQSVSSSYL A	GASSRAT	QRYGSSRT

Antibody ID.	VL Group	VL Amino Acid Sequence	CDRL1	CDRL2	CDRL3
		IYGASSRATGIPDRFSNSGSGTDFT LTISRLEPEDFAVYYCQRYGSSRT FGQGTKVEIKR (SEQ ID NO: 46)	(SEQ ID NO: 6)	(SEQ ID NO: 17)	(SEQ ID NO: 23)
22	LV-20	DIVMTQSPLSLPVTPGEPASISCRS SQSLLHSNGYNYLDWYLQKPGQS PQLLLYLGSNRASGVPDRFSGSGS GTDFTLQISRVEAEDVGVYYCMQ TLQTPFTFGPGTKVDIKR (SEQ ID NO: 47)	RSSQSLLHSNG YNYLD (SEQ ID NO: 7)	LGSNRAS (SEQ ID NO: 18)	MQTLQTPF T (SEQ ID NO: 24)
23	LV-21	DIVMTQSPLSLPVTPGEPASISCRS SQSLLHSNGYNYLDWYLQKPGQS PQLLLYLGSNRASGVPDRFSGSGS GTDFTLKISRVEAEDVGVYYCMQ TLQTPFTFGPGTKVDIKR (SEQ ID NO: 48)	RSSQSLLHSNG YNYLD (SEQ ID NO: 7)	LGSNRAS (SEQ ID NO: 18)	MQTLQTPF T (SEQ ID NO: 24)
24	LV-22	EIVLTQSPGTLSLSPGERATLSCRA SQTVSRSYLAWYQQKPGQAPRLL IYGASSRATGIPDRFSGSGSGTDFT LTISRLEPEDFAVFYCQQFGSSPW TFGQGTKVEIKR (SEQ ID NO: 49)	RASQTVSRSYL A (SEQ ID NO: 8)	GASSRAT (SEQ ID NO: 17)	QQFGSSPW T (SEQ ID NO: 25)
25	LV-23	DIVMTQSPDSLAVSLGERATIHCK SSQNVLYSSNNKNFLTWYQQKPG QPPKLLIYRASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVYFCQ QYYSAPFTFGPGTKVDIKR (SEQ ID NO: 50)	KSSQNVLYSSN NKNFLT (SEQ ID NO: 9)	RASTRES (SEQ ID NO: 16)	QQYYSAPF T (SEQ ID NO: 22)
26	LV-24	DIVMTQSPDSLAVSLGERTTIKCK SSQSVLYRSNNNNFLAWYQQKPG QPPKLLIYWASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVYFCQ QYYISPLTFGGGTKVEIKR (SEQ ID NO: 51)	KSSQSVLYRSN NNNFLA (SEQ ID NO: 10)	WASTRES (SEQ ID NO: 19)	QQYYISPLT (SEQ ID NO: 26)
27	LV-25	DIVMTQSPDSLAVSLGERATINCK SSQSVLYSSNNKHYLAWYRQKPG QPPKLLIYRASTRESGVPDRFSGS GSGTDFTLTISSLQPEDVAVYYCQ QYYSSPFTFGPGTKVDIKR (SEQ ID NO: 52)	KSSQSVLYSSN NKHYLA (SEQ ID NO: 11)	RASTRES (SEQ ID NO: 16)	QQYYSSPF T (SEQ ID NO: 27)
28	LV-26	DIVMTQSPDSLAVSLGERATIHCK SSQSVLYSSNNRNFLSWYQQKPG QPPKLLIYRASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVYFCQ QYYSAPFTFGPGTTVDIKR (SEQ ID NO: 53)	KSSQSVLYSSN NRNFLS (SEQ ID NO: 12)	RASTRES (SEQ ID NO: 16)	QQYYSAPF T (SEQ ID NO: 22)
29	LV-27	DIVMTQSPDSLAVSLGERATINCK SSQSVLYSSNNKNYLAWYRQKPG QPPKLLIYRASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVYHCQ QYYSSPFTFGPGTKVDIKR (SEQ ID NO: 54)	KSSQSVLYSSN NKNYLA (SEQ ID NO: 13)	RASTRES (SEQ ID NO: 16)	QQYYSSPF T (SEQ ID NO: 27)

Table 1B. Exemplary Anti-PAC1 Receptor Heavy Chain Variable Region Amino Acid Sequences

Antibody ID.	VH Group	VH Amino Acid Sequence	CDRH1	CDRH2	CDRH3
01A, 01C, 01D, 02A, 02C	HV-01	QVQLQQSGPGLVKPSQTLSLTCAI SGDSVSSNSATWNWIRQSPSRGL EWLGRTYYRSKWSNHYAVSVKS RITINPDTSKSQFSLQLNSVTPEDT AVYYCARGTWKQLWFLDHWGQ GTLVTVSS (SEQ ID NO: 83)	SNSATWN (SEQ ID NO: 55)	RTYYRSKW SNHYAVSV KS (SEQ ID NO: 66)	GTWKQLW FLDH (SEQ ID NO: 74)
01B	HV-02	QVQLQQSGPGLVKPSQTLSLTCAI SGDSVSSNSATWNWIRQSPSRKL EWLGRTYYRSKWSNHYAVSVKS RITINPDTSKSQFSLQLNSVTPEDT AVYYCARGTWKQLWFLDHWGQ GTLVTVSS (SEQ ID NO: 84)	SNSATWN (SEQ ID NO: 55)	RTYYRSKW SNHYAVSV KS (SEQ ID NO: 66)	GTWKQLW FLDH (SEQ ID NO: 74)
03A, 03C, 03D, 09, 13, 15	HV-03	QVQLVESGAEVVKPGASVKVSCK ASGFTFSRFAMHWVRQAPGQGLE WMGVISYDGGNKYYAESVKGRV TMTRDTSTSTLYMELSSLRSEDTA VYYCARGYDVLTGYPDYWGQGT LVTVSS (SEQ ID NO: 85)	RFAMH (SEQ ID NO: 56)	VISYDGGN KYYAESVK G (SEQ ID NO: 67)	GYDVLTGY PDY (SEQ ID NO: 75)
03B	HV-04	QVQLVESGAEVVKPGASVKVSCK ASGFTFSRFAMHWVRQAPGQKLE WMGVISYDGGNKYYAESVKGRV TMTRDTSTSTLYMELSSLRSEDTA VYYCARGYDVLTGYPDYWGQGT LVTVSS (SEQ ID NO: 86)	RFAMH (SEQ ID NO: 56)	VISYDGGN KYYAESVK G (SEQ ID NO: 67)	GYDVLTGY PDY (SEQ ID NO: 75)
04A, 04C, 04D	HV-05	QVQLVESGGGVVQPGRSLRLSCA ASGFTFSRFAMHWVRQAPGKGLE WVAVISYDGGNKYYAESVKGRF TISRDNSKNTLYLQMNSLRAEDT ALFYCARGYDVLTGYPDYWGQG TLVTVSS (SEQ ID NO: 87)	RFAMH (SEQ ID NO: 56)	VISYDGGN KYYAESVK G (SEQ ID NO: 67)	GYDVLTGY PDY (SEQ ID NO: 75)
04B	HV-06	QVQLVESGGGVVQPGRSLRLSCA ASGFTFSRFAMHWVRQAPGKKLE WVAVISYDGGNKYYAESVKGRF TISRDNSKNTLYLQMNSLRAEDT ALFYCARGYDVLTGYPDYWGQG TLVTVSS (SEQ ID NO: 88)	RFAMH (SEQ ID NO: 56)	VISYDGGN KYYAESVK G (SEQ ID NO: 67)	GYDVLTGY PDY (SEQ ID NO: 75)
05A, 05C, 05D	HV-07	QVQLQESGPGLVKPSQTLSLTCTV SGGSISSGGYYWSWIRQHPGKGL EWIGYIYYSGNTYYNPSLKSRVTI SGDTSKNQFSLKLRSVTAADTAV YYCTRGGAARGMDVWGQGTTV TVSS (SEQ ID NO: 89)	SGGYYWS (SEQ ID NO: 57)	YIYYSGNT YYNPSLKS (SEQ ID NO: 68)	GGAARGM DV (SEQ ID NO: 76)
05B	HV-08	QVQLQESGPGLVKPSQTLSLTCTV SGGSISSGGYYWSWIRQHPGKKL EWIGYIYYSGNTYYNPSLKSRVTI SGDTSKNQFSLKLRSVTAADTAV YYCTRGGAARGMDVWGQGTTV TVSS (SEQ ID NO: 90)	SGGYYWS (SEQ ID NO: 57)	YIYYSGNT YYNPSLKS (SEQ ID NO: 68)	GGAARGM DV (SEQ ID NO: 76)

Antibody ID.	VH Group	VH Amino Acid Sequence	CDRH1	CDRH2	CDRH3
06A, 06C	HV-09	QVQLQESGPGLVKPSETLSLTCTV SGGSISSGGYYWSWIRQPPGKGLE WIGYIYYSGNTYYNPSLKSRVTIS VDTSKNQFSLKLRSVTAADTAVY YCTRGGAARGMDVWGQGTTVT VSS (SEQ ID NO: 91)	SGGYYWS (SEQ ID NO: 57)	YIYYSGNT YYNPSLKS (SEQ ID NO: 68)	GGAARGM DV (SEQ ID NO: 76)
06B	HV-10	QVQLQESGPGLVKPSETLSLTCTV SGGSISSGGYYWSWIRQPPGKKLE WIGYIYYSGNTYYNPSLKSRVTIS VDTSKNQFSLKLRSVTAADTAVY YCTRGGAARGMDVWGQGTTVT VSS (SEQ ID NO: 92)	SGGYYWS (SEQ ID NO: 57)	YIYYSGNT YYNPSLKS (SEQ ID NO: 68)	GGAARGM DV (SEQ ID NO: 76)
07	HV-11	QVQLVESGGGVVQPGRSLRLSCA ASGFTFSYYAIHWVRQAPGKGLE WVAVISYDGSNKYYADSVKGRF TISRDNSKNTLYLQMNSLRAEDT AVYYCARGYDLLTGYPDYWGQG TLVTVSS (SEQ ID NO: 93)	YYAIH (SEQ ID NO: 58)	VISYDGSN KYYADSVK G (SEQ ID NO: 69)	GYDLLTGY PDY (SEQ ID NO: 77)
11, 14	HV-12	QVQLVESGGGVVQPGRSLRLSCA ASGFTFSRFAMHWVRRAPGKGLE WVAVISYDGGNKYYAESVKGRF TISRDNSKNTLNLLMNSLRAEDT ALFYCARGYDVLTGYPDYWGQG TLVTVSS (SEQ ID NO: 94)	RFAMH (SEQ ID NO: 56)	VISYDGGN KYYAESVK G (SEQ ID NO: 67)	GYDVLTGY PDY (SEQ ID NO: 75)
08, 12	HV-13	QVQLVESGGGVVQPGRSLRLSCA ASGFTFSRFAMHWVRQAPGKGLE WVAVISYDGGNKYYAESVKGRF TISRDNSKNTLNLLMNSLRAEDT ALFYCARGYDVLTGYPDYWGQG TLVTVSS (SEQ ID NO: 95)	RFAMH (SEQ ID NO: 56)	VISYDGGN KYYAESVK G (SEQ ID NO: 67)	GYDVLTGY PDY (SEQ ID NO: 75)
10	HV-14	QVQLVESGGGVVQPGRSLRLSCA ASGFTFSRFAMHWVRRAPGKGLE WVAVISYDGGNKYYAESVKGRF TISRDNSKNTLNLLMDSLRAEDT ALFYCARGYDVLTGYPDYWGQG TLVTVSS (SEQ ID NO: 96)	RFAMH (SEQ ID NO: 56)	VISYDGGN KYYAESVK G (SEQ ID NO: 67)	GYDVLTGY PDY (SEQ ID NO: 75)
16	HV-15	QVQLVQSGAEVKKPGASVKVSC KASGFTFSRFAMHWVRQAPGQG LEWMGVISYDGGNKYYAESVKG RVTMTRDTSTSTAYMELSSLRSE DTAVYYCARGYDVLTGYPDYWG QGTLVTVSS (SEQ ID NO: 97)	RFAMH (SEQ ID NO: 56)	VISYDGGN KYYAESVK G (SEQ ID NO: 67)	GYDVLTGY PDY (SEQ ID NO: 75)
17	HV-16	QVQLVQSGAEVKKPGASVKVSC AASGFTFSRFAMHWVRQAPGQG LEWMGVISYDGGNKYYAESVKG RVTMTRDNSKNTAYMELSSLRSE DTAVYYCARGYDVLTGYPDYWG QGTLVTVSS (SEQ ID NO: 98)	RFAMH (SEQ ID NO: 56)	VISYDGGN KYYAESVK G (SEQ ID NO: 67)	GYDVLTGY PDY (SEQ ID NO: 75)
18	HV-17	EVQLLESGGGLVQPGGSLRLSCA ASGFTFSRFAMHWVRQAPGKGLE WVAVISYDGGNKYYAESVKGRF TISRDNSKNTLYLQMNSLRAEDT AVYYCARGYDVLTGYPDYWGQ	RFAMH (SEQ ID NO: 56)	VISYDGGN KYYAESVK G (SEQ ID NO:	GYDVLTGY PDY (SEQ ID NO: 75)

Antibody ID.	VH Group	VH Amino Acid Sequence	CDRH1	CDRH2	CDRH3
		GTLVTVSS (SEQ ID NO: 99)		67)	
19, 20	HV-18	QVQLVESGGGVVQPGRSLRLSCA ASGFTFSRYAMHWVRQASGKGL EWVAVISYDGSNKYYADSVKGR FTISRDNSKNTLYLLMSSLRAEDT AVFYCARGYDILTGYPDYWGQG TLVTVSS (SEQ ID NO: 100)	RYAMH (SEQ ID NO: 59)	VISYDGSN KYYADSVK G (SEQ ID NO: 69)	GYDILTGY PDY (SEQ ID NO: 78)
21	HV-19	QVQLVQSGAEVKKPGASVKVSC KASGYTFTSYGISWVRQAPGQGL EWMGWINAYNGHTNYAQTFQGR VTMTTDTSTSTAYMELRSLRSDD TAVYYCARELELRSFYYFGMDV WGQGTTVPVSS (SEQ ID NO: 101)	SYGIS (SEQ ID NO: 60)	WINAYNGH TNYAQTFQ G (SEQ ID NO: 70)	ELELRSFYY FGMDV (SEQ ID NO: 79)
22	HV-20	QVQLVQSGAEVKKSGASLKVSCK ASGYIFTRYGVSWVRQAPGQGLE WMGWITTYNGNTNYAQKLQGR VTMTIDTSTSTAYMELRSLRSDDT AVYYCARRVRYSGGYSFDNWGQ GTLVTVSS (SEQ ID NO: 102)	RYGVS (SEQ ID NO: 61)	WITTYNGN TNYAQKLQ G (SEQ ID NO: 71)	RVRYSGGY SFDN (SEQ ID NO: 80)
23	HV-21	QVQLVQSGAEVKKSGASLKVSCK ASGYIFTRYGVSWVRQAPGQGLE WMGWITTYNGNTNYAQKLQGR VTMTTDTSTSTAYMELRSLRSDD TAVYYCARRVRYSGGYSFDNWG QGTLVTVSS (SEQ ID NO: 103)	RYGVS (SEQ ID NO: 61)	WITTYNGN TNYAQKLQ G (SEQ ID NO: 71)	RVRYSGGY SFDN (SEQ ID NO: 80)
24	HV-22	QVQLQESGPGLVKPSETLSLTCTV SGGSISSYYWSWIRQPAGKGLEWI GRIYTSGSTNYNPSLKSRVTMSIG TSKNQFSLKLSSVTAADTAVYYC AIIASRGWYFDLWGRGTLVTVSS (SEQ ID NO: 104)	SYYWS (SEQ ID NO: 62)	RIYTSGSTN YNPSLKS (SEQ ID NO: 72)	IASRGWYF DL (SEQ ID NO: 81)
25, 28	HV-23	QVQLQESGPGLVKPSQTLSLTCTV SGGSISSGGYYWSWIRQHPGKGL EWIGYIYYSGNTYYNPSLKSRVTI SGDTSKNQFSLKLRSVTAADTAV YYCARGGAARGMDVWGQGTTV TVSS (SEQ ID NO: 105)	SGGYYWS (SEQ ID NO: 57)	YIYYSGNT YYNPSLKS (SEQ ID NO: 68)	GGAARGM DV (SEQ ID NO: 76)
26	HV-24	QVQLQQSGPGLVKPSQTLSLTCAI SGDSVSSNSAAWNWIRQSPSRGL EWLGRTYYRSRWYNDYAVSVKS RITINPDTSKNQFSLQLNSVTPEDT AVYYCARGVFYSKGAFDIWGQG TMVTVSS (SEQ ID NO: 106)	SNSAAWN (SEQ ID NO: 63)	RTYYRSRW YNDYAVSV KS (SEQ ID NO: 73)	GVFYSKGA FDI (SEQ ID NO: 82)
27	HV-25	QVQLQESGPGLVKPSQTLSLTCTV SGGSISRGGYYWSWIRQHPGKGL EWIGYIYYSGNTYYNPSLKSRVIIS GDTSKNQLSLKLRSVTAADTAVY YCARGGAARGMDVWGQGTTVT VSS (SEQ ID NO: 107)	RGGYYWS (SEQ ID NO: 64)	YIYYSGNT YYNPSLKS (SEQ ID NO: 68)	GGAARGM DV (SEQ ID NO: 76)
29	HV-26	QVQLQESGPGLVKPSQTLSLTCTV SGGSISSGGFYWSWIRQHPGKGLE WIGYIYYSGNTYYNPSLKSRVIIS	SGGFYWS (SEQ ID NO: 65)	YIYYSGNT YYNPSLKS	GGAARGM DV

Antibody ID.	VH Group	VH Amino Acid Sequence	CDRH1	CDRH2	CDRH3
		GDTSKNQFSLKLSSVTAADTAVY YCARGGAARGMDVWGQGTTVT VSS (SEQ ID NO: 108)		(SEQ ID NO: 68)	(SEQ ID NO: 76)

[0060] The anti-PAC1 receptor binding domain of the bispecific antigen binding proteins may comprise one or more of the CDRs presented in Table 1A (light chain CDRs; i.e. CDRLs) and Table 1B (heavy chain CDRs, i.e. CDRHs). For instance, in certain embodiments, the anti-PAC1 receptor binding domain comprises one or more light chain CDRs selected from (i) a CDRL1 selected from SEQ ID NOs: 1 to 13, (ii) a CDRL2 selected from SEQ ID NOs: 14 to 19, and (iii) a CDRL3 selected from SEQ ID NOs: 20 to 27, and (iv) a CDRL of (i), (ii) and (iii) that contains one or more, e.g., one, two, three, four or more amino acid substitutions (e.g., conservative amino acid substitutions), deletions or insertions of no more than five, four, three, two, or one amino acids. In these and other embodiments, the anti-PAC1 receptor binding domain comprises one or more heavy chain CDRs selected from (i) a CDRH1 selected from SEQ ID NOs: 55 to 65, (ii) a CDRH2 selected from SEQ ID NOs: 66 to 73, and (iii) a CDRH3 selected from SEQ ID NOs: 74 to 82, and (iv) a CDRH of (i), (ii) and (iii) that contains one or more, e.g., one, two, three, four or more amino acid substitutions (e.g., conservative amino acid substitutions), deletions or insertions of no more than five, four, three, two, or one amino acids amino acids.

[0061] In certain embodiments, the anti-PAC1 receptor binding domain may comprise 1, 2, 3, 4, 5, or 6 variant forms of the CDRs listed in Tables 1A and 1B, each having at least 80%, 85%, 90% or 95% sequence identity to a CDR sequence listed in Tables 1A and 1B. In some embodiments, the anti-PAC1 receptor binding domain includes 1, 2, 3, 4, 5, or 6 of the CDRs listed in Tables 1A and 1B, each differing by no more than 1, 2, 3, 4 or 5 amino acids from the CDRs listed in these tables.

[0062] In particular embodiments, the anti-PAC1 receptor binding domain of the bispecific antigen binding proteins of the invention comprises a light chain variable region comprising a CDRL1, a CDRL2, and a CDRL3, wherein: (a) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 1, 14 and 20, respectively; (b) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 2, 15 and 21, respectively; (c) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 3, 15 and 21, respectively; (d) CDRL1, CDRL2, and CDRL3 have the sequence

of SEQ ID NOs: 4, 16 and 22, respectively; (e) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 5, 15 and 21, respectively; (f) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 6, 17 and 23, respectively; (g) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 7, 18 and 24, respectively; (h) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 8, 17 and 25, respectively; (i) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 9, 16 and 22, respectively; (j) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 10, 19 and 26, respectively; (k) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 11, 16 and 27, respectively; (l) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 12, 16 and 22, respectively; or (m) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 13, 16 and 27, respectively.

[0063] In other particular embodiments, the anti-PAC1 receptor binding domain of the bispecific antigen binding proteins of the invention comprises a heavy chain variable region comprising a CDRH1, a CDRH2, and a CDRH3, wherein: (a) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 55, 66 and 74, respectively; (b) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 56, 67 and 75, respectively; (c) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 57, 68 and 76, respectively; (d) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 58, 69 and 77, respectively; (e) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 59, 69 and 78, respectively; (f) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 60, 70 and 79, respectively; (g) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 61, 71 and 80, respectively; (h) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 62, 72 and 81, respectively; (i) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 63, 73 and 82, respectively; (j) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 64, 68 and 76, respectively; or (k) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 65, 68 and 76, respectively.

[0064] In certain embodiments, the anti-PAC1 receptor binding domain of the bispecific antigen binding proteins of the invention comprises a light chain variable region comprising a CDRL1, a CDRL2, and a CDRL3 and a heavy chain variable region comprising a CDRH1, a CDRH2, and a CDRH3, wherein:

(a) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 1, 14 and 20, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 55, 66 and 74, respectively;

(b) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 2, 15 and 21, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 56, 67 and 75, respectively;

(c) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 3, 15 and 21, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 56, 67 and 75, respectively;

(d) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 4, 16 and 22, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 57, 68 and 76, respectively;

(e) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 5, 15 and 21, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 58, 69 and 77, respectively;

(f) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 2, 15 and 21, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 59, 69 and 78, respectively;

(g) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 6, 17 and 23, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 60, 70 and 79, respectively;

(h) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 7, 18 and 24, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 61, 71 and 80, respectively;

(i) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 8, 17 and 25, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 62, 72 and 81, respectively;

(j) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 9, 16 and 22, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 57, 68 and 76, respectively;

(k) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 10, 19 and 26, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 63, 73 and 82, respectively;

(l) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 11, 16 and 27, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 64, 68 and 76, respectively;

(m) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 12, 16 and 22, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 57, 68 and 76, respectively; or

(n) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 13, 16 and 27, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 65, 68 and 76, respectively.

[0065] In some embodiments, the anti-PAC1 receptor binding domain of the bispecific antigen binding proteins of the invention comprises a light chain variable region comprising a CDRL1, a CDRL2, and a CDRL3 and a heavy chain variable region comprising a CDRH1, a CDRH2, and a CDRH3, wherein:

(a) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 1, 14 and 20, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 55, 66 and 74, respectively;

(b) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 2, 15 and 21, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 56, 67 and 75, respectively;

(c) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 3, 15 and 21, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 56, 67 and 75, respectively; or

(d) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 4, 16 and 22, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 57, 68 and 76, respectively.

[0066] The anti-PAC1 receptor binding domain of the antigen binding proteins of the invention may comprise a light chain variable region selected from the group consisting of LV-01, LV-02, LV-03, LV-04, LV-05, LV-06, LV-07, LV-08, LV-09, LV-10, LV-11, LV-12, LV-13, LV-14,

LV-15, LV-16, LV-17, LV-18, LV-19, LV-20, LV-21, LV-22, LV-23, LV-24, LV-25, LV-26, and LV-27, as shown in Table 1A, and/or a heavy chain variable region selected from the group consisting of HV-01, HV-02, HV-03, HV-04, HV-05, HV-06, HV-07, HV-08, HV-09, HV-10, HV-11, HV-12, HV-13, HV-14, HV-15, HV-16, HV-17, HV-18, HV-19, HV-20, HV-21, HV-22, HV-23, HV-24, HV-25, and HV-26 as shown in Table 1B, and functional fragments, derivatives, muteins and variants of these light chain and heavy chain variable regions.

[0067] Each of the light chain variable regions listed in Table 1A may be combined with any of the heavy chain variable regions shown in Table 1B to form an anti-PAC1 receptor binding domain suitable for incorporation into the bispecific antigen binding proteins of the invention. Examples of such combinations include, but are not limited to: LV-01 and HV-01; LV-02 and HV-02; LV-03 and HV-01; LV-04 and HV-03; LV-05 and HV-04; LV-06 and HV-05; LV-07 and HV-06; LV-08 and HV-07; LV-09 and HV-08; LV-10 and HV-09; LV-11 and HV-10; LV-12 and HV-11; LV-13 and HV-13; LV-13 and HV-03; LV-13 and HV-14; LV-14 and HV-12; LV-15 and HV-13; LV-15 and HV-03; LV-15 and HV-12; LV-16 and HV-03; LV-16 and HV-15; LV-16 and HV-16; LV-16 and HV-17; LV-17 and HV-18; LV-18 and HV-18; LV-19 and HV-19; LV-20 and HV-20; LV-21 and HV-21; LV-22 and HV-22; LV-23 and HV-23; LV-24 and HV-24; LV-25 and HV-25; LV-26 and HV-23; and LV-27 and HV-26. In certain embodiments, the anti-PAC1 receptor binding domain comprises: (a) LV-01 (SEQ ID NO: 28) and HV-01 (SEQ ID NO: 83); (b) LV-03 (SEQ ID NO: 30) and HV-01 (SEQ ID NO: 83); (c) LV-04 (SEQ ID NO: 31) and HV-03 (SEQ ID NO: 85); (d) LV-06 (SEQ ID NO: 33) and HV-05 (SEQ ID NO: 87); (e) LV-08 (SEQ ID NO: 35) and HV-07 (SEQ ID NO: 89); or (f) LV-10 (SEQ ID NO: 37) and HV-09 (SEQ ID NO: 91).

[0068] In some embodiments, the anti-PAC1 receptor binding domain comprises a light chain variable region comprising a sequence of contiguous amino acids that differs from the sequence of a light chain variable region in Table 1A, i.e. a VL selected from LV-01, LV-02, LV-03, LV-04, LV-05, LV-06, LV-07, LV-08, LV-09, LV-10, LV-11, LV-12, LV-13, LV-14, LV-15, LV-16, LV-17, LV-18, LV-19, LV-20, LV-21, LV-22, LV-23, LV-24, LV-25, LV-26, and LV-27 at only 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15 amino acid residues, wherein each such sequence difference is independently either a deletion, insertion or substitution of one amino acid, with the deletions, insertions and/or substitutions resulting in no more than 15 amino acid changes relative to the foregoing variable domain sequences. The light chain variable region in

some anti-PAC1 binding domains comprises a sequence of amino acids that has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97% or at least 99% sequence identity to the amino acid sequences of SEQ ID NOs: 28-54 (i.e. the light chain variable regions in Table 1A).

[0069] In these and other embodiments, the anti-PAC1 receptor binding domain comprises a heavy chain variable region comprising a sequence of contiguous amino acids that differs from the sequence of a heavy chain variable region in Table 1B, i.e., a VH selected from HV-01, HV-02, HV-03, HV-04, HV-05, HV-06, HV-07, HV-08, HV-09, HV-10, HV-11, HV-12, HV-13, HV-14, HV-15, HV-16, HV-17, HV-18, HV-19, HV-20, HV-21, HV-22, HV-23, HV-24, HV-25, and HV-26 at only 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15 amino acid residues, wherein each such sequence difference is independently either a deletion, insertion or substitution of one amino acid, with the deletions, insertions and/or substitutions resulting in no more than 15 amino acid changes relative to the foregoing variable domain sequences. The heavy chain variable region in some anti-PAC1 receptor binding domains comprises a sequence of amino acids that has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97% or at least 99% sequence identity to the amino acid sequences of SEQ ID NOs: 83-108 (i.e. the heavy chain variable regions in Table 1B).

[0070] The term "identity," as used herein, refers to a relationship between the sequences of two or more polypeptide molecules or two or more nucleic acid molecules, as determined by aligning and comparing the sequences. "Percent identity," as used herein, means the percent of identical residues between the amino acids or nucleotides in the compared molecules and is calculated based on the size of the smallest of the molecules being compared. For these calculations, gaps in alignments (if any) must be addressed by a particular mathematical model or computer program (i.e., an "algorithm"). Methods that can be used to calculate the identity of the aligned nucleic acids or polypeptides include those described in Computational Molecular Biology, (Lesk, A. M., ed.), 1988, New York: Oxford University Press; Biocomputing Informatics and Genome Projects, (Smith, D. W., ed.), 1993, New York: Academic Press; Computer Analysis of Sequence Data, Part I, (Griffin, A. M., and Griffin, H. G., eds.), 1994, New Jersey: Humana Press; von Heinje, G., 1987, Sequence Analysis in Molecular Biology, New York: Academic Press; Sequence Analysis Primer, (Gribskov, M. and Devereux, J., eds.), 1991, New York: M. Stockton Press; and Carillo et al., 1988, SIAM J. Applied Math. 48:1073. For example, sequence

identity can be determined by standard methods that are commonly used to compare the similarity in position of the amino acids of two polypeptides. Using a computer program such as BLAST or FASTA, two polypeptide or two polynucleotide sequences are aligned for optimal matching of their respective residues (either along the full length of one or both sequences, or along a pre-determined portion of one or both sequences). The programs provide a default opening penalty and a default gap penalty, and a scoring matrix such as PAM 250 (a standard scoring matrix; see Dayhoff et al., in Atlas of Protein Sequence and Structure, vol. 5, supp. 3 (1978)) can be used in conjunction with the computer program. For example, the percent identity can then be calculated as: the total number of identical matches multiplied by 100 and then divided by the sum of the length of the longer sequence within the matched span and the number of gaps introduced into the longer sequences in order to align the two sequences. In calculating percent identity, the sequences being compared are aligned in a way that gives the largest match between the sequences.

[0071] The GCG program package is a computer program that can be used to determine percent identity, which package includes GAP (Devereux et al., 1984, Nucl. Acid Res. 12:387; Genetics Computer Group, University of Wisconsin, Madison, WI). The computer algorithm GAP is used to align the two polypeptides or two polynucleotides for which the percent sequence identity is to be determined. The sequences are aligned for optimal matching of their respective amino acid or nucleotide (the "matched span", as determined by the algorithm). A gap opening penalty (which is calculated as 3x the average diagonal, wherein the "average diagonal" is the average of the diagonal of the comparison matrix being used; the "diagonal" is the score or number assigned to each perfect amino acid match by the particular comparison matrix) and a gap extension penalty (which is usually 1/10 times the gap opening penalty), as well as a comparison matrix such as PAM 250 or BLOSUM 62 are used in conjunction with the algorithm. In certain embodiments, a standard comparison matrix (see, Dayhoff et al., 1978, Atlas of Protein Sequence and Structure 5:345-352 for the PAM 250 comparison matrix; Henikoff et al., 1992, Proc. Natl. Acad. Sci. U.S.A. 89:10915-10919 for the BLOSUM 62 comparison matrix) is also used by the algorithm.

[0072] Recommended parameters for determining percent identity for polypeptides or nucleotide sequences using the GAP program include the following:

Algorithm: Needleman et al., 1970, J. Mol. Biol. 48:443-453;

Comparison matrix: BLOSUM 62 from Henikoff et al., 1992, *supra*;

Gap Penalty: 12 (but with no penalty for end gaps)

Gap Length Penalty: 4

Threshold of Similarity: 0

[0073] Certain alignment schemes for aligning two amino acid sequences may result in matching of only a short region of the two sequences, and this small aligned region may have very high sequence identity even though there is no significant relationship between the two full-length sequences. Accordingly, the selected alignment method (GAP program) can be adjusted if so desired to result in an alignment that spans at least 50 contiguous amino acids of the target polypeptide.

[0074] The bispecific antigen binding proteins of the invention comprise a binding domain that specifically binds to the human CGRP receptor. The human CGRP receptor (also referred to herein as "CGRPR," "CGRP R," "hCGRPR," and "huCGRPR") is a heterodimer that comprises the human calcitonin receptor-like receptor (CRLR) polypeptide (Genbank Accession No. U17473.1) and the human receptor activity modifying protein 1 (RAMP1) polypeptide (Genbank Accession No. AJ001014). The amino acid sequences for the full-length human CRLR and RAMP1 polypeptides as well as extracellular domains from both polypeptides are set forth in Table 2 below.

Table 2. Sequences of human CRLR and human RAMP1 polypeptides

Polypeptide	Sequence
Human CRLR	MLYSIFHFGLMMEKKCTLYFLVLLPFFMILVTAELEESPEDSIQLGVTRNKIMTAQYE CYQKIMQDPIQQAEGVYCNRTWDGWLCWNDVAAGTESMQLCPDYFQDFDPSEKVT KICDQDGNWFRHPASNRTWTNYTQCNVNTHEKVKTALNLFYLTIIGHGLSIASLLISL GIFFYFKSLSCQRITLHKNLFFSFVCNSVVTIIHLTAVANNQALVATNPVSCKVSQFIH LYLMGCNYFWMLCEGIYLHTLIVVAVFAEKQHLMWYYFLGWGFPLIPACIHAIARS LYYNDNCWISSDTHLLYIIHGPICAALLVNLFFLLNIVRVLITKLKVTHQAESNLYMK AVRATLILVPLLGIEFVLIPWRPEGKIAEEVYDYIMHILMHFQGLLVSTIFCFFNGEVQ AILRRNWNQYKIQFGNSFSNSEALRSASYTVSTISDGPGYSHDCPSEHLNGKSIHDIEN VLLKPENLYN (SEQ ID NO: 340)
Human RAMP1	MARALCRLPRRGLWLLLAHHLFMTTACQEANYGALLRELCLTQFQVDMEAVGETL WCDWGRTIRSYRELADCTWHMAEKLGCFWPNAEVDRFFLAVHGRYFRSCPISGRA VRDPPGSILYPFIVVPITVTLLVTALVVWQSKRTEGIV (SEQ ID NO: 341)
Extracellular Domain of Human CRLR	ELEESPEDSIQLGVTRNKIMTAQYECYQKIMQDPIQQAEGVYCNRTWDGWLCWNDV AAGTESMQLCPDYFQDFDPSEKVTKICDQDGNWFRHPASNRTWTNYTQCNVNTHE KVKTA (SEQ ID NO: 342)
Extracellular Domain of Human RAMP1	CQEANYGALLRELCLTQFQVDMEAVGETLWCDWGRTIRSYRELADCTWHMAEKL GCFWPNAEVDRFFLAVHGRYFRSCPISGRAVRDPPGS (SEQ ID NO: 343)

[0075] In certain embodiments, the anti-CGRP receptor binding domain of the bispecific antigen binding proteins of the invention comprises the VH region and/or the VL region or CDR regions from an anti-CGRP receptor antibody or functional fragment thereof. Preferably, the anti-CGRP receptor antibody or functional fragment thereof specifically binds to human CGRP receptor and prevents or reduces binding of the receptor to CGRP. In certain embodiments, the anti-CGRP receptor antibody or functional fragment thereof specifically binds to residues or sequences of residues, or regions in both human CRLR and human RAMP1 polypeptides. In one embodiment, the anti-CGRP receptor antibody or functional fragment thereof specifically binds to an epitope formed from amino acids in both human CRLR and human RAMP1 polypeptides. As used herein, an "epitope" refers to any determinant capable of being specifically bound by an antibody or functional fragment thereof. An epitope can be contiguous or non-contiguous (e.g., (i) in a single-chain polypeptide, amino acid residues that are not contiguous to one another in the polypeptide sequence but that within in context of the molecule are bound by the antibody or functional fragment, or (ii) in a multimeric protein, e.g., comprising two or more individual components, amino acid residues present on two or more of the individual components, but that within the context of the multimeric protein are bound by the antibody or functional fragment). In some embodiments, the epitope formed from amino acids in both human CRLR and human RAMP1 polypeptides comprises one or more cleavage sites for AspN protease, which cleaves peptides after aspartic acid residues and some glutamic acid residues at the amino end.

[0076] In certain embodiments, the anti-CGRP receptor antibody or functional fragment thereof from which the anti-CGRP receptor binding domain is derived specifically binds to an extracellular domain of human CRLR polypeptide comprising the amino acid sequence of SEQ ID NO: 342. Alternatively or additionally, the anti-CGRP receptor antibody or functional fragment thereof specifically binds to an extracellular domain of human RAMP1 polypeptide comprising the amino acid sequence of SEQ ID NO: 343. In some embodiments, the anti-CGRP receptor antibody or binding fragment specifically binds to an epitope within the human CRLR polypeptide comprising at least one sequence selected from SEQ ID NO: 344 (DSIQLGVTRNKIMTAQY; corresponding to amino acids 8-24 of SEQ ID NO: 342), SEQ ID NO: 345 (DVAAGTESMQLCP; corresponding to amino acids 55-67 of SEQ ID NO: 342), SEQ ID NO: 346 (DGNWFRHPASNRTWTNYTQCNVNTH; corresponding to amino acids 86-110 of SEQ ID NO: 342), SEQ ID NO: 347 (ECYQKIMQ; corresponding to amino acids 25-32 of

SEQ ID NO: 342), or SEQ ID NO: 348 (DGWLCWN; corresponding to amino acids 48-54 of SEQ ID NO: 342). For example, in some embodiments, the anti-CGRP receptor antibody or functional fragment thereof binds an epitope within a subregion of human CRLR polypeptide of SEQ ID NO: 342, wherein the epitope comprises SEQ ID NOs: 344-348, optionally in its native three-dimensional conformation. Alternatively or additionally, the anti-CGRP receptor antibody or functional fragment specifically binds to at least one epitope within the human RAMP1 polypeptide selected from SEQ ID NO: 349 (RELADCTWHMAE; corresponding to amino acids 41-52 of SEQ ID NO: 343), SEQ ID NO: 350 (DWGRTIRSYRELA; corresponding to amino acids 32-44 of SEQ ID NO: 343), SEQ ID NO: 351 (ELCLTQFQV; corresponding to amino acids 12-20 of SEQ ID NO: 343), or SEQ ID NO: 352 (DCTWHMA; corresponding to amino acids 45-51 of SEQ ID NO: 343). In some embodiments, the anti-CGRP receptor antibody or functional fragment thereof binds to an epitope within a subregion of human RAMP1 polypeptide of SEQ ID NO: 343, wherein the epitope comprises SEQ ID NOs: 349-352, optionally in its native three-dimensional conformation.

[0077] In some embodiments, the anti-CGRP receptor antibody or functional fragment thereof from which the anti-CGRP receptor binding domain of the bispecific antigen binding proteins of the invention is derived selectively inhibits the human CGRP receptor relative to the human adrenomedullin 1(AM1), human adrenomedullin 2 (AM2), or human amylin receptors (e.g. human AMY1 receptor). The human AM1 receptor is comprised of a human CRLR polypeptide and a RAMP2 polypeptide, whereas the human AM2 receptor is comprised of a human CRLR polypeptide and a RAMP3 polypeptide. Thus, an antibody or other binding protein that binds only CRLR (and not RAMP1) would not be expected to *selectively* inhibit the CGRP receptor because the CRLR polypeptide is also a component of the AM1 and AM2 receptors. The human amylin (AMY) receptors are comprised of a human calcitonin receptor (CT) polypeptide and one of the RAMP1, RAMP2, or RAMP3 subunits. Specifically, the human AMY1 receptor is composed of the CT polypeptide and the RAMP1 polypeptide, the human AMY2 receptor is composed of the CT polypeptide and the RAMP2 polypeptide, and the human AMY3 receptor is composed of the CT polypeptide and the RAMP3 polypeptide. Thus, an antibody or other binding protein that binds only RAMP1 (and not CRLR) would not be expected to *selectively* inhibit the CGRP receptor because the RAMP1 polypeptide is also a component of the human AMY1 receptor. As described above, the ability of any antibody or functional fragment thereof

to selectively inhibit a particular receptor (e.g. human CGRP receptor) relative to a reference receptor (e.g. human AM1, AM2, or AMY1 receptors) can be assessed by determining the IC50 value of the antibody or functional fragment in an inhibition assay for the target and reference receptors. The IC50 value for any anti-CGRP receptor antibody or functional fragment thereof can be calculated by determining the concentration of the antibody or fragment needed to inhibit half of the maximum biological response of the CGRP ligand in activating the human CGRP receptor in any functional assay, such as the cAMP assay described in the Examples. In some embodiments, the anti-CGRP receptor antibody or functional fragment thereof from which the anti-CGRP receptor binding domain of the bispecific antigen binding proteins of the invention is derived is a neutralizing antibody or fragment of the human CGRP receptor.

[0078] The variable regions or CDR regions of any anti-CGRP receptor antibody or functional fragment thereof can be used to construct the anti-CGRP receptor binding domain of any of the bispecific antigen binding proteins described herein. For instance, the anti-CGRP receptor binding domain of the bispecific antigen binding proteins of the invention may comprise VH and/or VL regions or one or more CDRs from any of the anti-human CGRP receptor antibodies described in WO 2010/075238. In some embodiments, the anti-CGRP receptor antibody from which the anti-CGRP receptor binding domain is derived competes for binding of the human CGRP receptor with one or more of the human anti-CGRP receptor antibodies described in WO 2010/075238 or one or more of the anti-CGRP receptor antibodies described below. In some embodiments, a competing antibody or binding fragment thereof reduces human CGRP receptor binding of a reference antibody between about 40% and 100%, such as about 60% and about 100%, specifically between about 70% and 100%, and more specifically between about 80% and 100%. A particularly suitable quantitative assay for detecting competitive binding uses a Biacore machine which measures the extent of interactions using surface plasmon resonance technology. Another suitable quantitative competition binding assay uses a FACS-based approach to measure competition between antibodies in terms of their binding to the human CGRP receptor.

[0079] Light chain and heavy chain variable regions and associated CDRs of exemplary human anti-CGRP receptor antibodies from which the anti-CGRP receptor binding domain of the bispecific antigen binding proteins of the invention can be derived or constructed are set forth below in Tables 3A and 3B, respectively.

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Table 3A. Exemplary Anti-CGRP Receptor Light Chain Variable Region Amino Acid Sequences

Antibody ID.	VL Group	VL Amino Acid Sequence	CDRL1	CDRL2	CDRL3
50A, 50C, 50D, 70	LV-101	QSVLTQPPSASGTPGQRVTISCSG SSSNIGSNYVYWYQQLPGAAPKL LIFRNNQRPSGVPDRFSGSKSGTS ASLAISGLRSEDEADYYCAAWDD SLSGWVFGGGTKLTVLG (SEQ ID NO: 136)	SGSSSNIGSNYVY (SEQ ID NO: 109)	RNNQRPS (SEQ ID NO: 120)	AAWDDSLS GWV (SEQ ID NO: 127)
50B	LV-102	QSVLTQPPSASGTPGQRVTISCSG SSSNIGSNYVYWYQQLPGAAPKL LIFRNNQRPSGVPDRFSGSKSGTS ASLAISGLRSEDEADYYCAAWDD SLSGWVFGKGTKLTVLG (SEQ ID NO: 137)	SGSSSNIGSNYVY (SEQ ID NO: 109)	RNNQRPS (SEQ ID NO: 120)	AAWDDSLS GWV (SEQ ID NO: 127)
51A, 51C, 51D	LV-103	QSVLTQSPSASGTPGQRVTISCSG SSSNIGSNYVYWYQQLPGAAPKL LILRNNQRPSGVPDRFSGSKSGTS ASLTISGLRSEDEADYYCAAWDD SLSGWVFGGGTKLTVLG (SEQ ID NO: 138)	SGSSSNIGSNYVY (SEQ ID NO: 109)	RNNQRPS (SEQ ID NO: 120)	AAWDDSLS GWV (SEQ ID NO: 127)
51B	LV-104	QSVLTQSPSASGTPGQRVTISCSG SSSNIGSNYVYWYQQLPGAAPKL LILRNNQRPSGVPDRFSGSKSGTS ASLTISGLRSEDEADYYCAAWDD SLSGWVFGKGTKLTVLG (SEQ ID NO: 139)	SGSSSNIGSNYVY (SEQ ID NO: 109)	RNNQRPS (SEQ ID NO: 120)	AAWDDSLS GWV (SEQ ID NO: 127)
52A, 52C, 52D, 53A, 53C	LV-105	QSVLTQPPSVSAAPGQKVTISCSG SSSNIGNNYVSWYQQLPGTAPKL LIYDNNKRPSGIPDRFSGSKSGTST TLGITGLQTGDEADYYCGTWDSR LSAVVFGGGTKLTVLG (SEQ ID NO: 140)	SGSSSNIGNNYVS (SEQ ID NO: 110)	DNNKRPS (SEQ ID NO: 121)	GTWDSRLS AVV (SEQ ID NO: 128)
52B, 53B	LV-106	QSVLTQPPSVSAAPGQKVTISCSG SSSNIGNNYVSWYQQLPGTAPKL LIYDNNKRPSGIPDRFSGSKSGTST TLGITGLQTGDEADYYCGTWDSR LSAVVFGKGTKLTVLG (SEQ ID NO: 141)	SGSSSNIGNNYVS (SEQ ID NO: 110)	DNNKRPS (SEQ ID NO: 121)	GTWDSRLS AVV (SEQ ID NO: 128)
54A, 54C, 56A, 56C, 71	LV-107	QSVLTQPPSVSAAPGQKVTISCSG SSSNIGNNYVSWYQQLPGTAPKL LIYDNNKRPSGIPDRFSGSKSGTS ATLGITGLQTGDEADYYCGTWDS RLSAVVFGGGTKLTVLG (SEQ ID NO: 142)	SGSSSNIGNNYVS (SEQ ID NO: 110)	DNNKRPS (SEQ ID NO: 121)	GTWDSRLS AVV (SEQ ID NO: 128)
54B, 56B	LV-108	QSVLTQPPSVSAAPGQKVTISCSG SSSNIGNNYVSWYQQLPGTAPKL LIYDNNKRPSGIPDRFSGSKSGTS ATLGITGLQTGDEADYYCGTWDS RLSAVVFGKGTKLTVLG (SEQ ID	SGSSSNIGNNYVS (SEQ ID NO: 110)	DNNKRPS (SEQ ID NO: 121)	GTWDSRLS AVV (SEQ ID NO: 128)

Antibody ID.	VL Group	VL Amino Acid Sequence	CDRL1	CDRL2	CDRL3
		NO: 143)			
55A, 55C	LV-109	QSVLTQPPSVSAAPGQKVTISCSG SSSNIGNNYVSWYQQLPGTAPKL LIYDNNKRPSGIPDRFSGSKSGTS ATLAITGLQTGDEADYYCGTWDS RLSAVVFGGGTKLTVLG (SEQ ID NO: 144)	SGSSSNIGNNY VS (SEQ ID NO: 110)	DNNKRPS (SEQ ID NO: 121)	GTWDSRLS AVV (SEQ ID NO: 128)
55B	LV-110	QSVLTQPPSVSAAPGQKVTISCSG SSSNIGNNYVSWYQQLPGTAPKL LIYDNNKRPSGIPDRFSGSKSGTS ATLAITGLQTGDEADYYCGTWDS RLSAVVFGKGTKLTVLG (SEQ ID NO: 145)	SGSSSNIGNNY VS (SEQ ID NO: 110)	DNNKRPS (SEQ ID NO: 121)	GTWDSRLS AVV (SEQ ID NO: 128)
57A, 57C, 57D, 58A, 58C	LV-111	EIVLTQSPGTLSLSPGERATLSCRA SQSVSSGYLTWYQQKPGQAPRLL IYGASSRATGIPDRFSGSGSGTDFT LTISRLEPEDFAVYYCQQYGNSLS RFGQGTKLEIKR (SEQ ID NO: 146)	RASQSVSSGYL T (SEQ ID NO: 111)	GASSRAT (SEQ ID NO: 17)	QQYGNSLS R (SEQ ID NO: 129)
57B, 58B	LV-112	EIVLTQSPGTLSLSPGERATLSCRA SQSVSSGYLTWYQQKPGQAPRLL IYGASSRATGIPDRFSGSGSGTDFT LTISRLEPEDFAVYYCQQYGNSLS RFGKGTKLEIKR (SEQ ID NO: 147)	RASQSVSSGYL T (SEQ ID NO: 111)	GASSRAT (SEQ ID NO: 17)	QQYGNSLS R (SEQ ID NO: 129)
59	LV-113	QSVLTQPPSVSEAPGQKVTISCSG SSSNIGNNYVSWYQQLPGTAPKL LIYDNNKRPSGIPDRFSGSKSGTS ATLGITGLQTGDEADYYCGTWDS RLSAVVFGGGTKLTVL (SEQ ID NO: 148)	SGSSSNIGNNY VS (SEQ ID NO: 110)	DNNKRPS (SEQ ID NO: 121)	GTWDSRLS AVV (SEQ ID NO: 128)
60	LV-114	QSVLTQPPSASGTPGQRVTISCSG SSSNIGSNYVYWYQQLPGAAPKL LIFRSNQRPSGVPDRFSGSKSGTS ASLAISGLRSEDEADYYCAAWDD SLSGWVFGGGTKLTVL (SEQ ID NO: 149)	SGSSSNIGSNYV Y (SEQ ID NO: 109)	RSNQRPS (SEQ ID NO: 122)	AAWDDSLS GWV (SEQ ID NO: 127)
61	LV-115	DIQMTQSPSSLSASVGDRVTITCR ASQGIRNDLGWFQQKPGKAPKRL IYAASSLQSGVPSRFSGSGSGTEFT LTISSLQPEDLATYYCLQYNIYPW TFGQGTKVEIK (SEQ ID NO: 150)	RASQGIRNDLG (SEQ ID NO: 112)	AASSLQS (SEQ ID NO: 14)	LQYNIYPW T (SEQ ID NO: 130)
62	LV-116	SSELTQDPTVSVALGQTVKITCQG DSLRSFYASWYQQKPGQAPVLVF YGKNNRPSGIPDRFSGSSSGNTAS LTITGAQAEDEADYYCNSRDSSV YHLVLGGGTKLTVL (SEQ ID NO: 151)	QGDSLRSFYAS (SEQ ID NO: 113)	GKNNRPS (SEQ ID NO: 123)	NSRDSSVY HLV (SEQ ID NO: 131)
63	LV-117	DIILAQTPLSLSVTPGQPASISCKSS QSLLHSAGKTYLYWYLQKPGQPP QLLIYEVSNRFSGVPDRFSGSGSG TDFTLKISRVEAEDVGIYYCMQSF PLPLTFGGGTKVEIK (SEQ ID NO: 152)	KSSQSLLHSAG KTYLY (SEQ ID NO: 114)	EVSNRFS (SEQ ID NO: 124)	MQSFPLPLT (SEQ ID NO: 132)
64	LV-	DIVMTQSPLSLPVTPGEPASISCRS	RSSQSLLHSFG	LGSNRAS	MQALQTPF

Antibody ID.	VL Group	VL Amino Acid Sequence	CDRL1	CDRL2	CDRL3
	118	SQSLLHSFGYNYLDWYLQKPGQS PQLLIYLGSNRASGVPDRFSGSGS GTDFTLKISRVEAEDVGVYYCMQ ALQTPFTFGPGTKVDIK (SEQ ID NO: 153)	YNYLD (SEQ ID NO: 115)	(SEQ ID NO: 18)	T (SEQ ID NO: 133)
65	LV-119	DIILTQTPLSLSVTPGQPASISCKSS QSLLHSDGKTYLYWYLQKPGQPP QLLIYEVSNRFSGEPDRFSGSGSG TDFTLKISRVEAEDVGTYYCMQS FPLPLTFGGGTKVEIK (SEQ ID NO: 154)	KSSQSLLHSDG KTYLY (SEQ ID NO: 116)	EVSNRFS (SEQ ID NO: 124)	MQSFPLPLT (SEQ ID NO: 132)
66	LV-120	QSVLTQPPSVSAAPGQKVTISCSG SSSNIGNNYVSWYQQFPGTAPKL LIYDNNKRPSGIPDRFSGSKSGTS ATLGITGLQTGDEADYYCGTWDS RLSAVVFGGGTKLTVL (SEQ ID NO: 155)	SGSSSNIGNNY VS (SEQ ID NO: 110)	DNNKRPS (SEQ ID NO: 121)	GTWDSRLS AVV (SEQ ID NO: 128)
67	LV-121	QSVLTQPPSASGTPGQRVTISCSG SSSNIGSNTVNWYQQLPGTAPKL LIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADFYCAARDES LNGVVFGGGTKLTVL (SEQ ID NO: 156)	SGSSSNIGSNTV N (SEQ ID NO: 117)	TNNQRPS (SEQ ID NO: 125)	AARDESLN GVV (SEQ ID NO: 134)
68	LV-122	DITLTQTPLSLSVSPGQPASISCKS SQSLLHSDGRNYLYWYLQKPGQP PQLLIYEVSNRFSGLPDRFSGSGS GTDFTLKISRVEAEDVGIYYCMQS FPLPLTFGGGTKVEIK (SEQ ID NO: 157)	KSSQSLLHSDG RNYLY (SEQ ID NO: 118)	EVSNRFS (SEQ ID NO: 124)	MQSFPLPLT (SEQ ID NO: 132)
69	LV-123	DIQMTQSPSSLSASVGDRVTITCR ASQGIRKDLGWYQQKPGKAPKR LIYGASSLQSGVPSRFSGSGSGTEF TLTISSLQPEDFATYYCLQYNSFP WTFGQGTKVEIK (SEQ ID NO: 158)	RASQGIRKDLG (SEQ ID NO: 119)	GASSLQS (SEQ ID NO: 126)	LQYNSFPW T (SEQ ID NO: 135)

Table 3B. Exemplary Anti-CGRP Receptor Heavy Chain Variable Region Amino Acid Sequences

Antibody ID.	VH Group	VH Amino Acid Sequence	CDRH1	CDRH2	CDRH3
50A, 50C, 50D	HV-101	EVQLVESGGGLVKPGGSLRLSCA ASGFTFGNAWMSWVRQAPGKGL EWVGRIKSKTDGGTTDYAAPVK GRFTISRDDSKNTLYLQMNSLKTE DTAVYFCTTDRTGYSISWSSYYY YYGMDVWGQGTTVTVSS (SEQ ID NO: 190)	NAWMS (SEQ ID NO: 159)	RIKSKTDG GTTDYAAP VKG (SEQ ID NO: 167)	DRTGYSIS WSSYYYYY GMDV (SEQ ID NO: 179)
50B	HV-102	EVQLVESGGGLVKPGGSLRLSCA ASGFTFGNAWMSWVRQAPGKEL EWVGRIKSKTDGGTTDYAAPVK	NAWMS (SEQ ID NO:	RIKSKTDG GTTDYAAP VKG	DRTGYSIS WSSYYYYY GMDV

Antibody ID.	VH Group	VH Amino Acid Sequence	CDRH1	CDRH2	CDRH3
		GRFTISRDDSKNTLYLQMNSLKTE DTAVYFCTTDRTGYSISWSSYYY YYGMDVWGQGTTVTVSS (SEQ ID NO: 191)	159)	(SEQ ID NO: 167)	(SEQ ID NO: 179)
51A, 51C, 51D	HV-103	EVQLVESGGGLVKPGGSLRLSCA ASGFTFSNAWMSWVRQAPGKGL EWVGRIKSKTDGGTTDYTAPVKG RFTISRDDSKNTLYLQMNSLKAE DTAVYYCTTDRTGYSISWSSYYY YYGMDVWGQGTTVTVSS (SEQ ID NO: 192)	NAWMS (SEQ ID NO: 159)	RIKSKTDG GTTDYTAP VKG (SEQ ID NO: 168)	DRTGYSIS WSSYYYYY GMDV (SEQ ID NO: 179)
51B	HV-104	EVQLVESGGGLVKPGGSLRLSCA ASGFTFSNAWMSWVRQAPGKEL EWVGRIKSKTDGGTTDYTAPVKG RFTISRDDSKNTLYLQMNSLKAE DTAVYYCTTDRTGYSISWSSYYY YYGMDVWGQGTTVTVSS (SEQ ID NO: 193)	NAWMS (SEQ ID NO: 159)	RIKSKTDG GTTDYTAP VKG (SEQ ID NO: 168)	DRTGYSIS WSSYYYYY GMDV (SEQ ID NO: 179)
52A, 52C, 52D, 54A, 54C, 55A, 55C, 59, 66	HV-105	QVQLVESGGGVVQPGRSLRLSCA ASGFTFSSFGMHWVRQAPGKGLE WVAVISFDGSIKYSVDSVKGRFTI SRDNSKNTLFLQMNSLRAEDTAV YYCARDRLNYYDSSGYYHYKYY GMAVWGQGTTVTVSS (SEQ ID NO: 194)	SFGMH (SEQ ID NO: 160)	VISFDGSIK YSVDSVKG (SEQ ID NO: 169)	DRLNYYDS SGYYHYKY YGMAV (SEQ ID NO: 180)
52B, 54B, 55B	HV-106	QVQLVESGGGVVQPGRSLRLSCA ASGFTFSSFGMHWVRQAPGKELE WVAVISFDGSIKYSVDSVKGRFTI SRDNSKNTLFLQMNSLRAEDTAV YYCARDRLNYYDSSGYYHYKYY GMAVWGQGTTVTVSS (SEQ ID NO: 195)	SFGMH (SEQ ID NO: 160)	VISFDGSIK YSVDSVKG (SEQ ID NO: 169)	DRLNYYDS SGYYHYKY YGMAV (SEQ ID NO: 180)
53A, 53C, 56A, 56C	HV-107	QVQLVESGGGVVQPGRSLRLSCA ASGFTFSSFGMHWVRQAPGKGLE WVAVISFDGSIKYSVDSVKGRFTI SRDNSKNTLFLQMNSLRAEDTAV YYCARDRLNYYESSGYYHYKYY GMAVWGQGTTVTVSS (SEQ ID NO: 196)	SFGMH (SEQ ID NO: 160)	VISFDGSIK YSVDSVKG (SEQ ID NO: 169)	DRLNYYES SGYYHYKY YGMAV (SEQ ID NO: 181)
53B, 56B	HV-108	QVQLVESGGGVVQPGRSLRLSCA ASGFTFSSFGMHWVRQAPGKELE WVAVISFDGSIKYSVDSVKGRFTI SRDNSKNTLFLQMNSLRAEDTAV YYCARDRLNYYESSGYYHYKYY GMAVWGQGTTVTVSS (SEQ ID NO: 197)	SFGMH (SEQ ID NO: 160)	VISFDGSIK YSVDSVKG (SEQ ID NO: 169)	DRLNYYES SGYYHYKY YGMAV (SEQ ID NO: 181)
57A, 57C, 57D	HV-109	QVQLVESGGGVVQPGRSLRLSCA ASGFTFSSYGMHWVRQAPGKGL EWVAVIWYDGSNKYYADSVKGR FIISRDKSKNTLYLQMNSLRAEDT AVYYCARAGGIAAAGLYYYYGM DVWGQGTTVTVSS (SEQ ID NO: 198)	SYGMH (SEQ ID NO: 161)	VIWYDGSN KYYADSVK G (SEQ ID NO: 170)	AGGIAAAG LYYYYGM DV (SEQ ID NO: 182)

Antibody ID.	VH Group	VH Amino Acid Sequence	CDRH1	CDRH2	CDRH3
57B	HV-110	QVQLVESGGGVVQPGRSLRLSCA ASGFTFSSYGMHWVRQAPGKELE WVAVIWYDGSNKYYADSVKGRF IISRDKSKNTLYLQMNSLRAEDTA VYYCARAGGIAAAGLYYYYGMD VWGQGTTVTVSS (SEQ ID NO: 199)	SYGMH (SEQ ID NO: 161)	VIWYDGSN KYYADSVK G (SEQ ID NO: 170)	AGGIAAAG LYYYYGM DV (SEQ ID NO: 182)
58A, 58C	HV-111	QVQLVESGGGVVQPGRSLRLSCA ASGFTFSSYGMHWVRQAPGKGL EWVAVIWYDGSNKYYAESVKGR FIISRDKSKNTLYLQMNSLRAEDT AVYYCARAGGIAAAGLYYYYGM DVWGQGTTVTVSS (SEQ ID NO: 200)	SYGMH (SEQ ID NO: 161)	VIWYDGSN KYYAESVK G (SEQ ID NO: 171)	AGGIAAAG LYYYYGM DV (SEQ ID NO: 182)
58B	HV-112	QVQLVESGGGVVQPGRSLRLSCA ASGFTFSSYGMHWVRQAPGKELE WVAVIWYDGSNKYYAESVKGRF IISRDKSKNTLYLQMNSLRAEDTA VYYCARAGGIAAAGLYYYYGMD VWGQGTTVTVSS (SEQ ID NO: 201)	SYGMH (SEQ ID NO: 161)	VIWYDGSN KYYAESVK G (SEQ ID NO: 171)	AGGIAAAG LYYYYGM DV (SEQ ID NO: 182)
60	HV-113	EVQLVESGGGLVKPGGSLRLSCA ASGFTFSNAWMSWVRQAPGKGL EWVGRIKSTTDGGTTDYAAPVKG RFTISRDDSKNTLYLQMNSLKTED TAVYYCTTDRTGYSISWSSYYYY YGMDVWGQGTTVTVSS (SEQ ID NO: 202)	NAWMS (SEQ ID NO: 159)	RIKSTTDGG TTDYAAPV KG (SEQ ID NO: 172)	DRTGYSIS WSSYYYYY GMDV (SEQ ID NO: 179)
61	HV-114	EVQLLESGGGLVQPGESLRLSCA ASGFTFSSYAMSWVRQAPGKGLE WVSAISGSGGRTYYADSVKGRFT ISRDNSKNTLYLQMNSLRAEDTA VYYCAKDQREVGPYSSGWYDYY YGMDVWGQGTTVTVSS (SEQ ID NO: 203)	SYAMS (SEQ ID NO: 162)	AISGSGGRT YYADSVKG (SEQ ID NO: 173)	DQREVGPY SSGWYDYY YGMDV (SEQ ID NO: 183)
62	HV-115	QVQLVQSGAEVKKPGASVKVSC KASGYTFTGYYMHWVRQAPGQG LEWMGWINPNSGGTNYAQKFQG RVTMTRDTSISTAYMELSRLRSD DTAVYFCARDQMSIIMLRGVFPP YYYGMDVWGQGTTVTVSS (SEQ ID NO: 204)	GYYMH (SEQ ID NO: 163)	WINPNSGG TNYAQKFQ G (SEQ ID NO: 174)	DQMSIIML RGVFPPYY YGMDV (SEQ ID NO: 184)
63, 65, 68	HV-116	QVQLVESGGGVVQPGRSLRLSCA ASGFTFSSYGMHWVRQAPGKGL EWVAVISYDGSHESYADSVKGRF TISRDISKNTLYLQMNSLRAEDTA VYFCARERKRVTMSTLYYYFYY GMDVWGQGTTVTVSS (SEQ ID NO: 205)	SYGMH (SEQ ID NO: 161)	VISYDGSHE SYADSVKG (SEQ ID NO: 175)	ERKRVTMS TLYYYFYY GMDV (SEQ ID NO: 185)
64	HV-117	EVQLVESGGGLVKPGRSLRLSCT ASGFTFGDYAMSWFRQAPGKGL EWIGFIRSRAYGGTPEYAASVKG RFTISRDDSKTIAYLQMNSLKTED	DYAMS (SEQ ID NO: 164)	FIRSRAYGG TPEYAASV KG	GRGIAARW DY (SEQ ID NO:

Antibody ID.	VH Group	VH Amino Acid Sequence	CDRH1	CDRH2	CDRH3
		TAVYFCARGRGIAARWDYWGQG TLVTVSS (SEQ ID NO: 206)		(SEQ ID NO: 176)	186)
67	HV-118	QVQLVQSGAEVKKPGASVKVSC KASGYTFTDYYMYWVRQAPGQG LEWMGWISPNSGGTNYAQKFQG RVTMTRDTSISTAYMELSRLRSD DTAVYYCVRGGYSGYAGLYSHY YGMDVWGQGTTVTVSS (SEQ ID NO: 207)	DYYMY (SEQ ID NO: 165)	WISPNSGG TNYAQKFQ G (SEQ ID NO: 177)	GGYSGYAG LYSHYYGM DV (SEQ ID NO: 187)
69	HV-119	EVQLVESGGGLVKPGGSLRLSCA ASGYTFSTYSMNWVRQAPGKGL EWVSSISSSSSYRYYADSVKGRFT ISRDNAKNSLYLQMSSLRAEDTA VYYCAREGVSGSSPYSISWYDYY YGMDVWGQGTTVTVSS (SEQ ID NO: 208)	TYSMN (SEQ ID NO: 166)	SISSSSSYR YYADSVKG (SEQ ID NO: 178)	EGVSGSSP YSISWYDY YYGMDV (SEQ ID NO: 188)
70	HV-120	EVQLVESGGGLVKPGGSLRLSCA ASGFTFGNAWMSWVRQAPGKGL EWVGRIKSKTDGGTTDYAAPVK GRFTISRDDSKNTLYLQMNSLKTE DTAVYYCTTDRTGYSISWSSYYY YYGMDVWGQGTTVTVSS (SEQ ID NO: 209)	NAWMS (SEQ ID NO: 159)	RIKSKTDG GTTDYAAP VKG (SEQ ID NO: 167)	DRTGYSIS WSSYYYYY GMDV (SEQ ID NO: 179)
71	HV-121	QVQLVESGGGVVQPGRSLRLSCA ASGFTFSSFGMHWVRQAPGKGLE WVAVISFDGSIKYSVDSVKGRFTI SRDNSKNTLFLQMNSLRAEDTAV YYCARDRLNYYDSSGYYHYKYY GLAVWGQGTTVTVSS (SEQ ID NO: 210)	SFGMH (SEQ ID NO: 160)	VISFDGSIK YSVDSVKG (SEQ ID NO: 169)	DRLNYYDS SGYYHYKY YGLAV (SEQ ID NO: 189)

[0080] The anti-CGRP receptor binding domain of the bispecific antigen binding proteins may comprise one or more of the CDRs presented in Table 3A (light chain CDRs; i.e. CDRLs) and Table 3B (heavy chain CDRs, i.e. CDRHs). For instance, in certain embodiments, the anti-CGRP receptor binding domain comprises one or more light chain CDRs selected from (i) a CDRL1 selected from SEQ ID NOs: 109 to 119, (ii) a CDRL2 selected from SEQ ID NOs: 14, 17, 18, 120 to 126, and (iii) a CDRL3 selected from SEQ ID NOs: 127 to 135, and (iv) a CDRL of (i), (ii) and (iii) that contains one or more, e.g., one, two, three, four or more amino acid substitutions (e.g., conservative amino acid substitutions), deletions or insertions of no more than five, four, three, two, or one amino acids. In these and other embodiments, the anti-CGRP receptor binding domain comprises one or more heavy chain CDRs selected from (i) a CDRH1 selected from SEQ ID NOs: 159 to 166, (ii) a CDRH2 selected from SEQ ID NOs: 167 to 178, and (iii) a CDRH3 selected from SEQ ID NOs: 179 to 189, and (iv) a CDRH of (i), (ii) and (iii)

that contains one or more, e.g., one, two, three, four or more amino acid substitutions (e.g., conservative amino acid substitutions), deletions or insertions of no more than five, four, three, two, or one amino acids amino acids.

[0081] In certain embodiments, the anti-CGRP receptor binding domain may comprise 1, 2, 3, 4, 5, or 6 variant forms of the CDRs listed in Tables 3A and 3B, each having at least 80%, 85%, 90% or 95% sequence identity to a CDR sequence listed in Tables 3A and 3B. In some embodiments, the anti-CGRP receptor binding domain includes 1, 2, 3, 4, 5, or 6 of the CDRs listed in Tables 3A and 3B, each differing by no more than 1, 2, 3, 4 or 5 amino acids from the CDRs listed in these tables.

[0082] In particular embodiments, the anti-CGRP receptor binding domain of the bispecific antigen binding proteins of the invention comprises a light chain variable region comprising a CDRL1, a CDRL2, and a CDRL3, wherein: (a) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 109, 120 and 127, respectively; (b) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 110, 121 and 128, respectively; (c) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 111, 17 and 129, respectively; (d) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 109, 122 and 127, respectively; (e) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 112, 14 and 130, respectively; (f) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 113, 123 and 131, respectively; (g) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 114, 124 and 132, respectively; (h) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 115, 18 and 133, respectively; (i) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 116, 124 and 132, respectively; (j) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 117, 125 and 134, respectively; (k) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 118, 124 and 132, respectively; or (l) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 119, 126 and 135, respectively.

[0083] In other particular embodiments, the anti-CGRP receptor binding domain of the bispecific antigen binding proteins of the invention comprises a heavy chain variable region comprising a CDRH1, a CDRH2, and a CDRH3, wherein: (a) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 159, 167 and 179, respectively; (b) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 159, 168 and 179, respectively; (c) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 160, 169 and 180, respectively; (d)

CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 160, 169 and 181, respectively; (e) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 161, 170 and 182, respectively; (f) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 161, 171 and 182, respectively; (g) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 159, 172 and 179, respectively; (h) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 162, 173 and 183, respectively; (i) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 163, 174 and 184, respectively; (j) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 161, 175 and 185, respectively; (k) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 164, 176 and 186, respectively; (l) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 165, 177 and 187, respectively; (m) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 166, 178 and 188, respectively; or (n) CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 160, 169 and 189, respectively.

[0084] In certain embodiments, the anti-CGRP receptor binding domain of the bispecific antigen binding proteins of the invention comprises a light chain variable region comprising a CDRL1, a CDRL2, and a CDRL3 and a heavy chain variable region comprising a CDRH1, a CDRH2, and a CDRH3, wherein:

(a) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 109, 120 and 127, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 159, 167 and 179, respectively;

(b) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 109, 120 and 127, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 159, 168 and 179, respectively;

(c) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 110, 121 and 128, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 160, 169 and 180, respectively;

(d) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 110, 121 and 128, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 160, 169 and 181, respectively;

(e) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 111, 17 and 129, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 161, 170 and 182, respectively;

(f) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 111, 17 and 129, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 161, 171 and 182, respectively;

(g) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 109, 122 and 127, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 159, 172 and 179, respectively;

(h) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 112, 14 and 130, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 162, 173 and 183, respectively;

(i) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 113, 123 and 131, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 163, 174 and 184, respectively;

(j) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 114, 124 and 132, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 161, 175 and 185, respectively;

(k) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 115, 18 and 133, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 164, 176 and 186, respectively;

(l) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 116, 124 and 132, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 161, 175 and 185, respectively;

(m) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 117, 125 and 134, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 165, 177 and 187, respectively;

(n) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 118, 124 and 132, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 161, 175 and 185, respectively;

(o) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 119, 126 and 135, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 166, 178 and 188, respectively; or

(p) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 110, 121 and 128, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 160, 169 and 189, respectively.

[0085] In some embodiments, the anti-CGRP receptor binding domain of the bispecific antigen binding proteins of the invention comprises a light chain variable region comprising a CDRL1, a CDRL2, and a CDRL3 and a heavy chain variable region comprising a CDRH1, a CDRH2, and a CDRH3, wherein:

(a) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 109, 120 and 127, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 159, 167 and 179, respectively;

(b) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 109, 120 and 127, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 159, 168 and 179, respectively;

(c) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 110, 121 and 128, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 160, 169 and 180, respectively;

(d) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 110, 121 and 128, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 160, 169 and 181, respectively;

(e) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 111, 17 and 129, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 161, 170 and 182, respectively; or

(f) CDRL1, CDRL2, and CDRL3 have the sequence of SEQ ID NOs: 111, 17 and 129, respectively, and CDRH1, CDRH2, and CDRH3 have the sequence of SEQ ID NOs: 161, 171 and 182, respectively.

[0086] The anti-CGRP receptor binding domain of the antigen binding proteins of the invention may comprise a light chain variable region selected from the group consisting of LV-101, LV-102, LV-103, LV-104, LV-105, LV-106, LV-107, LV-108, LV-109, LV-110, LV-111, LV-112,

LV-113, LV-114, LV-115, LV-116, LV-117, LV-118, LV-119, LV-120, LV-121, LV-122, and LV-123, as shown in Table 3A, and/or a heavy chain variable region selected from the group consisting of HV-101, HV-102, HV-103, HV-104, HV-105, HV-106, HV-107, HV-108, HV-109, HV-110, HV-111, HV-112, HV-113, HV-114, HV-115, HV-116, HV-117, HV-118, HV-119, HV-120, and HV-121, as shown in Table 3B, and functional fragments, derivatives, muteins and variants of these light chain and heavy chain variable regions.

[0087] Each of the light chain variable regions listed in Table 3A may be combined with any of the heavy chain variable regions shown in Table 3B to form an anti-CGRP receptor binding domain suitable for incorporation into the bispecific antigen binding proteins of the invention. Examples of such combinations include, but are not limited to: LV-101 and HV-101; LV-102 and HV-102; LV-103 and HV-103; LV-104 and HV-104; LV-105 and HV-105; LV-106 and HV-106; LV-105 and HV-107; LV-106 and HV-108; LV-107 and HV-105; LV-108 and HV-106; LV-109 and HV-105; LV-110 and HV-106; LV-107 and HV-107; LV-108 and HV-108; LV-111 and HV-109; LV-112 and HV-110; LV-111 and HV-111; LV-112 and HV-112; LV-113 and HV-105; LV-114 and HV-113; LV-115 and HV-114; LV-116 and HV-115; LV-117 and HV-116; LV-118 and HV-117; LV-119 and HV-116; LV-120 and HV-105; LV-121 and HV-118; LV-122 and HV-116; LV-123 and HV-119; LV-101 and HV-120; and LV-107 and HV-121. In certain embodiments, the anti-CGRP receptor binding domain comprises: (a) LV-101 (SEQ ID NO: 136) and HV-101 (SEQ ID NO: 190); (b) LV-103 (SEQ ID NO: 138) and HV-103 (SEQ ID NO: 192); (c) LV-105 (SEQ ID NO: 140) and HV-105 (SEQ ID NO: 194); (d) LV-105 (SEQ ID NO: 140) and HV-107 (SEQ ID NO: 196); (e) LV-107 (SEQ ID NO: 142) and HV-105 (SEQ ID NO: 194); (f) LV-109 (SEQ ID NO: 144) and HV-105 (SEQ ID NO: 194); (g) LV-107 (SEQ ID NO: 142) and HV-107 (SEQ ID NO: 196); (h) LV-111 (SEQ ID NO: 146) and HV-109 (SEQ ID NO: 198); or (i) LV-111 (SEQ ID NO: 146) and HV-111 (SEQ ID NO: 200).

[0088] In some embodiments, the anti-CGRP receptor binding domain comprises a light chain variable region comprising a sequence of contiguous amino acids that differs from the sequence of a light chain variable region in Table 3A, i.e. a VL selected from LV-101, LV-102, LV-103, LV-104, LV-105, LV-106, LV-107, LV-108, LV-109, LV-110, LV-111, LV-112, LV-113, LV-114, LV-115, LV-116, LV-117, LV-118, LV-119, LV-120, LV-121, LV-122, and LV-123 at only 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15 amino acid residues, wherein each such sequence difference is independently either a deletion, insertion or substitution of one amino

acid, with the deletions, insertions and/or substitutions resulting in no more than 15 amino acid changes relative to the foregoing variable domain sequences. The light chain variable region in some anti-CGRP binding domains comprises a sequence of amino acids that has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97% or at least 99% sequence identity to the amino acid sequences of SEQ ID NOs: 136-158 (i.e. the light chain variable regions in Table 3A).

[0089] In these and other embodiments, the anti-CGRP receptor binding domain comprises a heavy chain variable region comprising a sequence of contiguous amino acids that differs from the sequence of a heavy chain variable region in Table 3B, i.e., a VH selected from HV-101, HV-102, HV-103, HV-104, HV-105, HV-106, HV-107, HV-108, HV-109, HV-110, HV-111, HV-112, HV-113, HV-114, HV-115, HV-116, HV-117, HV-118, HV-119, HV-120, and HV-121 at only 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15 amino acid residues, wherein each such sequence difference is independently either a deletion, insertion or substitution of one amino acid, with the deletions, insertions and/or substitutions resulting in no more than 15 amino acid changes relative to the foregoing variable domain sequences. The heavy chain variable region in some anti-CGRP receptor binding domains comprises a sequence of amino acids that has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97% or at least 99% sequence identity to the amino acid sequences of SEQ ID NOs: 190-210 (i.e. the heavy chain variable regions in Table 3B).

[0090] In certain embodiments, the bispecific antigen binding proteins of the invention are antibodies. As used herein, the term "antibody" refers to a tetrameric immunoglobulin protein comprising two light chain polypeptides (about 25 kDa each) and two heavy chain polypeptides (about 50-70 kDa each). The term "light chain" or "immunoglobulin light chain" refers to a polypeptide comprising, from amino terminus to carboxyl terminus, a single immunoglobulin light chain variable region (VL) and a single immunoglobulin light chain constant domain (CL). The immunoglobulin light chain constant domain (CL) can be kappa (κ) or lambda (λ).The term "heavy chain" or "immunoglobulin heavy chain" refers to a polypeptide comprising, from amino terminus to carboxyl terminus, a single immunoglobulin heavy chain variable region (VH), an immunoglobulin heavy chain constant domain 1 (CH1), an immunoglobulin hinge region, an immunoglobulin heavy chain constant domain 2 (CH2), an immunoglobulin heavy chain constant domain 3 (CH3), and optionally an immunoglobulin heavy chain constant domain 4

(CH4). Heavy chains are classified as mu (μ), delta (Δ), gamma (γ), alpha (α), and epsilon (ε), and define the antibody's isotype as IgM, IgD, IgG, IgA, and IgE, respectively. The IgG-class and IgA-class antibodies are further divided into subclasses, namely, IgG1, IgG2, IgG3, and IgG4, and IgA1 and IgA2, respectively. The heavy chains in IgG, IgA, and IgD antibodies have three domains (CH1, CH2, and CH3), whereas the heavy chains in IgM and IgE antibodies have four domains (CH1, CH2, CH3, and CH4). The immunoglobulin heavy chain constant domains can be from any immunoglobulin isotype, including subtypes. The antibody chains are linked together via inter-polypeptide disulfide bonds between the CL domain and the CH1 domain (i.e. between the light and heavy chain) and between the hinge regions of the antibody heavy chains.

[0091] In particular embodiments, the bispecific antigen binding proteins of the invention are heterodimeric antibodies (used interchangeably herein with "hetero immunoglobulins" or "hetero Igs"), which refer to antibodies comprising two different light chains and two different heavy chains. For instance, in some embodiments, the heterodimeric antibody comprises a light chain and heavy chain from an anti-PAC1 receptor antibody and a light chain and heavy chain from an anti-CGRP receptor antibody. *See* Figure 1.

[0092] The heterodimeric antibodies can comprise any immunoglobulin constant region. The term "constant region" as used herein refers to all domains of an antibody other than the variable region. The constant region is not involved directly in binding of an antigen, but exhibits various effector functions. As described above, antibodies are divided into particular isotypes (IgA, IgD, IgE, IgG, and IgM) and subtypes (IgG1, IgG2, IgG3, IgG4, IgA1 IgA2) depending on the amino acid sequence of the constant region of their heavy chains. The light chain constant region can be, for example, a kappa- or lambda-type light chain constant region, e.g., a human kappa- or lambda-type light chain constant region, which are found in all five antibody isotypes. Examples of human immunoglobulin light chain constant region sequences are shown in the following table.

Table 4. Exemplary Human Immunoglobulin Light Chain Constant Regions

Designation	SEQ ID NO:	CL Domain Amino Acid Sequence
CL-1	353	GQPKANPTVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADGSPVKAG VETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTEC S
CL-2	354	GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
CL-3	355	GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV

Designation	SEQ ID NO:	CL Domain Amino Acid Sequence
		ETTTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS
CL-7	356	GQPKAAPSVTLFPPSSEELQANKATLVCLVSDFYPGAVTVAWKADGSPVKVG VETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCRVTHEGSTVEKTVAPAEC S

[0093] The heavy chain constant region of the heterodimeric antibodies can be, for example, an alpha-, delta-, epsilon-, gamma-, or mu-type heavy chain constant region, e.g., a human alpha-, delta-, epsilon-, gamma-, or mu-type heavy chain constant region. In some embodiments, the heterodimeric antibodies comprise a heavy chain constant region from an IgG1, IgG2, IgG3, or IgG4 immunoglobulin. In one embodiment, the heterodimeric antibody comprises a heavy chain constant region from a human IgG1 immunoglobulin. In another embodiment, the heterodimeric antibody comprises a heavy chain constant region from a human IgG2 immunoglobulin. Examples of human IgG1 and IgG2 heavy chain constant region sequences are shown below in Table 5.

Table 5. Exemplary Human Immunoglobulin Heavy Chain Constant Regions

Ig isotype	SEQ ID NO:	Heavy Chain Constant Region Amino Acid Sequence
Human IgG1z	357	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCP APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
Human IgG1za	358	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCP APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
Human IgG1f	359	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
Human IgG1fa	360	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
Human	361	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV

Ig isotype	SEQ ID NO:	Heavy Chain Constant Region Amino Acid Sequence
Human IgG2	361	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAP PVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAK TKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPR EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

[0094] Each of the variable regions disclosed in Tables 1A, 1B, 3A, and 3B may be attached to the above light and heavy chain constant regions to form complete antibody light and heavy chains, respectively. Further, each of the so generated heavy and light chain polypeptides may be combined to form a complete bispecific antibody structure, e.g. a heterodimeric antibody. It should be understood that the heavy chain and light chain variable regions provided herein can also be attached to other constant domains having different sequences than the exemplary sequences listed above.

[0095] To facilitate assembly of the light and heavy chains from the anti-PAC1 receptor antibody and the light and heavy chains from the anti-CGRP receptor antibody into a bispecific, heterodimeric antibody, the light chains and/or heavy chains from each antibody can be engineered to reduce the formation of mispaired molecules. For example, one approach to promote heterodimer formation over homodimer formation is the so-called "knobs-into-holes" method, which involves introducing mutations into the CH3 domains of two different antibody heavy chains at the contact interface. Specifically, one or more bulky amino acids in one heavy chain are replaced with amino acids having short side chains (e.g. alanine or threonine) to create a "hole," whereas one or more amino acids with large side chains (e.g. tyrosine or tryptophan) are introduced into the other heavy chain to create a "knob." When the modified heavy chains are co-expressed, a greater percentage of heterodimers (knob-hole) are formed as compared to homodimers (hole-hole or knob-knob). The "knobs-into-holes" methodology is described in detail in WO 96/027011; Ridgway *et al.*, Protein Eng., Vol. 9: 617-621, 1996; and Merchant *et al.*, Nat, Biotechnol., Vol. 16: 677-681, 1998.

[0096] Another approach for promoting heterodimer formation to the exclusion of homodimer formation entails utilizing an electrostatic steering mechanism (*see* Gunasekaran *et al.*, J. Biol. Chem., Vol. 285: 19637-19646, 2010). This approach involves introducing or exploiting charged residues in the CH3 domain in each heavy chain so that the two different heavy chains

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associate through opposite charges that cause electrostatic attraction. Homodimerization of the identical heavy chains are disfavored because the identical heavy chains have the same charge and therefore are repelled. This same electrostatic steering technique can be used to prevent mispairing of light chains with the non-cognate heavy chains by introducing residues having opposite charges in the correct light chain – heavy chain pair at the binding interface. The electrostatic steering technique and suitable charge pair mutations for promoting heterodimers and correct light chain/heavy chain pairing is described in WO2009089004 and WO2014081955.

[0097] In embodiments in which the bispecific antigen binding proteins of the invention are heterodimeric antibodies comprising a first light chain (LC1) and first heavy chain (HC1) from a first antibody that specifically binds to human CGRP receptor and a second light chain (LC2) and second heavy chain (HC2) from a second antibody that specifically binds to human PAC1 receptor, HC1 or HC2 may comprise one or more amino acid substitutions to replace a positively-charged amino acid with a negatively-charged amino acid. For instance, in one embodiment, the CH3 domain of HC1 or the CH3 domain of HC2 comprises an amino acid sequence differing from a wild-type IgG amino acid sequence such that one or more positively-charged amino acids (e.g., lysine, histidine and arginine) in the wild-type human IgG amino acid sequence are replaced with one or more negatively-charged amino acids (e.g., aspartic acid and glutamic acid) at the corresponding position(s) in the CH3 domain. In these and other embodiments, amino acids (e.g. lysine) at one or more positions selected from 370, 392 and 409 (EU numbering system) are replaced with a negatively-charged amino acid (e.g., aspartic acid and glutamic acid). Unless indicated otherwise, throughout the present specification and claims, the numbering of the residues in an immunoglobulin heavy chain or light chain is according to Kabat-EU numbering as described in Kabat *et al.*, Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD (1991). An amino acid substitution in an amino acid sequence is typically designated herein with a one-letter abbreviation for the amino acid residue in a particular position, followed by the numerical amino acid position relative to an original sequence of interest, which is then followed by the one-letter symbol for the amino acid residue substituted in. For example, "T30D" symbolizes a substitution of a threonine residue by an aspartate residue at amino acid position 30, relative to

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the original sequence of interest. Another example, "S218G" symbolizes a substitution of a serine residue by a glycine residue at amino acid position 218, relative to the original amino acid sequence of interest.

[0098] In certain embodiments, HC1 or HC2 of the heterodimeric antibodies may comprise one or more amino acid substitutions to replace a negatively-charged amino acid with a positively-charged amino acid. For instance, in one embodiment, the CH3 domain of HC1 or the CH3 domain of HC2 comprises an amino acid sequence differing from wild-type IgG amino acid sequence such that one or more negatively-charged amino acids in the wild-type human IgG amino acid sequence are replaced with one or more positively-charged amino acids at the corresponding position(s) in the CH3 domain. In these and other embodiments, amino acids (e.g., aspartic acid or glutamic acid) at one or more positions selected from 356, 357, and 399 (EU numbering system) of the CH3 domain are replaced with a positively-charged amino acid (e.g., lysine, histidine and arginine).

[0099] In particular embodiments, the heterodimeric antibody comprises a first heavy chain comprising negatively-charged amino acids at positions 392 and 409 (e.g., K392D and K409D substitutions), and a second heavy chain comprising positively-charged amino acids at positions 356 and 399 (e.g., E356K and D399K substitutions). In other particular embodiments, the heterodimeric antibody comprises a first heavy chain comprising negatively-charged amino acids at positions 392, 409, and 370 (e.g., K392D, K409D, and K370D substitutions), and a second heavy chain comprising positively-charged amino acids at positions 356, 399, and 357 (e.g., E356K, D399K, and E357K substitutions). In related embodiments, the first heavy chain is from an anti-CGRP receptor antibody and the second heavy chain is from an anti-PAC1 receptor antibody. In other related embodiments, the first heavy chain is from an anti-PAC1 receptor antibody and the second heavy chain is from an anti-CGRP receptor antibody.

[0100] To facilitate the association of a particular heavy chain with its cognate light chain, both the heavy and light chains may contain complimentary amino acid substitutions. As used herein, "complimentary amino acid substitutions" refer to a substitution to a positively-charged amino acid in one chain paired with a negatively-charged amino acid substitution in the other chain. For example, in some embodiments, the heavy chain comprises at least one amino acid substitution to introduce a charged amino acid and the corresponding light chain comprises at least one amino acid substitution to introduce a charged amino acid, wherein the charged amino

acid introduced into the heavy chain has the opposite charge of the amino acid introduced into the light chain. In certain embodiments, one or more positively-charged residues (e.g., lysine, histidine or arginine) can be introduced into a first light chain (LC1) and one or more negatively-charged residues (e.g., aspartic acid or glutamic acid) can be introduced into the companion heavy chain (HC1) at the binding interface of LC1/HC1, whereas one or more negatively-charged residues (e.g., aspartic acid or glutamic acid) can be introduced into a second light chain (LC2) and one or more positively-charged residues (e.g., lysine, histidine or arginine) can be introduced into the companion heavy chain (HC2) at the binding interface of LC2/HC2. The electrostatic interactions will direct the LC1 to pair with HC1 and LC2 to pair with HC2, as the opposite charged residues (polarity) at the interface attract. The heavy/light chain pairs having the same charged residues (polarity) at an interface (e.g. LC1/HC2 and LC2/HC1) will repel, resulting in suppression of the unwanted HC/LC pairings.

[0101] In these and other embodiments, the CH1 domain of the heavy chain or the CL domain of the light chain comprises an amino acid sequence differing from wild-type IgG amino acid sequence such that one or more positively-charged amino acids in wild-type IgG amino acid sequence is replaced with one or more negatively-charged amino acids. Alternatively, the CH1 domain of the heavy chain or the CL domain of the light chain comprises an amino acid sequence differing from wild-type IgG amino acid sequence such that one or more negatively-charged amino acids in wild-type IgG amino acid sequence is replaced with one or more positively-charged amino acids. In some embodiments, one or more amino acids in the CH1 domain of the first and/or second heavy chain in the heterodimeric antibody at an EU position selected from F126, P127, L128, A141, L145, K147, D148, H168, F170, P171, V173, Q175, S176, S183, V185 and K213 is replaced with a charged amino acid. In certain embodiments, a preferred residue for substitution with a negatively- or positively- charged amino acid is S183 (EU numbering system). In some embodiments, S183 is substituted with a positively-charged amino acid. In alternative embodiments, S183 is substituted with a negatively-charged amino acid. For instance, in one embodiment, S183 is substituted with a negatively-charged amino acid (e.g. S183E) in the first heavy chain, and S183 is substituted with a positively-charged amino acid (e.g. S183K) in the second heavy chain.

[0102] In embodiments in which the light chain is a kappa light chain, one or more amino acids in the CL domain of the first and/or second light chain in the heterodimeric antibody at a position

(EU and Kabat numbering in a kappa light chain) selected from F116, F118, S121, D122, E123, Q124, S131, V133, L135, N137, N138, Q160, S162, T164, S174 and S176 is replaced with a charged amino acid. In embodiments in which the light chain is a lambda light chain, one or more amino acids in the CL domain of the first and/or second light chain in the heterodimeric antibody at a position (Kabat numbering in a lambda chain) selected from T116, F118, S121, E123, E124, K129, T131, V133, L135, S137, E160, T162, S165, Q167, A174, S176 and Y178 is replaced with a charged amino acid. In some embodiments, a preferred residue for substitution with a negatively- or positively- charged amino acid is S176 (EU and Kabat numbering system) of the CL domain of either a kappa or lambda light chain. In certain embodiments, S176 of the CL domain is replaced with a positively-charged amino acid. In alternative embodiments, S176 of the CL domain is replaced with a negatively-charged amino acid. In one embodiment, S176 is substituted with a positively-charged amino acid (e.g. S176K) in the first light chain, and S176 is substituted with a negatively-charged amino acid (e.g. S176E) in the second light chain.

[0103] In addition to or as an alternative to the complimentary amino acid substitutions in the CH1 and CL domains, the variable regions of the light and heavy chains in the heterodimeric antibody may contain one or more complimentary amino acid substitutions to introduce charged amino acids. For instance, in some embodiments, the VH region of the heavy chain or the VL region of the light chain of a heterodimeric antibody comprises an amino acid sequence differing from wild-type IgG amino acid sequence such that one or more positively-charged amino acids in wild-type IgG amino acid sequence is replaced with one or more negatively-charged amino acids. Alternatively, the VH region of the heavy chain or the VL region of the light chain comprises an amino acid sequence differing from wild-type IgG amino acid sequence such that one or more negatively-charged amino acids in wild-type IgG amino acid sequence is replaced with one or more positively-charged amino acids.

[0104] V region interface residues (i.e., amino acid residues that mediate assembly of the VH and VL regions) within the VH region include Kabat positions 1, 3, 35, 37, 39, 43, 44, 45, 46, 47, 50, 59, 89, 91, and 93. One or more of these interface residues in the VH region can be substituted with a charged (positively- or negatively-charged) amino acid. In certain embodiments, the amino acid at Kabat position 39 in the VH region of the first and/or second heavy chain is substituted for a positively-charged amino acid, e.g., lysine. In alternative embodiments, the amino acid at Kabat position 39 in the VH region of the first and/or second

heavy chain is substituted for a negatively-charged amino acid, e.g., glutamic acid. In some embodiments, the amino acid at Kabat position 39 in the VH region of the first heavy chain is substituted for a negatively-charged amino acid (e.g. G39E), and the amino acid at Kabat position 39 in the VH region of the second heavy chain is substituted for a positively-charged amino acid (e.g. G39K). In some embodiments, the amino acid at Kabat position 44 in the VH region of the first and/or second heavy chain is substituted for a positively-charged amino acid, e.g., lysine. In alternative embodiments, the amino acid at Kabat position 44 in the VH region of the first and/or second heavy chain is substituted for a negatively-charged amino acid, e.g., glutamic acid. In certain embodiments, the amino acid at Kabat position 44 in the VH region of the first heavy chain is substituted for a negatively-charged amino acid (e.g. G44E), and the amino acid at Kabat position 44 in the VH region of the second heavy chain is substituted for a positively-charged amino acid (e.g. G44K).

[0105] V region interface residues (i.e., amino acid residues that mediate assembly of the VH and VL regions) within the VL region include Kabat positions 32, 34, 35, 36, 38, 41, 42, 43, 44, 45, 46, 48, 49, 50, 51, 53, 54, 55, 56, 57, 58, 85, 87, 89, 90, 91, and 100. One or more interface residues in the VL region can be substituted with a charged amino acid, preferably an amino acid that has an opposite charge to those introduced into the VH region of the cognate heavy chain. In some embodiments, the amino acid at Kabat position 100 in the VL region of the first and/or second light chain is substituted for a positively-charged amino acid, e.g., lysine. In alternative embodiments, the amino acid at Kabat position 100 in the VL region of the first and/or second light chain is substituted for a negative-charged amino acid, e.g., glutamic acid. In certain embodiments, the amino acid at Kabat position 100 in the VL region of the first light chain is substituted for a positively-charged amino acid (e.g. G100K), and the amino acid at Kabat position 100 in the VL region of the second light chain is substituted for a negatively-charged amino acid (e.g. G100E).

[0106] In certain embodiments, a heterodimeric antibody of the invention comprises a first heavy chain and a second heavy chain and a first light chain and a second light chain, wherein the first heavy chain comprises amino acid substitutions at positions 44 (Kabat), 183 (EU), 392 (EU) and 409 (EU), wherein the second heavy chain comprises amino acid substitutions at positions 44 (Kabat), 183 (EU), 356 (EU) and 399 (EU), wherein the first and second light chains comprise an amino acid substitution at positions 100 (Kabat) and 176 (EU), and wherein

the amino acid substitutions introduce a charged amino acid at said positions. In related embodiments, the glycine at position 44 (Kabat) of the first heavy chain is replaced with glutamic acid, the glycine at position 44 (Kabat) of the second heavy chain is replaced with lysine, the glycine at position 100 (Kabat) of the first light chain is replaced with lysine, the glycine at position 100 (Kabat) of the second light chain is replaced with glutamic acid, the serine at position 176 (EU) of the first light chain is replaced with lysine, the serine at position 176 (EU) of the second light chain is replaced with glutamic acid, the serine at position 183 (EU) of the first heavy chain is replaced with glutamic acid, the lysine at position 392 (EU) of the first heavy chain is replaced with aspartic acid, the lysine at position 409 (EU) of the first heavy chain is replaced with aspartic acid, the serine at position 183 (EU) of the second heavy chain is replaced with lysine, the glutamic acid at position 356 (EU) of the second heavy chain is replaced with lysine, and/or the aspartic acid at position 399 (EU) of the second heavy chain is replaced with lysine.

[0107] In other embodiments, a heterodimeric antibody of the invention comprises a first heavy chain and a second heavy chain and a first light chain and a second light chain, wherein the first heavy chain comprises amino acid substitutions at positions 183 (EU), 392 (EU) and 409 (EU), wherein the second heavy chain comprises amino acid substitutions at positions 183 (EU), 356 (EU) and 399 (EU), wherein the first and second light chains comprise an amino acid substitution at position 176 (EU), and wherein the amino acid substitutions introduce a charged amino acid at said positions. In related embodiments, the serine at position 176 (EU) of the first light chain is replaced with lysine, the serine at position 176 (EU) of the second light chain is replaced with glutamic acid, the serine at position 183 (EU) of the first heavy chain is replaced with glutamic acid, the lysine at position 392 (EU) of the first heavy chain is replaced with aspartic acid, the lysine at position 409 (EU) of the first heavy chain is replaced with aspartic acid, the serine at position 183 (EU) of the second heavy chain is replaced with lysine, the glutamic acid at position 356 (EU) of the second heavy chain is replaced with lysine, and/or the aspartic acid at position 399 (EU) of the second heavy chain is replaced with lysine.

[0108] In still other embodiments, a heterodimeric antibody of the invention comprises a first heavy chain and a second heavy chain and a first light chain and a second light chain, wherein the first heavy chain comprises amino acid substitutions at positions 183 (EU), 392 (EU), 409 (EU), and 370 (EU), wherein the second heavy chain comprises amino acid substitutions at

positions 183 (EU), 356 (EU), 399 (EU), and 357 (EU), wherein the first and second light chains comprise an amino acid substitution at position 176 (EU), and wherein the amino acid substitutions introduce a charged amino acid at said positions. In related embodiments, the serine at position 176 (EU) of the first light chain is replaced with lysine, the serine at position 176 (EU) of the second light chain is replaced with glutamic acid, the serine at position 183 (EU) of the first heavy chain is replaced with glutamic acid, the lysine at position 392 (EU) of the first heavy chain is replaced with aspartic acid, the lysine at position 409 (EU) of the first heavy chain is replaced with aspartic acid, the lysine at position 370 (EU) of the first heavy chain is replaced with aspartic acid, the serine at position 183 (EU) of the second heavy chain is replaced with lysine, the glutamic acid at position 356 (EU) of the second heavy chain is replaced with lysine, the aspartic acid at position 399 (EU) of the second heavy chain is replaced with lysine, and/or the glutamic acid at position 357 (EU) of the second heavy chain is replaced with lysine.

[0109] Any of the constant domains, anti-PAC1 receptor variable regions, and anti-CGRP receptor variable regions described herein can be modified to contain one or more of the charge pair mutations described above to facilitate correct assembly of a heterodimeric antibody. Exemplary full-length light chain sequences and full-length heavy chain sequences from anti-PAC1 receptor antibodies containing one or more charge pair mutations suitable for use in the heterodimeric antibodies of the invention are shown in Table 6A and Table 6B, respectively.

Table 6A. Exemplary Anti-PAC1 Receptor Light Chain Sequences

Antibody ID.	LC Group	Light Chain Amino Acid Sequence	Light Chain Nucleic Acid Sequence
01A, 01C, 01D	LC-01	DIQMTQSPSSLSASVGDRITITCRA SQSISRYLNWYQQKPGKAPKLLIY AASSLQSGIPSRFSGSGSGTDFTLT INSLQPEDFATYFCQQSYSPPFTFG PGTKVDIKRTVAAPSVFIFPPSDEQ LKSGTASVVCLLNNFYPREAKVQ WKVDNALQSGNSQESVTEQDSK DSTYSLESTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 211)	GACATCCAGATGACCCAGTCTCCATCCTCCC TGTCTGCATCTGTAGGAGACAGAATCACCA TCACTTGCCGGGCAAGTCAGAGCATTAGCA GGTATTTAAATTGGTATCAACAGAAACCAG GGAAAGCCCCTAAACTCCTGATCTATGCTG CATCCAGTTTGCAAAGTGGGATCCCATCAA GGTTCAGCGGCAGTGGATCTGGGACAGATT TCACTCTCACCATCAACAGTCTGCAACCTGA AGATTTTGCAACTTACTTCTGTCAACAGAGT TACAGTCCCCCATTCACTTTCGGCCCTGGGA CCAAAGTGGATATCAAACGTACGGTGGCTG CACCATCTGTCTTCATCTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCTCTGTT GTGTGCCTGCTGAATAACTTCTATCCCAGAG AGGCCAAAGTACAGTGGAAGGTGGATAAC GCCCTCCAATCGGGTAACTCCCAGGAGAGT GTCACAGAGCAGGACAGCAAGGACAGCAC

Antibody ID.	LC Group	Light Chain Amino Acid Sequence	Light Chain Nucleic Acid Sequence
			CTACAGCCTCGAGAGCACCCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAAGTCTA CGCCTGCGAAGTCACCCATCAGGGCCTGAG CTCGCCCGTCACAAAGAGCTTCAACAGGGG AGAGTGT (SEQ ID NO: 222)
01B	LC-02	DIQMTQSPSSLSASVGDRITITCRA SQSISRYLNWYQQKPGKAPKLLIY AASSLQSGIPSRFSGSGSGTDFTLT INSLQPEDFATYFCQQSYSPPFTFG EGTKVDIKRTVAAPSVFIFPPSDE QLKSGTASVVCLLNNFYPREAKV QWKVDNALQSGNSQESVTEQDS KDSTYSLESTLTLSKADYEKHKV YACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 212)	GACATCCAGATGACCCAGTCTCCATCCTCCC TGTCTGCATCTGTAGGAGACAGAATCACCA TCACTTGCCGGGCAAGTCAGAGCATTAGCA GGTATTTAAATTGGTATCAACAGAAACCAG GGAAAGCCCCTAAACTCCTGATCTATGCTG CATCCAGTTTGCAAAGTGGGATCCCATCAA GGTTCAGCGGCAGTGGATCTGGGACAGATT TCACTCTCACCATCAACAGTCTGCAACCTGA AGATTTTGCAACTTACTTCTGTCAACAGAGT TACAGTCCCCCATTCACTTTCGGCGAGGGG ACCAAAGTGGATATCAAACGTACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTG ATGAGCAGTTGAAATCTGGAACTGCCTCTG TTGTGTGCCTGCTGAATAACTTCTATCCCAG AGAGGCCAAAGTACAGTGGAAGGTGGATA ACGCCCTCCAATCGGGTAACTCCCAGGAGA GTGTCACAGAGCAGGACAGCAAGGACAGC ACCTACAGCCTCGAGAGCACCCTGACGCTG AGCAAAGCAGACTACGAGAAACACAAAGT CTACGCCTGCGAAGTCACCCATCAGGGCCT GAGCTCGCCCGTCACAAAGAGCTTCAACAG GGGAGAGTGT (SEQ ID NO: 223)
02A, 02C	LC-03	DIQMTQSPSSLSASVGDRITITCRA SQSISRYLNWYQQKPGKAPKLLIY AASSLQSGIPSRFSGSGSGTDFTLT INSLQPEDFATYFCQQSYSPPFTFG QGTKVDIKRTVAAPSVFIFPPSDE QLKSGTASVVCLLNNFYPREAKV QWKVDNALQSGNSQESVTEQDS KDSTYSLESTLTLSKADYEKHKV YACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 213)	GACATCCAGATGACCCAGTCTCCATCCTCCC TGTCTGCATCTGTAGGAGACAGAATCACCA TCACTTGCCGGGCAAGTCAGAGCATTAGCA GGTATTTAAATTGGTATCAACAGAAACCAG GGAAAGCCCCTAAACTCCTGATCTATGCTG CATCCAGTTTGCAAAGTGGGATCCCATCAA GGTTCAGCGGCAGTGGATCTGGGACAGATT TCACTCTCACCATCAACAGTCTGCAACCTGA AGATTTTGCAACTTACTTCTGTCAACAGAGT TACAGTCCCCCATTCACTTTCGGCCAGGGG ACCAAAGTGGATATCAAACGTACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTG ATGAGCAGTTGAAATCTGGAACTGCCTCTG TTGTGTGCCTGCTGAATAACTTCTATCCCAG AGAGGCCAAAGTACAGTGGAAGGTGGATA ACGCCCTCCAATCGGGTAACTCCCAGGAGA GTGTCACAGAGCAGGACAGCAAGGACAGC ACCTACAGCCTCGAAAGCACCCTGACGCTG AGCAAAGCAGACTACGAGAAACACAAAGT CTACGCCTGCGAAGTCACCCATCAGGGCCT GAGCTCGCCCGTCACAAAGAGCTTCAACAG GGGAGAGTGT (SEQ ID NO: 224)
03A, 03C, 03D	LC-04	DIQLTQSPSFLSASVGDRVTITCRA SQSIGRSLHWYQQKPGKAPKLLIK YASQSLSGVPSRFSGSGSGTEFTL TISSLQPEDFATYYCHQSSRLPFTF GPGTKVDIKRTVAAPSVFIFPPSDE	GATATCCAGCTCACTCAATCGCCATCATTTC TCTCCGCTTCGGTAGGCGACCGGGTCACGA TCACATGCAGGGCGTCGCAAAGCATTGGGA GGTCGTTGCATTGGTATCAGCAGAAACCCG GAAAGGCCCCGAAACTTCTGATCAAATACG

Antibody ID.	LC Group	Light Chain Amino Acid Sequence	Light Chain Nucleic Acid Sequence
		QLKSGTASVVCLLNNFYPREAKV QWKVDNALQSGNSQESVTEQDS KDSTYSLESTLTLSKADYEKHKV YACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 214)	CATCACAAAGCTTGAGCGGTGTGCCGTCGC GCTTCTCCGGTTCCGGAAGCGGAACGGAAT TCACGCTTACAATCTCCTCACTGCAGCCCGA GGATTTCGCGACCTATTACTGTCACCAGTCA TCCAGACTCCCGTTTACTTTTGGCCCTGGGA CCAAGGTGGACATTAAGCGTACGGTGGCTG CACCATCTGTCTTCATCTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCTCTGTT GTGTGCCTGCTGAATAACTTCTATCCCAGAG AGGCCAAAGTACAGTGGAAGGTGGATAAC GCCCTCCAATCGGGTAACTCCCAGGAGAGT GTCACAGAGCAGGACAGCAAGGACAGCAC CTACAGCCTCGAGAGCACCCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAAGTCTA CGCCTGCGAAGTCACCCATCAGGGCCTGAG CTCGCCCGTCACAAAGAGCTTCAACAGGGG AGAGTGT (SEQ ID NO: 225)
03B	LC-05	DIQLTQSPSFLSASVGDRVTITCRA SQSIGRSLHWYQQKPGKAPKLLIK YASQSLSGVPSRFSGSGSGTEFTL TISSLQPEDFATYYCHQSSRLPFTF GEGTKVDIKRTVAAPSVFIFPPSD EQLKSGTASVVCLLNNFYPREAK VQWKVDNALQSGNSQESVTEQD SKDSTYSLESTLTLSKADYEKHK VYACEVTHQGLSSPVTKSFNRGE C (SEQ ID NO: 215)	GATATCCAGCTCACTCAATCGCCATCATTTC TCTCCGCTTCGGTAGGCGACCGGGTCACGA TCACATGCAGGGCGTCGCAAAGCATTGGGA GGTCGTTGCATTGGTATCAGCAGAAACCCG GAAAGGCCCCGAAACTTCTGATCAAATACG CATCACAAAGCTTGAGCGGTGTGCCGTCGC GCTTCTCCGGTTCCGGAAGCGGAACGGAAT TCACGCTTACAATCTCCTCACTGCAGCCCGA GGATTTCGCGACCTATTACTGTCACCAGTCA TCCAGACTCCCGTTTACTTTTGGCGAGGGGA CCAAGGTGGACATTAAGCGTACGGTGGCTG CACCATCTGTCTTCATCTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCTCTGTT GTGTGCCTGCTGAATAACTTCTATCCCAGAG AGGCCAAAGTACAGTGGAAGGTGGATAAC GCCCTCCAATCGGGTAACTCCCAGGAGAGT GTCACAGAGCAGGACAGCAAGGACAGCAC CTACAGCCTCGAGAGCACCCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAAGTCTA CGCCTGCGAAGTCACCCATCAGGGCCTGAG CTCGCCCGTCACAAAGAGCTTCAACAGGGG AGAGTGT (SEQ ID NO: 226)
04A, 04C, 04D	LC-06	EIVLTQSPATLSLSPGERATLSCRA SQSVGRSLHWYQQKPGQAPRLLI KYASQSLSGIPARFSGSGSGTDFT LTISSLEPEDFAVYYCHQSSRLPFT FGPGTKVDIKRTVAAPSVFIFPPSD EQLKSGTASVVCLLNNFYPREAK VQWKVDNALQSGNSQESVTEQD SKDSTYSLESTLTLSKADYEKHK VYACEVTHQGLSSPVTKSFNRGE C (SEQ ID NO: 216)	GAGATCGTACTTACTCAGTCACCCGCCACA TTGTCCCTGAGCCCGGGTGAACGGGCGACC CTCAGCTGCCGAGCATCCCAGTCCGTCGGA CGATCATTGCACTGGTACCAACAAAAACCG GGCCAGGCCCCCAGACTTCTGATCAAGTAT GCGTCACAGAGCTTGTCGGGTATTCCCGCTC GCTTTTCGGGGTCGGGATCCGGGACAGATT TCACGCTCACAATCTCCTCGCTGGAACCCG AGGACTTCGCGGTCTACTATTGTCATCAGTC ATCGAGGTTGCCTTTCACGTTTGGACCAGG GACCAAGGTGGACATTAAGCGTACGGTGGC TGCACCATCTGTCTTCATCTTCCCGCCATCT GATGAGCAGTTGAAATCTGGAACTGCCTCT GTTGTGTGCCTGCTGAATAACTTCTATCCCA GAGAGGCCAAAGTACAGTGGAAGGTGGAT

Antibody ID.	LC Group	Light Chain Amino Acid Sequence	Light Chain Nucleic Acid Sequence
			AACGCCCTCCAATCGGGTAACTCCCAGGAG AGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCGAGAGCACCCTGACGCT GAGCAAAGCAGACTACGAGAAACACAAAG TCTACGCCTGCGAAGTCACCCATCAGGGCC TGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT (SEQ ID NO: 227)
04B	LC-07	EIVLTQSPATLSLSPGERATLSCRA SQSVGRSLHWYQQKPGQAPRLLI KYASQSLSGIPARFSGSGSGTDFT LTISSLEPEDFAVYYCHQSSRLPFT FGEGTKVDIKRTVAAPSVFIFPPSD EQLKSGTASVVCLLNNFYPREAK VQWKVDNALQSGNSQESVTEQD SKDSTYSLESTLTLSKADYEKHK VYACEVTHQGLSSPVTKSFNRGE C (SEQ ID NO: 217)	GAGATCGTACTTACTCAGTCACCCGCCACA TTGTCCCTGAGCCCGGGTGAACGGGCGACC CTCAGCTGCCGAGCATCCCAGTCCGTCGGA CGATCATTGCACTGGTACCAACAAAAACCG GGCCAGGCCCCCAGACTTCTGATCAAGTAT GCGTCACAGAGCTTGTCGGGTATTCCCGCTC GCTTTTCGGGGTCGGGATCCGGGACAGATT TCACGCTCACAATCTCCTCGCTGGAACCCG AGGACTTCGCGGTCTACTATTGTCATCAGTC ATCGAGGTTGCCTTTCACGTTTGGAGAAGG GACCAAGGTGGACATTAAGCGTACGGTGGC TGCACCATCTGTCTTCATCTTCCCGCCATCT GATGAGCAGTTGAAATCTGGAACTGCCTCT GTTGTGTGCCTGCTGAATAACTTCTATCCCA GAGAGGCCAAAGTACAGTGGAAGGTGGAT AACGCCCTCCAATCGGGTAACTCCCAGGAG AGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCGAGAGCACCCTGACGCT GAGCAAAGCAGACTACGAGAAACACAAAG TCTACGCCTGCGAAGTCACCCATCAGGGCC TGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT (SEQ ID NO: 228)
05A, 05C, 05D	LC-08	DIVMTQSPDSLAVSLGERATIHCK SSQSVLYSSNNKNFLTWYQQKPG QPPKLLIYRASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVYFCQ QYYSAPFTFGPGTRVDIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLN NFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLESTLTLSK ADYEKHKVYACEVTHQGLSSPVT KSFNRGEC (SEQ ID NO: 218)	GACATCGTGATGACCCAGTCTCCAGACTCC CTGGCTGTGTCTCTGGGCGAGAGGGCCACC ATCCACTGCAAGTCCAGCCAGAGTGTTTTAT ACAGCTCCAACAATAAGAACTTCTTAACTT GGTACCAGCAGAAACCAGGACAGCCTCCTA AACTTCTCATTTACCGGGCATCTACCCGGGA ATCCGGGGTTCCTGACCGATTCAGTGGCAG CGGGTCTGGGACAGATTTCACTCTCACCATC AGCAGCCTGCAGGCTGAAGATGTGGCAGTT TATTTCTGTCAGCAATATTATAGTGCTCCAT TCACTTTCGGCCCTGGGACCAGAGTGGATA TCAAACGTACGGTGGCTGCACCATCTGTCTT CATCTTCCCGCCATCTGATGAGCAGTTGAA ATCTGGAACTGCCTCTGTTGTGTGCCTGCTG AATAACTTCTATCCCAGAGAGGCCAAAGTA CAGTGGAAGGTGGATAACGCCCTCCAATCG GGTAACTCCCAGGAGAGTGTCACAGAGCAG GACAGCAAGGACAGCACCTACAGCCTCGAG AGCACCCTGACGCTGAGCAAAGCAGACTAC GAGAAACACAAAGTCTACGCCTGCGAAGTC ACCCATCAGGGCCTGAGCTCGCCCGTCACA AAGAGCTTCAACAGGGGAGAGTGT (SEQ ID NO: 229)
05B	LC-09	DIVMTQSPDSLAVSLGERATIHCK SSQSVLYSSNNKNFLTWYQQKPG	GACATCGTGATGACCCAGTCTCCAGACTCC CTGGCTGTGTCTCTGGGCGAGAGGGCCACC

Antibody ID.	LC Group	Light Chain Amino Acid Sequence	Light Chain Nucleic Acid Sequence
		QPPKLLIYRASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVYFCQ QYYSAPFTFGEGTRVDIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLN NFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLESTLTLSK ADYEKHKVYACEVTHQGLSSPVT KSFNRGEC (SEQ ID NO: 219)	ATCCACTGCAAGTCCAGCCAGAGTGTTTTAT ACAGCTCCAACAATAAGAACTTCTTAACTT GGTACCAGCAGAAACCAGGACAGCCTCCTA AACTTCTCATTTACCGGGCATCTACCCGGGA ATCCGGGGTTCCTGACCGATTCAGTGGCAG CGGGTCTGGGACAGATTTCACTCTCACCATC AGCAGCCTGCAGGCTGAAGATGTGGCAGTT TATTTCTGTCAGCAATATTATAGTGCTCCAT TCACTTTCGGCGAGGGGACCAGAGTGGATA TCAAACGTACGGTGGCTGCACCATCTGTCTT CATCTTCCCGCCATCTGATGAGCAGTTGAA ATCTGGAACTGCCTCTGTTGTGTGCCTGCTG AATAACTTCTATCCCAGAGAGGCCAAAGTA CAGTGGAAGGTGGATAACGCCCTCCAATCG GGTAACTCCCAGGAGAGTGTCACAGAGCAG GACAGCAAGGACAGCACCTACAGCCTCGAG AGCACCCTGACGCTGAGCAAAGCAGACTAC GAGAAACACAAAGTCTACGCCTGCGAAGTC ACCCATCAGGGCCTGAGCTCGCCCGTCACA AAGAGCTTCAACAGGGGAGAGTGT (SEQ ID NO: 230)
06A, 06C	LC-10	DIVMTQSPDSLAVSLGERATINCK SSQSVLYSSNNKNFLTWYQQKPG QPPKLLIYRASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVYFCQ QYYSAPFTFGPGTRVDIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLN NFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLESTLTLSK ADYEKHKVYACEVTHQGLSSPVT KSFNRGEC (SEQ ID NO: 220)	GACATCGTGATGACCCAGTCTCCAGACTCC CTGGCTGTGTCTCTGGGCGAGAGGGCCACC ATCAACTGCAAGTCCAGCCAGAGTGTTTTA TACAGCTCCAACAATAAGAACTTCTTAACTT GGTACCAGCAGAAACCAGGACAGCCTCCTA AACTTCTCATTTACCGGGCATCTACCCGGGA ATCCGGGGTTCCTGACCGATTCAGTGGCAG CGGGTCTGGGACAGATTTCACTCTCACCATC AGCAGCCTGCAGGCTGAAGATGTGGCAGTT TATTTCTGTCAGCAATATTATAGTGCTCCAT TCACTTTCGGCCCTGGGACCAGAGTGGATA TCAAACGTACGGTGGCTGCACCATCTGTCTT CATCTTCCCGCCATCTGATGAGCAGTTGAA ATCTGGAACTGCCTCTGTTGTGTGCCTGCTG AATAACTTCTATCCCAGAGAGGCCAAAGTA CAGTGGAAGGTGGATAACGCCCTCCAATCG GGTAACTCCCAGGAGAGTGTCACAGAGCAG GACAGCAAGGACAGCACCTACAGCCTCGAA AGCACCCTGACGCTGAGCAAAGCAGACTAC GAGAAACACAAAGTCTACGCCTGCGAAGTC ACCCATCAGGGCCTGAGCTCGCCCGTCACA AAGAGCTTCAACAGGGGAGAGTGT (SEQ ID NO: 231)
06B	LC-11	DIVMTQSPDSLAVSLGERATINCK SSQSVLYSSNNKNFLTWYQQKPG QPPKLLIYRASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVYFCQ QYYSAPFTFGEGTRVDIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLN NFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLESTLTLSK ADYEKHKVYACEVTHQGLSSPVT KSFNRGEC (SEQ ID NO: 221)	GACATCGTGATGACCCAGTCTCCAGACTCC CTGGCTGTGTCTCTGGGCGAGAGGGCCACC ATCAACTGCAAGTCCAGCCAGAGTGTTTTA TACAGCTCCAACAATAAGAACTTCTTAACTT GGTACCAGCAGAAACCAGGACAGCCTCCTA AACTTCTCATTTACCGGGCATCTACCCGGGA ATCCGGGGTTCCTGACCGATTCAGTGGCAG CGGGTCTGGGACAGATTTCACTCTCACCATC AGCAGCCTGCAGGCTGAAGATGTGGCAGTT TATTTCTGTCAGCAATATTATAGTGCTCCAT

Antibody ID.	LC Group	Light Chain Amino Acid Sequence	Light Chain Nucleic Acid Sequence
			TCACTTTCGGCGAGGGGACCAGAGTGGATA TCAAACGTACGGTGGCTGCACCATCTGTCTT CATCTTCCCGCCATCTGATGAGCAGTTGAA ATCTGGAACTGCCTCTGTTGTGTGCCTGCTG AATAACTTCTATCCCAGAGAGGCCAAAGTA CAGTGGAAGGTGGATAACGCCCTCCAATCG GGTAACTCCCAGGAGAGTGTCACAGAGCAG GACAGCAAGGACAGCACCTACAGCCTCGAA AGCACCCTGACGCTGAGCAAAGCAGACTAC GAGAAACACAAAGTCTACGCCTGCGAAGTC ACCCATCAGGGCCTGAGCTCGCCCGTCACA AAGAGCTTCAACAGGGGAGAGTGT (SEQ ID NO: 232)

Table 6B. Exemplary Anti-PAC1 Receptor Heavy Chain Sequences

Antibody ID.	HC Group	Heavy Chain Amino Acid Sequence	Heavy Chain Nucleic Acid Sequence
01A, 02A	HC-01	QVQLQQSGPGLVKPSQTL SLTCAISGDSVSSNSATW NWIRQSPSRGLEWLGRTY YRSKWSNHYAVSVKSRIT INPDTSKSQFSLQLNSVTP EDTAVYYCARGTWKQL WFLDHWGQGTLVTVSSA STKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPA VLQSSGLYSLKSVVTVPS SSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHT CPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYV DGVEVHNAKTKPCEEQY GSTYRCVSVLTVLHQDW LNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNG QPENNYDTTPPVLDSDGS FFLYSDLTVDKSRWQQG NVFSCSVMHEALHNHYT QKSLSLSPGK (SEQ ID NO: 233)	CAGGTACAGCTGCAGCAGTCAGGTCCAGGACTGGT GAAGCCCTCGCAGACCCTCTCACTCACCTGTGCCAT CTCCGGGGACAGTGTCTCTAGCAACAGTGCTACTTG GAACTGGATCAGGCAGTCCCCATCGAGAGGCCTTG AGTGGCTGGGAAGGACATATTACAGGTCCAAGTGG TCTAATCATTATGCAGTATCTGTGAAAAGTCGAATA ACCATCAACCCCGACACGTCCAAGAGCCAGTTCTCC CTGCAGCTGAACTCTGTGACTCCCGAGGACACGGCT GTGTATTACTGTGCAAGAGGAACGTGGAAACAGCT ATGGTTCCTTGACCACTGGGGCCAGGGAACCCTGGT CACCGTCTCTAGTGCCTCCACCAAGGGCCCATCGGT CTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGG GGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACT ACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCA GGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCT GTCCTACAGTCCTCAGGACTCTACTCCCTCAAGAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAGCCCAGCA ACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCT TGTGACAAAACTCACACATGCCCACCGTGCCCAGC ACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTT CCCCCCAAAACCCAAGGACACCCTCATGATCTCCCG GACCCCTGAGGTCACATGCGTGGTGGTGGACGTGA GCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAA GCCGTGTGAGGAGCAGTACGGCAGCACGTACCGTT GTGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGC TGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTC CAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGT ACACCCTGCCCCCATCCCGGGAGGAGATGACCAAG AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTC TATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAA TGGGCAGCCGGAGAACAACTACGATACCACGCCTC CCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATA

Antibody ID.	HC Group	Heavy Chain Amino Acid Sequence	Heavy Chain Nucleic Acid Sequence
			GCGATCTCACCGTGGACAAGAGCAGGTGGCAGCAG GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT CTGCACAACCACTACACGCAGAAGAGCCTCTCCCT GTCTCCGGGTAAA (SEQ ID NO: 252)
01B	HC-02	QVQLQQSGPGLVKPSQTL SLTCAISGDSVSSNSATW NWIRQSPSRKLEWLGRTY YRSKWSNHYAVSVKSRIT INPDTSKSQFSLQLNSVTP EDTAVYYCARGTWKQL WFLDHWGQGTLVTVSSA STKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPA VLQSSGLYSLKSVVTVPS SSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHT CPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYV DGVEVHNAKTKPCEEQY GSTYRCVSVLTVLHQDW LNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNG QPENNYDTTPPVLDSDGS FFLYSDLTVDKSRWQQG NVFSCSVMHEALHNHYT QKSLSLSPGK (SEQ ID NO: 234)	CAGGTACAGCTGCAGCAGTCAGGTCCAGGACTGGT GAAGCCCTCGCAGACCCTCTCACTCACCTGTGCCAT CTCCGGGGACAGTGTCTCTAGCAACAGTGCTACTTG GAACTGGATCAGGCAGTCCCCATCGAGAAAGCTTG AGTGGCTGGGAAGGACATATTACAGGTCCAAGTGG TCTAATCATTATGCAGTATCTGTGAAAAGTCGAATA ACCATCAACCCCGACACGTCCAAGAGCCAGTTCTCC CTGCAGCTGAACTCTGTGACTCCCGAGGACACGGCT GTGTATTACTGTGCAAGAGGAACGTGGAAACAGCT ATGGTTCCTTGACCACTGGGGCCAGGGAACCCTGGT CACCGTCTCTAGTGCCTCCACCAAGGGCCCATCGGT CTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGG GGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACT ACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCA GGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCT GTCCTACAGTCCTCAGGACTCTACTCCCTCAAGAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAGCCCAGCA ACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCT TGTGACAAAACTCACACATGCCCACCGTGCCCAGC ACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTT CCCCCCAAAACCCAAGGACACCCTCATGATCTCCCG GACCCCTGAGGTCACATGCGTGGTGGTGGACGTGA GCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAA GCCGTGTGAGGAGCAGTACGGCAGCACGTACCGTT GTGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGC TGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTC CAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGT ACACCCTGCCCCCATCCCGGGAGGAGATGACCAAG AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTC TATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAA TGGGCAGCCGGAGAACAACTACGATACCACGCCTC CCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATA GCGATCTCACCGTGGACAAGAGCAGGTGGCAGCAG GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT CTGCACAACCACTACACGCAGAAGAGCCTCTCCCT GTCTCCGGGTAAA (SEQ ID NO: 253)
01C, 02C	HC-03	QVQLQQSGPGLVKPSQTL SLTCAISGDSVSSNSATW NWIRQSPSRGLEWLGRTY YRSKWSNHYAVSVKSRIT INPDTSKSQFSLQLNSVTP EDTAVYYCARGTWKQL WFLDHWGQGTLVTVSSA STKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPA VLQSSGLYSLKSVVTVPS	CAGGTACAGCTGCAGCAGTCAGGTCCAGGACTGGT GAAGCCCTCGCAGACCCTCTCACTCACCTGTGCCAT CTCCGGGGACAGTGTCTCTAGCAACAGTGCTACTTG GAACTGGATCAGGCAGTCCCCATCGAGAGGCCTTG AGTGGCTGGGAAGGACATATTACAGGTCCAAGTGG TCTAATCATTATGCAGTATCTGTGAAAAGTCGAATA ACCATCAACCCCGACACGTCCAAGAGCCAGTTCTCC CTGCAGCTGAACTCTGTGACTCCCGAGGACACGGCT GTGTATTACTGTGCAAGAGGAACGTGGAAACAGCT ATGGTTCCTTGACCACTGGGGCCAGGGAACCCTGGT CACCGTCTCTAGTGCCTCCACCAAGGGCCCATCGGT

Antibody ID.	HC Group	Heavy Chain Amino Acid Sequence	Heavy Chain Nucleic Acid Sequence
		SSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHT CPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYV DGVEVHNAKTKPCEEQY GSTYRCVSVLTVLHQDW LNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTC LVDGFYPSDIAVEWESNG QPENNYDTTPPVLDSDGS FFLYSDLTVDKSRWQQG NVFSCSVMHEALHNHYT QKSLSLSPGK (SEQ ID NO: 235)	CTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGG GGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACT ACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCA GGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCT GTCCTACAGTCCTCAGGACTCTACTCCCTCAAGAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAGCCCAGCA ACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCT TGTGACAAAACTCACACATGCCCACCGTGCCCAGC ACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTT CCCCCCAAAACCCAAGGACACCCTCATGATCTCCCG GACCCCTGAGGTCACATGCGTGGTGGTGGACGTGA GCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAA GCCGTGTGAGGAGCAGTACGGCAGCACGTACCGTT GTGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGC TGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTC CAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGT ACACCCTGCCCCCATCCCGGGAGGAGATGACCAAG AACCAGGTCAGCCTGACCTGCCTGGTCGATGGCTTC TATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAA TGGGCAGCCGGAGAACAACTACGATACCACGCCTC CCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATA GCGATCTCACCGTGGACAAGAGCAGGTGGCAGCAG GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT CTGCACAACCACTACACGCAGAAGAGCCTCTCCCT GTCTCCGGGTAAA (SEQ ID NO: 254)
01D	HC-04	QVQLQQSGPGLVKPSQTL SLTCAISGDSVSSNSATW NWIRQSPSRGLEWLGRTY YRSKWSNHYAVSVKSRIT INPDTSKSQFSLQLNSVTP EDTAVYYCARGTWKQL WFLDHWGQGTLVTVSSA STKGPSVFPLAPCSRSTSE STAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPA VLQSSGLYSLKSVVTVPS SNFGTQTYTCNVDHKPSN TKVDKTVERKCCVECPPC PAPPVAGPSVFLFPPKPKD TLMISRTPEVTCVVVDVS HEDPEVQFNWYVDGVEV HNAKTKPREEQFNSTFRV VSVLTVVHQDWLNGKEY KCKVSNKGLPAPIEKTISK TKGQPREPQVYTLPPSRE EMTKNQVSLTCLVDGFY PSDIAVEWESNGQPENNY DTTPPMLDSDGSFFLYSD LTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSL SPGK (SEQ ID NO: 236)	CAGGTACAGCTGCAGCAGTCAGGTCCAGGACTGGT GAAGCCCTCGCAGACCCTCTCACTCACCTGTGCCAT CTCCGGGGACAGTGTCTCTAGCAACAGTGCTACTTG GAACTGGATCAGGCAGTCCCCATCGAGAGGCCTTG AGTGGCTGGGAAGGACATATTACAGGTCCAAGTGG TCTAATCATTATGCAGTATCTGTGAAAAGTCGAATA ACCATCAACCCCGACACGTCCAAGAGCCAGTTCTCC CTGCAGCTGAACTCTGTGACTCCCGAGGACACGGCT GTGTATTACTGTGCAAGAGGAACGTGGAAACAGCT ATGGTTCCTTGACCACTGGGGCCAGGGAACCCTGGT CACCGTCTCTAGTGCCTCCACCAAGGGCCCATCGGT CTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGA GAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACT ACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCA GGCGCTCTGACCAGCGGCGTGCACACCTTCCCAGCT GTCCTACAGTCCTCAGGACTCTACTCCCTCAAGAGC GTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAG ACCTACACCTGCAACGTAGATCACAAGCCCAGCAA CACCAAGGTGGACAAGACAGTTGAGCGCAAATGTT GTGTCGAGTGCCCACCGTGCCCAGCACCACCTGTGG CAGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCA AGGACACCCTCATGATCTCCCGGACCCCTGAGGTCA CGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCC GAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAAGCCACGGGAGGAGC AGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCA

Antibody ID.	HC Group	Heavy Chain Amino Acid Sequence	Heavy Chain Nucleic Acid Sequence
			CCGTTGTGCACCAGGACTGGCTGAACGGCAAGGAG TACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGC CCCCATCGAGAAAACCATCTCCAAAACCAAAGGGC AGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA TCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCT GACCTGCCTGGTCGATGGCTTCTACCCCAGCGACAT CGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGA ACAACTACGATACCACACCTCCCATGCTGGACTCCG ACGGCTCCTTCTTCCTCTACAGCGATCTCACCGTGG ACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCA TGCTCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA (SEQ ID NO: 255)
03A	HC-05	QVQLVESGAEVVKPGAS VKVSCKASGFTFSRFAMH WVRQAPGQGLEWMGVIS YDGGNKYYAESVKGRVT MTRDTSTSTLYMELSSLR SEDTAVYYCARGYDVLT GYPDYWGQGTLVTVSSA STKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPA VLQSSGLYSLKSVVTVPS SSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHT CPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYV DGVEVHNAKTKPCEEQY GSTYRCVSVLTVLHQDW LNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNG QPENNYDTTPPVLDSDGS FFLYSDLTVDKSRWQQG NVFSCSVMHEALHNHYT QKSLSLSPGK (SEQ ID NO: 237)	CAAGTTCAGTTGGTGGAGTCTGGAGCCGAAGTAGT AAAGCCAGGAGCTTCAGTGAAAGTCTCTTGTAAAG CAAGTGGATTCACGTTTAGCCGCTTTGCCATGCATT GGGTGCGGCAAGCTCCCGGTCAGGGGTTGGAGTGG ATGGGAGTTATTAGCTATGACGGGGGCAATAAGTA CTACGCCGAGTCTGTTAAGGGTCGGGTCACAATGA CACGGGACACCTCAACCAGTACACTCTATATGGAA CTGTCTAGCCTGAGATCCGAGGACACCGCTGTGTAT TATTGCGCTAGGGGGTACGATGTATTGACGGGTTAT CCTGATTACTGGGGGCAGGGGACACTCGTAACCGT CTCTAGTGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCAC AGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCC TGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTAC AGTCCTCAGGACTCTACTCCCTCAAGAGCGTGGTGA CCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACA TCTGCAACGTGAATCACAAGCCCAGCAACACCAAG GTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAA AACTCACACATGCCCACCGTGCCCAGCACCTGAACT CCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAA ACCCAAGGACACCCTCATGATCTCCCGGACCCCTGA GGTCACATGCGTGGTGGTGGACGTGAGCCACGAAG ACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGTGA GGAGCAGTACGGCAGCACGTACCGTTGTGTCAGCG TCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCA AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTC CCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAA AGGGCAGCCCCGAGAACCACAGGTGTACACCCTGC CCCCATCCCGGGAGGAGATGACCAAGAACCAGGTC AGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCC GGAGAACAACTACGATACCACGCCTCCCGTGCTGG ACTCCGACGGCTCCTTCTTCCTCTATAGCGATCTCA CCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTC TTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT AAA (SEQ ID NO: 256)
03B	HC-06	QVQLVESGAEVVKPGAS VKVSCKASGFTFSRFAMH	CAAGTTCAGTTGGTGGAGTCTGGAGCCGAAGTAGT AAAGCCAGGAGCTTCAGTGAAAGTCTCTTGTAAAG

Antibody ID.	HC Group	Heavy Chain Amino Acid Sequence	Heavy Chain Nucleic Acid Sequence
		WVRQAPGQKLEWMGVIS YDGGNKYYAESVKGRVT MTRDTSTSTLYMELSSLR SEDTAVYYCARGYDVLT GYPDYWGQGTLVTVSSA STKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPA VLQSSGLYSLKSVVTVPS SSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHT CPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYV DGVEVHNAKTKPCEEQY GSTYRCVSVLTVLHQDW LNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNG QPENNYDTTPPVLDSDGS FFLYSDLTVDKSRWQQG NVFSCSVMHEALHNHYT QKSLSLSPGK (SEQ ID NO: 238)	CAAGTGGATTCACGTTTAGCCGCTTTGCCATGCATT GGGTGCGGCAAGCTCCCGGTCAGAAGTTGGAGTGG ATGGGAGTTATTAGCTATGACGGGGGCAATAAGTA CTACGCCGAGTCTGTTAAGGGTCGGGTCACAATGA CACGGGACACCTCAACCAGTACACTCTATATGGAA CTGTCTAGCCTGAGATCCGAGGACACCGCTGTGTAT TATTGCGCTAGGGGGTACGATGTATTGACGGGTTAT CCTGATTACTGGGGGCAGGGGACACTCGTAACCGT CTCTAGTGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCAC AGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCC TGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTAC AGTCCTCAGGACTCTACTCCCTCAAGAGCGTGGTGA CCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACA TCTGCAACGTGAATCACAAGCCCAGCAACACCAAG GTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAA AACTCACACATGCCCACCGTGCCCAGCACCTGAACT CCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAA ACCCAAGGACACCCTCATGATCTCCCGGACCCCTGA GGTCACATGCGTGGTGGTGGACGTGAGCCACGAAG ACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGTGA GGAGCAGTACGGCAGCACGTACCGTTGTGTCAGCG TCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCA AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTC CCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAA AGGGCAGCCCCGAGAACCACAGGTGTACACCCTGC CCCCATCCCGGGAGGAGATGACCAAGAACCAGGTC AGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCC GGAGAACAACTACGATACCACGCCTCCCGTGCTGG ACTCCGACGGCTCCTTCTTCCTCTATAGCGATCTCA CCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTC TTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT AAA (SEQ ID NO: 257)
03C	HC-07	QVQLVESGAEVVKPGAS VKVSCKASGFTFSRFAMH WVRQAPGQGLEWMGVIS YDGGNKYYAESVKGRVT MTRDTSTSTLYMELSSLR SEDTAVYYCARGYDVLT GYPDYWGQGTLVTVSSA STKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPA VLQSSGLYSLKSVVTVPS SSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHT CPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYV DGVEVHNAKTKPCEEQY	CAAGTTCAGTTGGTGGAGTCTGGAGCCGAAGTAGT AAAGCCAGGAGCTTCAGTGAAAGTCTCTTGTAAAG CAAGTGGATTCACGTTTAGCCGCTTTGCCATGCATT GGGTGCGGCAAGCTCCCGGTCAGGGGTTGGAGTGG ATGGGAGTTATTAGCTATGACGGGGGCAATAAGTA CTACGCCGAGTCTGTTAAGGGTCGGGTCACAATGA CACGGGACACCTCAACCAGTACACTCTATATGGAA CTGTCTAGCCTGAGATCCGAGGACACCGCTGTGTAT TATTGCGCTAGGGGGTACGATGTATTGACGGGTTAT CCTGATTACTGGGGGCAGGGGACACTCGTAACCGT CTCTAGTGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCAC AGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCC TGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTAC AGTCCTCAGGACTCTACTCCCTCAAGAGCGTGGTGA CCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACA

Antibody ID.	HC Group	Heavy Chain Amino Acid Sequence	Heavy Chain Nucleic Acid Sequence
		GSTYRCVSVLTVLHQDW LNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTC LVDGFYPSDIAVEWESNG QPENNYDTTPPVLDSDGS FFLYSDLTVDKSRWQQG NVFSCSVMHEALHNHYT QKSLSLSPGK (SEQ ID NO: 239)	TCTGCAACGTGAATCACAAGCCCAGCAACACCAAG GTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAA AACTCACACATGCCCACCGTGCCCAGCACCTGAACT CCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAA ACCCAAGGACACCCTCATGATCTCCCGGACCCCTGA GGTCACATGCGTGGTGGTGGACGTGAGCCACGAAG ACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGTGA GGAGCAGTACGGCAGCACGTACCGTTGTGTCAGCG TCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCA AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTC CCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAA AGGGCAGCCCCGAGAACCACAGGTGTACACCCTGC CCCCATCCCGGGAGGAGATGACCAAGAACCAGGTC AGCCTGACCTGCCTGGTCGATGGCTTCTATCCCAGC GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCC GGAGAACAACTACGATACCACGCCTCCCGTGCTGG ACTCCGACGGCTCCTTCTTCCTCTATAGCGATCTCA CCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTC TTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT AAA (SEQ ID NO: 258)
03D	HC-08	QVQLVESGAEVVKPGAS VKVSCKASGFTFSRFAMH WVRQAPGQGLEWMGVIS YDGGNKYYAESVKGRVT MTRDTSTSTLYMELSSLR SEDTAVYYCARGYDVLT GYPDYWGQGTLVTVSSA STKGPSVFPLAPCSRSTSE STAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPA VLQSSGLYSLKSVVTVPS SNFGTQTYTCNVDHKPSN TKVDKTVERKCCVECPPC PAPPVAGPSVFLFPPKPKD TLMISRTPEVTCVVVDVS HEDPEVQFNWYVDGVEV HNAKTKPREEQFNSTFRV VSVLTVVHQDWLNGKEY KCKVSNKGLPAPIEKTISK TKGQPREPQVYTLPPSRE EMTKNQVSLTCLVDGFY PSDIAVEWESNGQPENNY DTTPPMLDSDGSFFLYSD LTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSL SPGK (SEQ ID NO: 240)	CAAGTTCAGTTGGTGGAGTCTGGAGCCGAAGTAGT AAAGCCAGGAGCTTCAGTGAAAGTCTCTTGTAAAG CAAGTGGATTCACGTTTAGCCGCTTTGCCATGCATT GGGTGCGGCAAGCTCCCGGTCAGGGGTTGGAGTGG ATGGGAGTTATTAGCTATGACGGGGGCAATAAGTA CTACGCCGAGTCTGTTAAGGGTCGGGTCACAATGA CACGGGACACCTCAACCAGTACACTCTATATGGAA CTGTCTAGCCTGAGATCCGAGGACACCGCTGTGTAT TATTGCGCTAGGGGGTACGATGTATTGACGGGTTAT CCTGATTACTGGGGGCAGGGGACACTCGTAACCGT CTCTAGTGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCA CAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCC CCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCT CTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTA CAGTCCTCAGGACTCTACTCCCTCAAGAGCGTGGTG ACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTAC ACCTGCAACGTAGATCACAAGCCCAGCAACACCAA GGTGGACAAGACAGTTGAGCGCAAATGTTGTGTCG AGTGCCCACCGTGCCCAGCACCACCTGTGGCAGGA CCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC ACCCTCATGATCTCCCGGACCCCTGAGGTCACGTGC GTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGT CCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGC ATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTC AACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTT GTGCACCAGGACTGGCTGAACGGCAAGGAGTACAA GTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCA TCGAGAAAACCATCTCCAAAACCAAAGGGCAGCCC CGAGAACCACAGGTGTACACCCTGCCCCCATCCCG GGAGGAGATGACCAAGAACCAGGTCAGCCTGACCT GCCTGGTCGATGGCTTCTACCCCAGCGACATCGCCG

Antibody ID.	HC Group	Heavy Chain Amino Acid Sequence	Heavy Chain Nucleic Acid Sequence
			TGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAA CTACGATACCACACCTCCCATGCTGGACTCCGACGG CTCCTTCTTCCTCTACAGCGATCTCACCGTGGACAA GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCT CCGTGATGCATGAGGCTCTGCACAACCACTACACG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA (SEQ ID NO: 259)
04A	HC-09	QVQLVESGGGVVQPGRS LRLSCAASGFTFSRFAMH WVRQAPGKGLEWVAVIS YDGGNKYYAESVKGRFT ISRDNSKNTLYLQMNSLR AEDTALFYCARGYDVLT GYPDYWGQGTLVTVSSA STKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPA VLQSSGLYSLKSVVTVPS SSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHT CPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYV DGVEVHNAKTKPCEEQY GSTYRCVSVLTVLHQDW LNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNG QPENNYDTTPPVLDSDGS FFLYSDLTVDKSRWQQG NVFSCSVMHEALHNHYT QKSLSLSPGK (SEQ ID NO: 241)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCCTGGGAGGTCCCTGCGACTCTCCTGTGCAGC CTCTGGATTCACCTTCAGTAGATTTGCCATGCACTG GGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGG TGGCAGTTATATCATATGATGGAGGAAATAAATAC TATGCAGAGTCCGTGAAGGGCCGGTTCACCATCTCC AGAGACAATTCCAAGAACACCCTGTATCTGCAAAT GAACAGCCTGAGAGCTGAGGACACGGCTCTGTTTT ACTGTGCGAGAGGATACGATGTTTTGACTGGTTACC CCGACTACTGGGGCCAGGGAACCCTGGTCACCGTC TCTAGTGCCTCCACCAAGGGCCCATCGGTCTTCCCC CTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCAC AGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCC TGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTAC AGTCCTCAGGACTCTACTCCCTCAAGAGCGTGGTGA CCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACA TCTGCAACGTGAATCACAAGCCCAGCAACACCAAG GTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAA AACTCACACATGCCCACCGTGCCCAGCACCTGAACT CCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAA ACCCAAGGACACCCTCATGATCTCCCGGACCCCTGA GGTCACATGCGTGGTGGTGGACGTGAGCCACGAAG ACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGTGA GGAGCAGTACGGCAGCACGTACCGTTGTGTCAGCG TCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCA AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTC CCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAA AGGGCAGCCCCGAGAACCACAGGTGTACACCCTGC CCCCATCCCGGGAGGAGATGACCAAGAACCAGGTC AGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCC GGAGAACAACTACGATACCACGCCTCCCGTGCTGG ACTCCGACGGCTCCTTCTTCCTCTATAGCGATCTCA CCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTC TTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT AAA (SEQ ID NO: 260)
04B	HC-10	QVQLVESGGGVVQPGRS LRLSCAASGFTFSRFAMH WVRQAPGKKLEWVAVIS YDGGNKYYAESVKGRFT ISRDNSKNTLYLQMNSLR AEDTALFYCARGYDVLT GYPDYWGQGTLVTVSSA STKGPSVFPLAPSSKSTSG	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCCTGGGAGGTCCCTGCGACTCTCCTGTGCAGC CTCTGGATTCACCTTCAGTAGATTTGCCATGCACTG GGTCCGCCAGGCTCCAGGCAAGAAGCTGGAGTGGG TGGCAGTTATATCATATGATGGAGGAAATAAATAC TATGCAGAGTCCGTGAAGGGCCGGTTCACCATCTCC AGAGACAATTCCAAGAACACCCTGTATCTGCAAAT GAACAGCCTGAGAGCTGAGGACACGGCTCTGTTTT

Antibody ID.	HC Group	Heavy Chain Amino Acid Sequence	Heavy Chain Nucleic Acid Sequence
		GTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPA VLQSSGLYSLKSVVTVPS SSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHT CPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYV DGVEVHNAKTKPCEEQY GSTYRCVSVLTVLHQDW LNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNG QPENNYDTTPPVLDSDGS FFLYSDLTVDKSRWQQG NVFSCSVMHEALHNHYT QKSLSLSPGK (SEQ ID NO: 242)	ACTGTGCGAGAGGATACGATGTTTTGACTGGTTACC CCGACTACTGGGGCCAGGGAACCCTGGTCACCGTC TCTAGTGCCTCCACCAAGGGCCCATCGGTCTTCCCC CTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCAC AGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCC TGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTAC AGTCCTCAGGACTCTACTCCCTCAAGAGCGTGGTGA CCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACA TCTGCAACGTGAATCACAAGCCCAGCAACACCAAG GTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAA AACTCACACATGCCCACCGTGCCCAGCACCTGAACT CCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAA ACCCAAGGACACCCTCATGATCTCCCGGACCCCTGA GGTCACATGCGTGGTGGTGGACGTGAGCCACGAAG ACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGTGA GGAGCAGTACGGCAGCACGTACCGTTGTGTCAGCG TCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCA AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTC CCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAA AGGGCAGCCCCGAGAACCACAGGTGTACACCCTGC CCCCATCCCGGGAGGAGATGACCAAGAACCAGGTC AGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCC GGAGAACAACTACGATACCACGCCTCCCGTGCTGG ACTCCGACGGCTCCTTCTTCCTCTATAGCGATCTCA CCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTC TTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT AAA (SEQ ID NO: 261)
04C	HC-11	QVQLVESGGGVVQPGRS LRLSCAASGFTFSRFAMH WVRQAPGKGLEWVAVIS YDGGNKYYAESVKGRFT ISRDNSKNTLYLQMNSLR AEDTALFYCARGYDVLT GYPDYWGQGTLVTVSSA STKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPA VLQSSGLYSLKSVVTVPS SSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHT CPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYV DGVEVHNAKTKPCEEQY GSTYRCVSVLTVLHQDW LNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTC LVDGFYPSDIAVEWESNG QPENNYDTTPPVLDSDGS	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCCTGGGAGGTCCCTGCGACTCTCCTGTGCAGC CTCTGGATTCACCTTCAGTAGATTTGCCATGCACTG GGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGG TGGCAGTTATATCATATGATGGAGGAAATAAATAC TATGCAGAGTCCGTGAAGGGCCGGTTCACCATCTCC AGAGACAATTCCAAGAACACCCTGTATCTGCAAAT GAACAGCCTGAGAGCTGAGGACACGGCTCTGTTTT ACTGTGCGAGAGGATACGATGTTTTGACTGGTTACC CCGACTACTGGGGCCAGGGAACCCTGGTCACCGTC TCTAGTGCCTCCACCAAGGGCCCATCGGTCTTCCCC CTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCAC AGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCC TGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTAC AGTCCTCAGGACTCTACTCCCTCAAGAGCGTGGTGA CCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACA TCTGCAACGTGAATCACAAGCCCAGCAACACCAAG GTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAA AACTCACACATGCCCACCGTGCCCAGCACCTGAACT CCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAA ACCCAAGGACACCCTCATGATCTCCCGGACCCCTGA GGTCACATGCGTGGTGGTGGACGTGAGCCACGAAG

Antibody ID.	HC Group	Heavy Chain Amino Acid Sequence	Heavy Chain Nucleic Acid Sequence
		FFLYSDLTVDKSRWQQG NVFSCSVMHEALHNHYT QKSLSLSPGK (SEQ ID NO: 243)	ACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGTGA GGAGCAGTACGGCAGCACGTACCGTTGTGTCAGCG TCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCA AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTC CCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAA AGGGCAGCCCCGAGAACCACAGGTGTACACCCTGC CCCCATCCCGGGAGGAGATGACCAAGAACCAGGTC AGCCTGACCTGCCTGGTCGATGGCTTCTATCCCAGC GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCC GGAGAACAACTACGATACCACGCCTCCCGTGCTGG ACTCCGACGGCTCCTTCTTCCTCTATAGCGATCTCA CCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTC TTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT AAA (SEQ ID NO: 262)
04D	HC-12	QVQLVESGGGVVQPGRS LRLSCAASGFTFSRFAMH WVRQAPGKGLEWVAVIS YDGGNKYYAESVKGRFT ISRDNSKNTLYLQMNSLR AEDTALFYCARGYDVLT GYPDYWGQGTLVTVSSA STKGPSVFPLAPCSRSTSE STAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPA VLQSSGLYSLKSVVTVPS SNFGTQTYTCNVDHKPSN TKVDKTVERKCCVECPPC PAPPVAGPSVFLFPPKPKD TLMISRTPEVTCVVVDVS HEDPEVQFNWYVDGVEV HNAKTKPREEQFNSTFRV VSVLTVVHQDWLNGKEY KCKVSNKGLPAPIEKTISK TKGQPREPQVYTLPPSRE EMTKNQVSLTCLVDGFY PSDIAVEWESNGQPENNY DTTPPMLDSDGSFFLYSD LTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSL SPGK (SEQ ID NO: 244)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCCTGGGAGGTCCCTGCGACTCTCCTGTGCAGC CTCTGGATTCACCTTCAGTAGATTTGCCATGCACTG GGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGG TGGCAGTTATATCATATGATGGAGGAAATAAATAC TATGCAGAGTCCGTGAAGGGCCGGTTCACCATCTCC AGAGACAATTCCAAGAACACCCTGTATCTGCAAAT GAACAGCCTGAGAGCTGAGGACACGGCTCTGTTTT ACTGTGCGAGAGGATACGATGTTTTGACTGGTTACC CCGACTACTGGGGCCAGGGAACCCTGGTCACCGTC TCTAGTGCCTCCACCAAGGGCCCATCGGTCTTCCCC CTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCAC AGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTC TGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTAC AGTCCTCAGGACTCTACTCCCTCAAGAGCGTGGTGA CCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACA CCTGCAACGTAGATCACAAGCCCAGCAACACCAAG GTGGACAAGACAGTTGAGCGCAAATGTTGTGTCGA GTGCCCACCGTGCCCAGCACCACCTGTGGCAGGAC CGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACA CCCTCATGATCTCCCGGACCCCTGAGGTCACGTGCG TGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTC CAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCA TAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCA ACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTG TGCACCAGGACTGGCTGAACGGCAAGGAGTACAAG TGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATC GAGAAAACCATCTCCAAAACCAAAGGGCAGCCCCG AGAACCACAGGTGTACACCCTGCCCCCATCCCGGG AGGAGATGACCAAGAACCAGGTCAGCCTGACCTGC CTGGTCGATGGCTTCTACCCCAGCGACATCGCCGTG GAGTGGGAGAGCAATGGGCAGCCGGAGAACAACT ACGATACCACACCTCCCATGCTGGACTCCGACGGCT CCTTCTTCCTCTACAGCGATCTCACCGTGGACAAGA GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACACGCA GAAGAGCCTCTCCCTGTCTCCGGGTAAA (SEQ ID

Antibody ID.	HC Group	Heavy Chain Amino Acid Sequence	Heavy Chain Nucleic Acid Sequence
			NO: 263)
05A	HC-13	QVQLQESGPGLVKPSQTL SLTCTVSGGSISSGGYYW SWIRQHPGKGLEWIGYIY YSGNTYYNPSLKSRVTIS GDTSKNQFSLKLRSVTAA DTAVYYCTRGGAARGM DVWGQGTTVTVSSASTK GPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVL QSSGLYSLKSVVTVPSSSL GTQTYICNVNHKPSNTKV DKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTY RCVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPS REEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPEN NYDTTPPVLDSDGSFFLY SDLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSL SLSPGK (SEQ ID NO: 245)	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGT GAAGCCTTCACAGACCCTGTCCCTCACCTGCACTGT CTCTGGTGGCTCCATCAGCAGTGGTGGTTACTACTG GAGCTGGATCCGCCAGCACCCAGGGAAGGGCCTGG AGTGGATTGGGTACATCTATTACAGTGGGAACACCT ACTACAACCCGTCCCTCAAGAGTCGAGTTACCATAT CAGGAGACACGTCTAAGAACCAGTTCTCCCTGAAG CTGAGGTCTGTGACTGCCGCGGACACGGCCGTGTAT TACTGTACGAGAGGAGGAGCAGCTCGCGGTATGGA CGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTA GTGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGG CACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAA CCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGAC CAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTC CTCAGGACTCTACTCCCTCAAGAGCGTGGTGACCGT GCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTG CAACGTGAATCACAAGCCCAGCAACACCAAGGTGG ACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACT CACACATGCCCACCGTGCCCAGCACCTGAACTCCTG GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCC AAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCC TGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGG AGGTGCATAATGCCAAGACAAAGCCGTGTGAGGAG CAGTACGGCAGCACGTACCGTTGTGTCAGCGTCCTC ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGA GTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAG CCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGG CAGCCCCGAGAACCACAGGTGTACACCCTGCCCCC ATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCC TGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACA TCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAG AACAACTACGATACCACGCCTCCCGTGCTGGACTCC GACGGCTCCTTCTTCCTCTATAGCGATCTCACCGTG GACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCACTA CACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA (SEQ ID NO: 264)
05B	HC-14	QVQLQESGPGLVKPSQTL SLTCTVSGGSISSGGYYW SWIRQHPGKKLEWIGYIY YSGNTYYNPSLKSRVTIS GDTSKNQFSLKLRSVTAA DTAVYYCTRGGAARGM DVWGQGTTVTVSSASTK GPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVL QSSGLYSLKSVVTVPSSSL GTQTYICNVNHKPSNTKV DKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPK	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGT GAAGCCTTCACAGACCCTGTCCCTCACCTGCACTGT CTCTGGTGGCTCCATCAGCAGTGGTGGTTACTACTG GAGCTGGATCCGCCAGCACCCAGGGAAGAAGCTGG AGTGGATTGGGTACATCTATTACAGTGGGAACACCT ACTACAACCCGTCCCTCAAGAGTCGAGTTACCATAT CAGGAGACACGTCTAAGAACCAGTTCTCCCTGAAG CTGAGGTCTGTGACTGCCGCGGACACGGCCGTGTAT TACTGTACGAGAGGAGGAGCAGCTCGCGGTATGGA CGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTA GTGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGG CACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAA CCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGAC

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		DTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTY RCVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPS REEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPEN NYDTTPPVLDSDGSFFLY SDLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSL SLSPGK (SEQ ID NO: 246)	CAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTC CTCAGGACTCTACTCCCTCAAGAGCGTGGTGACCGT GCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTG CAACGTGAATCACAAGCCCAGCAACACCAAGGTGG ACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACT CACACATGCCCACCGTGCCCAGCACCTGAACTCCTG GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCC AAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCC TGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGG AGGTGCATAATGCCAAGACAAAGCCGTGTGAGGAG CAGTACGGCAGCACGTACCGTTGTGTCAGCGTCCTC ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGA GTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAG CCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGG CAGCCCCGAGAACCACAGGTGTACACCCTGCCCCC ATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCC TGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACA TCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAG AACAACTACGATACCACGCCTCCCGTGCTGGACTCC GACGGCTCCTTCTTCCTCTATAGCGATCTCACCGTG GACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCACTA CACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA (SEQ ID NO: 265)
05C	HC-15	QVQLQESGPGLVKPSQTL SLTCTVSGGSISSGGYYW SWIRQHPGKGLEWIGYIY YSGNTYYNPSLKSRVTIS GDTSKNQFSLKLRSVTAA DTAVYYCTRGGAARGM DVWGQGTTVTVSSASTK GPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVL QSSGLYSLKSVVTVPSSSL GTQTYICNVNHKPSNTKV DKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTY RCVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPS REEMTKNQVSLTCLVDG FYPSDIAVEWESNGQPEN NYDTTPPVLDSDGSFFLY SDLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSL SLSPGK (SEQ ID NO: 247)	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGT GAAGCCTTCACAGACCCTGTCCCTCACCTGCACTGT CTCTGGTGGCTCCATCAGCAGTGGTGGTTACTACTG GAGCTGGATCCGCCAGCACCCAGGGAAGGGCCTGG AGTGGATTGGGTACATCTATTACAGTGGGAACACCT ACTACAACCCGTCCCTCAAGAGTCGAGTTACCATAT CAGGAGACACGTCTAAGAACCAGTTCTCCCTGAAG CTGAGGTCTGTGACTGCCGCGGACACGGCCGTGTAT TACTGTACGAGAGGAGGAGCAGCTCGCGGTATGGA CGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTA GTGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGG CACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAA CCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGAC CAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTC CTCAGGACTCTACTCCCTCAAGAGCGTGGTGACCGT GCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTG CAACGTGAATCACAAGCCCAGCAACACCAAGGTGG ACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACT CACACATGCCCACCGTGCCCAGCACCTGAACTCCTG GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCC AAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCC TGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGG AGGTGCATAATGCCAAGACAAAGCCGTGTGAGGAG CAGTACGGCAGCACGTACCGTTGTGTCAGCGTCCTC ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGA GTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAG CCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGG

Antibody ID.	HC Group	Heavy Chain Amino Acid Sequence	Heavy Chain Nucleic Acid Sequence
			CAGCCCCGAGAACCACAGGTGTACACCCTGCCCCC ATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCC TGACCTGCCTGGTCGATGGCTTCTATCCCAGCGACA TCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAG AACAACTACGATACCACGCCTCCCGTGCTGGACTCC GACGGCTCCTTCTTCCTCTATAGCGATCTCACCGTG GACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCACTA CACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA (SEQ ID NO: 266)
05D	HC-16	QVQLQESGPGLVKPSQTL SLTCTVSGGSISSGGYYW SWIRQHPGKGLEWIGYIY YSGNTYYNPSLKSRVTIS GDTSKNQFSLKLRSVTAA DTAVYYCTRGGAARGM DVWGQGTTVTVSSASTK GPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVL QSSGLYSLKSVVTVPSSN FGTQTYTCNVDHKPSNT KVDKTVERKCCVECPPCP APPVAGPSVFLFPPKPKD TLMISRTPEVTCVVVDVS HEDPEVQFNWYVDGVEV HNAKTKPREEQFNSTFRV VSVLTVVHQDWLNGKEY KCKVSNKGLPAPIEKTISK TKGQPREPQVYTLPPSRE EMTKNQVSLTCLVDGFY PSDIAVEWESNGQPENNY DTTPPMLDSDGSFFLYSD LTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSL SPGK (SEQ ID NO: 248)	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGT GAAGCCTTCACAGACCCTGTCCCTCACCTGCACTGT CTCTGGTGGCTCCATCAGCAGTGGTGGTTACTACTG GAGCTGGATCCGCCAGCACCCAGGGAAGGGCCTGG AGTGGATTGGGTACATCTATTACAGTGGGAACACCT ACTACAACCCGTCCCTCAAGAGTCGAGTTACCATAT CAGGAGACACGTCTAAGAACCAGTTCTCCCTGAAG CTGAGGTCTGTGACTGCCGCGGACACGGCCGTGTAT TACTGTACGAGAGGAGGAGCAGCTCGCGGTATGGA CGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTA GTGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGG CGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAA CCGGTGACGGTGTCGTGGAACTCAGGCGCTCTGAC CAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTC CTCAGGACTCTACTCCCTCAAGAGCGTGGTGACCGT GCCCTCCAGCAACTTCGGCACCCAGACCTACACCTG CAACGTAGATCACAAGCCCAGCAACACCAAGGTGG ACAAGACAGTTGAGCGCAAATGTTGTGTCGAGTGC CCACCGTGCCCAGCACCACCTGTGGCAGGACCGTC AGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCT CATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGT GGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGT TCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT GCCAAGACAAAGCCACGGGAGGAGCAGTTCAACAG CACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCA CCAGGACTGGCTGAACGGCAAGGAGTACAAGTGCA AGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAG AAAACCATCTCCAAAACCAAAGGGCAGCCCCGAGA ACCACAGGTGTACACCCTGCCCCCATCCCGGGAGG AGATGACCAAGAACCAGGTCAGCCTGACCTGCCTG GTCGATGGCTTCTACCCCAGCGACATCGCCGTGGAG TGGGAGAGCAATGGGCAGCCGGAGAACAACTACGA TACCACACCTCCCATGCTGGACTCCGACGGCTCCTT CTTCCTCTACAGCGATCTCACCGTGGACAAGAGCAG GTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGAT GCATGAGGCTCTGCACAACCACTACACGCAGAAGA GCCTCTCCCTGTCTCCGGGTAAA (SEQ ID NO: 267)
06A	HC-17	QVQLQESGPGLVKPSETL SLTCTVSGGSISSGGYYW SWIRQPPGKGLEWIGYIY YSGNTYYNPSLKSRVTIS VDTSKNQFSLKLRSVTAA DTAVYYCTRGGAARGM	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGT GAAGCCTTCAGAGACCCTGTCCCTCACCTGCACTGT CTCTGGTGGCTCCATCAGCAGTGGTGGTTACTACTG GAGCTGGATCCGCCAGCCCCCAGGGAAGGGCCTGG AGTGGATTGGGTACATCTATTACAGTGGGAACACCT ACTACAACCCGTCCCTCAAGAGTCGAGTTACCATAT

Antibody ID.	HC Group	Heavy Chain Amino Acid Sequence	Heavy Chain Nucleic Acid Sequence
		DVWGQGTTVTVSSASTK GPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVL QSSGLYSLKSVVTVPSSSL GTQTYICNVNHKPSNTKV DKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTY RCVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPS REEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPEN NYDTTPPVLDSDGSFFLY SDLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSL SLSPGK (SEQ ID NO: 249)	CAGTGGACACGTCTAAGAACCAGTTCTCCCTGAAG CTGAGGTCTGTGACTGCCGCGGACACGGCCGTGTAT TACTGTACGAGAGGAGGAGCAGCTCGCGGTATGGA CGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTA GTGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGG CACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAA CCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGAC CAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTC CTCAGGACTCTACTCCCTCAAGAGCGTGGTGACCGT GCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTG CAACGTGAATCACAAGCCCAGCAACACCAAGGTGG ACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACT CACACATGCCCACCGTGCCCAGCACCTGAACTCCTG GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCC AAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCC TGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGG AGGTGCATAATGCCAAGACAAAGCCGTGCGAGGAG CAGTACGGCAGCACGTACCGTTGCGTCAGCGTCCTC ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGA GTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAG CCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGG CAGCCCCGAGAACCACAGGTGTACACCCTGCCCCC ATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCC TGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACA TCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAG AACAACTACGACACCACGCCTCCCGTGCTGGACTCC GACGGCTCCTTCTTCCTCTATAGCGACCTCACCGTG GACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCACTA CACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA (SEQ ID NO: 268)
06B	HC-18	QVQLQESGPGLVKPSETL SLTCTVSGGSISSGGYYW SWIRQPPGKKLEWIGYIY YSGNTYYNPSLKSRVTIS VDTSKNQFSLKLRSVTAA DTAVYYCTRGGAARGM DVWGQGTTVTVSSASTK GPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVL QSSGLYSLKSVVTVPSSSL GTQTYICNVNHKPSNTKV DKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTY RCVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPS REEMTKNQVSLTCLVKG	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGT GAAGCCTTCAGAGACCCTGTCCCTCACCTGCACTGT CTCTGGTGGCTCCATCAGCAGTGGTGGTTACTACTG GAGCTGGATCCGCCAGCCCCCAGGGAAGAAGCTGG AGTGGATTGGGTACATCTATTACAGTGGGAACACCT ACTACAACCCGTCCCTCAAGAGTCGAGTTACCATAT CAGTAGACACGTCTAAGAACCAGTTCTCCCTGAAG CTGAGGTCTGTGACTGCCGCGGACACGGCCGTGTAT TACTGTACGAGAGGAGGAGCAGCTCGCGGTATGGA CGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTA GTGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGG CACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAA CCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGAC CAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTC CTCAGGACTCTACTCCCTCAAGAGCGTGGTGACCGT GCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTG CAACGTGAATCACAAGCCCAGCAACACCAAGGTGG ACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACT CACACATGCCCACCGTGCCCAGCACCTGAACTCCTG GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCC

Antibody ID.	HC Group	Heavy Chain Amino Acid Sequence	Heavy Chain Nucleic Acid Sequence
		FYPSDIAVEWESNGQPEN NYDTTPPVLDSDGSFFLY SDLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSL SLSPGK (SEQ ID NO: 250)	AAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCC TGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGG AGGTGCATAATGCCAAGACAAAGCCGTGCGAGGAG CAGTACGGCAGCACGTACCGTTGCGTCAGCGTCCTC ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGA GTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAG CCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGG CAGCCCCGAGAACCACAGGTGTACACCCTGCCCCC ATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCC TGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACA TCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAG AACAACTACGACACCACGCCTCCCGTGCTGGACTCC GACGGCTCCTTCTTCCTCTATAGCGACCTCACCGTG GACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCACTA CACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA (SEQ ID NO: 269)
06C	HC-19	QVQLQESGPGLVKPSETL SLTCTVSGGSISSGGYYW SWIRQPPGKGLEWIGYIY YSGNTYYNPSLKSRVTIS VDTSKNQFSLKLRSVTAA DTAVYYCTRGGAARGM DVWGQGTTVTVSSASTK GPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVL QSSGLYSLKSVVTVPSSSL GTQTYICNVNHKPSNTKV DKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTY RCVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPS REEMTKNQVSLTCLVDG FYPSDIAVEWESNGQPEN NYDTTPPVLDSDGSFFLY SDLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSL SLSPGK (SEQ ID NO: 251)	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGT GAAGCCTTCAGAGACCCTGTCCCTCACCTGCACTGT CTCTGGTGGCTCCATCAGCAGTGGTGGTTACTACTG GAGCTGGATCCGCCAGCCCCCAGGGAAGGGCCTGG AGTGGATTGGGTACATCTATTACAGTGGGAACACCT ACTACAACCCGTCCCTCAAGAGTCGAGTTACCATAT CAGTGGACACGTCTAAGAACCAGTTCTCCCTGAAG CTGAGGTCTGTGACTGCCGCGGACACGGCCGTGTAT TACTGTACGAGAGGAGGAGCAGCTCGCGGTATGGA CGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTA GTGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGG CACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAA CCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGAC CAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTC CTCAGGACTCTACTCCCTCAAGAGCGTGGTGACCGT GCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTG CAACGTGAATCACAAGCCCAGCAACACCAAGGTGG ACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACT CACACATGCCCACCGTGCCCAGCACCTGAACTCCTG GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCC AAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCC TGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGG AGGTGCATAATGCCAAGACAAAGCCGTGCGAGGAG CAGTACGGCAGCACGTACCGTTGCGTCAGCGTCCTC ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGA GTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAG CCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGG CAGCCCCGAGAACCACAGGTGTACACCCTGCCCCC ATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCC TGACCTGCCTGGTCGATGGCTTCTATCCCAGCGACA TCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAG AACAACTACGACACCACGCCTCCCGTGCTGGACTCC GACGGCTCCTTCTTCCTCTATAGCGACCTCACCGTG GACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC

Antibody ID.	HC Group	Heavy Chain Amino Acid Sequence	Heavy Chain Nucleic Acid Sequence
			ATGCTCCGTGATGCATGAGGCTCTGCACAACCACTA CACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA (SEQ ID NO: 270)

[0110] In some embodiments, the heterodimeric antibody of the invention comprises an anti-PAC1 receptor light chain from Table 6A and an anti-PAC1 receptor heavy chain from Table 6B. Exemplary pairs of anti-PAC1 receptor light and heavy chains that may be incorporated into a heterodimeric antibody include, but are not limited to: LC-01 (SEQ ID NO: 211) and HC-01 (SEQ ID NO: 233); LC-02 (SEQ ID NO: 212) and HC-02 (SEQ ID NO: 234); LC-01 (SEQ ID NO: 211) and HC-03 (SEQ ID NO: 235); LC-01 (SEQ ID NO: 211) and HC-04 (SEQ ID NO: 236); LC-03 (SEQ ID NO: 213) and HC-01 (SEQ ID NO: 233); LC-03 (SEQ ID NO: 213) and HC-03 (SEQ ID NO: 235); LC-04 (SEQ ID NO: 214) and HC-05 (SEQ ID NO: 237); LC-05 (SEQ ID NO: 215) and HC-06 (SEQ ID NO: 238); LC-04 (SEQ ID NO: 214) and HC-07 (SEQ ID NO: 239); LC-04 (SEQ ID NO: 214) and HC-08 (SEQ ID NO: 240); LC-06 (SEQ ID NO: 216) and HC-09 (SEQ ID NO: 241); LC-07 (SEQ ID NO: 217) and HC-10 (SEQ ID NO: 242); LC-06 (SEQ ID NO: 216) and HC-11 (SEQ ID NO: 243); LC-06 (SEQ ID NO: 216) and HC-12 (SEQ ID NO: 244); LC-08 (SEQ ID NO: 218) and HC-13 (SEQ ID NO: 245); LC-09 (SEQ ID NO: 219) and HC-14 (SEQ ID NO: 246); LC-08 (SEQ ID NO: 218) and HC-15 (SEQ ID NO: 247); LC-08 (SEQ ID NO: 218) and HC-16 (SEQ ID NO: 248); LC-10 (SEQ ID NO: 220) and HC-17 (SEQ ID NO: 249); LC-11(SEQ ID NO: 221) and HC-18 (SEQ ID NO: 250); and LC-10 (SEQ ID NO: 220) and HC-19 (SEQ ID NO: 251).

[0111] The anti-PAC1 receptor light chain and/or heavy chain incorporated into a heterodimeric antibody of the invention may comprise a sequence of contiguous amino acids that differs from the sequence of a light chain in Table 6A or a heavy chain in Table 6B by 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15 or more amino acid residues, wherein each such sequence difference is independently a deletion, insertion or substitution of one amino acid. In some embodiments, the anti-PAC1 receptor light chain incorporated into a heterodimeric antibody comprises a sequence of amino acids that has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97% or at least 99% sequence identity to the amino acid sequences of SEQ ID NOs: 211-221 (i.e. the anti-PAC1 receptor light chains in Table 6A). In certain embodiments, the anti-PAC1 receptor heavy chain incorporated into a heterodimeric antibody comprises a

sequence of amino acids that has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97% or at least 99% sequence identity to the amino acid sequences of SEQ ID NOs: 233-251 (i.e. the anti-PAC1 receptor heavy chains in Table 6B).

[0112] Exemplary full-length light chain sequences and full-length heavy chain sequences from anti-CGRP receptor antibodies containing one or more charge pair mutations suitable for use in the heterodimeric antibodies of the invention are shown in Table 7A and Table 7B, respectively.

Table 7A. Exemplary Anti-CGRP Receptor Light Chain Sequences

Antibody ID.	LC Group	Light Chain Amino Acid Sequence	Light Chain Nucleic Acid Sequence
50A, 50C, 50D	LC-101	QSVLTQPPSASGTPGQRVTI SCSGSSSNIGSNYVYWYQQ LPGAAPKLLIFRNNQRPSGV PDRFSGSKSGTSASLAISGL RSEDEADYYCAAWDDSLS GWVFGGGTKLTVLGQPKA NPTVTLFPPSSEELQANKAT LVCLISDFYPGAVTVAWKA DGSPVKAGVETTKPSKQSN NKYAAKSYLSLTPEQWKSH RSYSCQVTHEGSTVEKTVA PTECS (SEQ ID NO: 271)	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTGG GACCCCCGGGCAGAGAGTCACCATCTCTTGTTCT GGAAGCAGCTCCAACATCGGCAGTAATTATGTAT ACTGGTACCAGCAGCTCCCAGGAGCGGCCCCCAA ACTCCTCATCTTTAGGAATAATCAGCGGCCCTCAG GGGTCCCTGACCGCTTCTCTGGCTCCAAGTCTGGC ACCTCAGCCTCCCTGGCCATCAGTGGGCTCCGGTC CGAGGATGAGGCTGATTATTACTGTGCAGCATGG GATGACAGCCTGAGTGGTTGGGTGTTCGGCGGAG GGACCAAGCTGACCGTCCTAGGTCAGCCCAAGGC CAACCCCACTGTCACTCTGTTCCCGCCCTCCTCTG AGGAGCTCCAAGCCAACAAGGCCACACTAGTGTG TCTGATCAGTGACTTCTACCCGGGAGCTGTGACA GTGGCCTGGAAGGCAGATGGCAGCCCCGTCAAGG CGGGAGTGGAGACCACCAAACCCTCCAAACAGA GCAACAACAAGTACGCGGCCAAGAGCTACCTGAG CCTGACGCCCGAGCAGTGGAAGTCCCACAGAAGC TACAGCTGCCAGGTCACGCATGAAGGGAGCACCG TGGAGAAGACAGTGGCCCCTACAGAATGTTCA (SEQ ID NO: 283)
50B	LC-102	QSVLTQPPSASGTPGQRVTI SCSGSSSNIGSNYVYWYQQ LPGAAPKLLIFRNNQRPSGV PDRFSGSKSGTSASLAISGL RSEDEADYYCAAWDDSLS GWVFGKGTKLTVLGQPKA NPTVTLFPPSSEELQANKAT LVCLISDFYPGAVTVAWKA DGSPVKAGVETTKPSKQSN NKYAAKSYLSLTPEQWKSH RSYSCQVTHEGSTVEKTVA PTECS (SEQ ID NO: 272)	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTGG GACCCCCGGGCAGAGAGTCACCATCTCTTGTTCT GGAAGCAGCTCCAACATCGGCAGTAATTATGTAT ACTGGTACCAGCAGCTCCCAGGAGCGGCCCCCAA ACTCCTCATCTTTAGGAATAATCAGCGGCCCTCAG GGGTCCCTGACCGCTTCTCTGGCTCCAAGTCTGGC ACCTCAGCCTCCCTGGCCATCAGTGGGCTCCGGTC CGAGGATGAGGCTGATTATTACTGTGCAGCATGG GATGACAGCCTGAGTGGTTGGGTGTTCGGCAAGG GGACCAAGCTGACCGTCCTAGGTCAGCCCAAGGC CAACCCCACTGTCACTCTGTTCCCGCCCTCCTCTG AGGAGCTCCAAGCCAACAAGGCCACACTAGTGTG TCTGATCAGTGACTTCTACCCGGGAGCTGTGACA GTGGCCTGGAAGGCAGATGGCAGCCCCGTCAAGG CGGGAGTGGAGACCACCAAACCCTCCAAACAGA GCAACAACAAGTACGCGGCCAAGAGCTACCTGAG CCTGACGCCCGAGCAGTGGAAGTCCCACAGAAGC TACAGCTGCCAGGTCACGCATGAAGGGAGCACCG TGGAGAAGACAGTGGCCCCTACAGAATGTTCA

Antibody ID.	LC Group	Light Chain Amino Acid Sequence	Light Chain Nucleic Acid Sequence
			(SEQ ID NO: 284)
51A, 51C, 51D	LC-103	QSVLTQSPSASGTPGQRVTI SCSGSSSNIGSNYVYWYQQ LPGAAPKLLILRNNQRPSGV PDRFSGSKSGTSASLTISGL RSEDEADYYCAAWDDSLS GWVFGGGTKLTVLGQPKA NPTVTLFPPSSEELQANKAT LVCLISDFYPGAVTVAWKA DGSPVKAGVETTKPSKQSN NKYAAKSYLSLTPEQWKSH RSYSCQVTHEGSTVEKTVA PTECS (SEQ ID NO: 273)	CAGTCTGTGCTGACTCAGTCACCCTCAGCGTCTGG GACCCCCGGGCAGAGAGTCACCATCTCTTGTTCT GGAAGCAGCTCCAACATCGGCAGTAATTATGTAT ACTGGTACCAGCAGCTCCCAGGAGCGGCCCCCAA ACTCCTCATCCTTAGGAATAATCAGCGGCCCTCA GGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGG CACCTCAGCCTCCCTGACCATCAGTGGGCTCCGGT CCGAGGATGAGGCTGACTATTATTGTGCAGCATG GGATGACAGCCTGAGTGGTTGGGTGTTCGGCGGA GGGACCAAGCTGACCGTCCTAGGTCAGCCCAAGG CCAACCCCACTGTCACTCTGTTCCCGCCCTCCTCT GAGGAGCTCCAAGCCAACAAGGCCACACTAGTGT GTCTGATCAGTGACTTCTACCCGGGAGCTGTGAC AGTGGCCTGGAAGGCAGATGGCAGCCCCGTCAAG GCGGGAGTGGAGACCACCAAACCCTCCAAACAG AGCAACAACAAGTACGCGGCCAAGAGCTACCTGA GCCTGACGCCCGAGCAGTGGAAGTCCCACAGAAG CTACAGCTGCCAGGTCACGCATGAAGGGAGCACC GTGGAGAAGACAGTGGCCCCTACAGAATGTTCA (SEQ ID NO: 285)
51B	LC-104	QSVLTQSPSASGTPGQRVTI SCSGSSSNIGSNYVYWYQQ LPGAAPKLLILRNNQRPSGV PDRFSGSKSGTSASLTISGL RSEDEADYYCAAWDDSLS GWVFGKGTKLTVLGQPKA NPTVTLFPPSSEELQANKAT LVCLISDFYPGAVTVAWKA DGSPVKAGVETTKPSKQSN NKYAAKSYLSLTPEQWKSH RSYSCQVTHEGSTVEKTVA PTECS (SEQ ID NO: 274)	CAGTCTGTGCTGACTCAGTCACCCTCAGCGTCTGG GACCCCCGGGCAGAGAGTCACCATCTCTTGTTCT GGAAGCAGCTCCAACATCGGCAGTAATTATGTAT ACTGGTACCAGCAGCTCCCAGGAGCGGCCCCCAA ACTCCTCATCCTTAGGAATAATCAGCGGCCCTCA GGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGG CACCTCAGCCTCCCTGACCATCAGTGGGCTCCGGT CCGAGGATGAGGCTGACTATTATTGTGCAGCATG GGATGACAGCCTGAGTGGTTGGGTGTTCGGCAAG GGGACCAAGCTGACCGTCCTAGGTCAGCCCAAGG CCAACCCCACTGTCACTCTGTTCCCGCCCTCCTCT GAGGAGCTCCAAGCCAACAAGGCCACACTAGTGT GTCTGATCAGTGACTTCTACCCGGGAGCTGTGAC AGTGGCCTGGAAGGCAGATGGCAGCCCCGTCAAG GCGGGAGTGGAGACCACCAAACCCTCCAAACAG AGCAACAACAAGTACGCGGCCAAGAGCTACCTGA GCCTGACGCCCGAGCAGTGGAAGTCCCACAGAAG CTACAGCTGCCAGGTCACGCATGAAGGGAGCACC GTGGAGAAGACAGTGGCCCCTACAGAATGTTCA (SEQ ID NO: 286)
52A, 52C, 52D, 53A, 53C	LC-105	QSVLTQPPSVSAAPGQKVTI SCSGSSSNIGNNYVSWYQQ LPGTAPKLLIYDNNKRPSGI PDRFSGSKSGTSTTLGITGL QTGDEADYYCGTWDSRLS AVVFGGGTKLTVLGQPKA NPTVTLFPPSSEELQANKAT LVCLISDFYPGAVTVAWKA DGSPVKAGVETTKPSKQSN NKYAAKSYLSLTPEQWKSH RSYSCQVTHEGSTVEKTVA PTECS (SEQ ID NO: 275)	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGC GGCCCCAGGACAGAAGGTCACCATCTCCTGCTCT GGAAGCAGCTCCAACATTGGGAATAATTATGTAT CCTGGTACCAGCAGCTCCCAGGAACAGCCCCCAA ACTCCTCATTTATGACAATAATAAGCGACCCTCA GGGATTCCTGACCGATTCTCTGGCTCCAAGTCTGG CACGTCAACCACCCTGGGCATCACCGGACTCCAG ACTGGGGACGAGGCCGATTATTACTGCGGAACAT GGGATAGCCGCCTGAGTGCTGTGGTTTTCGGCGG AGGGACCAAGCTGACCGTCCTAGGTCAGCCCAAG GCCAACCCCACTGTCACTCTGTTCCCGCCCTCCTC TGAGGAGCTCCAAGCCAACAAGGCCACACTAGTG TGTCTGATCAGTGACTTCTACCCGGGAGCTGTGAC

Antibody ID.	LC Group	Light Chain Amino Acid Sequence	Light Chain Nucleic Acid Sequence
			AGTGGCCTGGAAGGCAGATGGCAGCCCCGTCAAG GCGGGAGTGGAGACCACCAAACCCTCCAAACAG AGCAACAACAAGTACGCGGCCAAGAGCTACCTGA GCCTGACGCCCGAGCAGTGGAAGTCCCACAGAAG CTACAGCTGCCAGGTCACGCATGAAGGGAGCACC GTGGAGAAGACAGTGGCCCCTACAGAATGTTCA (SEQ ID NO: 287)
52B, 53B	LC-106	QSVLTQPPSVSAAPGQKVTI SCSGSSSNIGNNYVSWYQQ LPGTAPKLLIYDNNKRPSGI PDRFSGSKSGTSTTLGITGL QTGDEADYYCGTWDSRLS AVVFGKGTKLTVLGQPKA NPTVTLFPPSSEELQANKAT LVCLISDFYPGAVTVAWKA DGSPVKAGVETTKPSKQSN NKYAAKSYLSLTPEQWKSH RSYSCQVTHEGSTVEKTVA PTECS (SEQ ID NO: 276)	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGC GGCCCCAGGACAGAAGGTCACCATCTCCTGCTCT GGAAGCAGCTCCAACATTGGGAATAATTATGTAT CCTGGTACCAGCAGCTCCCAGGAACAGCCCCCAA ACTCCTCATTTATGACAATAATAAGCGACCCTCA GGGATTCCTGACCGATTCTCTGGCTCCAAGTCTGG CACGTCAACCACCCTGGGCATCACCGGACTCCAG ACTGGGGACGAGGCCGATTATTACTGCGGAACAT GGGATAGCCGCCTGAGTGCTGTGGTTTTCGGCAA GGGGACCAAGCTGACCGTCCTAGGTCAGCCCAAG GCCAACCCCACTGTCACTCTGTTCCCGCCCTCCTC TGAGGAGCTCCAAGCCAACAAGGCCACACTAGTG TGTCTGATCAGTGACTTCTACCCGGGAGCTGTGAC AGTGGCCTGGAAGGCAGATGGCAGCCCCGTCAAG GCGGGAGTGGAGACCACCAAACCCTCCAAACAG AGCAACAACAAGTACGCGGCCAAGAGCTACCTGA GCCTGACGCCCGAGCAGTGGAAGTCCCACAGAAG CTACAGCTGCCAGGTCACGCATGAAGGGAGCACC GTGGAGAAGACAGTGGCCCCTACAGAATGTTCA (SEQ ID NO: 288)
54A, 54C, 56A, 56C	LC-107	QSVLTQPPSVSAAPGQKVTI SCSGSSSNIGNNYVSWYQQ LPGTAPKLLIYDNNKRPSGI PDRFSGSKSGTSATLGITGL QTGDEADYYCGTWDSRLS AVVFGGGTKLTVLGQPKA NPTVTLFPPSSEELQANKAT LVCLISDFYPGAVTVAWKA DGSPVKAGVETTKPSKQSN NKYAAKSYLSLTPEQWKSH RSYSCQVTHEGSTVEKTVA PTECS (SEQ ID NO: 277)	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGC GGCCCCAGGACAGAAGGTCACCATCTCCTGCTCT GGAAGCAGCTCCAACATTGGGAATAATTATGTAT CCTGGTACCAGCAGCTCCCAGGAACAGCCCCCAA ACTCCTCATTTATGACAATAATAAGCGACCCTCA GGGATTCCTGACCGATTCTCTGGCTCCAAGTCTGG CACGTCAGCCACCCTGGGCATCACCGGACTCCAG ACTGGGGACGAGGCCGATTATTACTGCGGAACAT GGGATAGCCGCCTGAGTGCTGTGGTTTTCGGCGG AGGGACCAAGCTGACCGTCCTAGGTCAGCCCAAG GCCAACCCCACTGTCACTCTGTTCCCGCCCTCCTC TGAGGAGCTCCAAGCCAACAAGGCCACACTAGTG TGTCTGATCAGTGACTTCTACCCGGGAGCTGTGAC AGTGGCCTGGAAGGCAGATGGCAGCCCCGTCAAG GCGGGAGTGGAGACCACCAAACCCTCCAAACAG AGCAACAACAAGTACGCGGCCAAGAGCTACCTGA GCCTGACGCCCGAGCAGTGGAAGTCCCACAGAAG CTACAGCTGCCAGGTCACGCATGAAGGGAGCACC GTGGAGAAGACAGTGGCCCCTACAGAATGTTCA (SEQ ID NO: 289)
54B, 56B	LC-108	QSVLTQPPSVSAAPGQKVTI SCSGSSSNIGNNYVSWYQQ LPGTAPKLLIYDNNKRPSGI PDRFSGSKSGTSATLGITGL QTGDEADYYCGTWDSRLS AVVFGKGTKLTVLGQPKA NPTVTLFPPSSEELQANKAT	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGC GGCCCCAGGACAGAAGGTCACCATCTCCTGCTCT GGAAGCAGCTCCAACATTGGGAATAATTATGTAT CCTGGTACCAGCAGCTCCCAGGAACAGCCCCCAA ACTCCTCATTTATGACAATAATAAGCGACCCTCA GGGATTCCTGACCGATTCTCTGGCTCCAAGTCTGG CACGTCAGCCACCCTGGGCATCACCGGACTCCAG

Antibody ID.	LC Group	Light Chain Amino Acid Sequence	Light Chain Nucleic Acid Sequence
		LVCLISDFYPGAVTVAWKA DGSPVKAGVETTKPSKQSN NKYAAKSYLSLTPEQWKSH RSYSCQVTHEGSTVEKTVA PTECS (SEQ ID NO: 278)	ACTGGGGACGAGGCCGATTATTACTGCGGAACAT GGGATAGCCGCCTGAGTGCTGTGGTTTTCGGCAA GGGGACCAAGCTGACCGTCCTAGGTCAGCCCAAG GCCAACCCCACTGTCACTCTGTTCCCGCCCTCCTC TGAGGAGCTCCAAGCCAACAAGGCCACACTAGTG TGTCTGATCAGTGACTTCTACCCGGGAGCTGTGAC AGTGGCCTGGAAGGCAGATGGCAGCCCCGTCAAG GCGGGAGTGGAGACCACCAAACCCTCCAAACAG AGCAACAACAAGTACGCGGCCAAGAGCTACCTGA GCCTGACGCCCGAGCAGTGGAAGTCCCACAGAAG CTACAGCTGCCAGGTCACGCATGAAGGGAGCACC GTGGAGAAGACAGTGGCCCCTACAGAATGTTCA (SEQ ID NO: 290)
55A, 55C	LC-109	QSVLTQPPSVSAAPGQKVTI SCSGSSSNIGNNYVSWYQQ LPGTAPKLLIYDNNKRPSGI PDRFSGSKSGTSATLAITGL QTGDEADYYCGTWDSRLS AVVFGGGTKLTVLGQPKA NPTVTLFPPSSEELQANKAT LVCLISDFYPGAVTVAWKA DGSPVKAGVETTKPSKQSN NKYAAKSYLSLTPEQWKSH RSYSCQVTHEGSTVEKTVA PTECS (SEQ ID NO: 279)	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGC GGCCCCAGGACAGAAGGTCACCATCTCCTGCTCT GGAAGCAGCTCCAACATTGGGAATAATTATGTAT CCTGGTACCAGCAGCTCCCAGGAACAGCCCCCAA ACTCCTCATTTATGACAATAATAAGCGACCCTCA GGGATTCCTGACCGATTCTCTGGCTCCAAGTCTGG CACGTCAGCCACCCTGGCCATCACCGGACTCCAG ACTGGGGACGAGGCCGATTATTACTGCGGAACAT GGGATAGCCGCCTGAGTGCTGTGGTTTTCGGCGG AGGGACCAAGCTGACCGTCCTAGGTCAGCCCAAG GCCAACCCCACTGTCACTCTGTTCCCGCCCTCCTC TGAGGAGCTCCAAGCCAACAAGGCCACACTAGTG TGTCTGATCAGTGACTTCTACCCGGGAGCTGTGAC AGTGGCCTGGAAGGCAGATGGCAGCCCCGTCAAG GCGGGAGTGGAGACCACCAAACCCTCCAAACAG AGCAACAACAAGTACGCGGCCAAGAGCTACCTGA GCCTGACGCCCGAGCAGTGGAAGTCCCACAGAAG CTACAGCTGCCAGGTCACGCATGAAGGGAGCACC GTGGAGAAGACAGTGGCCCCTACAGAATGTTCA (SEQ ID NO: 291)
55B	LC-110	QSVLTQPPSVSAAPGQKVTI SCSGSSSNIGNNYVSWYQQ LPGTAPKLLIYDNNKRPSGI PDRFSGSKSGTSATLAITGL QTGDEADYYCGTWDSRLS AVVFGKGTKLTVLGQPKA NPTVTLFPPSSEELQANKAT LVCLISDFYPGAVTVAWKA DGSPVKAGVETTKPSKQSN NKYAAKSYLSLTPEQWKSH RSYSCQVTHEGSTVEKTVA PTECS (SEQ ID NO: 280)	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGC GGCCCCAGGACAGAAGGTCACCATCTCCTGCTCT GGAAGCAGCTCCAACATTGGGAATAATTATGTAT CCTGGTACCAGCAGCTCCCAGGAACAGCCCCCAA ACTCCTCATTTATGACAATAATAAGCGACCCTCA GGGATTCCTGACCGATTCTCTGGCTCCAAGTCTGG CACGTCAGCCACCCTGGCCATCACCGGACTCCAG ACTGGGGACGAGGCCGATTATTACTGCGGAACAT GGGATAGCCGCCTGAGTGCTGTGGTTTTCGGCAA GGGGACCAAGCTGACCGTCCTAGGTCAGCCCAAG GCCAACCCCACTGTCACTCTGTTCCCGCCCTCCTC TGAGGAGCTCCAAGCCAACAAGGCCACACTAGTG TGTCTGATCAGTGACTTCTACCCGGGAGCTGTGAC AGTGGCCTGGAAGGCAGATGGCAGCCCCGTCAAG GCGGGAGTGGAGACCACCAAACCCTCCAAACAG AGCAACAACAAGTACGCGGCCAAGAGCTACCTGA GCCTGACGCCCGAGCAGTGGAAGTCCCACAGAAG CTACAGCTGCCAGGTCACGCATGAAGGGAGCACC GTGGAGAAGACAGTGGCCCCTACAGAATGTTCA (SEQ ID NO: 292)
57A, 57C,	LC-111	EIVLTQSPGTLSLSPGERAT	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGT

Antibody ID.	LC Group	Light Chain Amino Acid Sequence	Light Chain Nucleic Acid Sequence
57D, 58A, 58C		LSCRASQSVSSGYLTWYQQ KPGQAPRLLIYGASSRATGI PDRFSGSGSGTDFTLTISRLE PEDFAVYYCQQYGNSLSRF GQGTKLEIKRTVAAPSVFIF PPSDEQLKSGTASVVCLLN NFYPREAKVQWKVDNALQ SGNSQESVTEQDSKDSTYS LKSTLTLSKADYEKHKVYA CEVTHQGLSSPVTKSFNRG EC (SEQ ID NO: 281)	CTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGC AGGGCCAGTCAGAGTGTTAGCAGCGGCTACTTAA CCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAG ACTCCTCATCTATGGTGCATCCAGCAGGGCCACT GGCATCCCAGACAGGTTCAGTGGCAGTGGGTCTG GGACGGACTTCACTCTCACCATCAGCAGACTGGA GCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGT ATGGTAACTCACTGAGCAGGTTTGGCCAGGGGAC CAAGCTGGAAATCAAACGTACGGTGGCTGCACCA TCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTT GAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGA ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTG GAAGGTGGATAACGCCCTCCAATCGGGTAACTCC CAGGAGAGTGTCACAGAGCAGGACAGCAAGGAC AGCACCTACAGCCTCAAGAGCACCCTGACGCTGA GCAAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCC CGTCACAAAGAGCTTCAACAGGGGAGAGTGT (SEQ ID NO: 293)
57B, 58B	LC-112	EIVLTQSPGTLSLSPGERAT LSCRASQSVSSGYLTWYQQ KPGQAPRLLIYGASSRATGI PDRFSGSGSGTDFTLTISRLE PEDFAVYYCQQYGNSLSRF GKGTKLEIKRTVAAPSVFIF PPSDEQLKSGTASVVCLLN NFYPREAKVQWKVDNALQ SGNSQESVTEQDSKDSTYS LKSTLTLSKADYEKHKVYA CEVTHQGLSSPVTKSFNRG EC (SEQ ID NO: 282)	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGT CTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGC AGGGCCAGTCAGAGTGTTAGCAGCGGCTACTTAA CCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAG ACTCCTCATCTATGGTGCATCCAGCAGGGCCACT GGCATCCCAGACAGGTTCAGTGGCAGTGGGTCTG GTACGGACTTCACTCTCACCATCAGCAGACTGGA GCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGT ATGGTAACTCACTGAGCAGGTTTGGCAAGGGGAC CAAGCTGGAGATCAAACGTACGGTGGCTGCACCA TCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTT GAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGA ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTG GAAGGTGGATAACGCCCTCCAATCGGGTAACTCC CAGGAGAGTGTCACAGAGCAGGACAGCAAGGAC AGCACCTACAGCCTCAAGAGCACCCTGACGCTGA GCAAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCC CGTCACAAAGAGCTTCAACAGGGGAGAGTGT (SEQ ID NO: 294)

Table 7B. Exemplary Anti-CGRP Receptor Heavy Chain Sequences

Antibody ID.	HC Group	Heavy Chain Amino Acid Sequence	Heavy Chain Nucleic Acid Sequence
50A	HC-101	EVQLVESGGGLVKPGGSL RLSCAASGFTFGNAWMS WVRQAPGKGLEWVGRIKS KTDGGTTDYAAPVKGRFT ISRDDSKNTLYLQMNSLKT EDTAVYFCTTDRTGYSISW SSYYYYYGMDVWGQGTT VTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDY	GAGGTACAGCTGGTGGAGTCTGGGGGAGGCTTGG TAAAGCCTGGGGGGTCCCTCAGACTCTCCTGTGC AGCCTCTGGATTCACTTTCGGTAACGCCTGGATGA GCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGA GTGGGTTGGCCGTATTAAAAGCAAAACTGATGGT GGGACAACAGACTACGCTGCACCCGTGAAAGGCA GATTCACCATCTCAAGAGATGATTCAAAAAACAC GCTGTATCTGCAAATGAACAGCCTGAAAACCGAG GACACAGCCGTGTATTTCTGTACCACAGATCGGA

Antibody ID.	HC Group	Heavy Chain Amino Acid Sequence	Heavy Chain Nucleic Acid Sequence
		FPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLESVV TVPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSCDKT HTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQY GSTYRCVSVLTVLHQDWL NGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTL PPSRKEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPE NNYKTTPPVLKSDGSFFLY SKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSL SPGK (SEQ ID NO: 295)	CCGGGTATAGCATCAGCTGGTCTAGTTACTACTAC TACTACGGTATGGACGTCTGGGGCCAAGGAACAA CAGTTACCGTCTCTAGTGCCTCCACCAAGGGCCC ATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCA CCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGT CAAGGACTACTTCCCCGAACCGGTGACGGTGTCG TGGAACTCAGGCGCCCTGACCAGCGGCGTGCACA CCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTAC TCCCTCGAGAGCGTGGTGACCGTGCCCTCCAGCA GCTTGGGCACCCAGACCTACATCTGCAACGTGAA TCACAAGCCCAGCAACACCAAGGTGGACAAGAA AGTTGAGCCCAAATCTTGTGACAAAACTCACACA TGCCCACCGTGCCCAGCACCTGAACTCCTGGGGG GACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG GACACCCTCATGATCTCCCGGACCCCTGAGGTCA CATGCGTGGTGGTGGACGTGAGCCACGAAGACCC TGAGGTCAAGTTCAACTGGTACGTGGACGGCGTG GAGGTGCATAATGCCAAGACAAAGCCGTGCGAG GAGCAGTACGGCAGCACGTACCGTTGCGTCAGCG TCCTCACCGTCCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCC CTCCCAGCCCCCATCGAGAAAACCATCTCCAAAG CCAAAGGGCAGCCCCGAGAACCACAGGTGTACAC CCTGCCCCCATCCCGGAAGGAGATGACCAAGAAC CAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCT ATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAA TGGGCAGCCGGAGAACAACTACAAGACCACGCCT CCCGTGCTGAAGTCCGACGGCTCCTTCTTCCTCTA TAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCATG AGGCTCTGCACAACCACTACACGCAGAAGAGCCT CTCCCTGTCTCCGGGTAAA (SEQ ID NO: 317)
50B	HC-102	EVQLVESGGGLVKPGGSL RLSCAASGFTFGNAWMS WVRQAPGKELEWVGRIKS KTDGGTTDYAAPVKGRFT ISRDDSKNTLYLQMNSLKT EDTAVYFCTTDRTGYSISW SSYYYYYGMDVWGQGTT VTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLESVV TVPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSCDKT HTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQY GSTYRCVSVLTVLHQDWL NGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTL PPSRKEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPE	GAGGTACAGCTGGTGGAGTCTGGGGGAGGCTTGG TAAAGCCTGGGGGGTCCCTCAGACTCTCCTGTGC AGCCTCTGGATTCACTTTCGGTAACGCCTGGATGA GCTGGGTCCGCCAGGCTCCAGGGAAGGAGCTGGA GTGGGTTGGCCGTATTAAAAGCAAAACTGATGGT GGGACAACAGACTACGCTGCACCCGTGAAAGGCA GATTCACCATCTCAAGAGATGATTCAAAAAACAC GCTGTATCTGCAAATGAACAGCCTGAAAACCGAG GACACAGCCGTGTATTTCTGTACCACAGATCGGA CCGGGTATAGCATCAGCTGGTCTAGTTACTACTAC TACTACGGTATGGACGTCTGGGGCCAAGGAACAA CAGTTACCGTCTCTAGTGCCTCCACCAAGGGCCC ATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCA CCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGT CAAGGACTACTTCCCCGAACCGGTGACGGTGTCG TGGAACTCAGGCGCCCTGACCAGCGGCGTGCACA CCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTAC TCCCTCGAGAGCGTGGTGACCGTGCCCTCCAGCA GCTTGGGCACCCAGACCTACATCTGCAACGTGAA TCACAAGCCCAGCAACACCAAGGTGGACAAGAA AGTTGAGCCCAAATCTTGTGACAAAACTCACACA TGCCCACCGTGCCCAGCACCTGAACTCCTGGGGG

Antibody ID.	HC Group	Heavy Chain Amino Acid Sequence	Heavy Chain Nucleic Acid Sequence
		NNYKTTPPVLKSDGSFFLY SKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSL SPGK (SEQ ID NO: 296)	GACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG GACACCCTCATGATCTCCCGGACCCCTGAGGTCA CATGCGTGGTGGTGGACGTGAGCCACGAAGACCC TGAGGTCAAGTTCAACTGGTACGTGGACGGCGTG GAGGTGCATAATGCCAAGACAAAGCCGTGCGAG GAGCAGTACGGCAGCACGTACCGTTGCGTCAGCG TCCTCACCGTCCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCC CTCCCAGCCCCCATCGAGAAAACCATCTCCAAAG CCAAAGGGCAGCCCCGAGAACCACAGGTGTACAC CCTGCCCCCATCCCGGAAGGAGATGACCAAGAAC CAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCT ATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAA TGGGCAGCCGGAGAACAACTACAAGACCACGCCT CCCGTGCTGAAGTCCGACGGCTCCTTCTTCCTCTA TAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCATG AGGCTCTGCACAACCACTACACGCAGAAGAGCCT CTCCCTGTCTCCGGGTAAA (SEQ ID NO: 318)
50C	HC-103	EVQLVESGGGLVKPGGSL RLSCAASGFTFGNAWMS WVRQAPGKGLEWVGRIKS KTDGGTTDYAAPVKGRFT ISRDDSKNTLYLQMNSLKT EDTAVYFCTTDRTGYSISW SSYYYYYGMDVWGQGTT VTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLESVV TVPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSCDKT HTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQY GSTYRCVSVLTVLHQDWL NGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTL PPSRKKMTKNQVSLTCLV KGFYPSDIAVEWESNGQPE NNYKTTPPVLKSDGSFFLY SKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSL SPGK (SEQ ID NO: 297)	GAGGTACAGCTGGTGGAGTCTGGGGGAGGCTTGG TAAAGCCTGGGGGGGTCCCTCAGACTCTCCTGTGC AGCCTCTGGATTCACTTTCGGTAACGCCTGGATGA GCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGA GTGGGTTGGCCGTATTAAAAGCAAAACTGATGGT GGGACAACAGACTACGCTGCACCCGTGAAAGGCA GATTCACCATCTCAAGAGATGATTCAAAAAACAC GCTGTATCTGCAAATGAACAGCCTGAAAACCGAG GACACAGCCGTGTATTTCTGTACCACAGATCGGA CCGGGTATAGCATCAGCTGGTCTAGTTACTACTAC TACTACGGTATGGACGTCTGGGGCCAAGGAACAA CAGTTACCGTCTCTAGTGCCTCCACCAAGGGCCC ATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCA CCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGT CAAGGACTACTTCCCCGAACCGGTGACGGTGTCG TGGAACTCAGGCGCCCTGACCAGCGGCGTGCACA CCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTAC TCCCTCGAGAGCGTGGTGACCGTGCCCTCCAGCA GCTTGGGCACCCAGACCTACATCTGCAACGTGAA TCACAAGCCCAGCAACACCAAGGTGGACAAGAA AGTTGAGCCCAAATCTTGTGACAAAACTCACACA TGCCCACCGTGCCCAGCACCTGAACTCCTGGGGG GACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG GACACCCTCATGATCTCCCGGACCCCTGAGGTCA CATGCGTGGTGGTGGACGTGAGCCACGAAGACCC TGAGGTCAAGTTCAACTGGTACGTGGACGGCGTG GAGGTGCATAATGCCAAGACAAAGCCGTGCGAG GAGCAGTACGGCAGCACGTACCGTTGCGTCAGCG TCCTCACCGTCCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCC CTCCCAGCCCCCATCGAGAAAACCATCTCCAAAG CCAAAGGGCAGCCCCGAGAACCACAGGTGTACAC CCTGCCCCCATCCCGGAAGAAGATGACCAAGAAC CAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCT ATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAA

Antibody ID.	HC Group	Heavy Chain Amino Acid Sequence	Heavy Chain Nucleic Acid Sequence
			TGGGCAGCCGGAGAACAACTACAAGACCACGCCT CCCGTGCTGAAGTCCGACGGCTCCTTCTTCCTCTA TAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCATG AGGCTCTGCACAACCACTACACGCAGAAGAGCCT CTCCCTGTCTCCGGGTAAA (SEQ ID NO: 319)
50D	HC-104	EVQLVESGGGLVKPGGSL RLSCAASGFTFGNAWMS WVRQAPGKGLEWVGRIKS KTDGGTTDYAAPVKGRFT ISRDDSKNTLYLQMNSLKT EDTAVYFCTTDRTGYSISW SSYYYYYGMDVWGQGTT VTVSSASTKGPSVFPLAPC SRSTSESTAALGCLVKDYF PEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLESVVT VPSSNFGTQTYTCNVDHK PSNTKVDKTVERKCCVEC PPCPAPPVAGPSVFLFPPKP KDTLMISRTPEVTCVVVD VSHEDPEVQFNWYVDGVE VHNAKTKPREEQFNSTFR VVSVLTVVHQDWLNGKE YKCKVSNKGLPAPIEKTIS KTKGQPREPQVYTLPPSRK KMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYK TTPPMLKSDGSFFLYSKLT VDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPG K (SEQ ID NO: 298)	GAGGTACAGCTGGTGGAGTCTGGGGGAGGCTTGG TAAAGCCTGGGGGGTCCCTCAGACTCTCCTGTGC AGCCTCTGGATTCACTTTCGGTAACGCCTGGATGA GCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGA GTGGGTTGGCCGTATTAAAAGCAAAACTGATGGT GGGACAACAGACTACGCTGCACCCGTGAAAGGCA GATTCACCATCTCAAGAGATGATTCAAAAAACAC GCTGTATCTGCAAATGAACAGCCTGAAAACCGAG GACACAGCCGTGTATTTCTGTACCACAGATCGGA CCGGGTATAGCATCAGCTGGTCTAGTTACTACTAC TACTACGGTATGGACGTCTGGGGCCAAGGAACAA CAGTTACCGTCTCTAGTGCCTCCACCAAGGGCCC ATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCA CCTCCGAGAGCACAGCGGCCCTGGGCTGCCTGGT CAAGGACTACTTCCCCGAACCGGTGACGGTGTCG TGGAACTCAGGCGCTCTGACCAGCGGCGTGCACA CCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTAC TCCCTGGAGAGCGTGGTGACCGTGCCCTCCAGCA ACTTCGGCACCCAGACCTACACCTGCAACGTAGA TCACAAGCCCAGCAACACCAAGGTGGACAAGAC AGTTGAGCGCAAATGTTGTGTCGAGTGCCCACCG TGCCCAGCACCACCTGTGGCAGGACCGTCAGTCT TCCTCTTCCCCCCAAAACCCAAGGACACCCTCATG ATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGG TGGACGTGAGCCACGAAGACCCCGAGGTCCAGTT CAACTGGTACGTGGACGGCGTGGAGGTGCATAAT GCCAAGACAAAGCCACGGGAGGAGCAGTTCAAC AGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGT GCACCAGGACTGGCTGAACGGCAAGGAGTACAA GTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCC ATCGAGAAAACCATCTCCAAAACCAAAGGGCAGC CCCGAGAACCACAGGTGTACACCCTGCCCCCATC CCGGAAGAAGATGACCAAGAACCAGGTCAGCCT GACCTGCCTGGTCAAAGGCTTCTACCCCAGCGAC ATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCG GAGAACAACTACAAGACCACACCTCCCATGCTGA AGTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTC ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAAC GTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCA CAACCACTACACGCAGAAGAGCCTCTCCCTGTCT CCGGGTAAA (SEQ ID NO: 320)
51A	HC-105	EVQLVESGGGLVKPGGSL RLSCAASGFTFSNAWMSW VRQAPGKGLEWVGRIKSK TDGGTTDYTAPVKGRFTIS RDDSKNTLYLQMNSLKAE DTAVYYCTTDRTGYSISW SSYYYYYGMDVWGQGTT	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGG TAAAGCCTGGGGGGTCCCTTAGACTCTCCTGTGC AGCCTCTGGATTCACTTTCAGTAACGCCTGGATGA GCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGA GTGGGTTGGCCGTATTAAAAGCAAAACTGATGGT GGGACAACAGACTACACTGCACCCGTGAAAGGCA GATTCACCATCTCAAGAGATGATTCAAAAAACAC

Antibody ID.	HC Group	Heavy Chain Amino Acid Sequence	Heavy Chain Nucleic Acid Sequence
		VTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLESVV TVPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSCDKT HTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQY GSTYRCVSVLTVLHQDWL NGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTL PPSRKEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPE NNYKTTPPVLKSDGSFFLY SKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSL SPGK (SEQ ID NO: 299)	GCTGTATCTGCAAATGAATAGCCTGAAAGCCGAG GACACAGCCGTGTATTACTGTACCACAGATCGGA CCGGGTATAGCATCAGCTGGTCTAGTTACTACTAC TACTACGGTATGGACGTCTGGGGCCAAGGGACAA CAGTTACCGTCTCTAGTGCCTCCACCAAGGGCCC ATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCA CCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGT CAAGGACTACTTCCCCGAACCGGTGACGGTGTCG TGGAACTCAGGCGCCCTGACCAGCGGCGTGCACA CCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTAC TCCCTCGAGAGCGTGGTGACCGTGCCCTCCAGCA GCTTGGGCACCCAGACCTACATCTGCAACGTGAA TCACAAGCCCAGCAACACCAAGGTGGACAAGAA AGTTGAGCCCAAATCTTGTGACAAAACTCACACA TGCCCACCGTGCCCAGCACCTGAACTCCTGGGGG GACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG GACACCCTCATGATCTCCCGGACCCCTGAGGTCA CATGCGTGGTGGTGGACGTGAGCCACGAAGACCC TGAGGTCAAGTTCAACTGGTACGTGGACGGCGTG GAGGTGCATAATGCCAAGACAAAGCCGTGCGAG GAGCAGTACGGCAGCACGTACCGTTGCGTCAGCG TCCTCACCGTCCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCC CTCCCAGCCCCCATCGAGAAAACCATCTCCAAAG CCAAAGGGCAGCCCCGAGAACCACAGGTGTACAC CCTGCCCCCATCCCGGAAGGAGATGACCAAGAAC CAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCT ATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAA TGGGCAGCCGGAGAACAACTACAAGACCACGCCT CCCGTGCTGAAGTCCGACGGCTCCTTCTTCCTCTA TAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCATG AGGCTCTGCACAACCACTACACGCAGAAGAGCCT CTCCCTGTCTCCGGGTAAA (SEQ ID NO: 321)
51B	HC-106	EVQLVESGGGLVKPGGSL RLSCAASGFTFSNAWMSW VRQAPGKELEWVGRIKSK TDGGTTDYTAPVKGRFTIS RDDSKNTLYLQMNSLKAE DTAVYYCTTDRTGYSISW SSYYYYYGMDVWGQGTT VTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLESVV TVPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSCDKT HTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQY GSTYRCVSVLTVLHQDWL NGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTL	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGG TAAAGCCTGGGGGGTCCCTTAGACTCTCCTGTGC AGCCTCTGGATTCACTTTCAGTAACGCCTGGATGA GCTGGGTCCGCCAGGCTCCAGGGAAGGAGCTGGA GTGGGTTGGCCGTATTAAAAGCAAAACTGATGGT GGGACAACAGACTACACTGCACCCGTGAAAGGCA GATTCACCATCTCAAGAGATGATTCAAAAAACAC GCTGTATCTGCAAATGAATAGCCTGAAAGCCGAG GACACAGCCGTGTATTACTGTACCACAGATCGGA CCGGGTATAGCATCAGCTGGTCTAGTTACTACTAC TACTACGGTATGGACGTCTGGGGCCAAGGAACAA CAGTTACCGTCTCTAGTGCCTCCACCAAGGGCCC ATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCA CCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGT CAAGGACTACTTCCCCGAACCGGTGACGGTGTCG TGGAACTCAGGCGCCCTGACCAGCGGCGTGCACA CCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTAC TCCCTCGAGAGCGTGGTGACCGTGCCCTCCAGCA GCTTGGGCACCCAGACCTACATCTGCAACGTGAA TCACAAGCCCAGCAACACCAAGGTGGACAAGAA

Antibody ID.	HC Group	Heavy Chain Amino Acid Sequence	Heavy Chain Nucleic Acid Sequence
		PPSRKEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPE NNYKTTPPVLKSDGSFFLY SKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSL SPGK (SEQ ID NO: 300)	AGTTGAGCCCAAATCTTGTGACAAAACTCACACA TGCCCACCGTGCCCAGCACCTGAACTCCTGGGGG GACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG GACACCCTCATGATCTCCCGGACCCCTGAGGTCA CATGCGTGGTGGTGGACGTGAGCCACGAAGACCC TGAGGTCAAGTTCAACTGGTACGTGGACGGCGTG GAGGTGCATAATGCCAAGACAAAGCCGTGCGAG GAGCAGTACGGCAGCACGTACCGTTGCGTCAGCG TCCTCACCGTCCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCC CTCCCAGCCCCCATCGAGAAAACCATCTCCAAAG CCAAAGGGCAGCCCCGAGAACCACAGGTGTACAC CCTGCCCCCATCCCGGAAGGAGATGACCAAGAAC CAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCT ATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAA TGGGCAGCCGGAGAACAACTACAAGACCACGCCT CCCGTGCTGAAGTCCGACGGCTCCTTCTTCCTCTA TAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCATG AGGCTCTGCACAACCACTACACGCAGAAGAGCCT CTCCCTGTCTCCGGGTAAA (SEQ ID NO: 322)
51C	HC-107	EVQLVESGGGLVKPGGSL RLSCAASGFTFSNAWMSW VRQAPGKGLEWVGRIKSK TDGGTTDYTAPVKGRFTIS RDDSKNTLYLQMNSLKAE DTAVYYCTTDRTGYSISW SSYYYYYGMDVWGQGTT VTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLESVV TVPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSCDKT HTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQY GSTYRCVSVLTVLHQDWL NGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTL PPSRKKMTKNQVSLTCLV KGFYPSDIAVEWESNGQPE NNYKTTPPVLKSDGSFFLY SKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSL SPGK (SEQ ID NO: 301)	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGG TAAAGCCTGGGGGGTCCCTTAGACTCTCCTGTGC AGCCTCTGGATTCACTTTCAGTAACGCCTGGATGA GCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGA GTGGGTTGGCCGTATTAAAAGCAAAACTGATGGT GGGACAACAGACTACACTGCACCCGTGAAAGGCA GATTCACCATCTCAAGAGATGATTCAAAAAACAC GCTGTATCTGCAAATGAATAGCCTGAAAGCCGAG GACACAGCCGTGTATTACTGTACCACAGATCGGA CCGGGTATAGCATCAGCTGGTCTAGTTACTACTAC TACTACGGTATGGACGTCTGGGGCCAAGGGACAA CAGTTACCGTCTCTAGTGCCTCCACCAAGGGCCC ATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCA CCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGT CAAGGACTACTTCCCCGAACCGGTGACGGTGTCG TGGAACTCAGGCGCCCTGACCAGCGGCGTGCACA CCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTAC TCCCTCGAGAGCGTGGTGACCGTGCCCTCCAGCA GCTTGGGCACCCAGACCTACATCTGCAACGTGAA TCACAAGCCCAGCAACACCAAGGTGGACAAGAA AGTTGAGCCCAAATCTTGTGACAAAACTCACACA TGCCCACCGTGCCCAGCACCTGAACTCCTGGGGG GACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG GACACCCTCATGATCTCCCGGACCCCTGAGGTCA CATGCGTGGTGGTGGACGTGAGCCACGAAGACCC TGAGGTCAAGTTCAACTGGTACGTGGACGGCGTG GAGGTGCATAATGCCAAGACAAAGCCGTGCGAG GAGCAGTACGGCAGCACGTACCGTTGCGTCAGCG TCCTCACCGTCCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCC CTCCCAGCCCCCATCGAGAAAACCATCTCCAAAG CCAAAGGGCAGCCCCGAGAACCACAGGTGTACAC CCTGCCCCCATCCCGGAAGAAGATGACCAAGAAC

Antibody ID.	HC Group	Heavy Chain Amino Acid Sequence	Heavy Chain Nucleic Acid Sequence
			CAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCT ATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAA TGGGCAGCCGGAGAACAACTACAAGACCACGCCT CCCGTGCTGAAGTCCGACGGCTCCTTCTTCCTCTA TAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCATG AGGCTCTGCACAACCACTACACGCAGAAGAGCCT CTCCCTGTCTCCGGGTAAA (SEQ ID NO: 323)
51D	HC-108	EVQLVESGGGLVKPGGSL RLSCAASGFTFSNAWMSW VRQAPGKGLEWVGRIKSK TDGGTTDYTAPVKGRFTIS RDDSKNTLYLQMNSLKAE DTAVYYCTTDRTGYSISW SSYYYYYGMDVWGQGTT VTVSSASTKGPSVFPLAPC SRSTSESTAALGCLVKDYF PEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLESVVT VPSSNFGTQTYTCNVDHK PSNTKVDKTVERKCCVEC PPCPAPPVAGPSVFLFPPKP KDTLMISRTPEVTCVVVD VSHEDPEVQFNWYVDGVE VHNAKTKPREEQFNSTFR VVSVLTVVHQDWLNGKE YKCKVSNKGLPAPIEKTIS KTKGQPREPQVYTLPPSRK KMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYK TTPPMLKSDGSFFLYSKLT VDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPG K (SEQ ID NO: 302)	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGG TAAAGCCTGGGGGGTCCCTTAGACTCTCCTGTGC AGCCTCTGGATTCACTTTCAGTAACGCCTGGATGA GCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGA GTGGGTTGGCCGTATTAAAAGCAAAACTGATGGT GGGACAACAGACTACACTGCACCCGTGAAAGGCA GATTCACCATCTCAAGAGATGATTCAAAAAACAC GCTGTATCTGCAAATGAATAGCCTGAAAGCCGAG GACACAGCCGTGTATTACTGTACCACAGATCGGA CCGGGTATAGCATCAGCTGGTCTAGTTACTACTAC TACTACGGTATGGACGTCTGGGGCCAAGGAACAA CAGTTACCGTCTCTAGTGCCTCCACCAAGGGCCC ATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCA CCTCCGAGAGCACAGCGGCCCTGGGCTGCCTGGT CAAGGACTACTTCCCCGAACCGGTGACGGTGTCG TGGAACTCAGGCGCTCTGACCAGCGGCGTGCACA CCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTAC TCCCTGGAGAGCGTGGTGACCGTGCCCTCCAGCA ACTTCGGCACCCAGACCTACACCTGCAACGTAGA TCACAAGCCCAGCAACACCAAGGTGGACAAGAC AGTTGAGCGCAAATGTTGTGTCGAGTGCCCACCG TGCCCAGCACCACCTGTGGCAGGACCGTCAGTCT TCCTCTTCCCCCCAAAACCCAAGGACACCCTCATG ATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGG TGGACGTGAGCCACGAAGACCCCGAGGTCCAGTT CAACTGGTACGTGGACGGCGTGGAGGTGCATAAT GCCAAGACAAAGCCACGGGAGGAGCAGTTCAAC AGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGT GCACCAGGACTGGCTGAACGGCAAGGAGTACAA GTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCC ATCGAGAAAACCATCTCCAAAACCAAAGGGCAGC CCCGAGAACCACAGGTGTACACCCTGCCCCCATC CCGGAAGAAGATGACCAAGAACCAGGTCAGCCT GACCTGCCTGGTCAAAGGCTTCTACCCCAGCGAC ATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCG GAGAACAACTACAAGACCACACCTCCCATGCTGA AGTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTC ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAAC GTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCA CAACCACTACACGCAGAAGAGCCTCTCCCTGTCT CCGGGTAAA (SEQ ID NO: 324)
52A, 54A, 55A	HC-109	QVQLVESGGGVVQPGRSL RLSCAASGFTFSSFGMHW VRQAPGKGLEWVAVISFD GSIKYSVDSVKGRFTISRD NSKNTLFLQMNSLRAEDT	CAGGTGCAGCTGGTGGAATCTGGGGGAGGCGTGG TCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGC AGCCTCTGGATTCACCTTCAGTAGCTTTGGCATGC ACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGA GTGGGTGGCAGTTATATCATTTGATGGAAGTATT

Antibody ID.	HC Group	Heavy Chain Amino Acid Sequence	Heavy Chain Nucleic Acid Sequence
		AVYYCARDRLNYYDSSGY YHYKYYGMAVWGQGTT VTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLESVV TVPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSCDKT HTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQY GSTYRCVSVLTVLHQDWL NGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTL PPSRKEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPE NNYKTTPPVLKSDGSFFLY SKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSL SPGK (SEQ ID NO: 303)	AAGTATTCTGTAGACTCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAATTCAAAGAACACGCTGTT TCTGCAAATGAACAGCCTGCGAGCCGAGGACACG GCTGTGTATTACTGTGCGAGAGATCGGCTCAATT ACTATGATAGTAGTGGTTATTATCACTACAAATAC TACGGTATGGCCGTCTGGGGCCAAGGGACAACAG TTACCGTCTCTAGTGCCTCCACCAAGGGCCCATCG GTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTC TGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAG GACTACTTCCCCGAACCGGTGACGGTGTCGTGGA ACTCAGGCGCCCTGACCAGCGGCGTGCACACCTT CCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCC TCGAGAGCGTGGTGACCGTGCCCTCCAGCAGCTT GGGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGACAAGAAAGTT GAGCCCAAATCTTGTGACAAAACTCACACATGCC CACCGTGCCCAGCACCTGAACTCCTGGGGGGACC GTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACA CCCTCATGATCTCCCGGACCCCTGAGGTCACATGC GTGGTGGTGGACGTGAGCCACGAAGACCCTGAGG TAAAGTTCAACTGGTACGTGGACGGCGTGGAGGT GCATAATGCCAAGACAAAGCCGTGCGAGGAGCA GTACGGCAGCACGTACCGTTGCGTCAGCGTCCTC ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGG AGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCC AGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA GGGCAGCCCCGAGAACCACAGGTGTACACCCTGC CCCCATCCCGGAAGGAGATGACCAAGAACCAGGT CAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA GCGACATCGCCGTGGAGTGGGAGAGCAATGGGC AGCCGGAGAACAACTACAAGACCACGCCTCCCGT GCTGAAGTCCGACGGCTCCTTCTTCCTCTATAGCA AGCTCACCGTGGACAAGAGCAGGTGGCAGCAGG GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT CTGCACAACCACTACACGCAGAAGAGCCTCTCCC TGTCTCCGGGTAAA (SEQ ID NO: 325)
52B, 54B, 55B	HC-110	QVQLVESGGGVVQPGRSL RLSCAASGFTFSSFGMHW VRQAPGKELEWVAVISFD GSIKYSVDSVKGRFTISRD NSKNTLFLQMNSLRAEDT AVYYCARDRLNYYDSSGY YHYKYYGMAVWGQGTT VTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLESVV TVPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSCDKT HTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQY GSTYRCVSVLTVLHQDWL	CAGGTGCAGCTGGTGGAATCTGGGGGAGGCGTGG TCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGC AGCCTCTGGATTCACCTTCAGTAGCTTTGGCATGC ACTGGGTCCGCCAGGCTCCAGGGAAGGAGCTGGA GTGGGTGGCAGTTATATCATTTGATGGAAGTATT AAGTATTCTGTAGACTCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAATTCAAAGAACACGCTGTT TCTGCAAATGAACAGCCTGCGAGCCGAGGACACG GCTGTGTATTACTGTGCGAGAGATCGGCTCAATT ACTATGATAGTAGTGGTTATTATCACTACAAATAC TACGGTATGGCCGTCTGGGGCCAAGGGACAACAG TTACCGTCTCTAGTGCCTCCACCAAGGGCCCATCG GTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTC TGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAG GACTACTTCCCCGAACCGGTGACGGTGTCGTGGA ACTCAGGCGCCCTGACCAGCGGCGTGCACACCTT CCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCC TCGAGAGCGTGGTGACCGTGCCCTCCAGCAGCTT

Antibody ID.	HC Group	Heavy Chain Amino Acid Sequence	Heavy Chain Nucleic Acid Sequence
		NGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTL PPSRKEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPE NNYKTTPPVLKSDGSFFLY SKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSL SPGK (SEQ ID NO: 304)	GGGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGACAAGAAAGTT GAGCCCAAATCTTGTGACAAAACTCACACATGCC CACCGTGCCCAGCACCTGAACTCCTGGGGGGACC GTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACA CCCTCATGATCTCCCGGACCCCTGAGGTCACATGC GTGGTGGTGGACGTGAGCCACGAAGACCCTGAGG TCAAGTTCAACTGGTACGTGGACGGCGTGGAGGT GCATAATGCCAAGACAAAGCCGTGCGAGGAGCA GTACGGCAGCACGTACCGTTGCGTCAGCGTCCTC ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGG AGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCC AGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA GGGCAGCCCCGAGAACCACAGGTGTACACCCTGC CCCCATCCCGGAAGGAGATGACCAAGAACCAGGT CAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA GCGACATCGCCGTGGAGTGGGAGAGCAATGGGC AGCCGGAGAACAACTACAAGACCACGCCTCCCGT GCTGAAGTCCGACGGCTCCTTCTTCCTCTATAGCA AGCTCACCGTGGACAAGAGCAGGTGGCAGCAGG GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT CTGCACAACCACTACACGCAGAAGAGCCTCTCCC TGTCTCCGGGTAAA (SEQ ID NO: 326)
52C, 54C, 55C	HC-111	QVQLVESGGGVVQPGRSL RLSCAASGFTFSSFGMHW VRQAPGKGLEWVAVISFD GSIKYSVDSVKGRFTISRD NSKNTLFLQMNSLRAEDT AVYYCARDRLNYYDSSGY YHYKYYGMAVWGQGTT VTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLESVV TVPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSCDKT HTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQY GSTYRCVSVLTVLHQDWL NGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTL PPSRKKMTKNQVSLTCLV KGFYPSDIAVEWESNGQPE NNYKTTPPVLKSDGSFFLY SKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSL SPGK (SEQ ID NO: 305)	CAGGTGCAGCTGGTGGAATCTGGGGGAGGCGTGG TCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGC AGCCTCTGGATTCACCTTCAGTAGCTTTGGCATGC ACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGA GTGGGTGGCAGTTATATCATTTGATGGAAGTATT AAGTATTCTGTAGACTCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAATTCAAAGAACACGCTGTT TCTGCAAATGAACAGCCTGCGAGCCGAGGACACG GCTGTGTATTACTGTGCGAGAGATCGGCTCAATT ACTATGATAGTAGTGGTTATTATCACTACAAATAC TACGGTATGGCCGTCTGGGGCCAAGGAACAACAG TTACCGTCTCTAGTGCCTCCACCAAGGGCCCATCG GTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTC TGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAG GACTACTTCCCCGAACCGGTGACGGTGTCGTGGA ACTCAGGCGCCCTGACCAGCGGCGTGCACACCTT CCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCC TCGAGAGCGTGGTGACCGTGCCCTCCAGCAGCTT GGGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGACAAGAAAGTT GAGCCCAAATCTTGTGACAAAACTCACACATGCC CACCGTGCCCAGCACCTGAACTCCTGGGGGGACC GTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACA CCCTCATGATCTCCCGGACCCCTGAGGTCACATGC GTGGTGGTGGACGTGAGCCACGAAGACCCTGAGG TCAAGTTCAACTGGTACGTGGACGGCGTGGAGGT GCATAATGCCAAGACAAAGCCGTGCGAGGAGCA GTACGGCAGCACGTACCGTTGCGTCAGCGTCCTC ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGG AGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCC AGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA

Antibody ID.	HC Group	Heavy Chain Amino Acid Sequence	Heavy Chain Nucleic Acid Sequence
			GGGCAGCCCCGAGAACCACAGGTGTACACCCTGC CCCCATCCCGGAAGAAGATGACCAAGAACCAGGT CAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA GCGACATCGCCGTGGAGTGGGAGAGCAATGGGC AGCCGGAGAACAACTACAAGACCACGCCTCCCGT GCTGAAGTCCGACGGCTCCTTCTTCCTCTATAGCA AGCTCACCGTGGACAAGAGCAGGTGGCAGCAGG GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT CTGCACAACCACTACACGCAGAAGAGCCTCTCCC TGTCTCCGGGTAAA (SEQ ID NO: 327)
52D	HC-112	QVQLVESGGGVVQPGRSL RLSCAASGFTFSSFGMHW VRQAPGKGLEWVAVISFD GSIKYSVDSVKGRFTISRD NSKNTLFLQMNSLRAEDT AVYYCARDRLNYYDSSGY YHYKYYGMAVWGQGTT VTVSSASTKGPSVFPLAPC SRSTSESTAALGCLVKDYF PEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLESVVT VPSSNFGTQTYTCNVDHK PSNTKVDKTVERKCCVEC PPCPAPPVAGPSVFLFPPKP KDTLMISRTPEVTCVVVD VSHEDPEVQFNWYVDGVE VHNAKTKPREEQFNSTFR VVSVLTVVHQDWLNGKE YKCKVSNKGLPAPIEKTIS KTKGQPREPQVYTLPPSRK KMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYK TTPPMLKSDGSFFLYSKLT VDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPG K (SEQ ID NO: 306)	CAGGTGCAGCTGGTGGAATCTGGGGGAGGCGTGG TCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGC AGCCTCTGGATTCACCTTCAGTAGCTTTGGCATGC ACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGA GTGGGTGGCAGTTATATCATTTGATGGAAGTATT AAGTATTCTGTAGACTCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAATTCAAAGAACACGCTGTT TCTGCAAATGAACAGCCTGCGAGCCGAGGACACG GCTGTGTATTACTGTGCGAGAGATCGGCTCAATT ACTATGATAGTAGTGGTTATTATCACTACAAATAC TACGGTATGGCCGTCTGGGGCCAAGGGACAACAG TTACCGTCTCTAGTGCCTCCACCAAGGGCCCATCG GTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTC CGAGAGCACAGCGGCCCTGGGCTGCCTGGTCAAG GACTACTTCCCCGAACCGGTGACGGTGTCGTGGA ACTCAGGCGCTCTGACCAGCGGCGTGCACACCTT CCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCC TGGAGAGCGTGGTGACCGTGCCCTCCAGCAACTT CGGCACCCAGACCTACACCTGCAACGTAGATCAC AAGCCCAGCAACACCAAGGTGGACAAGACAGTT GAGCGCAAATGTTGTGTCGAGTGCCCACCGTGCC CAGCACCACCTGTGGCAGGACCGTCAGTCTTCCT CTTCCCCCCAAAACCCAAGGACACCCTCATGATC TCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGG ACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAA CTGGTACGTGGACGGCGTGGAGGTGCATAATGCC AAGACAAAGCCACGGGAGGAGCAGTTCAACAGC ACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCA CCAGGACTGGCTGAACGGCAAGGAGTACAAGTGC AAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCG AGAAAACCATCTCCAAAACCAAAGGGCAGCCCCG AGAACCACAGGTGTACACCCTGCCCCCATCCCGG AAGAAGATGACCAAGAACCAGGTCAGCCTGACCT GCCTGGTCAAAGGCTTCTACCCCAGCGACATCGC CGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAA CAACTACAAGACCACACCTCCCATGCTGAAGTCC GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGT GGACAAGAGCAGGTGGCAGCAGGGGAACGTCTT CTCATGCTCCGTGATGCATGAGGCTCTGCACAAC CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGG GTAAA (SEQ ID NO: 328)
53A, 56A	HC-113	QVQLVESGGGVVQPGRSL RLSCAASGFTFSSFGMHW VRQAPGKGLEWVAVISFD	CAGGTGCAGCTGGTGGAATCTGGGGGAGGCGTGG TCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGC AGCCTCTGGATTCACCTTCAGTAGCTTTGGCATGC

Antibody ID.	HC Group	Heavy Chain Amino Acid Sequence	Heavy Chain Nucleic Acid Sequence
		GSIKYSVDSVKGRFTISRD NSKNTLFLQMNSLRAEDT AVYYCARDRLNYYESSGY YHYKYYGMAVWGQGTT VTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLESVV TVPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSCDKT HTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQY GSTYRCVSVLTVLHQDWL NGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTL PPSRKEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPE NNYKTTPPVLKSDGSFFLY SKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSL SPGK (SEQ ID NO: 307)	ACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGA GTGGGTGGCAGTTATATCATTTGATGGAAGTATT AAGTATTCTGTAGACTCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAATTCAAAGAACACGCTGTT TCTGCAAATGAACAGCCTGCGAGCCGAGGACACG GCTGTGTATTACTGTGCGAGAGATCGGCTCAATT ACTATGAGAGTAGTGGTTATTATCACTACAAATA CTACGGTATGGCCGTCTGGGGCCAAGGGACAACA GTTACCGTCTCTAGTGCCTCCACCAAGGGCCCATC GGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCT CTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAA GGACTACTTCCCCGAACCGGTGACGGTGTCGTGG AACTCAGGCGCCCTGACCAGCGGCGTGCACACCT TCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCC CTCGAGAGCGTGGTGACCGTGCCCTCCAGCAGCT TGGGCACCCAGACCTACATCTGCAACGTGAATCA CAAGCCCAGCAACACCAAGGTGGACAAGAAAGT TGAGCCCAAATCTTGTGACAAAACTCACACATGC CCACCGTGCCCAGCACCTGAACTCCTGGGGGGAC CGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC ACCCTCATGATCTCCCGGACCCCTGAGGTCACAT GCGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTAAAGTTCAACTGGTACGTGGACGGCGTGGAG GTGCATAATGCCAAGACAAAGCCGTGCGAGGAGC AGTACGGCAGCACGTACCGTTGCGTCAGCGTCCT CACCGTCCTGCACCAGGACTGGCTGAATGGCAAG GAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCC CAGCCCCCATCGAGAAAACCATCTCCAAAGCCAA AGGGCAGCCCCGAGAACCACAGGTGTACACCCTG CCCCCATCCCGGAAGGAGATGACCAAGAACCAGG TCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC AGCGACATCGCCGTGGAGTGGGAGAGCAATGGG CAGCCGGAGAACAACTACAAGACCACGCCTCCCG TGCTGAAGTCCGACGGCTCCTTCTTCCTCTATAGC AAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG GGGAACGTCTTCTCATGCTCCGTGATGCATGAGG CTCTGCACAACCACTACACGCAGAAGAGCCTCTC CCTGTCTCCGGGTAAA (SEQ ID NO: 329)
53B, 56B	HC-114	QVQLVESGGGVVQPGRSL RLSCAASGFTFSSFGMHW VRQAPGKELEWVAVISFD GSIKYSVDSVKGRFTISRD NSKNTLFLQMNSLRAEDT AVYYCARDRLNYYESSGY YHYKYYGMAVWGQGTT VTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLESVV TVPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSCDKT HTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWY	CAGGTGCAGCTGGTGGAATCTGGGGGAGGCGTGG TCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGC AGCCTCTGGATTCACCTTCAGTAGCTTTGGCATGC ACTGGGTCCGCCAGGCTCCAGGGAAGGAGCTGGA GTGGGTGGCAGTTATATCATTTGATGGAAGTATT AAGTATTCTGTAGACTCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAATTCAAAGAACACGCTGTT TCTGCAAATGAACAGCCTGCGAGCCGAGGACACG GCTGTGTATTACTGTGCGAGAGATCGGCTCAATT ACTATGAGAGTAGTGGTTATTATCACTACAAATA CTACGGTATGGCCGTCTGGGGCCAAGGGACAACA GTTACCGTCTCTAGTGCCTCCACCAAGGGCCCATC GGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCT CTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAA GGACTACTTCCCCGAACCGGTGACGGTGTCGTGG AACTCAGGCGCCCTGACCAGCGGCGTGCACACCT

Antibody ID.	HC Group	Heavy Chain Amino Acid Sequence	Heavy Chain Nucleic Acid Sequence
		VDGVEVHNAKTKPCEEQY GSTYRCVSVLTVLHQDWL NGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTL PPSRKEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPE NNYKTTPPVLKSDGSFFLY SKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSL SPGK (SEQ ID NO: 308)	TCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCC CTCGAGAGCGTGGTGACCGTGCCCTCCAGCAGCT TGGGCACCCAGACCTACATCTGCAACGTGAATCA CAAGCCCAGCAACACCAAGGTGGACAAGAAAGT TGAGCCCAAATCTTGTGACAAAACTCACACATGC CCACCGTGCCCAGCACCTGAACTCCTGGGGGGAC CGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC ACCCTCATGATCTCCCGGACCCCTGAGGTCACAT GCGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGAG GTGCATAATGCCAAGACAAAGCCGTGCGAGGAGC AGTACGGCAGCACGTACCGTTGCGTCAGCGTCCT CACCGTCCTGCACCAGGACTGGCTGAATGGCAAG GAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCC CAGCCCCCATCGAGAAAACCATCTCCAAAGCCAA AGGGCAGCCCCGAGAACCACAGGTGTACACCCTG CCCCCATCCCGGAAGGAGATGACCAAGAACCAGG TCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC AGCGACATCGCCGTGGAGTGGGAGAGCAATGGG CAGCCGGAGAACAACTACAAGACCACGCCTCCCG TGCTGAAGTCCGACGGCTCCTTCTTCCTCTATAGC AAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG GGGAACGTCTTCTCATGCTCCGTGATGCATGAGG CTCTGCACAACCACTACACGCAGAAGAGCCTCTC CCTGTCTCCGGGTAAA (SEQ ID NO: 330)
53C, 56C	HC-115	QVQLVESGGGVVQPGRSL RLSCAASGFTFSSFGMHW VRQAPGKGLEWVAVISFD GSIKYSVDSVKGRFTISRD NSKNTLFLQMNSLRAEDT AVYYCARDRLNYYESSGY YHYKYYGMAVWGQGTT VTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLESVV TVPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSCDKT HTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQY GSTYRCVSVLTVLHQDWL NGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTL PPSRKKMTKNQVSLTCLV KGFYPSDIAVEWESNGQPE NNYKTTPPVLKSDGSFFLY SKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSL SPGK (SEQ ID NO: 309)	CAGGTGCAGCTGGTGGAATCTGGGGGAGGCGTGG TCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGC AGCCTCTGGATTCACCTTCAGTAGCTTTGGCATGC ACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGA GTGGGTGGCAGTTATATCATTTGATGGAAGTATT AAGTATTCTGTAGACTCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAATTCAAAGAACACGCTGTT TCTGCAAATGAACAGCCTGCGAGCCGAGGACACG GCTGTGTATTACTGTGCGAGAGATCGGCTCAATT ACTATGAGAGTAGTGGTTATTATCACTACAAATA CTACGGTATGGCCGTCTGGGGCCAAGGAACAACA GTTACCGTCTCTAGTGCCTCCACCAAGGGCCCATC GGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCT CTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAA GGACTACTTCCCCGAACCGGTGACGGTGTCGTGG AACTCAGGCGCCCTGACCAGCGGCGTGCACACCT TCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCC CTCGAGAGCGTGGTGACCGTGCCCTCCAGCAGCT TGGGCACCCAGACCTACATCTGCAACGTGAATCA CAAGCCCAGCAACACCAAGGTGGACAAGAAAGT TGAGCCCAAATCTTGTGACAAAACTCACACATGC CCACCGTGCCCAGCACCTGAACTCCTGGGGGGAC CGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC ACCCTCATGATCTCCCGGACCCCTGAGGTCACAT GCGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGAG GTGCATAATGCCAAGACAAAGCCGTGCGAGGAGC AGTACGGCAGCACGTACCGTTGCGTCAGCGTCCT CACCGTCCTGCACCAGGACTGGCTGAATGGCAAG

Antibody ID.	HC Group	Heavy Chain Amino Acid Sequence	Heavy Chain Nucleic Acid Sequence
			GAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCC CAGCCCCCATCGAGAAAACCATCTCCAAAGCCAA AGGGCAGCCCCGAGAACCACAGGTGTACACCCTG CCCCCATCCCGGAAGAAGATGACCAAGAACCAGG TCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC AGCGACATCGCCGTGGAGTGGGAGAGCAATGGG CAGCCGGAGAACAACTACAAGACCACGCCTCCCG TGCTGAAGTCCGACGGCTCCTTCTTCCTCTATAGC AAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG GGGAACGTCTTCTCATGCTCCGTGATGCATGAGG CTCTGCACAACCACTACACGCAGAAGAGCCTCTC CCTGTCTCCGGGTAAA (SEQ ID NO: 331)
57A	HC-116	QVQLVESGGGVVQPGRSL RLSCAASGFTFSSYGMHW VRQAPGKGLEWVAVIWY DGSNKYYADSVKGRFIISR DKSKNTLYLQMNSLRAED TAVYYCARAGGIAAAGLY YYYGMDVWGQGTTVTVS SASTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPA VLQSSGLYSLESVVTVPSS SLGTQTYICNVNHKPSNTK VDKKVEPKSCDKTHTCPP CPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYR CVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSR KEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNY KTTPPVLKSDGSFFLYSKL TVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSP GK (SEQ ID NO: 310)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGG TCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGC AGCGTCTGGATTCACCTTCAGTAGCTATGGCATGC ACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGA GTGGGTGGCAGTTATATGGTATGATGGAAGTAAT AAATACTATGCAGACTCCGTGAAGGGCCGATTCA TCATCTCCAGAGATAAATCCAAGAACACGCTGTA TCTGCAAATGAACAGCCTGAGAGCCGAGGACACG GCTGTGTATTACTGTGCGAGAGCGGGGGGTATAG CAGCAGCTGGCCTCTACTACTACTACGGTATGGA CGTCTGGGGCCAAGGGACAACAGTTACCGTCTCT AGTGCCTCCACCAAGGGCCCATCGGTCTTCCCCCT GGCACCCTCCTCCAAGAGCACCTCTGGGGGCACA GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCC CCGAACCGGTGACGGTGTCGTGGAACTCAGGCGC CCTGACCAGCGGCGTGCACACCTTCCCGGCTGTC CTACAGTCCTCAGGACTCTACTCCCTCGAGAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAG ACCTACATCTGCAACGTGAATCACAAGCCCAGCA ACACCAAGGTGGACAAGAAAGTTGAGCCCAAATC TTGTGACAAAACTCACACATGCCCACCGTGCCCA GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCC TCTTCCCCCCAAAACCCAAGGACACCCTCATGAT CTCCCGGACCCCTGAGGTCACATGCGTGGTGGTG GACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA ACTGGTACGTGGACGGCGTGGAGGTGCATAATGC CAAGACAAAGCCGTGCGAGGAGCAGTACGGCAG CACGTACCGTTGCGTCAGCGTCCTCACCGTCCTGC ACCAGGACTGGCTGAATGGCAAGGAGTACAAGTG CAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATC GAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCC GAGAACCACAGGTGTACACCCTGCCCCCATCCCG GAAGGAGATGACCAAGAACCAGGTCAGCCTGAC CTGCCTGGTCAAAGGCTTCTATCCCAGCGACATC GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAG AACAACTACAAGACCACGCCTCCCGTGCTGAAGT CCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACC GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTC TTCTCATGCTCCGTGATGCATGAGGCTCTGCACAA CCACTACACGCAGAAGAGCCTCTCCCTGTCTCCG GGTAAA (SEQ ID NO: 332)
57B	HC-117	QVQLVESGGGVVQPGRSL	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGG

Antibody ID.	HC Group	Heavy Chain Amino Acid Sequence	Heavy Chain Nucleic Acid Sequence
		RLSCAASGFTFSSYGMHW VRQAPGKELEWVAVIWY DGSNKYYADSVKGRFIISR DKSKNTLYLQMNSLRAED TAVYYCARAGGIAAAGLY YYYGMDVWGQGTTVTVS SASTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPA VLQSSGLYSLESVVTVPSS SLGTQTYICNVNHKPSNTK VDKKVEPKSCDKTHTCPP CPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYR CVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSR KEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNY KTTPPVLKSDGSFFLYSKL TVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSP GK (SEQ ID NO: 311)	TCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGC AGCGTCTGGATTCACCTTCAGTAGCTATGGCATGC ACTGGGTCCGCCAGGCTCCAGGGAAGGAGCTGGA GTGGGTGGCAGTTATATGGTATGATGGAAGTAAT AAATACTATGCAGACTCCGTGAAGGGCCGATTCA TCATCTCCAGAGATAAATCCAAGAACACGCTGTA TCTGCAAATGAACAGCCTGAGAGCCGAGGACACG GCTGTGTATTACTGTGCGAGAGCGGGGGGTATAG CAGCAGCTGGCCTCTACTACTACTACGGTATGGA CGTCTGGGGCCAAGGGACAACAGTTACCGTCTCT AGTGCCTCCACCAAGGGCCCATCGGTCTTCCCCCT GGCACCCTCCTCCAAGAGCACCTCTGGGGGCACA GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCC CCGAACCGGTGACGGTGTCGTGGAACTCAGGCGC CCTGACCAGCGGCGTGCACACCTTCCCGGCTGTC CTACAGTCCTCAGGACTCTACTCCCTCGAGAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAG ACCTACATCTGCAACGTGAATCACAAGCCCAGCA ACACCAAGGTGGACAAGAAAGTTGAGCCCAAATC TTGTGACAAAACTCACACATGCCCACCGTGCCCA GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCC TCTTCCCCCCAAAACCCAAGGACACCCTCATGAT CTCCCGGACCCCTGAGGTCACATGCGTGGTGGTG GACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA ACTGGTACGTGGACGGCGTGGAGGTGCATAATGC CAAGACAAAGCCGTGCGAGGAGCAGTACGGCAG CACGTACCGTTGCGTCAGCGTCCTCACCGTCCTGC ACCAGGACTGGCTGAATGGCAAGGAGTACAAGTG CAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATC GAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCC GAGAACCACAGGTGTACACCCTGCCCCCATCCCG GAAGGAGATGACCAAGAACCAGGTCAGCCTGAC CTGCCTGGTCAAAGGCTTCTATCCCAGCGACATC GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAG AACAACTACAAGACCACGCCTCCCGTGCTGAAGT CCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACC GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTC TTCTCATGCTCCGTGATGCATGAGGCTCTGCACAA CCACTACACGCAGAAGAGCCTCTCCCTGTCTCCG GGTAAA (SEQ ID NO: 333)
57C	HC-118	QVQLVESGGGVVQPGRSL RLSCAASGFTFSSYGMHW VRQAPGKGLEWVAVIWY DGSNKYYADSVKGRFIISR DKSKNTLYLQMNSLRAED TAVYYCARAGGIAAAGLY YYYGMDVWGQGTTVTVS SASTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPA VLQSSGLYSLESVVTVPSS SLGTQTYICNVNHKPSNTK VDKKVEPKSCDKTHTCPP CPAPELLGGPSVFLFPPKP	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGG TCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGC AGCGTCTGGATTCACCTTCAGTAGCTATGGCATGC ACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGA GTGGGTGGCAGTTATATGGTATGATGGAAGTAAT AAATACTATGCAGACTCCGTGAAGGGCCGATTCA TCATCTCCAGAGATAAATCCAAGAACACGCTGTA TCTGCAAATGAACAGCCTGAGAGCCGAGGACACG GCTGTGTATTACTGTGCGAGAGCGGGGGGTATAG CAGCAGCTGGCCTCTACTACTACTACGGTATGGA CGTCTGGGGCCAAGGAACAACAGTTACCGTCTCT AGTGCCTCCACCAAGGGCCCATCGGTCTTCCCCCT GGCACCCTCCTCCAAGAGCACCTCTGGGGGCACA GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCC

Antibody ID.	HC Group	Heavy Chain Amino Acid Sequence	Heavy Chain Nucleic Acid Sequence
		KDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYR CVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSR KKMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNY KTTPPVLKSDGSFFLYSKL TVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSP GK (SEQ ID NO: 312)	CCGAACCGGTGACGGTGTCGTGGAACTCAGGCGC CCTGACCAGCGGCGTGCACACCTTCCCGGCTGTC CTACAGTCCTCAGGACTCTACTCCCTCGAGAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAG ACCTACATCTGCAACGTGAATCACAAGCCCAGCA ACACCAAGGTGGACAAGAAAGTTGAGCCCAAATC TTGTGACAAAACTCACACATGCCCACCGTGCCCA GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCC TCTTCCCCCCAAAACCCAAGGACACCCTCATGAT CTCCCGGACCCCTGAGGTCACATGCGTGGTGGTT GACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA ACTGGTACGTGGACGGCGTGGAGGTGCATAATGC CAAGACAAAGCCGTGCGAGGAGCAGTACGGCAG CACGTACCGTTGCGTCAGCGTCCTCACCGTCCTGC ACCAGGACTGGCTGAATGGCAAGGAGTACAAGTG CAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATC GAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCC GAGAACCACAGGTGTACACCCTGCCCCCATCCCG GAAGAAGATGACCAAGAACCAGGTCAGCCTGAC CTGCCTGGTCAAAGGCTTCTATCCCAGCGACATC GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAG AACAACTACAAGACCACGCCTCCCGTGCTGAAGT CCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACC GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTC TTCTCATGCTCCGTGATGCATGAGGCTCTGCACAA CCACTACACGCAGAAGAGCCTCTCCCTGTCTCCG GGTAAA (SEQ ID NO: 334)
57D	HC-119	QVQLVESGGGVVQPGRSL RLSCAASGFTFSSYGMHW VRQAPGKGLEWVAVIWY DGSNKYYADSVKGRFIISR DKSKNTLYLQMNSLRAED TAVYYCARAGGIAAAGLY YYYGMDVWGQGTTVTVS SASTKGPSVFPLAPCSRSTS ESTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAV LQSSGLYSLESVVTVPSSN FGTQTYTCNVDHKPSNTK VDKTVERKCCVECPPCPA PPVAGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHE DPEVQFNWYVDGVEVHN AKTKPREEQFNSTFRVVSV LTVVHQDWLNGKEYKCK VSNKGLPAPIEKTISKTKG QPREPQVYTLPPSRKKMT KNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPP MLKSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK (SEQ ID NO: 313)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGG TCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGC AGCGTCTGGATTCACCTTCAGTAGCTATGGCATGC ACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGA GTGGGTGGCAGTTATATGGTATGATGGAAGTAAT AAATACTATGCAGACTCCGTGAAGGGCCGATTCA TCATCTCCAGAGATAAATCCAAGAACACGCTGTA TCTGCAAATGAACAGCCTGAGAGCCGAGGACACG GCTGTGTATTACTGTGCGAGAGCGGGGGGTATAG CAGCAGCTGGCCTCTACTACTACTACGGTATGGA CGTCTGGGGCCAAGGGACAACAGTTACCGTCTCT AGTGCCTCCACCAAGGGCCCATCGGTCTTCCCCCT GGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACA GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCC CCGAACCGGTGACGGTGTCGTGGAACTCAGGCGC TCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCC TACAGTCCTCAGGACTCTACTCCCTGGAGAGCGT GGTGACCGTGCCCTCCAGCAACTTCGGCACCCAG ACCTACACCTGCAACGTAGATCACAAGCCCAGCA ACACCAAGGTGGACAAGACAGTTGAGCGCAAAT GTTGTGTCGAGTGCCCACCGTGCCCAGCACCACC TGTGGCAGGACCGTCAGTCTTCCTCTTCCCCCCAA AACCCAAGGACACCCTCATGATCTCCCGGACCCC TGAGGTCACGTGCGTGGTGGTGGACGTGAGCCAC GAAGACCCCGAGGTCCAGTTCAACTGGTACGTGG ACGGCGTGGAGGTGCATAATGCCAAGACAAAGCC ACGGGAGGAGCAGTTCAACAGCACGTTCCGTGTG

Antibody ID.	HC Group	Heavy Chain Amino Acid Sequence	Heavy Chain Nucleic Acid Sequence
			GTCAGCGTCCTCACCGTTGTGCACCAGGACTGGC TGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAA CAAAGGCCTCCCAGCCCCCATCGAGAAAACCATC TCCAAAACCAAAGGGCAGCCCCGAGAACCACAG GTGTACACCCTGCCCCCATCCCGGAAGAAGATGA CCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAA AGGCTTCTACCCCAGCGACATCGCCGTGGAGTGG GAGAGCAATGGGCAGCCGGAGAACAACTACAAG ACCACACCTCCCATGCTGAAGTCCGACGGCTCCTT CTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG TGATGCATGAGGCTCTGCACAACCACTACACGCA GAAGAGCCTCTCCCTGTCTCCGGGTAAA (SEQ ID NO: 335)
58A	HC-120	QVQLVESGGGVVQPGRSL RLSCAASGFTFSSYGMHW VRQAPGKGLEWVAVIWY DGSNKYYAESVKGRFIISR DKSKNTLYLQMNSLRAED TAVYYCARAGGIAAAGLY YYYGMDVWGQGTTVTVS SASTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPA VLQSSGLYSLESVVTVPSS SLGTQTYICNVNHKPSNTK VDKKVEPKSCDKTHTCPP CPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYR CVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSR KEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNY KTTPPVLKSDGSFFLYSKL TVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSP GK (SEQ ID NO: 314)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGG TCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGC AGCGTCTGGATTCACCTTCAGTAGCTATGGCATGC ACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGA GTGGGTGGCAGTTATATGGTATGATGGAAGTAAT AAATACTATGCAGAGTCCGTGAAGGGCCGATTCA TCATCTCCAGAGATAAATCCAAGAACACGCTGTA TCTGCAAATGAACAGCCTGAGAGCCGAGGACACG GCTGTGTATTACTGTGCGAGAGCGGGGGGTATAG CAGCAGCTGGCCTCTACTACTACTACGGTATGGA CGTCTGGGGCCAAGGGACAACAGTTACCGTCTCT AGTGCCTCCACCAAGGGCCCATCGGTCTTCCCCCT GGCACCCTCCTCCAAGAGCACCTCTGGGGGCACA GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCC CCGAACCGGTGACGGTGTCGTGGAACTCAGGCGC CCTGACCAGCGGCGTGCACACCTTCCCGGCTGTC CTACAGTCCTCAGGACTCTACTCCCTCGAGAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAG ACCTACATCTGCAACGTGAATCACAAGCCCAGCA ACACCAAGGTGGACAAGAAAGTTGAGCCCAAATC TTGTGACAAAACTCACACATGCCCACCGTGCCCA GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCC TCTTCCCCCCAAAACCCAAGGACACCCTCATGAT CTCCCGGACCCCTGAGGTCACATGCGTGGTGGTG GACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA ACTGGTACGTGGACGGCGTGGAGGTGCATAATGC CAAGACAAAGCCGTGCGAGGAGCAGTACGGCAG CACGTACCGTTGCGTCAGCGTCCTCACCGTCCTGC ACCAGGACTGGCTGAATGGCAAGGAGTACAAGTG CAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATC GAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCC GAGAACCACAGGTGTACACCCTGCCCCCATCCCG GAAGGAGATGACCAAGAACCAGGTCAGCCTGAC CTGCCTGGTCAAAGGCTTCTATCCCAGCGACATC GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAG AACAACTACAAGACCACGCCTCCCGTGCTGAAGT CCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACC GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTC TTCTCATGCTCCGTGATGCATGAGGCTCTGCACAA CCACTACACGCAGAAGAGCCTCTCCCTGTCTCCG

Antibody ID.	HC Group	Heavy Chain Amino Acid Sequence	Heavy Chain Nucleic Acid Sequence
			GGTAAA (SEQ ID NO: 336)
58B	HC-121	QVQLVESGGGVVQPGRSL RLSCAASGFTFSSYGMHW VRQAPGKELEWVAVIWY DGSNKYYAESVKGRFIISR DKSKNTLYLQMNSLRAED TAVYYCARAGGIAAAGLY YYYGMDVWGQGTTVTVS SASTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPA VLQSSGLYSLESVVTVPSS SLGTQTYICNVNHKPSNTK VDKKVEPKSCDKTHTCPP CPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYR CVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSR KEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNY KTTPPVLKSDGSFFLYSKL TVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSP GK (SEQ ID NO: 315)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGG TCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGC AGCGTCTGGATTCACCTTCAGTAGCTATGGCATGC ACTGGGTCCGCCAGGCTCCAGGGAAGGAGCTGGA GTGGGTGGCAGTTATATGGTATGATGGAAGTAAT AAATACTATGCAGAGTCCGTGAAGGGCCGATTCA TCATCTCCAGAGATAAATCCAAGAACACGCTGTA TCTGCAAATGAACAGCCTGAGAGCCGAGGACACG GCTGTGTATTACTGTGCGAGAGCGGGGGGTATAG CAGCAGCTGGCCTCTACTACTACTACGGTATGGA CGTCTGGGGCCAAGGGACAACAGTTACCGTCTCT AGTGCCTCCACCAAGGGCCCATCGGTCTTCCCCCT GGCACCCTCCTCCAAGAGCACCTCTGGGGGCACA GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCC CCGAACCGGTGACGGTGTCGTGGAACTCAGGCGC CCTGACCAGCGGCGTGCACACCTTCCCGGCTGTC CTACAGTCCTCAGGACTCTACTCCCTCGAGAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAG ACCTACATCTGCAACGTGAATCACAAGCCCAGCA ACACCAAGGTGGACAAGAAAGTTGAGCCCAAATC TTGTGACAAAACTCACACATGCCCACCGTGCCCA GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCC TCTTCCCCCCAAAACCCAAGGACACCCTCATGAT CTCCCGGACCCCTGAGGTCACATGCGTGGTGGTG GACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA ACTGGTACGTGGACGGCGTGGAGGTGCATAATGC CAAGACAAAGCCGTGCGAGGAGCAGTACGGCAG CACGTACCGTTGCGTCAGCGTCCTCACCGTCCTGC ACCAGGACTGGCTGAATGGCAAGGAGTACAAGTG CAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATC GAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCC GAGAACCACAGGTGTACACCCTGCCCCCATCCCG GAAGGAGATGACCAAGAACCAGGTCAGCCTGAC CTGCCTGGTCAAAGGCTTCTATCCCAGCGACATC GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAG AACAACTACAAGACCACGCCTCCCGTGCTGAAGT CCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACC GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTC TTCTCATGCTCCGTGATGCATGAGGCTCTGCACAA CCACTACACGCAGAAGAGCCTCTCCCTGTCTCCG GGTAAA (SEQ ID NO: 337)
58C	HC-122	QVQLVESGGGVVQPGRSL RLSCAASGFTFSSYGMHW VRQAPGKGLEWVAVIWY DGSNKYYAESVKGRFIISR DKSKNTLYLQMNSLRAED TAVYYCARAGGIAAAGLY YYYGMDVWGQGTTVTVS SASTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPA VLQSSGLYSLESVVTVPSS SLGTQTYICNVNHKPSNTK	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGG TCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGC AGCGTCTGGATTCACCTTCAGTAGCTATGGCATGC ACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGA GTGGGTGGCAGTTATATGGTATGATGGAAGTAAT AAATACTATGCAGAGTCCGTGAAGGGCCGATTCA TCATCTCCAGAGATAAATCCAAGAACACGCTGTA TCTGCAAATGAACAGCCTGAGAGCCGAGGACACG GCTGTGTATTACTGTGCGAGAGCGGGGGGTATAG CAGCAGCTGGCCTCTACTACTACTACGGTATGGA CGTCTGGGGCCAAGGAACAACAGTTACCGTCTCT AGTGCCTCCACCAAGGGCCCATCGGTCTTCCCCCT

Antibody ID.	HC Group	Heavy Chain Amino Acid Sequence	Heavy Chain Nucleic Acid Sequence
		VDKKVEPKSCDKTHTCPP CPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYR CVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSR KKMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNY KTTPPVLKSDGSFFLYSKL TVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSP GK (SEQ ID NO: 316)	GGCACCCTCCTCCAAGAGCACCTCTGGGGGCACA GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCC CCGAACCGGTGACGGTGTCGTGGAACTCAGGCGC CCTGACCAGCGGCGTGCACACCTTCCCGGCTGTC CTACAGTCCTCAGGACTCTACTCCCTCGAGAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAG ACCTACATCTGCAACGTGAATCACAAGCCCAGCA ACACCAAGGTGGACAAGAAAGTTGAGCCCAAATC TTGTGACAAAACTCACACATGCCCACCGTGCCCA GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCC TCTTCCCCCCAAAACCCAAGGACACCCTCATGAT CTCCCGGACCCCTGAGGTCACATGCGTGGTGGTT GACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA ACTGGTACGTGGACGGCGTGGAGGTGCATAATGC CAAGACAAAGCCGTGCGAGGAGCAGTACGGCAG CACGTACCGTTGCGTCAGCGTCCTCACCGTCCTGC ACCAGGACTGGCTGAATGGCAAGGAGTACAAGTG CAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATC GAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCC GAGAACCACAGGTGTACACCCTGCCCCCATCCCG GAAGAAGATGACCAAGAACCAGGTCAGCCTGAC CTGCCTGGTCAAAGGCTTCTATCCCAGCGACATC GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAG AACAACTACAAGACCACGCCTCCCGTGCTGAAGT CCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACC GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTC TTCTCATGCTCCGTGATGCATGAGGCTCTGCACAA CCACTACACGCAGAAGAGCCTCTCCCTGTCTCCG GGTAAA (SEQ ID NO: 338)

[0113] In some embodiments, the heterodimeric antibody of the invention comprises an anti-CGRP receptor light chain from Table 7A and an anti-CGRP receptor heavy chain from Table 7B. Exemplary pairs of anti-CGRP receptor light and heavy chains that may be incorporated into a heterodimeric antibody include, but are not limited to: LC-101 (SEQ ID NO: 271) and HC-101 (SEQ ID NO: 295); LC-102 (SEQ ID NO: 272) and HC-102 (SEQ ID NO: 296); LC-101 (SEQ ID NO: 271) and HC-103 (SEQ ID NO: 297); LC-101 (SEQ ID NO: 271) and HC-104 (SEQ ID NO: 298); LC-103 (SEQ ID NO: 273) and HC-105 (SEQ ID NO: 299); LC-104 (SEQ ID NO: 274) and HC-106 (SEQ ID NO: 300); LC-103 (SEQ ID NO: 273) and HC-107 (SEQ ID NO: 301); LC-103 (SEQ ID NO: 273) and HC-108 (SEQ ID NO: 302); LC-105 (SEQ ID NO: 275) and HC-109 (SEQ ID NO: 303); LC-106 (SEQ ID NO: 276) and HC-110 (SEQ ID NO: 304); LC-105 (SEQ ID NO: 275) and HC-111 (SEQ ID NO: 305); LC-105 (SEQ ID NO: 275) and HC-112 (SEQ ID NO: 306); LC-105 (SEQ ID NO: 275) and HC-113 (SEQ ID NO: 307); LC-106 (SEQ ID NO: 276) and HC-114 (SEQ ID NO: 308); LC-105 (SEQ ID NO: 275) and

HC-115 (SEQ ID NO: 309); LC-107 (SEQ ID NO: 277) and HC-109 (SEQ ID NO: 303); LC-108 (SEQ ID NO: 278) and HC-110 (SEQ ID NO: 304); LC-107 (SEQ ID NO: 277) and HC-111 (SEQ ID NO: 305); LC-109 (SEQ ID NO: 279) and HC-109 (SEQ ID NO: 303); LC-110 (SEQ ID NO: 280) and HC-110 (SEQ ID NO: 304); LC-109 (SEQ ID NO: 279) and HC-111 (SEQ ID NO: 305); LC-107 (SEQ ID NO: 277) and HC-113 (SEQ ID NO: 307); LC-108 (SEQ ID NO: 278) and HC-114 (SEQ ID NO: 308); LC-107 (SEQ ID NO: 277) and HC-115 (SEQ ID NO: 309); LC-111 (SEQ ID NO: 281) and HC-116 (SEQ ID NO: 310); LC-112 (SEQ ID NO: 282) and HC-117 (SEQ ID NO: 311); LC-111 (SEQ ID NO: 281) and HC-118 (SEQ ID NO: 312); LC-111 (SEQ ID NO: 281) and HC-119 (SEQ ID NO: 313); LC-111 (SEQ ID NO: 281) and HC-120 (SEQ ID NO: 314); LC-112 (SEQ ID NO: 282) and HC-121 (SEQ ID NO: 315); and LC-111 (SEQ ID NO: 281) and HC-122 (SEQ ID NO: 316).

[0114] The anti-CGRP receptor light chain and/or heavy chain incorporated into a heterodimeric antibody of the invention may comprise a sequence of contiguous amino acids that differs from the sequence of a light chain in Table 7A or a heavy chain in Table 7B by 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15 or more amino acid residues, wherein each such sequence difference is independently a deletion, insertion or substitution of one amino acid. In some embodiments, the anti-CGRP receptor light chain incorporated into a heterodimeric antibody comprises a sequence of amino acids that has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97% or at least 99% sequence identity to the amino acid sequences of SEQ ID NOs: 271-282 (i.e. the anti-CGRP receptor light chains in Table 7A). In certain embodiments, the anti-CGRP receptor heavy chain incorporated into a heterodimeric antibody comprises a sequence of amino acids that has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97% or at least 99% sequence identity to the amino acid sequences of SEQ ID NOs: 295-316 (i.e. the anti-CGRP receptor heavy chains in Table 7B).

[0115] Any of the anti-PAC1 receptor light and heavy chains listed in Tables 6A and 6B may be combined with any of the anti-CGRP receptor light and heavy chains listed in Table 7A and 7B to form a bispecific, heterodimeric antibody of the invention. The structural features (e.g. component anti-PAC1 receptor light and heavy chains and anti-CGRP receptor light and heavy chains) of exemplary bispecific, heterodimeric antibodies of the invention are set forth in Table 8 below. These antibodies contain one or more charge pair mutations as described herein to promote correct pairing of heavy and light chains as well as heterodimerization between an anti-

PAC1 receptor heavy chain and an anti-CGRP receptor heavy chain. Antibodies having an "A" designation comprise the "v1" electrostatic steering strategy shown in Figure 1, whereas antibodies having a "B" designation comprise the "v3" electrostatic steering strategy shown in Figure 1. Antibodies having a "C" or "D" designation comprise the "v4" electrostatic steering strategy shown in Figure 1, with "C" antibodies having an IgG1 constant domain and "D" antibodies having an IgG2 constant domain. The variable light and heavy chain designations (e.g. LV-01, LV-02, LV-101, LV-102, HV-01, HV-02, HV-101, HV-102, etc.) in Table 8 are defined by amino acid sequence in Tables 1A, 1B, 3A, and 3B and nucleotide sequence in Tables 11 and 12. The light and heavy chain designations (e.g. LC-01, LC-02, LC-101, LC-102, HC-01, HC-02, HC-101, HC-102, etc.) in Table 8 are defined by amino acid and nucleotide sequence in Tables 6A, 6B, 7A, and 7B. Thus, the full sequence information for each of the four chains of the exemplary heterodimeric antibodies in Table 8 can be obtained by cross-reference to these tables. By way of illustration, heterodimeric antibody iPS: 326417 comprises an anti-PAC1 receptor light chain comprising the amino acid sequence of SEQ ID NO: 211 (LC-01), an anti-PAC1 receptor heavy chain comprising the amino acid sequence of SEQ ID NO: 233 (HC-01), an anti-CGRP receptor light chain comprising the amino acid sequence of SEQ ID NO: 281 (LC-111) and an anti-CGRP receptor heavy chain comprising the amino acid sequence of SEQ ID NO: 310 (HC-116).

Table 8. Exemplary Anti-PAC1 Receptor/Anti-CGRP Receptor Heterodimeric Antibodies

Heterodimeric Antibody Designation	Anti-PAC1 Receptor Antibody ID.	Anti-PAC1 Receptor Full Light Chain	Anti-PAC1 Receptor VL	Anti-PAC1 Receptor Full Heavy Chain	Anti-PAC1 Receptor VH	Anti-CGRP Receptor Antibody ID.	Anti- CGRP Receptor Full Light Chain	Anti- CGRP Receptor VL	Anti- CGRP Receptor Full Heavy Chain	Anti- CGRP Receptor VH
iPS:326417	01A	LC-01	LV-01	HC-01	HV-01	57A	LC-111	LV-111	HC-116	HV-109
iPS:326626	01D	LC-01	LV-01	HC-04	HV-01	50D	LC-101	LV-101	HC-104	HV-101
iPS:326628	03D	LC-04	LV-04	HC-08	HV-03	50D	LC-101	LV-101	HC-104	HV-101
iPS:326634	03D	LC-04	LV-04	HC-08	HV-03	51D	LC-103	LV-103	HC-108	HV-103
iPS:327870	01D	LC-01	LV-01	HC-04	HV-01	52D	LC-105	LV-105	HC-112	HV-105

Heterodimeric Antibody Designation	Anti-PAC1 Receptor Antibody ID.	Anti-PAC1 Receptor Full Light Chain	Anti-PAC1 Receptor VL	Anti-PAC1 Receptor Full Heavy Chain	Anti-PAC1 Receptor VH	Anti-CGRP Receptor Antibody ID.	Anti- CGRP Receptor Full Light Chain	Anti- CGRP Receptor VL	Anti- CGRP Receptor Full Heavy Chain	Anti- CGRP Receptor VH
iPS:327871	03D	LC-04	LV-04	HC-08	HV-03	52D	LC-105	LV-105	HC-112	HV-105
iPS:326645	05D	LC-08	LV-08	HC-16	HV-07	50D	LC-101	LV-101	HC-104	HV-101
iPS:326648	04D	LC-06	LV-06	HC-12	HV-05	50D	LC-101	LV-101	HC-104	HV-101
iPS:326651	05D	LC-08	LV-08	HC-16	HV-07	51D	LC-103	LV-103	HC-108	HV-103
iPS:326631	01D	LC-01	LV-01	HC-04	HV-01	51D	LC-103	LV-103	HC-108	HV-103
iPS:326654	04D	LC-06	LV-06	HC-12	HV-05	51D	LC-103	LV-103	HC-108	HV-103
iPS:328000	05D	LC-08	LV-08	HC-16	HV-07	52D	LC-105	LV-105	HC-112	HV-105
iPS:328001	04D	LC-06	LV-06	HC-12	HV-05	52D	LC-105	LV-105	HC-112	HV-105
iPS:326661	01D	LC-01	LV-01	HC-04	HV-01	57D	LC-111	LV-111	HC-119	HV-109
iPS:326663	03D	LC-04	LV-04	HC-08	HV-03	57D	LC-111	LV-111	HC-119	HV-109
iPS:326666	05D	LC-08	LV-08	HC-16	HV-07	57D	LC-111	LV-111	HC-119	HV-109
iPS:326669	04D	LC-06	LV-06	HC-12	HV-05	57D	LC-111	LV-111	HC-119	HV-109
iPS:327017	05A	LC-08	LV-08	HC-13	HV-07	57A	LC-111	LV-111	HC-116	HV-109
iPS:327018	03A	LC-04	LV-04	HC-05	HV-03	57A	LC-111	LV-111	HC-116	HV-109
iPS:327019	04A	LC-06	LV-06	HC-09	HV-05	57A	LC-111	LV-111	HC-116	HV-109
iPS:327023	01B	LC-02	LV-02	HC-02	HV-02	57B	LC-112	LV-112	HC-117	HV-110
iPS:327024	05B	LC-09	LV-09	HC-14	HV-08	57B	LC-112	LV-112	HC-117	HV-110
iPS:327025	03B	LC-05	LV-05	HC-06	HV-04	57B	LC-112	LV-112	HC-117	HV-110
iPS:327026	04B	LC-07	LV-07	HC-10	HV-06	57B	LC-112	LV-112	HC-117	HV-110
iPS:327091	01C	LC-01	LV-01	HC-03	HV-01	57C	LC-111	LV-111	HC-118	HV-109
iPS:327092	05C	LC-08	LV-08	HC-15	HV-07	57C	LC-111	LV-111	HC-118	HV-109
iPS:327093	03C	LC-04	LV-04	HC-07	HV-03	57C	LC-111	LV-111	HC-118	HV-109
iPS:327094	04C	LC-06	LV-06	HC-11	HV-05	57C	LC-111	LV-111	HC-118	HV-109
iPS:326414	01A	LC-01	LV-01	HC-01	HV-01	50A	LC-101	LV-101	HC-101	HV-101
iPS:327102	05A	LC-08	LV-08	HC-13	HV-07	50A	LC-101	LV-101	HC-101	HV-101
iPS:327103	03A	LC-04	LV-04	HC-05	HV-03	50A	LC-101	LV-101	HC-101	HV-101

Heterodimeric Antibody Designation	Anti-PAC1 Receptor Antibody ID.	Anti-PAC1 Receptor Full Light Chain	Anti-PAC1 Receptor VL	Anti-PAC1 Receptor Full Heavy Chain	Anti-PAC1 Receptor VH	Anti-CGRP Receptor Antibody ID.	Anti- CGRP Receptor Full Light Chain	Anti- CGRP Receptor VL	Anti- CGRP Receptor Full Heavy Chain	Anti- CGRP Receptor VH
iPS:327104	04A	LC-06	LV-06	HC-09	HV-05	50A	LC-101	LV-101	HC-101	HV-101
iPS:327105	01B	LC-02	LV-02	HC-02	HV-02	50B	LC-102	LV-102	HC-102	HV-102
iPS:327106	05B	LC-09	LV-09	HC-14	HV-08	50B	LC-102	LV-102	HC-102	HV-102
iPS:327107	03B	LC-05	LV-05	HC-06	HV-04	50B	LC-102	LV-102	HC-102	HV-102
iPS:327108	04B	LC-07	LV-07	HC-10	HV-06	50B	LC-102	LV-102	HC-102	HV-102
iPS:327109	01C	LC-01	LV-01	HC-03	HV-01	50C	LC-101	LV-101	HC-103	HV-101
iPS:327110	05C	LC-08	LV-08	HC-15	HV-07	50C	LC-101	LV-101	HC-103	HV-101
iPS:327111	03C	LC-04	LV-04	HC-07	HV-03	50C	LC-101	LV-101	HC-103	HV-101
iPS:327112	04C	LC-06	LV-06	HC-11	HV-05	50C	LC-101	LV-101	HC-103	HV-101
iPS:327267	01A	LC-01	LV-01	HC-01	HV-01	51A	LC-103	LV-103	HC-105	HV-103
iPS:327268	05A	LC-08	LV-08	HC-13	HV-07	51A	LC-103	LV-103	HC-105	HV-103
iPS:327269	03A	LC-04	LV-04	HC-05	HV-03	51A	LC-103	LV-103	HC-105	HV-103
iPS:327270	04A	LC-06	LV-06	HC-09	HV-05	51A	LC-103	LV-103	HC-105	HV-103
iPS:327272	01B	LC-02	LV-02	HC-02	HV-02	51B	LC-104	LV-104	HC-106	HV-104
iPS:327273	05B	LC-09	LV-09	HC-14	HV-08	51B	LC-104	LV-104	HC-106	HV-104
iPS:327274	03B	LC-05	LV-05	HC-06	HV-04	51B	LC-104	LV-104	HC-106	HV-104
iPS:327275	04B	LC-07	LV-07	HC-10	HV-06	51B	LC-104	LV-104	HC-106	HV-104
iPS:327276	01C	LC-01	LV-01	HC-03	HV-01	51C	LC-103	LV-103	HC-107	HV-103
iPS:327277	05C	LC-08	LV-08	HC-15	HV-07	51C	LC-103	LV-103	HC-107	HV-103
iPS:327278	03C	LC-04	LV-04	HC-07	HV-03	51C	LC-103	LV-103	HC-107	HV-103
iPS:327279	04C	LC-06	LV-06	HC-11	HV-05	51C	LC-103	LV-103	HC-107	HV-103
iPS:327280	01A	LC-01	LV-01	HC-01	HV-01	52A	LC-105	LV-105	HC-109	HV-105
iPS:327281	05A	LC-08	LV-08	HC-13	HV-07	52A	LC-105	LV-105	HC-109	HV-105
iPS:327282	03A	LC-04	LV-04	HC-05	HV-03	52A	LC-105	LV-105	HC-109	HV-105
iPS:327283	04A	LC-06	LV-06	HC-09	HV-05	52A	LC-105	LV-105	HC-109	HV-105

Heterodimeric Antibody Designation	Anti-PAC1 Receptor Antibody ID.	Anti-PAC1 Receptor Full Light Chain	Anti-PAC1 Receptor VL	Anti-PAC1 Receptor Full Heavy Chain	Anti-PAC1 Receptor VH	Anti-CGRP Receptor Antibody ID.	Anti- CGRP Receptor Full Light Chain	Anti- CGRP Receptor VL	Anti- CGRP Receptor Full Heavy Chain	Anti- CGRP Receptor VH
iPS:327284	01B	LC-02	LV-02	HC-02	HV-02	52B	LC-106	LV-106	HC-110	HV-106
iPS:327285	05B	LC-09	LV-09	HC-14	HV-08	52B	LC-106	LV-106	HC-110	HV-106
iPS:327286	03B	LC-05	LV-05	HC-06	HV-04	52B	LC-106	LV-106	HC-110	HV-106
iPS:327287	04B	LC-07	LV-07	HC-10	HV-06	52B	LC-106	LV-106	HC-110	HV-106
iPS:327288	01C	LC-01	LV-01	HC-03	HV-01	52C	LC-105	LV-105	HC-111	HV-105
iPS:327289	05C	LC-08	LV-08	HC-15	HV-07	52C	LC-105	LV-105	HC-111	HV-105
iPS:327290	03C	LC-04	LV-04	HC-07	HV-03	52C	LC-105	LV-105	HC-111	HV-105
iPS:327291	04C	LC-06	LV-06	HC-11	HV-05	52C	LC-105	LV-105	HC-111	HV-105
iPS:327677	01A	LC-01	LV-01	HC-01	HV-01	58A	LC-111	LV-111	HC-120	HV-111
iPS:327678	05A	LC-08	LV-08	HC-13	HV-07	58A	LC-111	LV-111	HC-120	HV-111
iPS:327679	03A	LC-04	LV-04	HC-05	HV-03	58A	LC-111	LV-111	HC-120	HV-111
iPS:327680	04A	LC-06	LV-06	HC-09	HV-05	58A	LC-111	LV-111	HC-120	HV-111
iPS:327681	01B	LC-02	LV-02	HC-02	HV-02	58B	LC-112	LV-112	HC-121	HV-112
iPS:327682	05B	LC-09	LV-09	HC-14	HV-08	58B	LC-112	LV-112	HC-121	HV-112
iPS:327683	03B	LC-05	LV-05	HC-06	HV-04	58B	LC-112	LV-112	HC-121	HV-112
iPS:327684	04B	LC-07	LV-07	HC-10	HV-06	58B	LC-112	LV-112	HC-121	HV-112
iPS:327685	01C	LC-01	LV-01	HC-03	HV-01	58C	LC-111	LV-111	HC-122	HV-111
iPS:327686	05C	LC-08	LV-08	HC-15	HV-07	58C	LC-111	LV-111	HC-122	HV-111
iPS:327687	03C	LC-04	LV-04	HC-07	HV-03	58C	LC-111	LV-111	HC-122	HV-111
iPS:327688	04C	LC-06	LV-06	HC-11	HV-05	58C	LC-111	LV-111	HC-122	HV-111
iPS:327689	01A	LC-01	LV-01	HC-01	HV-01	53A	LC-105	LV-105	HC-113	HV-107
iPS:327690	05A	LC-08	LV-08	HC-13	HV-07	53A	LC-105	LV-105	HC-113	HV-107
iPS:327691	03A	LC-04	LV-04	HC-05	HV-03	53A	LC-105	LV-105	HC-113	HV-107
iPS:327693	04A	LC-06	LV-06	HC-09	HV-05	53A	LC-105	LV-105	HC-113	HV-107
iPS:327694	01B	LC-02	LV-02	HC-02	HV-02	53B	LC-106	LV-106	HC-114	HV-108

Heterodimeric Antibody Designation	Anti-PAC1 Receptor Antibody ID.	Anti-PAC1 Receptor Full Light Chain	Anti-PAC1 Receptor VL	Anti-PAC1 Receptor Full Heavy Chain	Anti-PAC1 Receptor VH	Anti-CGRP Receptor Antibody ID.	Anti- CGRP Receptor Full Light Chain	Anti- CGRP Receptor VL	Anti- CGRP Receptor Full Heavy Chain	Anti- CGRP Receptor VH
iPS:327696	05B	LC-09	LV-09	HC-14	HV-08	53B	LC-106	LV-106	HC-114	HV-108
iPS:327697	03B	LC-05	LV-05	HC-06	HV-04	53B	LC-106	LV-106	HC-114	HV-108
iPS:327698	04B	LC-07	LV-07	HC-10	HV-06	53B	LC-106	LV-106	HC-114	HV-108
iPS:327699	01C	LC-01	LV-01	HC-03	HV-01	53C	LC-105	LV-105	HC-115	HV-107
iPS:327700	05C	LC-08	LV-08	HC-15	HV-07	53C	LC-105	LV-105	HC-115	HV-107
iPS:327701	03C	LC-04	LV-04	HC-07	HV-03	53C	LC-105	LV-105	HC-115	HV-107
iPS:327702	04C	LC-06	LV-06	HC-11	HV-05	53C	LC-105	LV-105	HC-115	HV-107
iPS:327703	01A	LC-01	LV-01	HC-01	HV-01	54A	LC-107	LV-107	HC-109	HV-105
iPS:327704	05A	LC-08	LV-08	HC-13	HV-07	54A	LC-107	LV-107	HC-109	HV-105
iPS:327705	03A	LC-04	LV-04	HC-05	HV-03	54A	LC-107	LV-107	HC-109	HV-105
iPS:327706	04A	LC-06	LV-06	HC-09	HV-05	54A	LC-107	LV-107	HC-109	HV-105
iPS:327707	01B	LC-02	LV-02	HC-02	HV-02	54B	LC-108	LV-108	HC-110	HV-106
iPS:327708	05B	LC-09	LV-09	HC-14	HV-08	54B	LC-108	LV-108	HC-110	HV-106
iPS:327709	03B	LC-05	LV-05	HC-06	HV-04	54B	LC-108	LV-108	HC-110	HV-106
iPS:327710	04B	LC-07	LV-07	HC-10	HV-06	54B	LC-108	LV-108	HC-110	HV-106
iPS:327711	01C	LC-01	LV-01	HC-03	HV-01	54C	LC-107	LV-107	HC-111	HV-105
iPS:327712	05C	LC-08	LV-08	HC-15	HV-07	54C	LC-107	LV-107	HC-111	HV-105
iPS:327713	03C	LC-04	LV-04	HC-07	HV-03	54C	LC-107	LV-107	HC-111	HV-105
iPS:327714	04C	LC-06	LV-06	HC-11	HV-05	54C	LC-107	LV-107	HC-111	HV-105
iPS:327717	01A	LC-01	LV-01	HC-01	HV-01	55A	LC-109	LV-109	HC-109	HV-105
iPS:327718	05A	LC-08	LV-08	HC-13	HV-07	55A	LC-109	LV-109	HC-109	HV-105
iPS:327719	03A	LC-04	LV-04	HC-05	HV-03	55A	LC-109	LV-109	HC-109	HV-105
iPS:327721	04A	LC-06	LV-06	HC-09	HV-05	55A	LC-109	LV-109	HC-109	HV-105
iPS:327722	01B	LC-02	LV-02	HC-02	HV-02	55B	LC-110	LV-110	HC-110	HV-106
iPS:327724	05B	LC-09	LV-09	HC-14	HV-08	55B	LC-110	LV-110	HC-110	HV-106

Heterodimeric Antibody Designation	Anti-PAC1 Receptor Antibody ID.	Anti-PAC1 Receptor Full Light Chain	Anti-PAC1 Receptor VL	Anti-PAC1 Receptor Full Heavy Chain	Anti-PAC1 Receptor VH	Anti-CGRP Receptor Antibody ID.	Anti- CGRP Receptor Full Light Chain	Anti- CGRP Receptor VL	Anti- CGRP Receptor Full Heavy Chain	Anti- CGRP Receptor VH
iPS:327725	03B	LC-05	LV-05	HC-06	HV-04	55B	LC-110	LV-110	HC-110	HV-106
iPS:327726	04B	LC-07	LV-07	HC-10	HV-06	55B	LC-110	LV-110	HC-110	HV-106
iPS:327727	01C	LC-01	LV-01	HC-03	HV-01	55C	LC-109	LV-109	HC-111	HV-105
iPS:327728	05C	LC-08	LV-08	HC-15	HV-07	55C	LC-109	LV-109	HC-111	HV-105
iPS:327729	03C	LC-04	LV-04	HC-07	HV-03	55C	LC-109	LV-109	HC-111	HV-105
iPS:327730	04C	LC-06	LV-06	HC-11	HV-05	55C	LC-109	LV-109	HC-111	HV-105
iPS:327731	01A	LC-01	LV-01	HC-01	HV-01	56A	LC-107	LV-107	HC-113	LV-107
iPS:327732	05A	LC-08	LV-08	HC-13	HV-07	56A	LC-107	LV-107	HC-113	LV-107
iPS:327733	03A	LC-04	LV-04	HC-05	HV-03	56A	LC-107	LV-107	HC-113	LV-107
iPS:327734	04A	LC-06	LV-06	HC-09	HV-05	56A	LC-107	LV-107	HC-113	LV-107
iPS:327735	01B	LC-02	LV-02	HC-02	HV-02	56B	LC-108	LV-108	HC-114	LV-108
iPS:327736	05B	LC-09	LV-09	HC-14	HV-08	56B	LC-108	LV-108	HC-114	LV-108
iPS:327737	03B	LC-05	LV-05	HC-06	HV-04	56B	LC-108	LV-108	HC-114	LV-108
iPS:327738	04B	LC-07	LV-07	HC-10	HV-06	56B	LC-108	LV-108	HC-114	LV-108
iPS:327739	01C	LC-01	LV-01	HC-03	HV-01	56C	LC-107	LV-107	HC-115	LV-107
iPS:327740	05C	LC-08	LV-08	HC-15	HV-07	56C	LC-107	LV-107	HC-115	LV-107
iPS:327741	03C	LC-04	LV-04	HC-07	HV-03	56C	LC-107	LV-107	HC-115	LV-107
iPS:327742	04C	LC-06	LV-06	HC-11	HV-05	56C	LC-107	LV-107	HC-115	LV-107
iPS:327872	02A	LC-03	LV-03	HC-01	HV-01	58A	LC-111	LV-111	HC-120	HV-111
iPS:327874	06A	LC-10	LV-10	HC-17	HV-09	58A	LC-111	LV-111	HC-120	HV-111
iPS:327875	06B	LC-11	LV-11	HC-18	HV-10	58B	LC-112	LV-112	HC-121	HV-112
iPS:327876	02C	LC-03	LV-03	HC-03	HV-01	58C	LC-111	LV-111	HC-122	HV-111
iPS:327877	06C	LC-10	LV-10	HC-19	HV-09	58C	LC-111	LV-111	HC-122	HV-111
iPS:327878	02A	LC-03	LV-03	HC-01	HV-01	53A	LC-105	LV-105	HC-113	HV-107
iPS:327879	06A	LC-10	LV-10	HC-17	HV-09	53A	LC-105	LV-105	HC-113	HV-107

Heterodimeric Antibody Designation	Anti-PAC1 Receptor Antibody ID.	Anti-PAC1 Receptor Full Light Chain	Anti-PAC1 Receptor VL	Anti-PAC1 Receptor Full Heavy Chain	Anti-PAC1 Receptor VH	Anti-CGRP Receptor Antibody ID.	Anti- CGRP Receptor Full Light Chain	Anti- CGRP Receptor VL	Anti- CGRP Receptor Full Heavy Chain	Anti- CGRP Receptor VH
iPS:327880	06B	LC-11	LV-11	HC-18	HV-10	53B	LC-106	LV-106	HC-114	HV-108
iPS:327881	02C	LC-03	LV-03	HC-03	HV-01	53C	LC-105	LV-105	HC-115	HV-107
iPS:327882	06C	LC-10	LV-10	HC-19	HV-09	53C	LC-105	LV-105	HC-115	HV-107
iPS:327883	02A	LC-03	LV-03	HC-01	HV-01	54A	LC-107	LV-107	HC-109	HV-105
iPS:327884	06A	LC-10	LV-10	HC-17	HV-09	54A	LC-107	LV-107	HC-109	HV-105
iPS:327885	06B	LC-11	LV-11	HC-18	HV-10	54B	LC-108	LV-108	HC-110	HV-106
iPS:327886	02C	LC-03	LV-03	HC-03	HV-01	54C	LC-107	LV-107	HC-111	HV-105
iPS:327887	06C	LC-10	LV-10	HC-19	HV-09	54C	LC-107	LV-107	HC-111	HV-105
iPS:327888	02A	LC-03	LV-03	HC-01	HV-01	55A	LC-109	LV-109	HC-109	HV-105
iPS:327889	06A	LC-10	LV-10	HC-17	HV-09	55A	LC-109	LV-109	HC-109	HV-105
iPS:327890	06B	LC-11	LV-11	HC-18	HV-10	55B	LC-110	LV-110	HC-110	HV-106
iPS:327891	02C	LC-03	LV-03	HC-03	HV-01	55C	LC-109	LV-109	HC-111	HV-105
iPS:327892	06C	LC-10	LV-10	HC-19	HV-09	55C	LC-109	LV-109	HC-111	HV-105
iPS:327893	02A	LC-03	LV-03	HC-01	HV-01	56A	LC-107	LV-107	HC-113	LV-107
iPS:327894	06A	LC-10	LV-10	HC-17	HV-09	56A	LC-107	LV-107	HC-113	LV-107
iPS:327895	06B	LC-11	LV-11	HC-18	HV-10	56B	LC-108	LV-108	HC-114	LV-108
iPS:327896	02C	LC-03	LV-03	HC-03	HV-01	56C	LC-107	LV-107	HC-115	LV-107
iPS:327897	06C	LC-10	LV-10	HC-19	HV-09	56C	LC-107	LV-107	HC-115	LV-107
iPS:328031	02A	LC-03	LV-03	HC-01	HV-01	57A	LC-111	LV-111	HC-116	HV-109
iPS:328033	06A	LC-10	LV-10	HC-17	HV-09	57A	LC-111	LV-111	HC-116	HV-109
iPS:328034	06B	LC-11	LV-11	HC-18	HV-10	57B	LC-112	LV-112	HC-117	HV-110
iPS:328035	02C	LC-03	LV-03	HC-03	HV-01	57C	LC-111	LV-111	HC-118	HV-109
iPS:328036	06C	LC-10	LV-10	HC-19	HV-09	57C	LC-111	LV-111	HC-118	HV-109
iPS:328037	02A	LC-03	LV-03	HC-01	HV-01	50A	LC-101	LV-101	HC-101	HV-101
iPS:328038	06A	LC-10	LV-10	HC-17	HV-09	50A	LC-101	LV-101	HC-101	HV-101
iPS:328039	06B	LC-11	LV-11	HC-18	HV-10	50B	LC-102	LV-102	HC-102	HV-102
iPS:328040	02C	LC-03	LV-03	HC-03	HV-01	50C	LC-101	LV-101	HC-103	HV-101

Heterodimeric Antibody Designation	Anti-PAC1 Receptor Antibody ID.	Anti-PAC1 Receptor Full Light Chain	Anti-PAC1 Receptor VL	Anti-PAC1 Receptor Full Heavy Chain	Anti-PAC1 Receptor VH	Anti-CGRP Receptor Antibody ID.	Anti- CGRP Receptor Full Light Chain	Anti- CGRP Receptor VL	Anti- CGRP Receptor Full Heavy Chain	Anti- CGRP Receptor VH
iPS:328041	06C	LC-10	LV-10	HC-19	HV-09	50C	LC-101	LV-101	HC-103	HV-101
iPS:328042	02A	LC-03	LV-03	HC-01	HV-01	51A	LC-103	LV-103	HC-105	HV-103
iPS:328043	06A	LC-10	LV-10	HC-17	HV-09	51A	LC-103	LV-103	HC-105	HV-103
iPS:328044	06B	LC-11	LV-11	HC-18	HV-10	51B	LC-104	LV-104	HC-106	HV-104
iPS:328045	02C	LC-03	LV-03	HC-03	HV-01	51C	LC-103	LV-103	HC-107	HV-103
iPS:328046	06C	LC-10	LV-10	HC-19	HV-09	51C	LC-103	LV-103	HC-107	HV-103
iPS:328047	02A	LC-03	LV-03	HC-01	HV-01	52A	LC-105	LV-105	HC-109	HV-105
iPS:328048	06A	LC-10	LV-10	HC-17	HV-09	52A	LC-105	LV-105	HC-109	HV-105
iPS:328049	06B	LC-11	LV-11	HC-18	HV-10	52B	LC-106	LV-106	HC-110	HV-106
iPS:328050	02C	LC-03	LV-03	HC-03	HV-01	52C	LC-105	LV-105	HC-111	HV-105
iPS:328051	06C	LC-10	LV-10	HC-19	HV-09	52C	LC-105	LV-105	HC-111	HV-105

[0116] In certain embodiments, the bispecific antigen binding protein of the invention is a heterodimeric antibody selected from the antibodies designated as iPS:326417, iPS:326626, iPS:326628, iPS:326631, iPS:326634, iPS:327870, iPS:327871, iPS:326645, iPS:326648, iPS:326651, iPS:326654, iPS:328000, iPS:328001, iPS:326661, iPS:326663, iPS:326666, iPS:326669, iPS:327017, iPS:327018, iPS:327019, iPS:327023, iPS:327024, iPS:327025, iPS:327026, iPS:327091, iPS:327092, iPS:327093, iPS:327094, iPS:326414, iPS:327102, iPS:327103, iPS:327104, iPS:327105, iPS:327106, iPS:327107, iPS:327108, iPS:327109, iPS:327110, iPS:327111, iPS:327112, iPS:327267, iPS:327268, iPS:327269, iPS:327270, iPS:327272, iPS:327273, iPS:327274, iPS:327275, iPS:327276, iPS:327277, iPS:327278, iPS:327279, iPS:327280, iPS:327281, iPS:327282, iPS:327283, iPS:327284, iPS:327285, iPS:327286, iPS:327287, iPS:327288, iPS:327289, iPS:327290, iPS:327291, iPS:327677, iPS:327678, iPS:327679, iPS:327680, iPS:327681, iPS:327682, iPS:327683, iPS:327684, iPS:327685, iPS:327686, iPS:327687, iPS:327688, iPS:327689, iPS:327690, iPS:327691, iPS:327693, iPS:327694, iPS:327696, iPS:327697, iPS:327698, iPS:327699, iPS:327700, iPS:327701, iPS:327702, iPS:327703, iPS:327704, iPS:327705, iPS:327706, iPS:327707,

iPS:327708, iPS:327709, iPS:327710, iPS:327711, iPS:327712, iPS:327713, iPS:327714, iPS:327717, iPS:327718, iPS:327719, iPS:327721, iPS:327722, iPS:327724, iPS:327725, iPS:327726, iPS:327727, iPS:327728, iPS:327729, iPS:327730, iPS:327731, iPS:327732, iPS:327733, iPS:327734, iPS:327735, iPS:327736, iPS:327737, iPS:327738, iPS:327739, iPS:327740, iPS:327741, iPS:327742, iPS:327872, iPS:327874, iPS:327875, iPS:327876, iPS:327877, iPS:327878, iPS:327879, iPS:327880, iPS:327881, iPS:327882, iPS:327883, iPS:327884, iPS:327885, iPS:327886, iPS:327887, iPS:327888, iPS:327889, iPS:327890, iPS:327891, iPS:327892, iPS:327893, iPS:327894, iPS:327895, iPS:327896, iPS:327897, iPS:328031, iPS:328033, iPS:328034, iPS:328035, iPS:328036, iPS:328037, iPS:328038, iPS:328039, iPS:328040, iPS:328041, iPS:328042, iPS:328043, iPS:328044, iPS:328045, iPS:328046, iPS:328047, iPS:328048, iPS:328049, iPS:328050, or iPS:328051 as set forth in Table 8. In some embodiments, the heterodimeric antibody is an antibody selected from the antibodies designated as iPS:327730, iPS:327680, iPS: 328001, iPS:327741, iPS:326648, iPS:327689, iPS:327111, iPS:327742, iPS:327698, iPS:327272, iPS:327717, iPS:327702, iPS:327270, iPS:327026, iPS:327112, iPS:327283, iPS:327688, or iPS:327714 as set forth in Table 8. In other embodiments, the heterodimeric antibody is an antibody selected from the antibodies designated as iPS:327730, iPS:327680, iPS: 328001, iPS:327741, iPS:326648, iPS:327689, iPS:327111, iPS:327742, iPS:327698, iPS:327272, iPS:327717, iPS:327702, or iPS:327270 as set forth in Table 8. In particular embodiments, the heterodimeric antibody is an antibody designated as iPS:327689 or iPS:327742 as set forth in Table 8.

[0117] The inventive heterodimeric antibodies also encompass antibodies comprising the heavy chain(s) and/or light chain(s) described herein, where one, two, three, four or five amino acid residues are lacking from the N-terminus or C-terminus, or both, in relation to any one of the heavy and light chains set forth in Tables 6A, 6B, 7A, and 7B, e.g., due to post-translational modifications resulting from the type of host cell in which the antibodies are expressed. For instance, Chinese Hamster Ovary (CHO) cells frequently cleave off a C-terminal lysine from antibody heavy chains.

[0118] In certain embodiments, the antigen binding proteins of the invention comprise (i) a first binding domain that specifically binds to human CGRP receptor, (ii) a second binding domain that specifically binds to human PAC1 receptor, and (iii) a human immunoglobulin Fc region, wherein one of the binding domains is positioned at the amino terminus of the Fc region and the

other binding domain is positioned at the carboxyl terminus of the Fc region. In some such embodiments, each of the first and second binding domains comprises immunoglobulin variable regions. For instance, in certain embodiments, the first binding domain comprises a first light chain variable region (VL1) and a first heavy chain variable region (VH1) from an anti-CGRP receptor antibody and the second binding domain comprises a second light chain variable region (VL2) and a second heavy chain variable region (VH2) from an anti-PAC1 receptor antibody.

[0119] As used herein, 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. The Fc region of an immunoglobulin generally comprises two constant domains, a CH2 domain and a CH3 domain, and optionally comprises a CH4 domain. In certain embodiments, the Fc region is an Fc region from an IgG1, IgG2, IgG3, or IgG4 immunoglobulin. In some embodiments, the Fc region comprises CH2 and CH3 domains from a human IgG1 or human IgG2 immunoglobulin. The Fc region may retain effector function, such as C1q binding, complement dependent cytotoxicity (CDC), Fc receptor binding, antibody-dependent cell-mediated cytotoxicity (ADCC), and phagocytosis. In other embodiments, the Fc region may be modified to reduce or eliminate effector function as described in further detail herein.

[0120] In some embodiments of the antigen binding proteins of the invention, the binding domain positioned at the carboxyl terminus of the Fc region (i.e. the carboxyl-terminal binding domain) is a scFv. In certain embodiments, the scFv comprises a heavy chain variable region (VH) and light chain variable region (VL) connected by a peptide linker. The variable regions may be oriented within the scFv in a VH-VL or VL-VH orientation. For instance, in one embodiment, the scFv comprises, from N-terminus to C-terminus, a VH region, a peptide linker, and a VL region. In another embodiment, the scFv comprises, from N-terminus to C-terminus, a VL region, a peptide linker, and a VH region. The VH and VL regions of the scFv may contain one or more cysteine substitutions to permit disulfide bond formation between the VH and VL regions. Such cysteine clamps stabilize the two variable domains in the antigen-binding configuration. In one embodiment, position 44 (Kabat numbering) in the VH region and position 100 (Kabat numbering) in the VL region are each substituted with a cysteine residue.

[0121] In certain embodiments, the scFv is fused or otherwise connected at its amino terminus to the carboxyl terminus of the Fc region (e.g. the carboxyl terminus of the CH3 domain) through a peptide linker. Thus, in one embodiment, the scFv is fused to an Fc region such that the resulting

fusion protein comprises, from N-terminus to C-terminus, a CH2 domain, a CH3 domain, a first peptide linker, a VH region, a second peptide linker, and a VL region. In another embodiment, the scFv is fused to an Fc region such that the resulting fusion protein comprises, from N-terminus to C-terminus, a CH2 domain, a CH3 domain, a first peptide linker, a VL region, a second peptide linker, and a VH region. A "fusion protein" is a protein that includes polypeptide components derived from more than one parental protein or polypeptide. Typically, a fusion protein is expressed from a fusion gene in which a nucleotide sequence encoding a polypeptide sequence from one protein is appended in frame with, and optionally separated by a linker from, a nucleotide sequence encoding a polypeptide sequence from a different protein. The fusion gene can then be expressed by a recombinant host cell to produce the single fusion protein.

[0122] A "peptide linker" refers to an oligopeptide of about 2 to about 50 amino acids that covalently joins one polypeptide to another polypeptide. The peptide linkers can be used to connect the VH and VL domains within the scFv. The peptide linkers can also be used to connect a scFv, Fab fragment, or other functional antibody fragment to the amino terminus or carboxyl terminus of an Fc region to create bispecific antigen binding proteins as described herein. Preferably, the peptide linkers are at least 5 amino acids in length. In certain embodiments, the peptide linkers are from about 5 amino acids in length to about 40 amino acids in length. In other embodiments, the peptide linkers are from about 8 amino acids in length to about 30 amino acids in length. In still other embodiments, the peptide linkers are from about 10 amino acids in length to about 20 amino acids in length.

[0123] Preferably, but not necessarily, the peptide linker comprises amino acids from among the twenty canonical amino acids, particularly cysteine, glycine, alanine, proline, asparagine, glutamine, and /or serine. In certain embodiments, the peptide linker is comprised of a majority of amino acids that are sterically unhindered, such as glycine, serine, and alanine. Thus, linkers that are preferred in some embodiments, include polyglycines, polyserines, and polyalanines, or combinations of any of these. Some exemplary peptide linkers include, but are not limited to, poly$(Gly)_{2-8}$, particularly $(Gly)_3$, $(Gly)_4$ (SEQ ID NO: 362), $(Gly)_5$ (SEQ ID NO: 363) and $(Gly)_7$ (SEQ ID NO: 364), as well as, poly$(Gly)_4Ser$ (SEQ ID NO: 365), poly$(Gly\text{-}Ala)_{2-4}$ and poly$(Ala)_{2-8}$. In certain embodiments, the peptide linker is $(Gly_xSer)_n$ where x=3 or 4 and n= 2, 3, 4, 5 or 6. Such peptide linkers include "L5" (GGGGS; or "G_4S"; SEQ ID NO: 366), "L9" (GGGSGGGGS; or "G_3SG_4S"; SEQ ID NO: 367), "L10" (GGGGSGGGGS; or "$(G_4S)_2$"; SEQ

ID NO: 368), "L15" (GGGGSGGGGSGGGGS; or "$(G_4S)_3$"; SEQ ID NO: 369), and "L25" (GGGGSGGGGSGGGGSGGGGSGGGGS; or "$(G_4S)_5$"; SEQ ID NO:370). In some embodiments, the peptide linker joining the VH and VL regions within the scFv is a L15 or $(G_4S)_3$ linker (SEQ ID NO: 369). In these and other embodiments, the peptide linker joining the carboxyl-terminal binding domain (e.g. scFv or Fab) to the C-terminus of the Fc region is a L9 or G_3SG_4S linker (SEQ ID NO: 367) or a L10 $(G_4S)_2$ linker (SEQ ID NO: 368).

[0124] Other specific examples of peptide linkers that may be used in the bispecific antigen binding proteins of the invention include $(Gly)_5Lys$ (SEQ ID NO: 371); $(Gly)_5LysArg$ (SEQ ID NO: 372); $(Gly)_3Lys(Gly)_4$ (SEQ ID NO: 373); $(Gly)_3AsnGlySer(Gly)_2$ (SEQ ID NO: 374); $(Gly)_3Cys(Gly)_4$ (SEQ ID NO: 375); GlyProAsnGlyGly (SEQ ID NO: 376); GGEGGG (SEQ ID NO: 377); GGEEEGGG (SEQ ID NO: 378); GEEEG (SEQ ID NO: 379); GEEE (SEQ ID NO: 380); GGDGGG (SEQ ID NO: 381); GGDDDGG (SEQ ID NO: 382); GDDDG (SEQ ID NO: 383); GDDD (SEQ ID NO: 384); GGGGSDDSDEGSDGEDGGGGS (SEQ ID NO: 385); WEWEW (SEQ ID NO: 386); FEFEF (SEQ ID NO: 387); EEEWWW (SEQ ID NO: 388); EEEFFF (SEQ ID NO: 389); WWEEEWW (SEQ ID NO: 390); and FFEEEFF (SEQ ID NO: 391).

[0125] In certain embodiments of the bispecific antigen binding proteins of the invention, the binding domain positioned at the amino terminus of the Fc region (i.e. the amino-terminal binding domain) is a Fab fragment fused to the amino terminus of the Fc region through a peptide linker described herein or through an immunoglobulin hinge region. An "immunoglobulin hinge region" refers to the amino acid sequence connecting the CH1 domain and the CH2 domain of an immunoglobulin heavy chain. The hinge region of human IgG1 is generally defined as the amino acid sequence from about Glu216 or about Cys226, to about Pro230. Hinge regions of other IgG isotypes may be aligned with the IgG1 sequence by placing the first and last cysteine residues forming inter-heavy chain disulfide bonds in the same positions and are determinable to those of skill in the art. In some embodiments, the amino-terminal binding domain is joined to the amino terminus of the Fc region through a human IgG1 hinge region. In other embodiments, the amino-terminal binding domain is joined to the amino terminus of the Fc region through a human IgG2 hinge region. Preferably, the amino-terminal binding domain (e.g. Fab fragment) is fused to the Fc region through the carboxyl terminus of the CH1 region of the Fab.

[0126] In some embodiments, the bispecific antigen binding protein of the invention comprises a first antibody that specifically binds to a first target (e.g. human CGRP receptor or human PAC1 receptor) where a scFv comprising variable domains from a second antibody that specifically binds to a second target (e.g. human CGRP receptor or human PAC1 receptor) is fused to the carboxyl terminus of the heavy chain of the first antibody. This format is referred to herein as the "IgG-scFv" format, and one embodiment of this type of molecule is shown schematically in Figure 2. Thus, in certain embodiments, the present invention includes a bispecific, multivalent antigen binding protein comprising: (i) a light chain and a heavy chain from a first antibody, and (ii) a scFv comprising VL and VH regions from a second antibody, wherein the scFv is fused at its amino terminus to the carboxyl terminus of the heavy chain through a peptide linker to form a modified heavy chain, and wherein the first or second antibody specifically binds to human CGRP receptor and the other antibody specifically binds to human PAC1 receptor. When dimerized, the bispecific antigen binding protein is a homotetramer comprising two light chains and two modified heavy chains.

[0127] As used herein, the term "modified heavy chain" refers to a fusion protein comprising an immunoglobulin heavy chain, particularly a human IgG1 or human IgG2 heavy chain, and a functional antibody fragment (e.g. scFv, Fab) or portion thereof (e.g. immunoglobulin light chain or Fd fragment), wherein the fragment or portion thereof is fused at its N-terminus, optionally through a peptide linker, to the C-terminus of the heavy chain.

[0128] In the IgG-scFv format of the bispecific antigen binding proteins of the invention, an anti-PAC1 receptor antibody can be the first antibody (i.e. the "IgG") or the second antibody (i.e. from which the scFv is derived). Similarly, an anti-CGRP receptor antibody can be the first antibody (i.e. the "IgG") or the second antibody (i.e. from which the scFv is derived). Any of the anti-PAC1 receptor antibody variable regions set forth in Tables 1A and 1B can be incorporated into either the IgG component or the scFv component of the bispecific antigen binding proteins of the invention. Any of the anti-CGRP receptor antibody variable regions set forth in Tables 3A and 3B can be incorporated into either the IgG component or the scFv component of the bispecific antigen binding proteins of the invention.

[0129] Amino acid sequences for light chains and modified heavy chains of exemplary antigen binding proteins of the invention in the IgG-scFv format are summarized in Table 9 below. The molecules listed in the first half of the table comprise an anti-PAC1 receptor IgG component and

an anti-CGRP receptor scFv, whereas the molecules listed in the second half of the table comprise an anti-CGRP receptor IgG component and an anti-PAC1 receptor scFv.

Table 9. Amino Acid Sequences of Exemplary Bispecific Antigen Binding Proteins in the IgG-scFv Format

IgG-scFv Molecule Designation	Light Chain Amino Acid Sequence	Modified Heavy Chain Amino Acid Sequence
Anti-PAC1 Receptor IgG x Anti-CGRP Receptor scFv		
iPS:386738	DIQLTQSPSFLSASVGD RVTITCRASQSIGRSLH WYQQKPGKAPKLLIK YASQSLSGVPSRFSGS GSGTEFTLTISSLQPED FATYYCHQSSRLPFTF GPGTKVDIKRTVAAPS VFIFPPSDEQLKSGTAS VVCLLNNFYPREAKV QWKVDNALQSGNSQE SVTEQDSKDSTYSLSS TLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC (SEQ ID NO: 392)	QVQLVESGAEVVKPGASVKVSCKASGFTFSRFAMHWVRQAP GQGLEWMGVISYDGGNKYYAESVKGRVTMTRDTSTSTLYME LSSLRSEDTAVYYCARGYDVLTGYPDYWGQGTLVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGGGGSQVQLVE SGGGVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPGKCLEW VAVISFDGSIKYSVDSVKGRFTISRDNSKNTLFLQMNSLRAEDT AVYYCARDRLNYYDSSGYYHYKYYGMAVWGQGTTVTVSSG GGGSGGGGSGGGGSQSVLTQPPSVSAAPGQKVTISCSGSSSNI GNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTST TLGITGLQTGDEADYYCGTWDSRLSAVVFGCGTKLTVL (SEQ ID NO: 396)
iPS:386764	SEQ ID NO: 392	QVQLVESGAEVVKPGASVKVSCKASGFTFSRFAMHWVRQAP GQGLEWMGVISYDGGNKYYAESVKGRVTMTRDTSTSTLYME LSSLRSEDTAVYYCARGYDVLTGYPDYWGQGTLVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGGGGSQSVLTQ PPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIY DNNKRPSGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWD SRLSAVVFGGGTKLTVLGGGGSGGGGSGGGGSQVQLVESGG GVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPGKGLEWVAVI SFDGSIKYSVDSVKGRFTISRDNSKNTLFLQMNSLRAEDTAVY YCARDRLNYYDSSGYYHYKYYGMAVWGQGTTVTVSS (SEQ ID NO: 397)
iPS:386762	SEQ ID NO: 392	QVQLVESGAEVVKPGASVKVSCKASGFTFSRFAMHWVRQAP GQGLEWMGVISYDGGNKYYAESVKGRVTMTRDTSTSTLYME LSSLRSEDTAVYYCARGYDVLTGYPDYWGQGTLVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL

IgG-scFv Molecule Designation	Light Chain Amino Acid Sequence	Modified Heavy Chain Amino Acid Sequence
		MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGGGGSQSVLTQ PPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIY DNNKRPSGIPDRFSGSKSGTSATLAITGLQTGDEADYYCGTWD SRLSAVVFGGGTKLTVLGGGGSGGGGSGGGGSQVQLVESGG GVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPGKGLEWVAVI SFDGSIKYSVDSVKGRFTISRDNSKNTLFLQMNSLRAEDTAVY YCARDRLNYYDSSGYYHYKYYGMAVWGQGTTVTVSS (SEQ ID NO: 398)
iPS:386760	SEQ ID NO: 392	QVQLVESGAEVVKPGASVKVSCKASGFTFSRFAMHWVRQAP GQGLEWMGVISYDGGNKYYAESVKGRVTMTRDTSTSTLYME LSSLRSEDTAVYYCARGYDVLTGYPDYWGQGTLVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGGGGSQSVLTQ PPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIY DNNKRPSGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWD SRLSAVVFGGGTKLTVLGGGGSGGGGSGGGGSQVQLVESGG GVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPGKGLEWVAVI SFDGSIKYSVDSVKGRFTISRDNSKNTLFLQMNSLRAEDTAVY YCARDRLNYYESSGYYHYKYYGMAVWGQGTTVTVSS (SEQ ID NO: 399)
iPS:386758	SEQ ID NO: 392	QVQLVESGAEVVKPGASVKVSCKASGFTFSRFAMHWVRQAP GQGLEWMGVISYDGGNKYYAESVKGRVTMTRDTSTSTLYME LSSLRSEDTAVYYCARGYDVLTGYPDYWGQGTLVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGGGGSQSVLTQ PPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIY DNNKRPSGIPDRFSGSKSGTSTTLGITGLQTGDEADYYCGTWD SRLSAVVFGGGTKLTVLGGGGSGGGGSGGGGSQVQLVESGG GVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPGKGLEWVAVI SFDGSIKYSVDSVKGRFTISRDNSKNTLFLQMNSLRAEDTAVY YCARDRLNYYESSGYYHYKYYGMAVWGQGTTVTVSS (SEQ ID NO: 400)
iPS:386756	SEQ ID NO: 392	QVQLVESGAEVVKPGASVKVSCKASGFTFSRFAMHWVRQAP GQGLEWMGVISYDGGNKYYAESVKGRVTMTRDTSTSTLYME LSSLRSEDTAVYYCARGYDVLTGYPDYWGQGTLVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN

IgG-scFv Molecule Designation	Light Chain Amino Acid Sequence	Modified Heavy Chain Amino Acid Sequence
		TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGGGGSQSVLTQ PPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIY DNNKRPSGIPDRFSGSKSGTSTTLGITGLQTGDEADYYCGTWD SRLSAVVFGGGTKLTVLGGGGSGGGGSGGGGSQVQLVESGG GVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPGKGLEWVAVI SFDGSIKYSVDSVKGRFTISRDNSKNTLFLQMNSLRAEDTAVY YCARDRLNYYDSSGYYHYKYYGMAVWGQGTTVTVSS (SEQ ID NO: 401)
iPS:386754	SEQ ID NO: 392	QVQLVESGAEVVKPGASVKVSCKASGFTFSRFAMHWVRQAP GQGLEWMGVISYDGGNKYYAESVKGRVTMTRDTSTSTLYME LSSLRSEDTAVYYCARGYDVLTGYPDYWGQGTLVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGGGGSQVQLVE SGGGVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPGKGLEW VAVISFDGSIKYSVDSVKGRFTISRDNSKNTLFLQMNSLRAEDT AVYYCARDRLNYYESSGYYHYKYYGMAVWGQGTTVTVSSG GGGSGGGGSGGGGSQSVLTQPPSVSAAPGQKVTISCSGSSSNI GNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTST TLGITGLQTGDEADYYCGTWDSRLSAVVFGGGTKLTVL (SEQ ID NO: 402)
iPS:386752	SEQ ID NO: 392	QVQLVESGAEVVKPGASVKVSCKASGFTFSRFAMHWVRQAP GQGLEWMGVISYDGGNKYYAESVKGRVTMTRDTSTSTLYME LSSLRSEDTAVYYCARGYDVLTGYPDYWGQGTLVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGGGGSQVQLVE SGGGVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPGKGLEW VAVISFDGSIKYSVDSVKGRFTISRDNSKNTLFLQMNSLRAEDT AVYYCARDRLNYYDSSGYYHYKYYGMAVWGQGTTVTVSSG GGGSGGGGSGGGGSQSVLTQPPSVSAAPGQKVTISCSGSSSNI GNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTSA TLGITGLQTGDEADYYCGTWDSRLSAVVFGGGTKLTVL (SEQ ID NO: 403)
iPS:386750	SEQ ID NO: 392	QVQLVESGAEVVKPGASVKVSCKASGFTFSRFAMHWVRQAP GQGLEWMGVISYDGGNKYYAESVKGRVTMTRDTSTSTLYME LSSLRSEDTAVYYCARGYDVLTGYPDYWGQGTLVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT

IgG-scFv Molecule Designation	Light Chain Amino Acid Sequence	Modified Heavy Chain Amino Acid Sequence
		SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGGGGSQVQLVE SGGGVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPGKCLEW VAVISFDGSIKYSVDSVKGRFTISRDNSKNTLFLQMNSLRAEDT AVYYCARDRLNYYDSSGYYHYKYYGMAVWGQGTTVTVSSG GGGSGGGGSGGGGSQSVLTQPPSVSAAPGQKVTISCSGSSSNI GNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTSA TLGITGLQTGDEADYYCGTWDSRLSAVVFGCGTKLTVL (SEQ ID NO: 404)
iPS:386748	SEQ ID NO: 392	QVQLVESGAEVVKPGASVKVSCKASGFTFSRFAMHWVRQAP GQGLEWMGVISYDGGNKYYAESVKGRVTMTRDTSTSTLYME LSSLRSEDTAVYYCARGYDVLTGYPDYWGQGTLVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGGGGSQVQLVE SGGGVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPGKGLEW VAVISFDGSIKYSVDSVKGRFTISRDNSKNTLFLQMNSLRAEDT AVYYCARDRLNYYESSGYYHYKYYGMAVWGQGTTVTVSSG GGGSGGGGSGGGGSQSVLTQPPSVSAAPGQKVTISCSGSSSNI GNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTSA TLGITGLQTGDEADYYCGTWDSRLSAVVFGGGTKLTVL (SEQ ID NO: 405)
iPS:386746	SEQ ID NO: 392	QVQLVESGAEVVKPGASVKVSCKASGFTFSRFAMHWVRQAP GQGLEWMGVISYDGGNKYYAESVKGRVTMTRDTSTSTLYME LSSLRSEDTAVYYCARGYDVLTGYPDYWGQGTLVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGGGGSQVQLVE SGGGVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPGKGLEW VAVISFDGSIKYSVDSVKGRFTISRDNSKNTLFLQMNSLRAEDT AVYYCARDRLNYYDSSGYYHYKYYGMAVWGQGTTVTVSSG GGGSGGGGSGGGGSQSVLTQPPSVSAAPGQKVTISCSGSSSNI GNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTSA TLAITGLQTGDEADYYCGTWDSRLSAVVFGGGTKLTVL (SEQ ID NO: 406)
iPS:386744	SEQ ID NO: 392	QVQLVESGAEVVKPGASVKVSCKASGFTFSRFAMHWVRQAP GQGLEWMGVISYDGGNKYYAESVKGRVTMTRDTSTSTLYME LSSLRSEDTAVYYCARGYDVLTGYPDYWGQGTLVTVSSASTK

IgG-scFv Molecule Designation	Light Chain Amino Acid Sequence	Modified Heavy Chain Amino Acid Sequence
		GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGGGGSQVQLVE SGGGVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPGKCLEW VAVISFDGSIKYSVDSVKGRFTISRDNSKNTLFLQMNSLRAEDT AVYYCARDRLNYYDSSGYYHYKYYGMAVWGQGTTVTVSSG GGGSGGGGSGGGGSQSVLTQPPSVSAAPGQKVTISCSGSSSNI GNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTSA TLAITGLQTGDEADYYCGTWDSRLSAVVFGCGTKLTVL (SEQ ID NO: 407)
iPS:386742	SEQ ID NO: 392	QVQLVESGAEVVKPGASVKVSCKASGFTFSRFAMHWVRQAP GQGLEWMGVISYDGGNKYYAESVKGRVTMTRDTSTSTLYME LSSLRSEDTAVYYCARGYDVLTGYPDYWGQGTLVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGGGGSQVQLVE SGGGVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPGKCLEW VAVISFDGSIKYSVDSVKGRFTISRDNSKNTLFLQMNSLRAEDT AVYYCARDRLNYYESSGYYHYKYYGMAVWGQGTTVTVSSG GGGSGGGGSGGGGSQSVLTQPPSVSAAPGQKVTISCSGSSSNI GNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTSA TLGITGLQTGDEADYYCGTWDSRLSAVVFGCGTKLTVL (SEQ ID NO: 408)
iPS:386740	SEQ ID NO: 392	QVQLVESGAEVVKPGASVKVSCKASGFTFSRFAMHWVRQAP GQGLEWMGVISYDGGNKYYAESVKGRVTMTRDTSTSTLYME LSSLRSEDTAVYYCARGYDVLTGYPDYWGQGTLVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGGGGSQVQLVE SGGGVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPGKCLEW VAVISFDGSIKYSVDSVKGRFTISRDNSKNTLFLQMNSLRAEDT AVYYCARDRLNYYESSGYYHYKYYGMAVWGQGTTVTVSSG GGGSGGGGSGGGGSQSVLTQPPSVSAAPGQKVTISCSGSSSNI GNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTST TLGITGLQTGDEADYYCGTWDSRLSAVVFGCGTKLTVL (SEQ ID NO: 409)
iPS:386736	SEQ ID NO: 392	QVQLVESGAEVVKPGASVKVSCKASGFTFSRFAMHWVRQAP GQGLEWMGVISYDGGNKYYAESVKGRVTMTRDTSTSTLYME

IgG-scFv Molecule Designation	Light Chain Amino Acid Sequence	Modified Heavy Chain Amino Acid Sequence
		LSSLRSEDTAVYYCARGYDVLTGYPDYWGQGTLVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGGGGSQVQLVE SGGGVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPGKGLEW VAVISFDGSIKYSVDSVKGRFTISRDNSKNTLFLQMNSLRAEDT AVYYCARDRLNYYDSSGYYHYKYYGMAVWGQGTTVTVSSG GGGSGGGGSGGGGSQSVLTQPPSVSAAPGQKVTISCSGSSSNI GNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTST TLGITGLQTGDEADYYCGTWDSRLSAVVFGGGTKLTVL (SEQ ID NO: 410)
Anti-CGRP Receptor IgG x Anti-PAC1 Receptor scFv		
iPS:386731	QSVLTQPPSVSAAPGQ KVTISCSGSSSNIGNNY VSWYQQLPGTAPKLLI YDNNKRPSGIPDRFSG SKSGTSTTLGITGLQTG DEADYYCGTWDSRLS AVVFGGGTKLTVLGQ PKANPTVTLFPPSSEEL QANKATLVCLISDFYP GAVTVAWKADGSPVK AGVETTKPSKQSNNK YAASSYLSLTPEQWKS HRSYSCQVTHEGSTVE KTVAPTECS (SEQ ID NO: 393)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPG KGLEWVAVISFDGSIKYSVDSVKGRFTISRDNSKNTLFLQMNS LRAEDTAVYYCARDRLNYYESSGYYHYKYYGMAVWGQGTT VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY ICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVF LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGG GGSDIQLTQSPSFLSASVGDRVTITCRASQSIGRSLHWYQQKPG KAPKLLIKYASQSLSGVPSRFSGSGSGTEFTLTISSLQPEDFATY YCHQSSRLPFTFGPGTKVDIKRGGGGSGGGGSGGGGSQVQLV ESGAEVVKPGASVKVSCKASGFTFSRFAMHWVRQAPGQGLE WMGVISYDGGNKYYAESVKGRVTMTRDTSTSTLYMELSSLR SEDTAVYYCARGYDVLTGYPDYWGQGTLVTVSS (SEQ ID NO: 411)
iPS:386725	SEQ ID NO: 393	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPG KGLEWVAVISFDGSIKYSVDSVKGRFTISRDNSKNTLFLQMNS LRAEDTAVYYCARDRLNYYDSSGYYHYKYYGMAVWGQGTT VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY ICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVF LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGG GGSDIQLTQSPSFLSASVGDRVTITCRASQSIGRSLHWYQQKPG KAPKLLIKYASQSLSGVPSRFSGSGSGTEFTLTISSLQPEDFATY YCHQSSRLPFTFGPGTKVDIKRGGGGSGGGGSGGGGSQVQLV ESGAEVVKPGASVKVSCKASGFTFSRFAMHWVRQAPGQGLE WMGVISYDGGNKYYAESVKGRVTMTRDTSTSTLYMELSSLR SEDTAVYYCARGYDVLTGYPDYWGQGTLVTVSS (SEQ ID NO: 412)

IgG-scFv Molecule Designation	Light Chain Amino Acid Sequence	Modified Heavy Chain Amino Acid Sequence
iPS:386717	SEQ ID NO: 393	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPG KGLEWVAVISFDGSIKYSVDSVKGRFTISRDNSKNTLFLQMNS LRAEDTAVYYCARDRLNYYESSGYYHYKYYGMAVWGQGTT VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY ICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVF LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGG GGSQVQLVESGAEVVKPGASVKVSCKASGFTFSRFAMHWVR QAPGQGLEWMGVISYDGGNKYYAESVKGRVTMTRDTSTSTL YMELSSLRSEDTAVYYCARGYDVLTGYPDYWGQGTLVTVSS GGGGSGGGGSGGGGSDIQLTQSPSFLSASVGDRVTITCRASQSI GRSLHWYQQKPGKCPKLLIKYASQSLSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCHQSSRLPFTFGCGTKVDIKR (SEQ ID NO: 413)
iPS:386715	SEQ ID NO: 393	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPG KGLEWVAVISFDGSIKYSVDSVKGRFTISRDNSKNTLFLQMNS LRAEDTAVYYCARDRLNYYDSSGYYHYKYYGMAVWGQGTT VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY ICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVF LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGG GGSQVQLVESGAEVVKPGASVKVSCKASGFTFSRFAMHWVR QAPGQGLEWMGVISYDGGNKYYAESVKGRVTMTRDTSTSTL YMELSSLRSEDTAVYYCARGYDVLTGYPDYWGQGTLVTVSS GGGGSGGGGSGGGGSDIQLTQSPSFLSASVGDRVTITCRASQSI GRSLHWYQQKPGKCPKLLIKYASQSLSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCHQSSRLPFTFGCGTKVDIKR (SEQ ID NO: 414)
iPS:386707	SEQ ID NO: 393	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPG KGLEWVAVISFDGSIKYSVDSVKGRFTISRDNSKNTLFLQMNS LRAEDTAVYYCARDRLNYYESSGYYHYKYYGMAVWGQGTT VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY ICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVF LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGG GGSQVQLVESGAEVVKPGASVKVSCKASGFTFSRFAMHWVR QAPGQGLEWMGVISYDGGNKYYAESVKGRVTMTRDTSTSTL YMELSSLRSEDTAVYYCARGYDVLTGYPDYWGQGTLVTVSS GGGGSGGGGSGGGGSDIQLTQSPSFLSASVGDRVTITCRASQSI GRSLHWYQQKPGKAPKLLIKYASQSLSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCHQSSRLPFTFGPGTKVDIKR (SEQ ID

IgG-scFv Molecule Designation	Light Chain Amino Acid Sequence	Modified Heavy Chain Amino Acid Sequence
		NO: 415)
iPS:386705	SEQ ID NO: 393	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPG KGLEWVAVISFDGSIKYSVDSVKGRFTISRDNSKNTLFLQMNS LRAEDTAVYYCARDRLNYYDSSGYYHYKYYGMAVWGQGTT VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY ICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVF LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGG GGSQVQLVESGAEVVKPGASVKVSCKASGFTFSRFAMHWVR QAPGQGLEWMGVISYDGGNKYYAESVKGRVTMTRDTSTSTL YMELSSLRSEDTAVYYCARGYDVLTGYPDYWGQGTLVTVSS GGGGSGGGGSGGGGSDIQLTQSPSFLSASVGDRVTITCRASQSI GRSLHWYQQKPGKAPKLLIKYASQSLSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCHQSSRLPFTFGPGTKVDIKR (SEQ ID NO: 416)
iPS:386723	QSVLTQPPSVSAAPGQ KVTISCSGSSSNIGNNY VSWYQQLPGTAPKLLI YDNNKRPSGIPDRFSG SKSGTSATLGITGLQT GDEADYYCGTWDSRL SAVVFGGGTKLTVLG QPKANPTVTLFPPSSEE LQANKATLVCLISDFY PGAVTVAWKADGSPV KAGVETTKPSKQSNN KYAASSYLSLTPEQW KSHRSYSCQVTHEGST VEKTVAPTECS (SEQ ID NO: 394)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPG KGLEWVAVISFDGSIKYSVDSVKGRFTISRDNSKNTLFLQMNS LRAEDTAVYYCARDRLNYYESSGYYHYKYYGMAVWGQGTT VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY ICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVF LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGG GGSQVQLVESGAEVVKPGASVKVSCKASGFTFSRFAMHWVR QAPGQGLEWMGVISYDGGNKYYAESVKGRVTMTRDTSTSTL YMELSSLRSEDTAVYYCARGYDVLTGYPDYWGQGTLVTVSS GGGGSGGGGSGGGGSDIQLTQSPSFLSASVGDRVTITCRASQSI GRSLHWYQQKPGKCPKLLIKYASQSLSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCHQSSRLPFTFGCGTKVDIKR (SEQ ID NO: 417)
iPS:386719	SEQ ID NO: 394	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPG KGLEWVAVISFDGSIKYSVDSVKGRFTISRDNSKNTLFLQMNS LRAEDTAVYYCARDRLNYYDSSGYYHYKYYGMAVWGQGTT VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY ICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVF LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGG GGSQVQLVESGAEVVKPGASVKVSCKASGFTFSRFAMHWVR QAPGQGLEWMGVISYDGGNKYYAESVKGRVTMTRDTSTSTL YMELSSLRSEDTAVYYCARGYDVLTGYPDYWGQGTLVTVSS GGGGSGGGGSGGGGSDIQLTQSPSFLSASVGDRVTITCRASQSI GRSLHWYQQKPGKCPKLLIKYASQSLSGVPSRFSGSGSGTEFT

IgG-scFv Molecule Designation	Light Chain Amino Acid Sequence	Modified Heavy Chain Amino Acid Sequence
		LTISSLQPEDFATYYCHQSSRLPFTFGCGTKVDIKR (SEQ ID NO: 418)
iPS:386713	SEQ ID NO: 394	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPG KGLEWVAVISFDGSIKYSVDSVKGRFTISRDNSKNTLFLQMNS LRAEDTAVYYCARDRLNYYESSGYYHYKYYGMAVWGQGTT VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY ICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVF LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGG GGSQVQLVESGAEVVKPGASVKVSCKASGFTFSRFAMHWVR QAPGQGLEWMGVISYDGGNKYYAESVKGRVTMTRDTSTSTL YMELSSLRSEDTAVYYCARGYDVLTGYPDYWGQGTLVTVSS GGGGSGGGGSGGGGSDIQLTQSPSFLSASVGDRVTITCRASQSI GRSLHWYQQKPGKAPKLLIKYASQSLSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCHQSSRLPFTFGPGTKVDIKR (SEQ ID NO: 419)
iPS:386709	SEQ ID NO: 394	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPG KGLEWVAVISFDGSIKYSVDSVKGRFTISRDNSKNTLFLQMNS LRAEDTAVYYCARDRLNYYDSSGYYHYKYYGMAVWGQGTT VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY ICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVF LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGG GGSQVQLVESGAEVVKPGASVKVSCKASGFTFSRFAMHWVR QAPGQGLEWMGVISYDGGNKYYAESVKGRVTMTRDTSTSTL YMELSSLRSEDTAVYYCARGYDVLTGYPDYWGQGTLVTVSS GGGGSGGGGSGGGGSDIQLTQSPSFLSASVGDRVTITCRASQSI GRSLHWYQQKPGKAPKLLIKYASQSLSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCHQSSRLPFTFGPGTKVDIKR (SEQ ID NO: 420)
iPS:386727	SEQ ID NO: 394	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPG KGLEWVAVISFDGSIKYSVDSVKGRFTISRDNSKNTLFLQMNS LRAEDTAVYYCARDRLNYYDSSGYYHYKYYGMAVWGQGTT VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY ICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVF LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGG GGSDIQLTQSPSFLSASVGDRVTITCRASQSIGRSLHWYQQKPG KAPKLLIKYASQSLSGVPSRFSGSGSGTEFTLTISSLQPEDFATY YCHQSSRLPFTFGPGTKVDIKRGGGGSGGGGSGGGGSGGGGSQVQLV ESGAEVVKPGASVKVSCKASGFTFSRFAMHWVRQAPGQGLE

IgG-scFv Molecule Designation	Light Chain Amino Acid Sequence	Modified Heavy Chain Amino Acid Sequence
		WMGVISYDGGNKYYAESVKGRVTMTRDTSTSTLYMELSSLR SEDTAVYYCARGYDVLTGYPDYWGQGTLVTVSS (SEQ ID NO: 421)
iPS:386721	QSVLTQPPSVSAAPGQ KVTISCSGSSSNIGNNY VSWYQQLPGTAPKLLI YDNNKRPSGIPDRFSG SKSGTSATLAITGLQT GDEADYYCGTWDSRL SAVVFGGGTKLTVLG QPKANPTVTLFPPSSEE LQANKATLVCLISDFY PGAVTVAWKADGSPV KAGVETTKPSKQSNN KYAASSYLSLTPEQW KSHRSYSCQVTHEGST VEKTVAPTECS (SEQ ID NO: 395)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPG KGLEWVAVISFDGSIKYSVDSVKGRFTISRDNSKNTLFLQMNS LRAEDTAVYYCARDRLNYYDSSGYYHYKYYGMAVWGQGTT VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY ICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVF LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGG GGSQVQLVESGAEVVKPGASVKVSCKASGFTFSRFAMHWVR QAPGQGLEWMGVISYDGGNKYYAESVKGRVTMTRDTSTSTL YMELSSLRSEDTAVYYCARGYDVLTGYPDYWGQGTLVTVSS GGGGSGGGGSGGGGSDIQLTQSPSFLSASVGDRVTITCRASQSI GRSLHWYQQKPGKCPKLLIKYASQSLSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCHQSSRLPFTFGCGTKVDIKR (SEQ ID NO: 422)
iPS:386711	SEQ ID NO: 395	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPG KGLEWVAVISFDGSIKYSVDSVKGRFTISRDNSKNTLFLQMNS LRAEDTAVYYCARDRLNYYDSSGYYHYKYYGMAVWGQGTT VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY ICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVF LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGG GGSQVQLVESGAEVVKPGASVKVSCKASGFTFSRFAMHWVR QAPGQGLEWMGVISYDGGNKYYAESVKGRVTMTRDTSTSTL YMELSSLRSEDTAVYYCARGYDVLTGYPDYWGQGTLVTVSS GGGGSGGGGSGGGGSDIQLTQSPSFLSASVGDRVTITCRASQSI GRSLHWYQQKPGKAPKLLIKYASQSLSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCHQSSRLPFTFGPGTKVDIKR (SEQ ID NO: 423)
iPS:386733	SEQ ID NO: 395	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPG KGLEWVAVISFDGSIKYSVDSVKGRFTISRDNSKNTLFLQMNS LRAEDTAVYYCARDRLNYYESSGYYHYKYYGMAVWGQGTT VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY ICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVF LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGG GGSDIQLTQSPSFLSASVGDRVTITCRASQSIGRSLHWYQQKPG KAPKLLIKYASQSLSGVPSRFSGSGSGTEFTLTISSLQPEDFATY YCHQSSRLPFTFGPGTKVDIKRGGGGSGGGGSGGGGSQVQLV

IgG-scFv Molecule Designation	Light Chain Amino Acid Sequence	Modified Heavy Chain Amino Acid Sequence
		ESGAEVVKPGASVKVSCKASGFTFSRFAMHWVRQAPGQGLE WMGVISYDGGNKYYAESVKGRVTMTRDTSTSTLYMELSSLR SEDTAVYYCARGYDVLTGYPDYWGQGTLVTVSS (SEQ ID NO: 424)
iPS:386729	SEQ ID NO: 395	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPG KGLEWVAVISFDGSIKYSVDSVKGRFTISRDNSKNTLFLQMNS LRAEDTAVYYCARDRLNYYDSSGYYHYKYYGMAVWGQGTT VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY ICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVF LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGG GGSDIQLTQSPSFLSASVGDRVTITCRASQSIGRSLHWYQQKPG KAPKLLIKYASQSLSGVPSRFSGSGSGTEFTLTISSLQPEDFATY YCHQSSRLPFTFGPGTKVDIKRGGGGSGGGGSGGGGSQVQLV ESGAEVVKPGASVKVSCKASGFTFSRFAMHWVRQAPGQGLE WMGVISYDGGNKYYAESVKGRVTMTRDTSTSTLYMELSSLR SEDTAVYYCARGYDVLTGYPDYWGQGTLVTVSS (SEQ ID NO: 425)

[0130] In certain embodiments, the first antibody (i.e. the IgG component) of the IgG-scFv bispecific antigen binding proteins is an anti-PAC1 receptor antibody and the second antibody (i.e. from which the scFv is derived) is an anti-CGRP receptor antibody. In such embodiments, the anti-PAC1 receptor antibody comprises a VL region from any of those described in Table 1A and a VH region from any of those described in Table 1B. For instance, in one embodiment, the anti-PAC1 receptor antibody from which the IgG component is derived comprises a LV-04 (SEQ ID NO: 31) VL region and a HV-03 (SEQ ID NO: 85) VH region.

[0131] In embodiments in which the scFv component is derived from an anti-CGRP receptor antibody, the anti-CGRP receptor antibody may comprise a VL region from any of those described in Table 3A and a VH region from any of those described in Table 3B. In one embodiment, the anti-CGRP receptor scFv comprises a LV-105 (SEQ ID NO: 140) VL region and a HV-105 (SEQ ID NO: 194) VH region. In another embodiment, the anti-CGRP receptor scFv comprises a LV-105 (SEQ ID NO: 140) VL region and a HV-107 (SEQ ID NO: 196) VH region. In another embodiment, the anti-CGRP receptor scFv comprises a LV-107 (SEQ ID NO: 142) VL region and a HV-105 (SEQ ID NO: 194) VH region. In yet another embodiment, the anti-CGRP receptor scFv comprises a LV-109 (SEQ ID NO: 144) VL region and a HV-105

(SEQ ID NO: 194) VH region. In still another embodiment, the anti-CGRP receptor scFv comprises a LV-107 (SEQ ID NO: 142) VL region and a HV-107 (SEQ ID NO: 196) VH region.

[0132] In embodiments in which the IgG component of the bispecific antigen binding proteins is derived from an anti-PAC1 receptor antibody and the scFv component is derived from an anti-CGRP receptor antibody, the modified heavy chain of the bispecific antigen binding proteins comprises a sequence selected from SEQ ID NOs: 396 to 410. In related embodiments, the light chain of the bispecific antigen binding proteins comprises the sequence of SEQ ID NO: 392. In certain embodiments, the bispecific, multivalent antigen binding protein is an antigen binding protein designated as iPS:386738, iPS:386764, iPS:386762, iPS:386760, iPS:386758, iPS:386756, iPS:386754, iPS:386752, iPS:386750, iPS:386748, iPS:386746, iPS:386744, iPS:386742, iPS:386740, or iPS:386736 as set forth in Table 9. In other embodiments, the bispecific, multivalent antigen binding protein is an antigen binding protein designated as iPS:386738, iPS:386754, iPS:386750, iPS:386748, iPS:386746, iPS:386744, iPS:386740, or iPS:386736 as set forth in Table 9. In still other embodiments, the bispecific, multivalent antigen binding protein is an antigen binding protein designated as iPS:386744, iPS:386746, or iPS:386748 as set forth in Table 9.

[0133] In other embodiments of the invention, the first antibody (i.e. the IgG component) of the IgG-scFv bispecific antigen binding proteins is an anti-CGRP receptor antibody and the second antibody (i.e. from which the scFv is derived) is an anti-PAC1 receptor antibody. In such embodiments, the anti-CGRP receptor antibody comprises a VL region from any of those described in Table 3A and a VH region from any of those described in Table 3B. For example, in one embodiment, the anti-CGRP receptor antibody from which the IgG component is derived comprises a LV-105 (SEQ ID NO: 140) VL region and a HV-105 (SEQ ID NO: 194) VH region. In another embodiment, the anti-CGRP receptor antibody from which the IgG component is derived comprises a LV-105 (SEQ ID NO: 140) VL region and a HV-107 (SEQ ID NO: 196) VH region. In another embodiment, the anti-CGRP receptor antibody from which the IgG component is derived comprises a LV-107 (SEQ ID NO: 142) VL region and a HV-105 (SEQ ID NO: 194) VH region. In yet another embodiment, the anti-CGRP receptor antibody from which the IgG component is derived comprises a LV-109 (SEQ ID NO: 144) VL region and a HV-105 (SEQ ID NO: 194) VH region. In still another embodiment, the anti-CGRP receptor antibody

from which the IgG component is derived comprises a LV-107 (SEQ ID NO: 142) VL region and a HV-107 (SEQ ID NO: 196) VH region.

[0134] In embodiments in which the scFv component is derived from an anti-PAC1 receptor antibody, the anti-PAC1 receptor antibody may comprise a VL region from any of those described in Table 1A and a VH region from any of those described in Table 1B. In one embodiment, the anti-PAC1 receptor scFv comprises a LV-04 (SEQ ID NO: 31) VL region and a HV-03 (SEQ ID NO: 85) VH region.

[0135] In embodiments in which the IgG component of the bispecific antigen binding proteins is derived from an anti-CGRP receptor antibody and the scFv component is derived from an anti-PAC1 receptor antibody, the modified heavy chain of the bispecific antigen binding proteins comprises a sequence selected from SEQ ID NOs: 411 to 425. In related embodiments, the light chain of the bispecific antigen binding proteins comprises a sequence selected from SEQ ID NOs: 393 to 395. In one embodiment, the modified heavy chain comprises a sequence selected from SEQ ID NOs: 411 to 416 and the light chain comprises the sequence of SEQ ID NO: 393. In another embodiment, the modified heavy chain comprises a sequence selected from SEQ ID NOs: 417 to 421 and the light chain comprises the sequence of SEQ ID NO: 394. In yet another embodiment, the modified heavy chain comprises a sequence selected from SEQ ID NOs: 422 to 425 and the light chain comprises the sequence of SEQ ID NO: 395.

[0136] In certain embodiments, the bispecific, multivalent antigen binding protein is an antigen binding protein designated as iPS:386731, iPS:386725, iPS:386717, iPS:386715, iPS:386707, iPS:386705, iPS:386723, iPS:386719, iPS:386713, iPS:386709, iPS:386727, iPS:386721, iPS:386711, iPS:386733, or iPS:386729 as set forth in Table 9. In some embodiments, the bispecific, multivalent antigen binding protein is an antigen binding protein designated as iPS:386721, iPS:386723, or iPS:386733 as set forth in Table 9.

[0137] In some embodiments of the antigen binding proteins of the invention, the binding domain positioned at the carboxyl terminus of the Fc region (i.e. the carboxyl-terminal binding domain) is a Fab fragment. In such embodiments, the Fab is fused or otherwise connected to the carboxyl terminus of the Fc region (e.g. the carboxyl terminus of the CH3 domain) through a peptide linker through the amino terminus of the VL region or VH region of the Fab fragment. Thus, in one embodiment, the Fab is fused to an Fc region through the amino terminus of the VL region of the Fab such that the resulting fusion protein comprises, from N-terminus to C-

terminus, a CH2 domain, a CH3 domain, a peptide linker, a VL region, and a CL region. In another embodiment, the Fab is fused to an Fc region through the amino terminus of the VH region of the Fab such that the resulting fusion protein comprises, from N-terminus to C-terminus, a CH2 domain, a CH3 domain, a peptide linker, a VH region, and a CH1 region.

[0138] The peptide linker joining the Fc region to the carboxyl-terminal Fab can be any of the peptide linkers described herein. In particular embodiments, the peptide linker joining the Fc region to the carboxyl-terminal Fab fragment is at least 5 amino acids in length. In other embodiments, the peptide linker joining the Fc region to the carboxyl-terminal Fab fragment is at least 8 amino acids in length. Particularly suitable peptide linkers for joining the Fc region to the carboxyl-terminal Fab fragment are glycine-serine linkers, such as $(Gly_xSer)_n$ where x=3 or 4 and n= 2, 3, 4, 5 or 6. In one embodiment, the peptide linker connecting the Fc region to the carboxyl-terminal Fab fragment is a L10 $(G_4S)_2$ linker (SEQ ID NO: 368). In another embodiment, the peptide linker connecting the Fc region to the carboxyl-terminal Fab fragment is a L9 or G_3SG_4S linker (SEQ ID NO: 367).

[0139] In some embodiments of the bispecific antigen binding proteins of the invention in which the carboxyl-terminal binding domain is a Fab fragment, the binding domain positioned at the amino terminus of the Fc region (i.e. the amino-terminal binding domain) is also a Fab fragment. The amino-terminal Fab fragment can be fused to the amino terminus of the Fc region through a peptide linker or an immunoglobulin hinge region described herein. In some embodiments, the amino-terminal Fab fragment is joined to the amino terminus of the Fc region through a human IgG1 hinge region. In other embodiments, the amino-terminal Fab fragment is joined to the amino terminus of the Fc region through a human IgG2 hinge region. Preferably, the amino-terminal Fab fragment is fused to the Fc region through the carboxyl terminus of the CH1 region of the Fab.

[0140] In some embodiments, the bispecific antigen binding protein of the invention comprises a first antibody that specifically binds to a first target (e.g. human CGRP receptor or human PAC1 receptor) where one polypeptide chain (e.g. the light chain (VL-CL)) of a Fab fragment from a second antibody that specifically binds to a second target (e.g. human CGRP receptor or human PAC1 receptor) is fused to the carboxyl terminus of the heavy chain of the first antibody. The bispecific antigen binding protein in such embodiments also comprises a polypeptide chain containing the other half of the Fab fragment from the second antibody (e.g. the Fd chain (VH-

CH1)). This format is referred to herein as the "IgG-Fab" format, and one embodiment of this type of molecule is shown schematically in Figure 3. Thus, in certain embodiments, the present invention includes a bispecific, multivalent antigen binding protein comprising: (i) a light chain from a first antibody, (ii) a heavy chain from the first antibody, wherein the heavy chain is fused at its carboxyl terminus through a peptide linker to a first polypeptide comprising VL-CL domains or VH-CH1 domains of a second antibody to form a modified heavy chain, and (iii) a second polypeptide comprising VH-CH1 domains or VL-CL domains of the second antibody, wherein the first or second antibody specifically binds to human CGRP receptor and the other antibody specifically binds to human PAC1 receptor. When dimerized, the bispecific antigen binding protein is a homohexamer comprising two modified heavy chains, two light chains from the first antibody, and two polypeptide chains containing the other half of the Fab fragment from the second antibody (either the Fd fragment or light chain). In one embodiment, the first polypeptide, which is fused to the carboxyl terminus of the heavy chain, comprises VL and CL domains from the second antibody, and the second polypeptide comprises VH and CH1 domains from the second antibody. In another embodiment, the first polypeptide, which is fused to the carboxyl terminus of the heavy chain, comprises VH and CH1 domains from the second antibody, and the second polypeptide comprises VL and CL domains from the second antibody.

[0141] Charge pair mutations or complimentary amino acid substitutions as described herein can be introduced into the Fab regions of the first antibody (Fab 1) or second antibody (Fab 2) to promote correct heavy chain-light chain pairing. For instance, in some embodiments, the amino acid at Kabat position 38 of the VL domain in Fab 1 is replaced with a negatively-charged amino acid (e.g. glutamic acid) and the amino acid at Kabat position 39 of the VH domain in Fab 1 is replaced with a positively-charged amino acid (e.g. lysine). In other embodiments, the amino acid at Kabat position 38 of the VL domain in Fab 1 is replaced with a positively-charged amino acid (e.g. lysine) and the amino acid at Kabat position 39 of the VH domain in Fab 1 is replaced with a negatively-charged amino acid (e.g. glutamic acid). In certain embodiments, the amino acid at Kabat position 38 of the VL domain in Fab 2 is replaced with a negatively-charged amino acid (e.g. glutamic acid) and the amino acid at Kabat position 39 of the VH domain in Fab 2 is replaced with a positively-charged amino acid (e.g. lysine). In other embodiments, the amino acid at Kabat position 38 of the VL domain in Fab 2 is replaced with a positively-charged amino

acid (e.g. lysine) and the amino acid at Kabat position 39 of the VH domain in Fab 2 is replaced with a negatively-charged amino acid (e.g. glutamic acid).

[0142] In embodiments in which the VH-CH1 region (i.e. Fd fragment) from the second antibody is fused to the heavy chain of the first antibody, the heavy chain from the first antibody comprises a S183E mutation (EU numbering), the light chain from the first antibody comprises a S176K mutation (EU numbering), the light chain from the second antibody comprises a S176E mutation (EU numbering), and the Fd region from the second antibody (which is fused to the C-terminus of the heavy chain from the first antibody) comprises a S183K mutation (EU numbering). In other embodiments, the heavy chain from the first antibody comprises a G44E mutation (Kabat) and S183E mutation (EU numbering), the light chain from the first antibody comprises a G100K mutation (Kabat) and S176K mutation (EU numbering), the light chain from the second antibody comprises a G100E mutation (Kabat) and S176E mutation (EU numbering), and the Fd region from the second antibody (which is fused to the C-terminus of the heavy chain from the first antibody) comprises a G44K mutation (Kabat) and S183K mutation (EU numbering). The charges in the foregoing examples may be reversed so long as the charge on the corresponding light or heavy chain is also reversed so that the correct heavy/light chain pairs have opposite charges.

[0143] Additionally or alternatively, correct heavy-light chain pairing may be facilitated by swapping the CH1 and CL domains in the carboxyl-terminal Fab binding domain. By way of example, the first polypeptide, which is fused to the carboxyl terminus of the heavy chain, may comprise a VL domain and CH1 domain from the second antibody, and the second polypeptide may comprise a VH domain and CL domain from the second antibody. In another embodiment, the first polypeptide, which is fused to the carboxyl terminus of the heavy chain, may comprise a VH domain and a CL domain from the second antibody, and the second polypeptide may comprise a VL domain and CH1 domain from the second antibody.

[0144] In the IgG-Fab format of the bispecific antigen binding proteins of the invention, an anti-PAC1 receptor antibody can be the first antibody (i.e. the "IgG") or the second antibody (i.e. from which the C-terminal Fab is derived). Similarly, an anti-CGRP receptor antibody can be the first antibody (i.e. the "IgG") or the second antibody (i.e. from which the C-terminal Fab is derived). Any of the anti-PAC1 receptor antibody variable regions set forth in Tables 1A and 1B can be incorporated into either the IgG component or the C-terminal Fab component of the

bispecific antigen binding proteins of the invention. Any of the anti-CGRP receptor antibody variable regions set forth in Tables 3A and 3B can be incorporated into either the IgG component or the C-terminal Fab component of the bispecific antigen binding proteins of the invention.

[0145] Amino acid sequences for light chains, modified heavy chains, and second polypeptides of exemplary antigen binding proteins of the invention in the IgG-Fab format are summarized in Table 10 below. The molecules listed in the first half of the table comprise an anti-PAC1 receptor IgG component and an anti-CGRP receptor C-terminal Fab fragment, whereas the molecules listed in the second half of the table comprise an anti-CGRP receptor IgG component and an anti-PAC1 receptor C-terminal Fab fragment.

Table 10. Amino Acid Sequences of Exemplary Bispecific Antigen Binding Proteins in the IgG-Fab Format

IgG-Fab Molecule Designation	Light Chain Amino Acid Sequence	Modified Heavy Chain Amino Acid Sequence	Second Polypeptide Amino Acid Sequence
Anti-PAC1 Receptor IgG x Anti-CGRP Receptor Fab			
iPS:392513	DIQLTQSPSFLSA SVGDRVTITCRAS QSIGRSLHWYQQ KPGKAPKLLIKY ASQSLSGVPSRFS GSGSGTEFTLTISS LQPEDFATYYCH QSSRLPFTFGPGT KVDIKRTVAAPS VFIFPPSDEQLKS GTASVVCLLNNF YPREAKVQWKV DNALQSGNSQES VTEQDSKDSTYS LESTLTLSKADYE KHKVYACEVTH QGLSSPVTKSFNR GEC (SEQ ID NO: 214)	QVQLVESGAEVVKPGASVKVSCKASGFTFSRF AMHWVRQAPGQGLEWMGVISYDGGNKYYAE SVKGRVTMTRDTSTSTLYMELSSLRSEDTAVY YCARGYDVLTGYPDYWGQGTLVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLKSVVT VPSSSLGTQTYICNVNHKPSNTKVDKKVEPKS CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPCEEQYGSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEALHNHYTQKSLSL SPGGGGSGGGGSQSVLTQPPSVSAAPGQKVTIS CSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNN KRPSGIPDRFSGSKSGTSTTLGITGLQTGDEAD YYCGTWDSRLSAVVFGGGTKLTVLASTKGPS VFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLKSVVTVP SSSLGTQTYICNVNHKPSNTKVDKKV (SEQ ID NO: 428)	QVQLVESGGGVVQP GRSLRLSCAASGFTF SSFGMHWVRQAPG KGLEWVAVISFDGSI KYSVDSVKGRFTISR DNSKNTLFLQMNSL RAEDTAVYYCARDR LNYYDSSGYYHYKY YGMAVWGQGTTVT VSSGQPKANPTVTLF PPSSEELQANKATLV CLISDFYPGAVTVA WKADGSPVKAGVE TTKPSKQSNNKYAA ESYLSLTPEQWKSH RSYSCQVTHEGSTV EKTVAPTECS (SEQ ID NO: 452)
iPS:392514	SEQ ID NO: 214	QVQLVESGAEVVKPGASVKVSCKASGFTFSRF AMHWVRQAPGQGLEWMGVISYDGGNKYYAE SVKGRVTMTRDTSTSTLYMELSSLRSEDTAVY YCARGYDVLTGYPDYWGQGTLVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLKSVVT VPSSSLGTQTYICNVNHKPSNTKVDKKVEPKS	QVQLVESGGGVVQP GRSLRLSCAASGFTF SSFGMHWVREAPGK GLEWVAVISFDGSIK YSVDSVKGRFTISRD NSKNTLFLQMNSLR AEDTAVYYCARDRL

IgG-Fab Molecule Designation	Light Chain Amino Acid Sequence	Modified Heavy Chain Amino Acid Sequence	Second Polypeptide Amino Acid Sequence
		CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPCEEQYGSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEALHNHYTQKSLSL SPGGGGSGGGGSQSVLTQPPSVSAAPGQKVTIS CSGSSSNIGNNYVSWYQKLPGTAPKLLIYDNN KRPSGIPDRFSGSKSGTSTTLGITGLQTGDEAD YYCGTWDSRLSAVVFGGGTKLTVLASTKGPS VFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLKSVVTVP SSSLGTQTYICNVNHKPSNTKVDKKV (SEQ ID NO: 429)	NYYDSSGYYHYKY YGMAVWGQGTTVT VSSGQPKANPTVTLF PPSSEELQANKATLV CLISDFYPGAVTVA WKADGSPVKAGVE TTKPSKQSNNKYAA ESYLSLTPEQWKSH RSYSCQVTHEGSTV EKTVAPTECS (SEQ ID NO: 453)
iPS:392475	SEQ ID NO: 214	QVQLVESGAEVVKPGASVKVSCKASGFTFSRF AMHWVRQAPGQGLEWMGVISYDGGNKYYAE SVKGRVTMTRDTSTSTLYMELSSLRSEDTAVY YCARGYDVLTGYPDYWGQGTLVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLKSVVT VPSSSLGTQTYICNVNHKPSNTKVDKKVEPKS CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPCEEQYGSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEALHNHYTQKSLSL SPGGGGSGGGGSQSVLTQPPSVSAAPGQKVTIS CSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNN KRPSGIPDRFSGSKSGTSTTLGITGLQTGDEAD YYCGTWDSRLSAVVFGGGTKLTVLASTKGPS VFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLKSVVTVP SSSLGTQTYICNVNHKPSNTKVDKKV (SEQ ID NO: 430)	QVQLVESGGGVVQP GRSLRLSCAASGFTF SSFGMHWVRQAPG KGLEWVAVISFDGSI KYSVDSVKGRFTISR DNSKNTLFLQMNSL RAEDTAVYYCARDR LNYYESSGYYHYKY YGMAVWGQGTTVT VSSGQPKANPTVTLF PPSSEELQANKATLV CLISDFYPGAVTVA WKADGSPVKAGVE TTKPSKQSNNKYAA ESYLSLTPEQWKSH RSYSCQVTHEGSTV EKTVAPTECS (SEQ ID NO: 454)
iPS:392519	SEQ ID NO: 214	QVQLVESGAEVVKPGASVKVSCKASGFTFSRF AMHWVRQAPGQGLEWMGVISYDGGNKYYAE SVKGRVTMTRDTSTSTLYMELSSLRSEDTAVY YCARGYDVLTGYPDYWGQGTLVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLKSVVT VPSSSLGTQTYICNVNHKPSNTKVDKKVEPKS CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPCEEQYGSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEALHNHYTQKSLSL SPGGGGSGGGGSQSVLTQPPSVSAAPGQKVTIS CSGSSSNIGNNYVSWYQKLPGTAPKLLIYDNN	QVQLVESGGGVVQP GRSLRLSCAASGFTF SSFGMHWVREAPGK GLEWVAVISFDGSIK YSVDSVKGRFTISRD NSKNTLFLQMNSLR AEDTAVYYCARDRL NYYESSGYYHYKYY GMAVWGQGTTVTV SSGQPKANPTVTLFP PSSEELQANKATLV CLISDFYPGAVTVA WKADGSPVKAGVE TTKPSKQSNNKYAA ESYLSLTPEQWKSH RSYSCQVTHEGSTV

IgG-Fab Molecule Designation	Light Chain Amino Acid Sequence	Modified Heavy Chain Amino Acid Sequence	Second Polypeptide Amino Acid Sequence
		KRPSGIPDRFSGSKSGTSTTLGITGLQTGDEAD YYCGTWDSRLSAVVFGGGTKLTVLASTKGPS VFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLKSVVTVP SSSLGTQTYICNVNHKPSNTKVDKKV (SEQ ID NO: 431)	EKTVAPTECS (SEQ ID NO: 455)
iPS:392515	SEQ ID NO: 214	QVQLVESGAEVVKPGASVKVSCKASGFTFSRF AMHWVRQAPGQGLEWMGVISYDGGNKYYAE SVKGRVTMTRDTSTSTLYMELSSLRSEDTAVY YCARGYDVLTGYPDYWGQGTLVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLKSVVT VPSSSLGTQTYICNVNHKPSNTKVDKKVEPKS CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPCEEQYGSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEALHNHYTQKSLSL SPGGGGSGGGGSQSVLTQPPSVSAAPGQKVTIS CSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNN KRPSGIPDRFSGSKSGTSTTLGITGLQTGDEAD YYCGTWDSRLSAVVFGGGTKLTVLGQPKANP TVTLFPPSSEELQANKATLVCLISDFYPGAVTV AWKADGSPVKAGVETTKPSKQSNNKYAAKSY LSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPT ECS (SEQ ID NO: 432)	QVQLVESGGGVVQP GRSLRLSCAASGFTF SSFGMHWVRQAPG KGLEWVAVISFDGSI KYSVDSVKGRFTISR DNSKNTLFLQMNSL RAEDTAVYYCARDR LNYYDSSGYYHYKY YGMAVWGQGTTVT VSSASTKGPSVFPLA PSSKSTSGGTAALGC LVKDYFPEPVTVSW NSGALTSGVHTFPA VLQSSGLYSLESVVT VPSSSLGTQTYICNV NHKPSNTKVDKKV (SEQ ID NO: 456)
iPS:392516	SEQ ID NO: 214	QVQLVESGAEVVKPGASVKVSCKASGFTFSRF AMHWVRQAPGQGLEWMGVISYDGGNKYYAE SVKGRVTMTRDTSTSTLYMELSSLRSEDTAVY YCARGYDVLTGYPDYWGQGTLVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLKSVVT VPSSSLGTQTYICNVNHKPSNTKVDKKVEPKS CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPCEEQYGSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEALHNHYTQKSLSL SPGGGGSGGGGSQSVLTQPPSVSAAPGQKVTIS CSGSSSNIGNNYVSWYQKLPGTAPKLLIYDNN KRPSGIPDRFSGSKSGTSTTLGITGLQTGDEAD YYCGTWDSRLSAVVFGGGTKLTVLGQPKANP TVTLFPPSSEELQANKATLVCLISDFYPGAVTV AWKADGSPVKAGVETTKPSKQSNNKYAAKSY LSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPT ECS (SEQ ID NO: 433)	QVQLVESGGGVVQP GRSLRLSCAASGFTF SSFGMHWVREAPGK GLEWVAVISFDGSIK YSVDSVKGRFTISRD NSKNTLFLQMNSLR AEDTAVYYCARDRL NYYDSSGYYHYKY YGMAVWGQGTTVT VSSASTKGPSVFPLA PSSKSTSGGTAALGC LVKDYFPEPVTVSW NSGALTSGVHTFPA VLQSSGLYSLESVVT VPSSSLGTQTYICNV NHKPSNTKVDKKV (SEQ ID NO: 457)
iPS:392521	SEQ ID NO: 214	QVQLVESGAEVVKPGASVKVSCKASGFTFSRF AMHWVRQAPGQGLEWMGVISYDGGNKYYAE SVKGRVTMTRDTSTSTLYMELSSLRSEDTAVY	QVQLVESGGGVVQP GRSLRLSCAASGFTF SSFGMHWVREAPGK

IgG-Fab Molecule Designation	Light Chain Amino Acid Sequence	Modified Heavy Chain Amino Acid Sequence	Second Polypeptide Amino Acid Sequence
		YCARGYDVLTGYPDYWGQGTLVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLKSVVT VPSSSLGTQTYICNVNHKPSNTKVDKKVEPKS CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPCEEQYGSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEALHNHYTQKSLSL SPGGGGSGGGGSQSVLTQPPSVSAAPGQKVTIS CSGSSSNIGNNYVSWYQKLPGTAPKLLIYDNN KRPSGIPDRFSGSKSGTSTTLGITGLQTGDEAD YYCGTWDSRLSAVVFGGGTKLTVLGQPKANP TVTLFPPSSEELQANKATLVCLISDFYPGAVTV AWKADGSPVKAGVETTKPSKQSNNKYAAKSY LSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPT ECS (SEQ ID NO: 434)	GLEWVAVISFDGSIK YSVDSVKGRFTISRD NSKNTLFLQMNSLR AEDTAVYYCARDRL NYYESSGYYHYKYY GMAVWGQGTTVTV SSASTKGPSVFPLAP SSKSTSGGTAALGCL VKDYFPEPVTVSWN SGALTSGVHTFPAV LQSSGLYSLESVVTV PSSSLGTQTYICNVN HKPSNTKVDKKV (SEQ ID NO: 458)
iPS:392520	SEQ ID NO: 214	QVQLVESGAEVVKPGASVKVSCKASGFTFSRF AMHWVRQAPGQGLEWMGVISYDGGNKYYAE SVKGRVTMTRDTSTSTLYMELSSLRSEDTAVY YCARGYDVLTGYPDYWGQGTLVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLKSVVT VPSSSLGTQTYICNVNHKPSNTKVDKKVEPKS CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPCEEQYGSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEALHNHYTQKSLSL SPGGGGSGGGGSQSVLTQPPSVSAAPGQKVTIS CSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNN KRPSGIPDRFSGSKSGTSTTLGITGLQTGDEAD YYCGTWDSRLSAVVFGGGTKLTVLGQPKANP TVTLFPPSSEELQANKATLVCLISDFYPGAVTV AWKADGSPVKAGVETTKPSKQSNNKYAAKSY LSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPT ECS (SEQ ID NO: 435)	QVQLVESGGGVVQP GRSLRLSCAASGFTF SSFGMHWVRQAPG KGLEWVAVISFDGSI KYSVDSVKGRFTISR DNSKNTLFLQMNSL RAEDTAVYYCARDR LNYYESSGYYHYKY YGMAVWGQGTTVT VSSASTKGPSVFPLA PSSKSTSGGTAALGC LVKDYFPEPVTVSW NSGALTSGVHTFPA VLQSSGLYSLESVVT VPSSSLGTQTYICNV NHKPSNTKVDKKV (SEQ ID NO: 459)
iPS:392517	DIQLTQSPSFLSA SVGDRVTITCRAS QSIGRSLHWYQE KPGKAPKLLIKY ASQSLSGVPSRFS GSGSGTEFTLTISS LQPEDFATYYCH QSSRLPFTFGPGT KVDIKRTVAAPS VFIFPPSDEQLKS GTASVVCLLNNF YPREAKVQWKV	QVQLVESGAEVVKPGASVKVSCKASGFTFSRF AMHWVRKAPGQGLEWMGVISYDGGNKYYAE SVKGRVTMTRDTSTSTLYMELSSLRSEDTAVY YCARGYDVLTGYPDYWGQGTLVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLKSVVT VPSSSLGTQTYICNVNHKPSNTKVDKKVEPKS CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPCEEQYGSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE	SEQ ID NO: 456

IgG-Fab Molecule Designation	Light Chain Amino Acid Sequence	Modified Heavy Chain Amino Acid Sequence	Second Polypeptide Amino Acid Sequence
	DNALQSGNSQES VTEQDSKDSTYS LESTLTLSKADYE KHKVYACEVTH QGLSSPVTKSFNR GEC (SEQ ID NO: 426)	WESNGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEALHNHYTQKSLSL SPGGGGSGGGGSQSVLTQPPSVSAAPGQKVTIS CSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNN KRPSGIPDRFSGSKSGTSTTLGITGLQTGDEAD YYCGTWDSRLSAVVFGGGTKLTVLGQPKANP TVTLFPPSSEELQANKATLVCLISDFYPGAVTV AWKADGSPVKAGVETTKPSKQSNNKYAAKSY LSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPT ECS (SEQ ID NO: 436)	
iPS:392518	SEQ ID NO: 426	QVQLVESGAEVVKPGASVKVSCKASGFTFSRF AMHWVRKAPGQGLEWMGVISYDGGNKYYAE SVKGRVTMTRDTSTSTLYMELSSLRSEDTAVY YCARGYDVLTGYPDYWGQGTLVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLKSVVT VPSSSLGTQTYICNVNHKPSNTKVDKKVEPKS CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPCEEQYGSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEALHNHYTQKSLSL SPGGGGSGGGGSQSVLTQPPSVSAAPGQKVTIS CSGSSSNIGNNYVSWYQKLPGTAPKLLIYDNN KRPSGIPDRFSGSKSGTSTTLGITGLQTGDEAD YYCGTWDSRLSAVVFGGGTKLTVLGQPKANP TVTLFPPSSEELQANKATLVCLISDFYPGAVTV AWKADGSPVKAGVETTKPSKQSNNKYAAKSY LSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPT ECS (SEQ ID NO: 437)	SEQ ID NO: 457
iPS:392522	SEQ ID NO: 426	QVQLVESGAEVVKPGASVKVSCKASGFTFSRF AMHWVRKAPGQGLEWMGVISYDGGNKYYAE SVKGRVTMTRDTSTSTLYMELSSLRSEDTAVY YCARGYDVLTGYPDYWGQGTLVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLKSVVT VPSSSLGTQTYICNVNHKPSNTKVDKKVEPKS CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPCEEQYGSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEALHNHYTQKSLSL SPGGGGSGGGGSQSVLTQPPSVSAAPGQKVTIS CSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNN KRPSGIPDRFSGSKSGTSTTLGITGLQTGDEAD YYCGTWDSRLSAVVFGGGTKLTVLGQPKANP TVTLFPPSSEELQANKATLVCLISDFYPGAVTV AWKADGSPVKAGVETTKPSKQSNNKYAAKSY LSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPT	SEQ ID NO: 459

IgG-Fab Molecule Designation	Light Chain Amino Acid Sequence	Modified Heavy Chain Amino Acid Sequence	Second Polypeptide Amino Acid Sequence
		ECS (SEQ ID NO: 438)	
iPS:392523	SEQ ID NO: 426	QVQLVESGAEVVKPGASVKVSCKASGFTFSRF AMHWVRKAPGQGLEWMGVISYDGGNKYYAE SVKGRVTMTRDTSTSTLYMELSSLRSEDTAVY YCARGYDVLTGYPDYWGQGTLVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLKSVVT VPSSSLGTQTYICNVNHKPSNTKVDKKVEPKS CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPCEEQYGSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEALHNHYTQKSLSL SPGGGGSGGGGSQSVLTQPPSVSAAPGQKVTIS CSGSSSNIGNNYVSWYQKLPGTAPKLLIYDNN KRPSGIPDRFSGSKSGTSTTLGITGLQTGDEAD YYCGTWDSRLSAVVFGGGTKLTVLGQPKANP TVTLFPPSSEELQANKATLVCLISDFYPGAVTV AWKADGSPVKAGVETTKPSKQSNNKYAAKSY LSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPT ECS (SEQ ID NO: 439)	SEQ ID NO: 458
Anti-CGRP Receptor IgG x Anti-PAC1 Receptor Fab			
iPS:392524	QSVLTQPPSVSAA PGQKVTISCSGSS SNIGNNYVSWYQ QLPGTAPKLLIYD NNKRPSGIPDRFS GSKSGTSTTLGIT GLQTGDEADYYC GTWDSRLSAVVF GGGTKLTVLGQP KANPTVTLFPPSS EELQANKATLVC LISDFYPGAVTVA WKADGSPVKAG VETTKPSKQSNN KYAAKSYLSLTP EQWKSHRSYSCQ VTHEGSTVEKTV APTECS (SEQ ID NO: 275)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSF GMHWVRQAPGKGLEWVAVISFDGSIKYSVDS VKGRFTISRDNSKNTLFLQMNSLRAEDTAVYY CARDRLNYYDSSGYYHYKYYGMAVWGQGTT VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLESVVTVPSSSLGTQTYICNVNHKPSNTK VDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPCEEQYGSTYRCVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGGGGSGGGGSDIQLTQSPSFLSA SVGDRVTITCRASQSIGRSLHWYQQKPGKAPK LLIKYASQSLSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCHQSSRLPFTFGPGTKVDIKRASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLESVVT VPSSSLGTQTYICNVNHKPSNTKVDKKV (SEQ ID NO: 440)	QVQLVESGAEVVKP GASVKVSCKASGFT FSRFAMHWVRQAP GQGLEWMGVISYD GGNKYYAESVKGR VTMTRDTSTSTLYM ELSSLRSEDTAVYYC ARGYDVLTGYPDY WGQGTLVTVSSTVA APSVFIFPPSDEQLKS GTASVVCLLNNFYP REAKVQWKVDNAL QSGNSQESVTEQDS KDSTYSLKSTLTLSK ADYEKHKVYACEV THQGLSSPVTKSFNR GEC (SEQ ID NO: 460)
iPS:392525	SEQ ID NO: 275	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSF GMHWVRQAPGKGLEWVAVISFDGSIKYSVDS VKGRFTISRDNSKNTLFLQMNSLRAEDTAVYY CARDRLNYYDSSGYYHYKYYGMAVWGQGTT VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLESVVTVPSSSLGTQTYICNVNHKPSNTK	QVQLVESGAEVVKP GASVKVSCKASGFT FSRFAMHWVRKAP GQGLEWMGVISYD GGNKYYAESVKGR VTMTRDTSTSTLYM ELSSLRSEDTAVYYC

IgG-Fab Molecule Designation	Light Chain Amino Acid Sequence	Modified Heavy Chain Amino Acid Sequence	Second Polypeptide Amino Acid Sequence
		VDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPCEEQYGSTYRCVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGGGGSGGGGSDIQLTQSPSFLSA SVGDRVTITCRASQSIGRSLHWYQEKPGKAPK LLIKYASQSLSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCHQSSRLPFTFGPGTKVDIKRASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLESVVT VPSSSLGTQTYICNVNHKPSNTKVDKKV (SEQ ID NO: 441)	ARGYDVLTGYPDY WGQGTLVTVSSTVA APSVFIFPPSDEQLKS GTASVVCLLNNFYP REAKVQWKVDNAL QSGNSQESVTEQDS KDSTYSLKSTLTLSK ADYEKHKVYACEV THQGLSSPVTKSFNR GEC (SEQ ID NO: 461)
iPS:392526	SEQ ID NO: 275	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSF GMHWVRQAPGKGLEWVAVISFDGSIKYSVDS VKGRFTISRDNSKNTLFLQMNSLRAEDTAVYY CARDRLNYYESSGYYHYKYYGMAVWGQGTT VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLESVVTVPSSSLGTQTYICNVNHKPSNTK VDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPCEEQYGSTYRCVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGGGGSGGGGSDIQLTQSPSFLSA SVGDRVTITCRASQSIGRSLHWYQQKPGKAPK LLIKYASQSLSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCHQSSRLPFTFGPGTKVDIKRASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLESVVT VPSSSLGTQTYICNVNHKPSNTKVDKKV (SEQ ID NO: 442)	SEQ ID NO: 460
iPS:392527	SEQ ID NO: 275	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSF GMHWVRQAPGKGLEWVAVISFDGSIKYSVDS VKGRFTISRDNSKNTLFLQMNSLRAEDTAVYY CARDRLNYYESSGYYHYKYYGMAVWGQGTT VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLESVVTVPSSSLGTQTYICNVNHKPSNTK VDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPCEEQYGSTYRCVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGGGGSGGGGSDIQLTQSPSFLSA SVGDRVTITCRASQSIGRSLHWYQEKPGKAPK	SEQ ID NO: 461

IgG-Fab Molecule Designation	Light Chain Amino Acid Sequence	Modified Heavy Chain Amino Acid Sequence	Second Polypeptide Amino Acid Sequence
		LLIKYASQSLSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCHQSSRLPFTFGPGTKVDIKRASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLESVVT VPSSSLGTQTYICNVNHKPSNTKVDKKV (SEQ ID NO: 443)	
iPS:392528	SEQ ID NO: 275	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSF GMHWVRQAPGKGLEWVAVISFDGSIKYSVDS VKGRFTISRDNSKNTLFLQMNSLRAEDTAVYY CARDRLNYYDSSGYYHYKYYGMAVWGQGTT VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLESVVTVPSSSLGTQTYICNVNHKPSNTK VDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPCEEQYGSTYRCVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGGGGSGGGGSDIQLTQSPSFLSA SVGDRVTITCRASQSIGRSLHWYQQKPGKAPK LLIKYASQSLSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCHQSSRLPFTFGPGTKVDIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKV QWKVDNALQSGNSQESVTEQDSKDSTYSLEST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC (SEQ ID NO: 444)	QVQLVESGAEVVKP GASVKVSCKASGFT FSRFAMHWVRQAP GQGLEWMGVISYD GGNKYYAESVKGR VTMTRDTSTSTLYM ELSSLRSEDTAVYYC ARGYDVLTGYPDY WGQGTLVTVSSAST KGPSVFPLAPSSKST SGGTAALGCLVKDY FPEPVTVSWNSGAL TSGVHTFPAVLQSSG LYSLKSVVTVPSSSL GTQTYICNVNHKPS NTKVDKKV (SEQ ID NO: 462)
iPS:392529	SEQ ID NO: 275	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSF GMHWVRQAPGKGLEWVAVISFDGSIKYSVDS VKGRFTISRDNSKNTLFLQMNSLRAEDTAVYY CARDRLNYYDSSGYYHYKYYGMAVWGQGTT VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLESVVTVPSSSLGTQTYICNVNHKPSNTK VDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPCEEQYGSTYRCVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGGGGSGGGGSDIQLTQSPSFLSA SVGDRVTITCRASQSIGRSLHWYQEKPGKAPK LLIKYASQSLSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCHQSSRLPFTFGPGTKVDIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKV QWKVDNALQSGNSQESVTEQDSKDSTYSLEST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC (SEQ ID NO: 445)	QVQLVESGAEVVKP GASVKVSCKASGFT FSRFAMHWVRKAP GQGLEWMGVISYD GGNKYYAESVKGR VTMTRDTSTSTLYM ELSSLRSEDTAVYYC ARGYDVLTGYPDY WGQGTLVTVSSAST KGPSVFPLAPSSKST SGGTAALGCLVKDY FPEPVTVSWNSGAL TSGVHTFPAVLQSSG LYSLKSVVTVPSSSL GTQTYICNVNHKPS NTKVDKKV (SEQ ID NO: 463)
iPS:392532	SEQ ID NO: 275	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSF GMHWVRQAPGKGLEWVAVISFDGSIKYSVDS VKGRFTISRDNSKNTLFLQMNSLRAEDTAVYY	SEQ ID NO: 462

IgG-Fab Molecule Designation	Light Chain Amino Acid Sequence	Modified Heavy Chain Amino Acid Sequence	Second Polypeptide Amino Acid Sequence
		CARDRLNYYESSGYYHYKYYGMAVWGQGTT VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLESVVTVPSSSLGTQTYICNVNHKPSNTK VDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPCEEQYGSTYRCVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGGGGSGGGGSDIQLTQSPSFLSA SVGDRVTITCRASQSIGRSLHWYQQKPGKAPK LLIKYASQSLSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCHQSSRLPFTFGPGTKVDIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKV QWKVDNALQSGNSQESVTEQDSKDSTYSLEST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC (SEQ ID NO: 446)	
iPS:392533	SEQ ID NO: 275	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSF GMHWVRQAPGKGLEWVAVISFDGSIKYSVDS VKGRFTISRDNSKNTLFLQMNSLRAEDTAVYY CARDRLNYYESSGYYHYKYYGMAVWGQGTT VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLESVVTVPSSSLGTQTYICNVNHKPSNTK VDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPCEEQYGSTYRCVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGGGGSGGGGSDIQLTQSPSFLSA SVGDRVTITCRASQSIGRSLHWYQEKPGKAPK LLIKYASQSLSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCHQSSRLPFTFGPGTKVDIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKV QWKVDNALQSGNSQESVTEQDSKDSTYSLEST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC (SEQ ID NO: 447)	SEQ ID NO: 463
iPS:392530	QSVLTQPPSVSAA PGQKVTISCSGSS SNIGNNYVSWYQ KLPGTAPKLLIYD NNKRPSGIPDRFS GSKSGTSTTLGIT GLQTGDEADYYC GTWDSRLSAVVF GGGTKLTVLGQP KANPTVTLFPPSS EELQANKATLVC LISDFYPGAVTVA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSF GMHWVREAPGKGLEWVAVISFDGSIKYSVDS VKGRFTISRDNSKNTLFLQMNSLRAEDTAVYY CARDRLNYYDSSGYYHYKYYGMAVWGQGTT VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLESVVTVPSSSLGTQTYICNVNHKPSNTK VDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPCEEQYGSTYRCVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKG	SEQ ID NO: 462

IgG-Fab Molecule Designation	Light Chain Amino Acid Sequence	Modified Heavy Chain Amino Acid Sequence	Second Polypeptide Amino Acid Sequence
	WKADGSPVKAG VETTKPSKQSNN KYAAKSYLSLTP EQWKSHRSYSCQ VTHEGSTVEKTV APTECS (SEQ ID NO: 427)	FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGGGGSGGGGSDIQLTQSPSFLSA SVGDRVTITCRASQSIGRSLHWYQQKPGKAPK LLIKYASQSLSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCHQSSRLPFTFGPGTKVDIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKV QWKVDNALQSGNSQESVTEQDSKDSTYSLEST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC (SEQ ID NO: 448)	
iPS:392531	SEQ ID NO: 427	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSF GMHWVREAPGKGLEWVAVISFDGSIKYSVDS VKGRFTISRDNSKNTLFLQMNSLRAEDTAVYY CARDRLNYYDSSGYYHYKYYGMAVWGQGTT VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLESVVTVPSSSLGTQTYICNVNHKPSNTK VDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPCEEQYGSTYRCVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGGGGSGGGGSDIQLTQSPSFLSA SVGDRVTITCRASQSIGRSLHWYQEKPGKAPK LLIKYASQSLSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCHQSSRLPFTFGPGTKVDIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKV QWKVDNALQSGNSQESVTEQDSKDSTYSLEST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC (SEQ ID NO: 449)	SEQ ID NO: 463
iPS:392534	SEQ ID NO: 427	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSF GMHWVREAPGKGLEWVAVISFDGSIKYSVDS VKGRFTISRDNSKNTLFLQMNSLRAEDTAVYY CARDRLNYYESSGYYHYKYYGMAVWGQGTT VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLESVVTVPSSSLGTQTYICNVNHKPSNTK VDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPCEEQYGSTYRCVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGGGGSGGGGSDIQLTQSPSFLSA SVGDRVTITCRASQSIGRSLHWYQQKPGKAPK LLIKYASQSLSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCHQSSRLPFTFGPGTKVDIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKV QWKVDNALQSGNSQESVTEQDSKDSTYSLEST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFN	SEQ ID NO: 462

IgG-Fab Molecule Designation	Light Chain Amino Acid Sequence	Modified Heavy Chain Amino Acid Sequence	Second Polypeptide Amino Acid Sequence
		RGEC (SEQ ID NO: 450)	
iPS:392535	SEQ ID NO: 427	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSF GMHWVREAPGKGLEWVAVISFDGSIKYSVDS VKGRFTISRDNSKNTLFLQMNSLRAEDTAVYY CARDRLNYYESSGYYHYKYYGMAVWGQGTT VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLESVVTVPSSSLGTQTYICNVNHKPSNTK VDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPCEEQYGSTYRCVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGGGGSGGGGSDIQLTQSPSFLSA SVGDRVTITCRASQSIGRSLHWYQEKPGKAPK LLIKYASQSLSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCHQSSRLPFTFGPGTKVDIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKV QWKVDNALQSGNSQESVTEQDSKDSTYSLEST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC (SEQ ID NO: 451)	SEQ ID NO: 463

[0146] In certain embodiments, the first antibody (i.e. the IgG component) of the IgG-Fab bispecific antigen binding proteins is an anti-PAC1 receptor antibody and the second antibody (i.e. from which the carboxyl-terminal Fab is derived) is an anti-CGRP receptor antibody. In such embodiments, the anti-PAC1 receptor antibody comprises a VL region from any of those described in Table 1A and a VH region from any of those described in Table 1B. For instance, in one embodiment, the anti-PAC1 receptor antibody from which the IgG component is derived comprises a LV-04 (SEQ ID NO: 31) VL region and a HV-03 (SEQ ID NO: 85) VH region.

[0147] In embodiments in which the carboxyl-terminal Fab component is derived from an anti-CGRP receptor antibody, the anti-CGRP receptor antibody may comprise a VL region from any of those described in Table 3A and a VH region from any of those described in Table 3B. In one embodiment, the anti-CGRP receptor Fab comprises a LV-105 (SEQ ID NO: 140) VL region and a HV-105 (SEQ ID NO: 194) VH region. In another embodiment, the anti-CGRP receptor Fab comprises a LV-105 (SEQ ID NO: 140) VL region and a HV-107 (SEQ ID NO: 196) VH region.

[0148] In embodiments in which the IgG component of the bispecific antigen binding proteins is derived from an anti-PAC1 receptor antibody and the carboxyl-terminal Fab component is

derived from an anti-CGRP receptor antibody, the modified heavy chain of the bispecific antigen binding proteins comprises a sequence selected from SEQ ID NOs: 428 to 439. In related embodiments, the light chain of the bispecific antigen binding proteins comprises the sequence of SEQ ID NO: 214 or SEQ ID NO: 426 and the second polypeptide (which contains the other half of the carboxyl-terminal Fab fragment) comprises a sequence selected from SEQ ID NOs: 452 to 459. In some embodiments, the bispecific, multivalent antigen binding protein comprises a light chain, a modified heavy chain, and a second polypeptide, wherein:

(a) the light chain comprises the sequence of SEQ ID NO: 214, the modified heavy chain comprises the sequence of SEQ ID NO: 428, and the second polypeptide comprises the sequence of SEQ ID NO: 452;

(b) the light chain comprises the sequence of SEQ ID NO: 214, the modified heavy chain comprises the sequence of SEQ ID NO: 429, and the second polypeptide comprises the sequence of SEQ ID NO: 453;

(c) the light chain comprises the sequence of SEQ ID NO: 214, the modified heavy chain comprises the sequence of SEQ ID NO: 430, and the second polypeptide comprises the sequence of SEQ ID NO: 454;

(d) the light chain comprises the sequence of SEQ ID NO: 214, the modified heavy chain comprises the sequence of SEQ ID NO: 431, and the second polypeptide comprises the sequence of SEQ ID NO: 455;

(e) the light chain comprises the sequence of SEQ ID NO: 214, the modified heavy chain comprises the sequence of SEQ ID NO: 432, and the second polypeptide comprises the sequence of SEQ ID NO: 456;

(f) the light chain comprises the sequence of SEQ ID NO: 214, the modified heavy chain comprises the sequence of SEQ ID NO: 433, and the second polypeptide comprises the sequence of SEQ ID NO: 457;

(g) the light chain comprises the sequence of SEQ ID NO: 214, the modified heavy chain comprises the sequence of SEQ ID NO: 434, and the second polypeptide comprises the sequence of SEQ ID NO: 458;

(h) the light chain comprises the sequence of SEQ ID NO: 214, the modified heavy chain comprises the sequence of SEQ ID NO: 435, and the second polypeptide comprises the sequence of SEQ ID NO: 459;

(i) the light chain comprises the sequence of SEQ ID NO: 426, the modified heavy chain comprises the sequence of SEQ ID NO: 436, and the second polypeptide comprises the sequence of SEQ ID NO: 456;

(j) the light chain comprises the sequence of SEQ ID NO: 426, the modified heavy chain comprises the sequence of SEQ ID NO: 437, and the second polypeptide comprises the sequence of SEQ ID NO: 457;

(k) the light chain comprises the sequence of SEQ ID NO: 426, the modified heavy chain comprises the sequence of SEQ ID NO: 438, and the second polypeptide comprises the sequence of SEQ ID NO: 459; or

(l) the light chain comprises the sequence of SEQ ID NO: 426, the modified heavy chain comprises the sequence of SEQ ID NO: 439, and the second polypeptide comprises the sequence of SEQ ID NO: 458. In certain embodiments, the bispecific, multivalent antigen binding protein is an antigen binding protein designated as iPS:392513, iPS:392514, iPS:392475, iPS:392519, iPS:392515, iPS:392516, iPS:392521, iPS:392520, iPS:392517, iPS:392518, iPS:392522, or iPS:392523 as set forth in Table 10.

[0149] In other embodiments of the invention, the first antibody (i.e. the IgG component) of the IgG-Fab bispecific antigen binding proteins is an anti-CGRP receptor antibody and the second antibody (i.e. from which the carboxyl-terminal Fab is derived) is an anti-PAC1 receptor antibody. In such embodiments, the anti-CGRP receptor antibody comprises a VL region from any of those described in Table 3A and a VH region from any of those described in Table 3B. For example, in one embodiment, the anti-CGRP receptor antibody from which the IgG component is derived comprises a LV-105 (SEQ ID NO: 140) VL region and a HV-105 (SEQ ID NO: 194) VH region. In another embodiment, the anti-CGRP receptor antibody from which the IgG component is derived comprises a LV-105 (SEQ ID NO: 140) VL region and a HV-107 (SEQ ID NO: 196) VH region. In embodiments in which the carboxyl-terminal Fab component is derived from an anti-PAC1 receptor antibody, the anti-PAC1 receptor antibody may comprise a VL region from any of those described in Table 1A and a VH region from any of those described in Table 1B. In one embodiment, the anti-PAC1 receptor Fab comprises a LV-04 (SEQ ID NO: 31) VL region and a HV-03 (SEQ ID NO: 85) VH region.

[0150] In embodiments in which the IgG component of the bispecific antigen binding proteins is derived from an anti-CGRP receptor antibody and the carboxyl-terminal Fab component is

derived from an anti-PAC1 receptor antibody, the modified heavy chain of the bispecific antigen binding proteins comprises a sequence selected from SEQ ID NOs: 440 to 451. In related embodiments, the light chain of the bispecific antigen binding proteins comprises the sequence of SEQ ID NO: 275 or SEQ ID NO: 427 and the second polypeptide (which contains the other half of the carboxyl-terminal Fab fragment) comprises a sequence selected from SEQ ID NOs: 460 to 463. In some embodiments, the bispecific, multivalent antigen binding protein comprises a light chain, a modified heavy chain, and a second polypeptide, wherein:

(a) the light chain comprises the sequence of SEQ ID NO: 275, the modified heavy chain comprises the sequence of SEQ ID NO: 440, and the second polypeptide comprises the sequence of SEQ ID NO: 460;

(b) the light chain comprises the sequence of SEQ ID NO: 275, the modified heavy chain comprises the sequence of SEQ ID NO: 441, and the second polypeptide comprises the sequence of SEQ ID NO: 461;

(c) the light chain comprises the sequence of SEQ ID NO: 275, the modified heavy chain comprises the sequence of SEQ ID NO: 442, and the second polypeptide comprises the sequence of SEQ ID NO: 460;

(d) the light chain comprises the sequence of SEQ ID NO: 275, the modified heavy chain comprises the sequence of SEQ ID NO: 443, and the second polypeptide comprises the sequence of SEQ ID NO: 461;

(e) the light chain comprises the sequence of SEQ ID NO: 275, the modified heavy chain comprises the sequence of SEQ ID NO: 444, and the second polypeptide comprises the sequence of SEQ ID NO: 462;

(f) the light chain comprises the sequence of SEQ ID NO: 275, the modified heavy chain comprises the sequence of SEQ ID NO: 445, and the second polypeptide comprises the sequence of SEQ ID NO: 463;

(g) the light chain comprises the sequence of SEQ ID NO: 275, the modified heavy chain comprises the sequence of SEQ ID NO: 446, and the second polypeptide comprises the sequence of SEQ ID NO: 462;

(h) the light chain comprises the sequence of SEQ ID NO: 275, the modified heavy chain comprises the sequence of SEQ ID NO: 447, and the second polypeptide comprises the sequence of SEQ ID NO: 463;

(i) the light chain comprises the sequence of SEQ ID NO: 427, the modified heavy chain comprises the sequence of SEQ ID NO: 448, and the second polypeptide comprises the sequence of SEQ ID NO: 462;

(j) the light chain comprises the sequence of SEQ ID NO: 427, the modified heavy chain comprises the sequence of SEQ ID NO: 449, and the second polypeptide comprises the sequence of SEQ ID NO: 463;

(k) the light chain comprises the sequence of SEQ ID NO: 427, the modified heavy chain comprises the sequence of SEQ ID NO: 450, and the second polypeptide comprises the sequence of SEQ ID NO: 462; or

(l) the light chain comprises the sequence of SEQ ID NO: 427, the modified heavy chain comprises the sequence of SEQ ID NO: 451, and the second polypeptide comprises the sequence of SEQ ID NO: 463. In certain embodiments, the bispecific, multivalent antigen binding protein is an antigen binding protein designated as iPS:392524, iPS:392525, iPS:392526, iPS:392527, iPS:392528, iPS:392529, iPS:392532, iPS:392533, iPS:392530, iPS:392531, iPS:392534, or iPS:392535 as set forth in Table 10. In other embodiments, the bispecific, multivalent antigen binding protein is an antigen binding protein designated as iPS:392524, iPS:392525, iPS:392526, iPS:392527, iPS:392532, iPS:392533, iPS:392534, or iPS:392535 as set forth in Table 10.

[0151] The heavy chain constant regions or the Fc regions of the bispecific antigen binding proteins described herein may comprise one or more amino acid substitutions that affect the glycosylation and/or effector function of the antigen binding protein. One of the functions of the Fc region of an immunoglobulin is to communicate to the immune system when the immunoglobulin binds its target. This is commonly referred to as "effector function." Communication leads to antibody-dependent cellular cytotoxicity (ADCC), antibody-dependent cellular phagocytosis (ADCP), and/or complement dependent cytotoxicity (CDC). ADCC and ADCP are mediated through the binding of the Fc region to Fc receptors on the surface of cells of the immune system. CDC is mediated through the binding of the Fc with proteins of the complement system, e.g., C1q. In some embodiments, the bispecific antigen binding proteins of the invention comprise one or more amino acid substitutions in the constant region to enhance effector function, including ADCC activity, CDC activity, ADCP activity, and/or the clearance or half-life of the antigen binding protein. Exemplary amino acid substitutions (EU numbering) that can enhance effector function include, but are not limited to, E233L, L234I, L234Y, L235S,

G236A, S239D, F243L, F243V, P247I, D280H, K290S, K290E, K290N, K290Y, R292P, E294L, Y296W, S298A, S298D, S298V, S298G, S298T, T299A, Y300L, V305I, Q311M, K326A, K326E, K326W, A330S, A330L, A330M, A330F, I332E, D333A, E333S, E333A, K334A, K334V, A339D, A339Q, P396L, or combinations of any of the foregoing.

[0152] In other embodiments, the bispecific antigen binding proteins of the invention comprise one or more amino acid substitutions in the constant region to reduce effector function. Exemplary amino acid substitutions (EU numbering) that can reduce effector function include, but are not limited to, C220S, C226S, C229S, E233P, L234A, L234V, V234A, L234F, L235A, L235E, G237A, P238S, S267E, H268Q, N297A, N297G, V309L, E318A, L328F, A330S, A331S, P331S or combinations of any of the foregoing.

[0153] Glycosylation can contribute to the effector function of antibodies, particularly IgG1 antibodies. Thus, in some embodiments, the bispecific antigen binding proteins of the invention may comprise one or more amino acid substitutions that affect the level or type of glycosylation of the binding proteins. Glycosylation of polypeptides is typically either N-linked or O-linked. N-linked refers to the attachment of the carbohydrate moiety to the side chain of an asparagine residue. The tri-peptide sequences asparagine-X-serine and asparagine-X-threonine, where X is any amino acid except proline, are the recognition sequences for enzymatic attachment of the carbohydrate moiety to the asparagine side chain. Thus, the presence of either of these tri-peptide sequences in a polypeptide creates a potential glycosylation site. O-linked glycosylation refers to the attachment of one of the sugars N-acetylgalactosamine, galactose, or xylose, to a hydroxyamino acid, most commonly serine or threonine, although 5-hydroxyproline or 5-hydroxylysine may also be used.

[0154] In certain embodiments, glycosylation of the bispecific antigen binding proteins described herein is increased by adding one or more glycosylation sites, e.g., to the Fc region of the binding protein. Addition of glycosylation sites to the antigen binding protein can be conveniently accomplished by altering the amino acid sequence such that it contains one or more of the above-described tri-peptide sequences (for N-linked glycosylation sites). The alteration may also be made by the addition of, or substitution by, one or more serine or threonine residues to the starting sequence (for O-linked glycosylation sites). For ease, the antigen binding protein amino acid sequence may be altered through changes at the DNA level, particularly by mutating

the DNA encoding the target polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

[0155] The invention also encompasses production of bispecific antigen binding protein molecules with altered carbohydrate structure resulting in altered effector activity, including antigen binding proteins with absent or reduced fucosylation that exhibit improved ADCC activity. Various methods are known in the art to reduce or eliminate fucosylation. For example, ADCC effector activity is mediated by binding of the antibody molecule to the FcγRIII receptor, which has been shown to be dependent on the carbohydrate structure of the N-linked glycosylation at the N297 residue of the CH2 domain. Non-fucosylated antibodies bind this receptor with increased affinity and trigger FcγRIII-mediated effector functions more efficiently than native, fucosylated antibodies. For example, recombinant production of non-fucosylated antibody in CHO cells in which the alpha-1,6-fucosyl transferase enzyme has been knocked out results in antibody with 100-fold increased ADCC activity (*see* Yamane-Ohnuki *et al.*, Biotechnol Bioeng. 87(5):614-22, 2004). Similar effects can be accomplished through decreasing the activity of alpha-1,6-fucosyl transferase enzyme or other enzymes in the fucosylation pathway, e.g., through siRNA or antisense RNA treatment, engineering cell lines to knockout the enzyme(s), or culturing with selective glycosylation inhibitors (*see* Rothman *et al.*, Mol Immunol. 26(12):1113-23, 1989). Some host cell strains, e.g. Lec13 or rat hybridoma YB2/0 cell line naturally produce antibodies with lower fucosylation levels (*see* Shields *et al.*, J Biol Chem. 277(30):26733-40, 2002 and Shinkawa *et al.*, J Biol Chem. 278(5):3466-73, 2003). An increase in the level of bisected carbohydrate, e.g. through recombinantly producing antibody in cells that overexpress GnTIII enzyme, has also been determined to increase ADCC activity (*see* Umana *et al.*, Nat Biotechnol. 17(2):176-80, 1999).

[0156] In other embodiments, glycosylation of the bispecific antigen binding proteins described herein is decreased or eliminated by removing one or more glycosylation sites, e.g., from the Fc region of the binding protein. Amino acid substitutions that eliminate or alter N-linked glycosylation sites can reduce or eliminate N-linked glycosylation of the antigen binding protein. In certain embodiments, the bispecific antigen binding proteins described herein comprise a mutation at position N297 (EU numbering), such as N297Q, N297A, or N297G. In one particular embodiment, the bispecific antigen binding proteins of the invention comprise a Fc region from a human IgG1 antibody with a N297G mutation. To improve the stability of

molecules comprising a N297 mutation, the Fc region of the molecules may be further engineered. For instance, in some embodiments, one or more amino acids in the Fc region are substituted with cysteine to promote disulfide bond formation in the dimeric state. Residues corresponding to V259, A287, R292, V302, L306, V323, or I332 (EU numbering) of an IgG1 Fc region may thus be substituted with cysteine. Preferably, specific pairs of residues are substituted with cysteine such that they preferentially form a disulfide bond with each other, thus limiting or preventing disulfide bond scrambling. Preferred pairs include, but are not limited to, A287C and L306C, V259C and L306C, R292C and V302C, and V323C and I332C. In particular embodiments, the bispecific antigen binding proteins described herein comprise a Fc region from a human IgG1 antibody with mutations at R292C and V302C. In such embodiments, the Fc region may also comprise a N297G mutation.

[0157] Modifications of the bispecific antigen binding proteins of the invention to increase serum half-life also may desirable, for example, by incorporation of or addition of a salvage receptor binding epitope (e.g., by mutation of the appropriate region or by incorporating the epitope into a peptide tag that is then fused to the antigen binding protein at either end or in the middle, e.g., by DNA or peptide synthesis; *see, e.g.*, WO96/32478) or adding molecules such as PEG or other water soluble polymers, including polysaccharide polymers. The salvage receptor binding epitope preferably constitutes a region wherein any one or more amino acid residues from one or two loops of a Fc region are transferred to an analogous position in the antigen binding protein. Even more preferably, three or more residues from one or two loops of the Fc region are transferred. Still more preferred, the epitope is taken from the CH2 domain of the Fc region (e.g., an IgG Fc region) and transferred to the CH1, CH3, or VH region, or more than one such region, of the antigen binding protein. Alternatively, the epitope is taken from the CH2 domain of the Fc region and transferred to the CL region or VL region, or both, of the antigen binding protein. *See* International applications WO 97/34631 and WO 96/32478 for a description of Fc variants and their interaction with the salvage receptor.

[0158] The present invention includes one or more isolated nucleic acids encoding the bispecific antigen binding proteins and components thereof described herein. Nucleic acid molecules of the invention include DNA and RNA in both single-stranded and double-stranded form, as well as the corresponding complementary sequences. DNA includes, for example, cDNA, genomic DNA, chemically synthesized DNA, DNA amplified by PCR, and combinations thereof. The

nucleic acid molecules of the invention include full-length genes or cDNA molecules as well as a combination of fragments thereof. The nucleic acids of the invention are preferentially derived from human sources, but the invention includes those derived from non-human species, as well.

[0159] Relevant amino acid sequences from an immunoglobulin or region thereof (e.g. variable region, Fc region, etc.) or polypeptide of interest may be determined by direct protein sequencing, and suitable encoding nucleotide sequences can be designed according to a universal codon table. Alternatively, genomic or cDNA encoding monoclonal antibodies from which the binding domains of the bispecific antigen binding proteins of the invention may be derived can be isolated and sequenced from cells producing such antibodies using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of the monoclonal antibodies).

[0160] An "isolated nucleic acid," which is used interchangeably herein with "isolated polynucleotide," is a nucleic acid that has been separated from adjacent genetic sequences present in the genome of the organism from which the nucleic acid was isolated, in the case of nucleic acids isolated from naturally- occurring sources. In the case of nucleic acids synthesized enzymatically from a template or chemically, such as PCR products, cDNA molecules, or oligonucleotides for example, it is understood that the nucleic acids resulting from such processes are isolated nucleic acids. An isolated nucleic acid molecule refers to a nucleic acid molecule in the form of a separate fragment or as a component of a larger nucleic acid construct. In one preferred embodiment, the nucleic acids are substantially free from contaminating endogenous material. The nucleic acid molecule has preferably been derived from DNA or RNA isolated at least once in substantially pure form and in a quantity or concentration enabling identification, manipulation, and recovery of its component nucleotide sequences by standard biochemical methods (such as those outlined in Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, NY (1989)). Such sequences are preferably provided and/or constructed in the form of an open reading frame uninterrupted by internal non-translated sequences, or introns, that are typically present in eukaryotic genes. Sequences of non-translated DNA can be present 5' or 3' from an open reading frame, where the same do not interfere with manipulation or expression of the coding region. Unless specified otherwise, the left-hand end of any single-stranded polynucleotide sequence discussed herein is the 5' end; the left-hand direction of double-stranded polynucleotide

sequences is referred to as the 5' direction. The direction of 5' to 3' production of nascent RNA transcripts is referred to as the transcription direction; sequence regions on the DNA strand having the same sequence as the RNA transcript that are 5' to the 5' end of the RNA transcript are referred to as "upstream sequences;" sequence regions on the DNA strand having the same sequence as the RNA transcript that are 3' to the 3' end of the RNA transcript are referred to as "downstream sequences."

[0161] The present invention also includes nucleic acids that hybridize under moderately stringent conditions, and more preferably highly stringent conditions, to nucleic acids encoding polypeptides as described herein. The basic parameters affecting the choice of hybridization conditions and guidance for devising suitable conditions are set forth by Sambrook,, Fritsch, and Maniatis (1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., chapters 9 and 11; and Current Protocols in Molecular Biology, 1995, Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4), and can be readily determined by those having ordinary skill in the art based on, for example, the length and/or base composition of the DNA. One way of achieving moderately stringent conditions involves the use of a prewashing solution containing 5 x SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0), hybridization buffer of about 50% formamide, 6 x SSC, and a hybridization temperature of about 55°C (or other similar hybridization solutions, such as one containing about 50% formamide, with a hybridization temperature of about 42°C), and washing conditions of about 60°C, in 0.5 x SSC, 0.1% SDS. Generally, highly stringent conditions are defined as hybridization conditions as above, but with washing at approximately 68°C, 0.2 x SSC, 0.1% SDS. SSPE (1 x SSPE is 0.15M NaCl, 10 mM NaH_2PO_4, and 1.25 mM EDTA, pH 7.4) can be substituted for SSC (1 x SSC is 0.15M NaCl and 15 mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete. It should be understood that the wash temperature and wash salt concentration can be adjusted as necessary to achieve a desired degree of stringency by applying the basic principles that govern hybridization reactions and duplex stability, as known to those skilled in the art and described further below (*see, e.g.*, Sambrook *et al.*, 1989). When hybridizing a nucleic acid to a target nucleic acid of unknown sequence, the hybrid length is assumed to be that of the hybridizing nucleic acid. When nucleic acids of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the nucleic acids and identifying the region or regions of optimal sequence

complementarity. The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5 to 10°C less than the melting temperature (Tm) of the hybrid, where Tm is determined according to the following equations. For hybrids less than 18 base pairs in length, Tm (°C) = 2(# of A + T bases) + 4(# of G + C bases). For hybrids above 18 base pairs in length, Tm (°C) = 81.5 + 16.6(log10 [Na+]) + 0.41(% G + C) - (600/N), where N is the number of bases in the hybrid, and [Na+] is the concentration of sodium ions in the hybridization buffer ([Na+] for 1 x SSC = 0.165M). Preferably, each such hybridizing nucleic acid has a length that is at least 15 nucleotides (or more preferably at least 18 nucleotides, or at least 20 nucleotides, or at least 25 nucleotides, or at least 30 nucleotides, or at least 40 nucleotides, or most preferably at least 50 nucleotides), or at least 25% (more preferably at least 50%, or at least 60%, or at least 70%, and most preferably at least 80%) of the length of the nucleic acid of the present invention to which it hybridizes, and has at least 60% sequence identity (more preferably at least 70%, at least 75%, at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, and most preferably at least 99.5%) with the nucleic acid of the present invention to which it hybridizes, where sequence identity is determined by comparing the sequences of the hybridizing nucleic acids when aligned so as to maximize overlap and identity while minimizing sequence gaps as described in more detail above.

[0162] Variants of the antigen binding proteins described herein can be prepared by site-specific mutagenesis of nucleotides in the DNA encoding the polypeptide, using cassette or PCR mutagenesis or other techniques well known in the art, to produce DNA encoding the variant, and thereafter expressing the recombinant DNA in cell culture as outlined herein. However, antigen binding proteins comprising variant CDRs having up to about 100-150 residues may be prepared by *in vitro* synthesis using established techniques. The variants typically exhibit the same qualitative biological activity as the naturally occurring analogue, e.g., binding to antigen. Such variants include, for example, deletions and/or insertions and/or substitutions of residues within the amino acid sequences of the antigen binding proteins. Any combination of deletion, insertion, and substitution is made to arrive at the final construct, provided that the final construct possesses the desired characteristics. The amino acid changes also may alter post-translational processes of the antigen binding protein, such as changing the number or position of

glycosylation sites. In certain embodiments, antigen binding protein variants are prepared with the intent to modify those amino acid residues which are directly involved in epitope binding. In other embodiments, modification of residues which are not directly involved in epitope binding or residues not involved in epitope binding in any way, is desirable, for purposes discussed herein. Mutagenesis within any of the CDR regions and/or framework regions is contemplated. Covariance analysis techniques can be employed by the skilled artisan to design useful modifications in the amino acid sequence of the antigen binding protein. *See, e.g.*, Choulier, *et al.*, Proteins 41:475-484, 2000; Demarest *et al.*, J. Mol. Biol. 335:41-48, 2004; Hugo *et al.*, Protein Engineering 16(5):381-86, 2003; Aurora *et al.*, US Patent Publication No. 2008/0318207 A1; Glaser *et al.*, US Patent Publication No. 2009/0048122 A1; Urech *et al.*, WO 2008/110348 A1; Borras *et al.*, WO 2009/000099 A2. Such modifications determined by covariance analysis can improve potency, pharmacokinetic, pharmacodynamic, and/or manufacturability characteristics of an antigen binding protein.

[0163] Table 11 shows exemplary nucleic acid sequences encoding light and heavy chain variable regions of anti-PAC1 receptor antibodies, and Table 12 shows exemplary nucleic acid sequences encoding light and heavy chain variable regions of anti-CGRP receptor antibodies. Polynucleotides encoding the anti-PAC1 receptor and anti-CGRP receptor variable regions can be used to construct the anti-PAC1 receptor and anti-CGRP receptor binding domains, respectively, of the bispecific antigen binding proteins described herein.

Table 11. Exemplary Anti-PAC1 Receptor Variable Region Nucleic Acid Sequences

Antibody ID	Designation	Nucleic Acid Sequence	SEQ ID NO:
		Light chain variable regions	
01A, 01C, 01D	LV-01	GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAG GAGACAGAATCACCATCACTTGCCGGGCAAGTCAGAGCATTAGCA GGTATTTAAATTGGTATCAACAGAAACCAGGGAAAGCCCCTAAAC TCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGATCCCATCAAG GTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAAC AGTCTGCAACCTGAAGATTTTGCAACTTACTTCTGTCAACAGAGTT ACAGTCCCCCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAA ACGT	464
01B	LV-02	GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAG GAGACAGAATCACCATCACTTGCCGGGCAAGTCAGAGCATTAGCA GGTATTTAAATTGGTATCAACAGAAACCAGGGAAAGCCCCTAAAC TCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGATCCCATCAAG GTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAAC AGTCTGCAACCTGAAGATTTTGCAACTTACTTCTGTCAACAGAGTT	465

Antibody ID	Designation	Nucleic Acid Sequence	SEQ ID NO:
		ACAGTCCCCCATTCACTTTCGGCGAGGGGACCAAAGTGGATATCA AACGT	
02A, 02C	LV-03	GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAG GAGACAGAATCACCATCACTTGCCGGGCAAGTCAGAGCATTAGCA GGTATTTAAATTGGTATCAACAGAAACCAGGGAAAGCCCCTAAAC TCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGATCCCATCAAG GTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAAC AGTCTGCAACCTGAAGATTTTGCAACTTACTTCTGTCAACAGAGTT ACAGTCCCCCATTCACTTTCGGCCAGGGGACCAAAGTGGATATCA AACGT	466
03A, 03C, 03D	LV-04	GATATCCAGCTCACTCAATCGCCATCATTTCTCTCCGCTTCGGTAG GCGACCGGGTCACGATCACATGCAGGGCGTCGCAAAGCATTGGGA GGTCGTTGCATTGGTATCAGCAGAAACCCGGAAAGGCCCCGAAAC TTCTGATCAAATACGCATCACAAAGCTTGAGCGGTGTGCCGTCGC GCTTCTCCGGTTCCGGAAGCGGAACGGAATTCACGCTTACAATCTC CTCACTGCAGCCCGAGGATTTCGCGACCTATTACTGTCACCAGTCA TCCAGACTCCCGTTTACTTTTGGCCCTGGGACCAAGGTGGACATTA AGCGT	467
03B	LV-05	GATATCCAGCTCACTCAATCGCCATCATTTCTCTCCGCTTCGGTAG GCGACCGGGTCACGATCACATGCAGGGCGTCGCAAAGCATTGGGA GGTCGTTGCATTGGTATCAGCAGAAACCCGGAAAGGCCCCGAAAC TTCTGATCAAATACGCATCACAAAGCTTGAGCGGTGTGCCGTCGC GCTTCTCCGGTTCCGGAAGCGGAACGGAATTCACGCTTACAATCTC CTCACTGCAGCCCGAGGATTTCGCGACCTATTACTGTCACCAGTCA TCCAGACTCCCGTTTACTTTTGGCGAGGGGACCAAGGTGGACATTA AGCGT	468
04A, 04C, 04D	LV-06	GAGATCGTACTTACTCAGTCACCCGCCACATTGTCCCTGAGCCCGG GTGAACGGGCGACCCTCAGCTGCCGAGCATCCCAGTCCGTCGGAC GATCATTGCACTGGTACCAACAAAAACCGGGCCAGGCCCCCAGAC TTCTGATCAAGTATGCGTCACAGAGCTTGTCGGGTATTCCCGCTCG CTTTTCGGGGTCGGGATCCGGGACAGATTTCACGCTCACAATCTCC TCGCTGGAACCCGAGGACTTCGCGGTCTACTATTGTCATCAGTCAT CGAGGTTGCCTTTCACGTTTGGACCAGGGACCAAGGTGGACATTA AGCGT	469
04B	LV-07	GAGATCGTACTTACTCAGTCACCCGCCACATTGTCCCTGAGCCCGG GTGAACGGGCGACCCTCAGCTGCCGAGCATCCCAGTCCGTCGGAC GATCATTGCACTGGTACCAACAAAAACCGGGCCAGGCCCCCAGAC TTCTGATCAAGTATGCGTCACAGAGCTTGTCGGGTATTCCCGCTCG CTTTTCGGGGTCGGGATCCGGGACAGATTTCACGCTCACAATCTCC TCGCTGGAACCCGAGGACTTCGCGGTCTACTATTGTCATCAGTCAT CGAGGTTGCCTTTCACGTTTGGAGAAGGGACCAAGGTGGACATTA AGCGT	470
05A, 05C, 05D	LV-08	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGG GCGAGAGGGCCACCATCCACTGCAAGTCCAGCCAGAGTGTTTTAT ACAGCTCCAACAATAAGAACTTCTTAACTTGGTACCAGCAGAAAC CAGGACAGCCTCCTAAACTTCTCATTTACCGGGCATCTACCCGGGA ATCCGGGGTTCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGA TTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTT TATTTCTGTCAGCAATATTATAGTGCTCCATTCACTTTCGGCCCTGG GACCAGAGTGGATATCAAACGT	471
05B	LV-09	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGG GCGAGAGGGCCACCATCCACTGCAAGTCCAGCCAGAGTGTTTTAT	472

Antibody ID	Designation	Nucleic Acid Sequence	SEQ ID NO:
		ACAGCTCCAACAATAAGAACTTCTTAACTTGGTACCAGCAGAAAC CAGGACAGCCTCCTAAACTTCTCATTTACCGGGCATCTACCCGGGA ATCCGGGGTTCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGA TTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTT TATTTCTGTCAGCAATATTATAGTGCTCCATTCACTTTCGGCGAGG GGACCAGAGTGGATATCAAACGT	
06A, 06C	LV-10	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGG GCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTGTTTTAT ACAGCTCCAACAATAAGAACTTCTTAACTTGGTACCAGCAGAAAC CAGGACAGCCTCCTAAACTTCTCATTTACCGGGCATCTACCCGGGA ATCCGGGGTTCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGA TTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTT TATTTCTGTCAGCAATATTATAGTGCTCCATTCACTTTCGGCCCTGG GACCAGAGTGGATATCAAACGT	473
06B	LV-11	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGG GCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTGTTTTAT ACAGCTCCAACAATAAGAACTTCTTAACTTGGTACCAGCAGAAAC CAGGACAGCCTCCTAAACTTCTCATTTACCGGGCATCTACCCGGGA ATCCGGGGTTCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGA TTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTT TATTTCTGTCAGCAATATTATAGTGCTCCATTCACTTTCGGCGAGG GGACCAGAGTGGATATCAAACGT	474
07	LV-12	GAAATTGTGCTGACTCAGTCTCCAGACTTTCAGTCTGTGACTCCAA AGGAGAAAGTCACCATCACCTGCCGGGCCAGTCAGAGCATTGGTA GTAGCTTACACTGGTACCAGCAGAAACCAGATCAGTCTCCAAAGC TCCTCATCAAGTATGCTTCCCAGTCCTTGTCAGGGATCCCCTCGAG GTTTAGTGGCAGTGGATCTGGGACACATTTCACCCTCACCATCAAT AGCCTGGAAGCTGAAGATGCTGCAACGTATTACTGTCATCAGAGT AGTCGTTTACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCA AACGAAC	475
08, 09, 10	LV-13	GAAATTGTGCTGACTCAGTCTCCAGACTTTCAGTCTGTGACTCCAA AGGAGAAAGTCACCATCACCTGCCGGGCCAGTCAGAGCGTTGGTC GTAGTTTACACTGGTACCATCAGAAACCAGATCAGTCTCCAAAGC TCCTCATCAAGTATGCTTCCCAGTCCTTATCAGGGGTCCCCTCGAG GTTCAGTGGCAGTGGATCTGGGACAGATTTCACCCTCATTATCAAT AGCCTGGAAGCTGAAGATGCTGCAACGTATTACTGTCATCAGAGT AGTCGTTTACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCA AACGAA	476
11	LV-14	GATATCCAGCTCACTCAATCGCCATCATTTCTCTCCGCTTCGGTAG GCGACCGGGTCACGATCACATGCAGGGCGTCGCAAAGCATTGGGA GGTCGTTGCATTGGTATCACCAGAAACCCGGAAAGGCCCCGAAAC TTCTGATCAAATACGCATCACAAAGCTTGAGCGGTGTGCCGTCGC GCTTCTCCGGTTCCGGAAGCGGAACGGAATTCACGCTTATCATCTC CTCACTGCAGCCCGAGGATTTCGCGACCTATTACTGTCACCAGTCA TCCAGACTCCCGTTTACTTTTGGCCCTGGGACCAAGGTGGACATTA AGCGTAC	477
12, 13, 14	LV-15	GAAATTGTGCTGACTCAGTCTCCAGACTTTCAGTCTGTGACTCCAA AGGAGAAAGTCACCATCACCTGCCGGGCCAGTCAGAGCGTTGGTC GTAGTTTACACTGGTACCAGCAGAAACCAGATCAGTCTCCAAAGC TCCTCATCAAGTATGCTTCCCAGTCCTTATCAGGGGTCCCCTCGAG GTTCAGTGGCAGTGGATCTGGGACAGATTTCACCCTCACTATCAAT AGCCTGGAAGCTGAAGATGCTGCAACGTATTACTGTCATCAGAGT	478

Antibody ID	Designation	Nucleic Acid Sequence	SEQ ID NO:
		AGTCGTTTACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCA AACGAAC	
15, 16, 17, 18	LV-16	GAGATCGTACTTACTCAGTCACCCGGCACATTGTCCCTGAGCCCGG GTGAACGGGCGACCCTCAGCTGCCGAGCATCCCAGTCCGTCGGAC GATCATTGCACTGGTACCAACAAAAACCGGGCCAGGCCCCCAGAC TTCTGATCAAGTATGCGTCACAGAGCTTGTCGGGTATTCCCGATCG CTTTTCGGGGTCGGGATCCGGGACAGATTTCACGCTCACAATCTCC CGACTGGAACCCGAGGACTTCGCGACCTACTATTGTCATCAGTCAT CGAGGTTGCCTTTCACGTTTGGACAGGGGACCAAGGTGGAGATTA AGCGTA	479
19	LV-17	GAAATTGTGCTGACTCAGTCTCCAGACTTTCAGTCTGTGACTCCAA AGGAGAAAGTCACCATCACCTGCCGGGCCAGTCAGAGCATTGGTC GTAGTTTACACTGGTACCAGCAGAAACCAGATCAGTCTCCAAAGC TCCTCTTCAAGTATGCTTCCCAGTCCTTATCAGGGGTCCCCTCGAG GTTCAGTGGCAGTGGATCTGGGACAGATTTCACCCTCACAATCAAT AGCCTGGAAGCTGAAGATGCTGCAACGTATTACTGTCATCAGAGT AGTCGTTTACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCA AACGAA	480
20	LV-18	GATATCCAGCTCACTCAATCGCCATCATTTCTCTCCGCTTCGGTAG GCGACCGGGTCACGATCACATGCAGGGCGTCGCAAAGCATTGGGA GGTCGTTGCATTGGTATCAGCAGAAACCCGGAAAGGCCCCGAAAC TTCTGTTCAAATACGCATCACAAAGCTTGAGCGGTGTGCCGTCGCG CTTCTCCGGTTCCGGAAGCGGAACGGAATTCACGCTTACAATCTCC TCACTGCAGCCCGAGGATTTCGCGACCTATTACTGTCACCAGTCAT CCAGACTCCCGTTTACTTTTGGCCCTGGGACCAAGGTGGACATTAA GCGTAC	481
21	LV-19	GAAATTGTGTTGACGCAGTCGCCAGGCACCCTGTCTTTGTCTCCAG GGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCA GCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCA GGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAG ACAGGTTCAGTAACAGTGGGTCTGGGACAGACTTCACTCTCACCA TCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGA GGTATGGTAGCTCACGGACGTTCGGCCAAGGGACCAAGGTGGAAA TCAAACGAA	482
22	LV-20	GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTG GAGAGCCGGCCTCCATCTCCTGCAGGTCTAGTCAGAGCCTCCTGCA TAGTAATGGATACAACTATTTGGATTGGTACCTGCAGAAGCCAGG GCAGTCTCCACAGCTCCTGCTCTATTTGGGTTCTAATCGGGCCTCC GGGGTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTT ACACTGCAAATCAGCAGAGTGGAGGCTGAGGATGTTGGGGTTTAT TACTGCATGCAAACTCTACAAACTCCATTCACTTTCGGCCCTGGGA CCAAAGTGGATATCAAACGT	483
23	LV-21	GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTG GAGAGCCGGCCTCCATCTCCTGCAGGTCTAGTCAGAGCCTCCTGCA TAGTAATGGATACAACTATTTGGATTGGTACCTGCAGAAGCCAGG GCAGTCTCCACAGCTCCTGCTCTATTTGGGTTCTAATCGGGCCTCC GGGGTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTT ACACTGAAAATCAGCAGAGTGGAGGCTGAGGATGTTGGGGTTTAT TACTGCATGCAAACTCTACAAACTCCATTCACTTTCGGCCCTGGGA CCAAAGTGGATATCAAACGT	484
24	LV-22	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAG GGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGACTGTTAGCA	485

Antibody ID	Designation	Nucleic Acid Sequence	SEQ ID NO:
		GGAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCA GGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAG ACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCA TCAGCAGACTGGAGCCTGAAGATTTTGCCGTGTTTTACTGTCAGCA GTTTGGTAGCTCACCGTGGACGTTCGGCCAAGGGACCAAGGTGGA AATCAAACGT	
25	LV-23	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGG GCGAGAGGGCCACCATCCATTGCAAGTCCAGCCAGAATGTTTTAT ACAGCTCCAACAATAAGAACTTCTTAACTTGGTACCAGCAGAAAC CAGGACAGCCCCCTAAACTGCTCATTTACCGGGCATCTACCCGGG AATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACGG ATTTCACTCTCACTATCAGCAGTCTGCAGGCTGAAGATGTGGCAGT TTATTTCTGTCAGCAATATTATAGTGCTCCATTCACTTTCGGCCCTG GGACCAAAGTGGATATCAAACGTAC	486
26	LV-24	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGG GCGAGAGGACCACCATCAAGTGCAAGTCCAGCCAGAGTGTTTTAT ACAGATCCAACAATAACAACTTCTTAGCTTGGTACCAGCAGAAAC CAGGACAGCCTCCTAAGCTGCTCATTTATTGGGCATCTACCCGGGA ATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGA TTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCTGTT TATTTCTGTCAGCAATATTATATTTCTCCGCTCACTTTCGGCGGAG GGACCAAGGTGGAGATCAAACGTA	487
27	LV-25	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGG GCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTGTTTTAT ACAGTTCCAACAATAAGCACTACTTAGCTTGGTACCGGCAGAAAC CAGGACAGCCTCCTAAACTGCTCATTTACAGGGCATCTACCCGGG AATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAG ATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTGGCAGT GTATTACTGTCAGCAATATTATAGTTCTCCATTCACTTTCGGCCCTG GGACCAAAGTGGATATCAAACGTA	488
28	LV-26	GACATCGTGATGACTCAGTCTCCAGACTCCCTGGCTGTGTCTCTGG GCGAGAGGGCCACCATCCACTGCAAGTCCAGCCAGAGTGTTTTAT ACAGCTCCAACAATAGGAACTTCTTAAGTTGGTACCAGCAGAAAC CAGGACAGCCTCCTAAACTGCTCATTTACCGGGCATCTACCCGGG AATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAG ATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGT TTATTTCTGTCAGCAATATTATAGTGCTCCATTCACTTTCGGCCCTG GGACCACAGTGGATATCAAACGTAC	489
29	LV-27	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGG GCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTGTTTTAT ACAGTTCCAACAATAAGAACTACTTAGCTTGGTACCGGCAGAAAC CAGGACAGCCTCCTAAGCTGCTCATTTACAGGGCATCTACCCGGG AATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAG ATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGT GTATCACTGTCAGCAATATTATAGTTCTCCATTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGTAC	490
Heavy chain variable regions			
01A, 01C, 01D, 02A, 02C	HV-01	CAGGTACAGCTGCAGCAGTCAGGTCCAGGACTGGTGAAGCCCTCG CAGACCCTCTCACTCACCTGTGCCATCTCCGGGGACAGTGTCTCTA GCAACAGTGCTACTTGGAACTGGATCAGGCAGTCCCCATCGAGAG GCCTTGAGTGGCTGGGAAGGACATATTACAGGTCCAAGTGGTCTA ATCATTATGCAGTATCTGTGAAAAGTCGAATAACCATCAACCCCG	491

Antibody ID	Designation	Nucleic Acid Sequence	SEQ ID NO:
		ACACGTCCAAGAGCCAGTTCTCCCTGCAGCTGAACTCTGTGACTCC CGAGGACACGGCTGTGTATTACTGTGCAAGAGGAACGTGGAAACA GCTATGGTTCCTTGACCACTGGGGCCAGGGAACCCTGGTCACCGTC TCTAGT	
01B	HV-02	CAGGTACAGCTGCAGCAGTCAGGTCCAGGACTGGTGAAGCCCTCG CAGACCCTCTCACTCACCTGTGCCATCTCCGGGGACAGTGTCTCTA GCAACAGTGCTACTTGGAACTGGATCAGGCAGTCCCCATCGAGAA AGCTTGAGTGGCTGGGAAGGACATATTACAGGTCCAAGTGGTCTA ATCATTATGCAGTATCTGTGAAAAGTCGAATAACCATCAACCCCG ACACGTCCAAGAGCCAGTTCTCCCTGCAGCTGAACTCTGTGACTCC CGAGGACACGGCTGTGTATTACTGTGCAAGAGGAACGTGGAAACA GCTATGGTTCCTTGACCACTGGGGCCAGGGAACCCTGGTCACCGTC TCTAGT	492
03A, 03C, 03D, 09, 13, 15	HV-03	CAAGTTCAGTTGGTGGAGTCTGGAGCCGAAGTAGTAAAGCCAGGA GCTTCAGTGAAAGTCTCTTGTAAAGCAAGTGGATTCACGTTTAGCC GCTTTGCCATGCATTGGGTGCGGCAAGCTCCCGGTCAGGGGTTGG AGTGGATGGGAGTTATTAGCTATGACGGGGGCAATAAGTACTACG CCGAGTCTGTTAAGGGTCGGGTCACAATGACACGGGACACCTCAA CCAGTACACTCTATATGGAACTGTCTAGCCTGAGATCCGAGGACA CCGCTGTGTATTATTGCGCTAGGGGGTACGATGTATTGACGGGTTA TCCTGATTACTGGGGGCAGGGGACACTCGTAACCGTCTCTAGT	493
03B	HV-04	CAAGTTCAGTTGGTGGAGTCTGGAGCCGAAGTAGTAAAGCCAGGA GCTTCAGTGAAAGTCTCTTGTAAAGCAAGTGGATTCACGTTTAGCC GCTTTGCCATGCATTGGGTGCGGCAAGCTCCCGGTCAGAAGTTGG AGTGGATGGGAGTTATTAGCTATGACGGGGGCAATAAGTACTACG CCGAGTCTGTTAAGGGTCGGGTCACAATGACACGGGACACCTCAA CCAGTACACTCTATATGGAACTGTCTAGCCTGAGATCCGAGGACA CCGCTGTGTATTATTGCGCTAGGGGGTACGATGTATTGACGGGTTA TCCTGATTACTGGGGGCAGGGGACACTCGTAACCGTCTCTAGT	494
04A, 04C, 04D	HV-05	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGG AGGTCCCTGCGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTA GATTTGCCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGG AGTGGGTGGCAGTTATATCATATGATGGAGGAAATAAATACTATG CAGAGTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCCA AGAACACCCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACA CGGCTCTGTTTTACTGTGCGAGAGGATACGATGTTTTGACTGGTTA CCCCGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCTAGT	495
04B	HV-06	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGG AGGTCCCTGCGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTA GATTTGCCATGCACTGGGTCCGCCAGGCTCCAGGCAAGAAGCTGG AGTGGGTGGCAGTTATATCATATGATGGAGGAAATAAATACTATG CAGAGTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCCA AGAACACCCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACA CGGCTCTGTTTTACTGTGCGAGAGGATACGATGTTTTGACTGGTTA CCCCGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCTAGT	496
05A, 05C, 05D	HV-07	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCA CAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGCA GTGGTGGTTACTACTGGAGCTGGATCCGCCAGCACCCAGGGAAGG GCCTGGAGTGGATTGGGTACATCTATTACAGTGGGAACACCTACT ACAACCCGTCCCTCAAGAGTCGAGTTACCATATCAGGAGACACGT CTAAGAACCAGTTCTCCCTGAAGCTGAGGTCTGTGACTGCCGCGG ACACGGCCGTGTATTACTGTACGAGAGGAGGAGCAGCTCGCGGTA	497

Antibody ID	Designation	Nucleic Acid Sequence	SEQ ID NO:
		TGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGT	
05B	HV-08	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCA CAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGCA GTGGTGGTTACTACTGGAGCTGGATCCGCCAGCACCCAGGGAAGA AGCTGGAGTGGATTGGGTACATCTATTACAGTGGGAACACCTACT ACAACCCGTCCCTCAAGAGTCGAGTTACCATATCAGGAGACACGT CTAAGAACCAGTTCTCCCTGAAGCTGAGGTCTGTGACTGCCGCGG ACACGGCCGTGTATTACTGTACGAGAGGAGGAGCAGCTCGCGGTA TGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGT	498
06A, 06C	HV-09	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCA GAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGCA GTGGTGGTTACTACTGGAGCTGGATCCGCCAGCCCCCAGGGAAGG GCCTGGAGTGGATTGGGTACATCTATTACAGTGGGAACACCTACT ACAACCCGTCCCTCAAGAGTCGAGTTACCATATCAGTGGACACGT CTAAGAACCAGTTCTCCCTGAAGCTGAGGTCTGTGACTGCCGCGG ACACGGCCGTGTATTACTGTACGAGAGGAGGAGCAGCTCGCGGTA TGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGT	499
06B	HV-10	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCA GAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGCA GTGGTGGTTACTACTGGAGCTGGATCCGCCAGCCCCCAGGGAAGA AGCTGGAGTGGATTGGGTACATCTATTACAGTGGGAACACCTACT ACAACCCGTCCCTCAAGAGTCGAGTTACCATATCAGTAGACACGT CTAAGAACCAGTTCTCCCTGAAGCTGAGGTCTGTGACTGCCGCGG ACACGGCCGTGTATTACTGTACGAGAGGAGGAGCAGCTCGCGGTA TGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGT	500
07	HV-11	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGG AGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTT ACTATGCCATACACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTAG AGTGGGTGGCAGTTATCTCATATGATGGAAGTAATAAATACTATG CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCA AGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACA CGGCTGTGTATTACTGTGCGAGAGGATACGATCTTTTGACTGGTTA CCCCGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG	501
11, 14	HV-12	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGG AGGTCCCTGCGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTA GATTTGCCATGCACTGGGTCCGCCGGGCTCCAGGCAAGGGGCTGG AGTGGGTGGCAGTTATATCATATGATGGAGGAAATAAATACTATG CAGAGTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCCA AGAACACCCTGAATCTGCTAATGAACAGCCTGAGAGCTGAGGACA CGGCTCTGTTTTACTGTGCGAGAGGATACGATGTTTTGACTGGTTA CCCCGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGC	502
08, 12	HV-13	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGG AGGTCCCTGCGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTA GATTTGCCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGG AGTGGGTGGCAGTTATATCATATGATGGAGGAAATAAATACTATG CAGAGTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCCA AGAACACCCTGAATCTGCTAATGAACAGCCTGAGAGCTGAGGACA CGGCTCTGTTTTACTGTGCGAGAGGATACGATGTTTTGACTGGTTA CCCCGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGC	503
10	HV-14	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGG AGGTCCCTGCGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTA GATTTGCCATGCACTGGGTCCGCCGGGCTCCAGGCAAGGGGCTGG	504

Antibody ID	Designation	Nucleic Acid Sequence	SEQ ID NO:
		AGTGGGTGGCAGTTATATCATATGATGGAGGAAATAAATACTATG CAGAGTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCCA AGAACACCCTGAATCTGCTAATGGACAGCCTGAGAGCTGAGGACA CGGCTCTGTTTTACTGTGCGAGAGGATACGATGTTTTGACTGGTTA CCCCGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA	
16	HV-15	CAAGTTCAGTTGGTGCAATCTGGAGCCGAAGTAAAGAAGCCAGGA GCTTCAGTGAAAGTCTCTTGTAAAGCAAGTGGATTCACGTTTAGCC GCTTTGCCATGCATTGGGTGCGGCAAGCTCCCGGTCAGGGGTTGG AGTGGATGGGAGTTATTAGCTATGACGGGGGCAATAAGTACTACG CCGAGTCTGTTAAGGGTCGGGTCACAATGACACGGGACACCTCAA CCAGTACAGCCTATATGGAACTGTCTAGCCTGAGATCCGAGGACA CCGCTGTGTATTATTGCGCTAGGGGGTACGATGTATTGACGGGTTA TCCTGATTACTGGGGGCAGGGGACACTCGTAACCGTCTCTAGT	505
17	HV-16	CAAGTTCAGTTGGTGCAATCTGGAGCCGAAGTAAAGAAGCCAGGA GCTTCAGTGAAAGTCTCTTGTGCCGCAAGTGGATTCACGTTTAGCC GCTTTGCCATGCATTGGGTGCGGCAAGCTCCCGGTCAGGGGTTGG AGTGGATGGGAGTTATTAGCTATGACGGGGGCAATAAGTACTACG CCGAGTCTGTTAAGGGTCGGGTCACAATGACACGGGACAACTCAA AAAATACAGCCTATATGGAACTGTCTAGCCTGAGATCCGAGGACA CCGCTGTGTATTATTGCGCTAGGGGGTACGATGTATTGACGGGTTA TCCTGATTACTGGGGGCAGGGGACACTCGTAACCGTCTCTAGT	506
18	HV-17	GAGGTGCAGCTGCTGGAGTCTGGGGGAGGCCTGGTCCAGCCTGGG GGGTCCCTGCGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTA GATTTGCCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGG AGTGGGTGGCAGTTATATCATATGATGGAGGAAATAAATACTATG CAGAGTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCCA AGAACACCCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACA CGGCTGTGTATTACTGTGCGAGAGGATACGATGTTTTGACTGGTTA CCCCGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGC	507
19, 20	HV-18	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGG AGGTCCCTGCGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTC GCTATGCCATGCACTGGGTCCGCCAGGCTTCAGGCAAGGGGCTGG AGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCA AGAACACCCTGTATCTGCTAATGAGCAGCCTGAGAGCTGAGGACA CGGCTGTGTTTTACTGTGCGAGAGGATACGATATTTTGACTGGTTA CCCCGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA	508
21	HV-19	CAGGTTCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGG GCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTTACCA GCTATGGTATCAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTG AGTGGATGGGATGGATCAACGCTTACAATGGTCACACAAACTATG CACAGACGTTCCAGGGCAGAGTCACCATGACCACAGACACATCCA CGAGCACAGCCTACATGGAGCTGAGGAGCCTGAGATCTGACGACA CGGCCGTGTATTACTGTGCGAGGGAACTGGAACTACGCTCCTTCTA TTACTTCGGTATGGACGTCTGGGGCCAAGGGACCACGGTCCCCGT CTCTAGTG	509
22	HV-20	CAGGTTCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGTCTGGG GCCTCTTTGAAGGTCTCCTGCAAGGCTTCTGGTTACATTTTTACCC GCTATGGTGTCAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTG AGTGGATGGGATGGATCACCACTTACAATGGTAACACAAACTATG CACAGAAGCTCCAGGGCAGAGTCACCATGACCATAGACACATCCA CGAGCACAGCCTACATGGAACTGAGAAGCCTCAGATCTGACGACA	510

Antibody ID	Designation	Nucleic Acid Sequence	SEQ ID NO:
		CGGCCGTGTATTACTGTGCGAGAAGAGTGCGGTATAGTGGGGGCT ACTCGTTTGACAACTGGGGCCAGGGAACCCTGGTCACCGTCTCTA GT	
23	HV-21	CAGGTTCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGTCTGGG GCCTCTTTGAAGGTCTCCTGCAAGGCTTCTGGTTACATTTTTACCC GCTATGGTGTCAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTG AGTGGATGGGATGGATCACCACTTACAATGGTAATACAAACTATG CACAGAAGCTCCAGGGCAGAGTCACCATGACCACAGACACATCCA CGAGCACAGCCTACATGGAACTGAGGAGCCTCAGATCTGACGACA CGGCCGTGTATTACTGTGCGAGAAGAGTGCGGTACAGTGGGGGCT ACTCGTTTGACAACTGGGGCCAGGGAACCCTGGTCACCGTCTCTA GTGC	511
24	HV-22	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCG GAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGTA GTTACTACTGGAGCTGGATCCGGCAGCCCGCCGGGAAGGGACTGG AATGGATTGGGCGTATCTATACCAGTGGGAGCACCAACTACAACC CCTCCCTCAAGAGTCGAGTCACCATGTCAATAGGCACGTCCAAGA ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGCCGCGGACACGG CCGTGTATTACTGTGCGATTATTGCATCTCGTGGCTGGTACTTCGA TCTCTGGGGCCGTGGCACCCTGGTCACCGTCTCTAGTG	512
25, 28	HV-23	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCA CAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGCA GTGGTGGTTACTACTGGAGCTGGATCCGCCAGCACCCAGGGAAGG GCCTGGAGTGGATTGGGTACATCTATTACAGTGGGAACACCTACT ACAACCCGTCCCTCAAGAGTCGAGTTACCATATCAGGAGACACGT CTAAGAACCAGTTCTCCCTGAAGCTGAGGTCTGTGACTGCCGCGG ACACGGCCGTGTATTACTGTGCGAGAGGAGGAGCAGCTCGCGGTA TGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGTGC	513
26	HV-24	CAGGTACAGCTGCAGCAGTCAGGTCCAGGACTGGTGAAGCCCTCG CAGACCCTCTCACTCACCTGTGCCATCTCCGGGGACAGTGTCTCTA GCAACAGTGCTGCTTGGAACTGGATCAGGCAGTCCCCATCGAGAG GCCTTGAGTGGCTGGGAAGGACATACTACAGGTCCAGGTGGTATA ATGATTATGCAGTATCTGTGAAAAGTCGAATAACCATCAACCCAG ACACATCCAAGAACCAGTTCTCCCTGCAGCTGAACTCTGTGACTCC CGAGGACACGGCTGTGTATTACTGTGCAAGAGGGGTCTTTTATAG CAAAGGTGCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGT CTCTAGTG	514
27	HV-25	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCA CAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGCC GTGGTGGTTACTACTGGAGCTGGATCCGCCAGCACCCAGGGAAGG GCCTGGAGTGGATTGGGTACATATATTACAGTGGGAATACCTACT ACAACCCGTCCCTCAAGAGTCGAGTTATCATATCAGGAGACACGT CTAAGAACCAGCTCTCCCTGAAGCTGAGGTCTGTGACTGCCGCGG ACACGGCCGTGTATTATTGTGCGAGAGGAGGAGCAGCTCGCGGTA TGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGTGC	515
29	HV-26	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCA CAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGCA GTGGTGGTTTCTACTGGAGCTGGATCCGCCAGCACCCAGGGAAGG GCCTGGAGTGGATTGGGTACATCTATTACAGTGGGAATACCTACT ACAACCCGTCCCTCAAGAGTCGAGTTATCATATCAGGAGACACGT CTAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACGGCCGCGG ACACGGCCGTGTATTACTGTGCGAGAGGAGGAGCAGCTCGCGGTA	516

Antibody ID	Designation	Nucleic Acid Sequence	SEQ ID NO:
		TGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGTGC	

Table 12. Exemplary Anti-CGRP Receptor Variable Region Nucleic Acid Sequences

Antibody ID	Designation	Nucleic Acid Sequence	SEQ ID NO:
		Light chain variable regions	
50A, 50C, 50D, 70	LV-101	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGC AGAGAGTCACCATCTCTTGTTCTGGAAGCAGCTCCAACATCGGCA GTAATTATGTATACTGGTACCAGCAGCTCCCAGGAGCGGCCCCCA AACTCCTCATCTTTAGGAATAATCAGCGGCCCTCAGGGGTCCCTGA CCGCTTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATC AGTGGGCTCCGGTCCGAGGATGAGGCTGATTATTACTGTGCAGCA TGGGATGACAGCCTGAGTGGTTGGGTGTTCGGCGGAGGGACCAAG CTGACCGTCCTAGGT	517
50B	LV-102	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGC AGAGAGTCACCATCTCTTGTTCTGGAAGCAGCTCCAACATCGGCA GTAATTATGTATACTGGTACCAGCAGCTCCCAGGAGCGGCCCCCA AACTCCTCATCTTTAGGAATAATCAGCGGCCCTCAGGGGTCCCTGA CCGCTTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATC AGTGGGCTCCGGTCCGAGGATGAGGCTGATTATTACTGTGCAGCA TGGGATGACAGCCTGAGTGGTTGGGTGTTCGGCAAGGGGACCAAG CTGACCGTCCTAGGT	518
51A, 51C, 51D	LV-103	CAGTCTGTGCTGACTCAGTCACCCTCAGCGTCTGGGACCCCCGGGC AGAGAGTCACCATCTCTTGTTCTGGAAGCAGCTCCAACATCGGCA GTAATTATGTATACTGGTACCAGCAGCTCCCAGGAGCGGCCCCCA AACTCCTCATCCTTAGGAATAATCAGCGGCCCTCAGGGGTCCCTGA CCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGACCATC AGTGGGCTCCGGTCCGAGGATGAGGCTGACTATTATTGTGCAGCA TGGGATGACAGCCTGAGTGGTTGGGTGTTCGGCGGAGGGACCAAG CTGACCGTCCTAGGT	519
51B	LV-104	CAGTCTGTGCTGACTCAGTCACCCTCAGCGTCTGGGACCCCCGGGC AGAGAGTCACCATCTCTTGTTCTGGAAGCAGCTCCAACATCGGCA GTAATTATGTATACTGGTACCAGCAGCTCCCAGGAGCGGCCCCCA AACTCCTCATCCTTAGGAATAATCAGCGGCCCTCAGGGGTCCCTGA CCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGACCATC AGTGGGCTCCGGTCCGAGGATGAGGCTGACTATTATTGTGCAGCA TGGGATGACAGCCTGAGTGGTTGGGTGTTCGGCAAGGGGACCAAG CTGACCGTCCTAGGT	520
52A, 52C, 52D, 53A, 53C	LV-105	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGAC AGAAGGTCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGA ATAATTATGTATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCCA AACTCCTCATTTATGACAATAATAAGCGACCCTCAGGGATTCCTGA CCGATTCTCTGGCTCCAAGTCTGGCACGTCAACCACCCTGGGCATC ACCGGACTCCAGACTGGGGACGAGGCCGATTATTACTGCGGAACA TGGGATAGCCGCCTGAGTGCTGTGGTTTTCGGCGGAGGGACCAAG CTGACCGTCCTAGGT	521
52B, 53B	LV-106	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGAC AGAAGGTCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGA ATAATTATGTATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCCA	522

Antibody ID	Designation	Nucleic Acid Sequence	SEQ ID NO:
		AACTCCTCATTTATGACAATAATAAGCGACCCTCAGGGATTCCTGA CCGATTCTCTGGCTCCAAGTCTGGCACGTCAACCACCCTGGGCATC ACCGGACTCCAGACTGGGGACGAGGCCGATTATTACTGCGGAACA TGGGATAGCCGCCTGAGTGCTGTGGTTTTCGGCAAGGGGACCAAG CTGACCGTCCTAGGT	
54A, 54C, 56A, 56C, 71	LV-107	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGAC AGAAGGTCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGA ATAATTATGTATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCCA AACTCCTCATTTATGACAATAATAAGCGACCCTCAGGGATTCCTGA CCGATTCTCTGGCTCCAAGTCTGGCACGTCAGCCACCCTGGGCATC ACCGGACTCCAGACTGGGGACGAGGCCGATTATTACTGCGGAACA TGGGATAGCCGCCTGAGTGCTGTGGTTTTCGGCGGAGGGACCAAG CTGACCGTCCTAGGT	523
54B, 56B	LV-108	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGAC AGAAGGTCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGA ATAATTATGTATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCCA AACTCCTCATTTATGACAATAATAAGCGACCCTCAGGGATTCCTGA CCGATTCTCTGGCTCCAAGTCTGGCACGTCAGCCACCCTGGGCATC ACCGGACTCCAGACTGGGGACGAGGCCGATTATTACTGCGGAACA TGGGATAGCCGCCTGAGTGCTGTGGTTTTCGGCAAGGGGACCAAG CTGACCGTCCTAGGT	524
55A, 55C	LV-109	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGAC AGAAGGTCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGA ATAATTATGTATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCCA AACTCCTCATTTATGACAATAATAAGCGACCCTCAGGGATTCCTGA CCGATTCTCTGGCTCCAAGTCTGGCACGTCAGCCACCCTGGCCATC ACCGGACTCCAGACTGGGGACGAGGCCGATTATTACTGCGGAACA TGGGATAGCCGCCTGAGTGCTGTGGTTTTCGGCGGAGGGACCAAG CTGACCGTCCTAGGT	525
55B	LV-110	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGAC AGAAGGTCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGA ATAATTATGTATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCCA AACTCCTCATTTATGACAATAATAAGCGACCCTCAGGGATTCCTGA CCGATTCTCTGGCTCCAAGTCTGGCACGTCAGCCACCCTGGCCATC ACCGGACTCCAGACTGGGGACGAGGCCGATTATTACTGCGGAACA TGGGATAGCCGCCTGAGTGCTGTGGTTTTCGGCAAGGGGACCAAG CTGACCGTCCTAGGT	526
57A, 57C, 57D, 58A, 58C	LV-111	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAG GGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCA GCGGCTACTTAACCTGGTACCAGCAGAAACCTGGCCAGGCTCCCA GACTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAG ACAGGTTCAGTGGCAGTGGGTCTGGGACGGACTTCACTCTCACCA TCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCA GTATGGTAACTCACTGAGCAGGTTTGGCCAGGGGACCAAGCTGGA AATCAAACGT	527
57B, 58B	LV-112	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAG GGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCA GCGGCTACTTAACCTGGTACCAGCAGAAACCTGGCCAGGCTCCCA GACTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAG ACAGGTTCAGTGGCAGTGGGTCTGGTACGGACTTCACTCTCACCAT CAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCA GTATGGTAACTCACTGAGCAGGTTTGGCAAGGGGACCAAGCTGGA	528

Antibody ID	Designation	Nucleic Acid Sequence	SEQ ID NO:
		GATCAAACGT	
59	LV-113	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGAGGCCCCAGGA CAGAAGGTCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGG AATAATTATGTATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCC AAACTCCTCATTTATGACAATAATAAGCGACCCTCAGGGATTCCTG ACCGATTCTCTGGCTCCAAGTCTGGCACGTCAGCCACCCTGGGCAT CACCGGACTCCAGACTGGGGACGAGGCCGATTATTACTGCGGAAC ATGGGATAGCCGCCTGAGTGCTGTGGTTTTCGGCGGAGGGACCAA GCTGACCGTCCTA	529
60	LV-114	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGC AGAGAGTCACCATCTCTTGTTCTGGAAGCAGCTCCAACATCGGCA GTAATTATGTATACTGGTACCAGCAGCTCCCAGGAGCGGCCCCCA AACTCCTCATCTTTAGGAGTAATCAGCGGCCCTCAGGGGTCCCTGA CCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATC AGTGGGCTCCGGTCCGAGGATGAGGCTGATTATTACTGTGCAGCA TGGGATGACAGCCTGAGTGGTTGGGTGTTCGGCGGAGGGACCAAG CTGACCGTCCTA	530
61	LV-115	GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAG GAGACAGAGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAA ATGATTTAGGCTGGTTTCAGCAGAAACCAGGGAAAGCCCCTAAGC GCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAG GTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACAATCAG CAGCCTGCAGCCTGAAGATTTAGCAACTTATTACTGTCTACAGTAT AATATTTACCCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATC AAA	531
62	LV-116	TCTTCTGAGCTGACTCAGGACCCTACTGTGTCTGTGGCCTTGGGAC AGACAGTCAAAATCACATGCCAAGGAGACAGCCTCAGAAGTTTTT ATGCAAGCTGGTACCAGCAGAAGCCAGGACAGGCCCCTGTACTTG TCTTCTATGGTAAAAACAACCGGCCCTCAGGGATCCCAGACCGAT TCTCTGGCTCCAGCTCAGGAAACACAGCTTCCTTGACCATCACTGG GGCTCAGGCGGAAGATGAGGCTGACTATTATTGTAATTCCCGGGA CAGCAGTGTTTACCATCTGGTACTCGGCGGAGGGACCAAGCTGAC CGTCCTA	532
63	LV-117	GATATTATACTGGCCCAGACTCCACTTTCTCTGTCCGTCACCCCTG GACAGCCGGCCTCCATCTCCTGCAAGTCTAGTCAGAGCCTCCTGCA CAGTGCTGGAAAGACCTATTTGTATTGGTACCTGCAGAAGCCAGG CCAGCCTCCACAGCTCCTGATCTATGAAGTTTCCAACCGGTTCTCT GGAGTGCCAGATAGGTTCAGTGGCAGCGGGTCAGGGACAGATTTC ACACTGAAAATCAGCCGGGTGGAGGCTGAGGATGTTGGGATTTAT TACTGCATGCAAAGTTTTCCGCTTCCGCTCACTTTCGGCGGAGGGA CCAAGGTGGAGATCAAA	533
64	LV-118	GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTG GAGAGCCGGCCTCCATCTCCTGCAGGTCTAGTCAGAGCCTCCTGCA TAGTTTTGGGTACAACTATTTGGATTGGTACCTGCAGAAGCCAGGG CAGTCTCCACAGCTCCTGATCTATTTGGGTTCTAATCGGGCCTCCG GGGTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTA CACTGAAAATCAGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATT ACTGCATGCAAGCTCTACAAACTCCATTCACTTTCGGCCCTGGGAC CAAAGTGGATATCAAA	534
65	LV-119	GATATTATTCTGACCCAGACTCCACTTTCTCTGTCCGTCACCCCTG GACAGCCGGCCTCCATCTCCTGCAAGTCTAGTCAGAGCCTCCTGCA CAGTGATGGAAAGACCTATTTGTATTGGTACCTGCAGAAGCCCGG	535

Antibody ID	Designation	Nucleic Acid Sequence	SEQ ID NO:
		CCAGCCTCCACAGCTCCTGATCTATGAAGTTTCCAACCGGTTCTCT GGAGAGCCAGATAGGTTCAGTGGCAGCGGGTCAGGGACAGATTTC ACACTGAAAATCAGCCGGGTGGAGGCTGAGGATGTTGGGACTTAT TATTGCATGCAAAGTTTTCCGCTTCCGCTCACTTTCGGCGGAGGGA CCAAGGTGGAGATCAAA	
66	LV-120	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGAC AGAAGGTCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGA ATAATTATGTATCCTGGTACCAGCAGTTCCCAGGAACAGCCCCCA AACTCCTCATTTATGACAATAATAAGCGACCCTCAGGGATTCCTGA CCGATTCTCTGGCTCCAAGTCTGGCACGTCAGCCACCCTGGGCATC ACCGGACTCCAGACTGGGGACGAGGCCGATTATTACTGCGGAACA TGGGATAGCCGCCTGAGTGCTGTGGTTTTCGGCGGAGGGACCAAG CTGACCGTCCTA	536
67	LV-121	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGC AGAGGGTCACCATCTCTTGTTCTGGAAGCAGTTCCAATATCGGAA GTAATACTGTGAACTGGTACCAGCAGCTCCCAGGAACGGCCCCCA AACTCCTCATCTATACTAATAATCAGCGGCCCTCAGGGGTCCCTGA CCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATC AGTGGACTCCAGTCTGAGGATGAGGCTGATTTTTACTGTGCAGCGC GGGATGAGAGCCTGAATGGTGTGGTATTCGGCGGAGGGACCAAGC TGACCGTCCTA	537
68	LV-122	GATATTACACTGACCCAGACTCCACTTTCTCTGTCCGTCTCCCCTG GACAGCCGGCCTCCATCTCCTGCAAGTCTAGTCAGAGCCTCCTGCA CAGTGATGGAAGGAACTATCTGTATTGGTACCTGCAGAAGCCAGG CCAGCCTCCACAGCTCCTGATCTATGAAGTGTCCAACCGGTTCTCT GGACTGCCAGATAGGTTCAGTGGCAGCGGGTCAGGGACAGATTTC ACACTGAAAATCAGCCGGGTGGAGGCTGAGGATGTTGGGATTTAT TACTGCATGCAAAGTTTTCCGCTTCCGCTCACTTTCGGCGGAGGGA CCAAGGTGGAGATCAAA	538
69	LV-123	GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAG GAGACAGAGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAA AGGATTTAGGCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGC GCCTGATCTATGGAGCATCCAGTTTGCAAAGTGGGGTCCCATCAA GGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACAATCA GCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGTCTACAGTA TAATAGTTTCCCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAAT CAAA	539
		Heavy chain variable regions	
50A, 50C, 50D	HV-101	GAGGTACAGCTGGTGGAGTCTGGGGGAGGCTTGGTAAAGCCTGGG GGGTCCCTCAGACTCTCCTGTGCAGCCTCTGGATTCACTTTCGGTA ACGCCTGGATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGG AGTGGGTTGGCCGTATTAAAAGCAAAACTGATGGTGGGACAACAG ACTACGCTGCACCCGTGAAAGGCAGATTCACCATCTCAAGAGATG ATTCAAAAAACACGCTGTATCTGCAAATGAACAGCCTGAAAACCG AGGACACAGCCGTGTATTTCTGTACCACAGATCGGACCGGGTATA GCATCAGCTGGTCTAGTTACTACTACTACTACGGTATGGACGTCTG GGGCCAAGGAACAACAGTTACCGTCTCTAGT	540
50B	HV-102	GAGGTACAGCTGGTGGAGTCTGGGGGAGGCTTGGTAAAGCCTGGG GGGTCCCTCAGACTCTCCTGTGCAGCCTCTGGATTCACTTTCGGTA ACGCCTGGATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGAGCTGG AGTGGGTTGGCCGTATTAAAAGCAAAACTGATGGTGGGACAACAG ACTACGCTGCACCCGTGAAAGGCAGATTCACCATCTCAAGAGATG	541

Antibody ID	Designation	Nucleic Acid Sequence	SEQ ID NO:
		ATTCAAAAAACACGCTGTATCTGCAAATGAACAGCCTGAAAACCG AGGACACAGCCGTGTATTTCTGTACCACAGATCGGACCGGGTATA GCATCAGCTGGTCTAGTTACTACTACTACTACGGTATGGACGTCTG GGGCCAAGGAACAACAGTTACCGTCTCTAGT	
51A, 51C, 51D	HV-103	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTAAAGCCTGGG GGGTCCCTTAGACTCTCCTGTGCAGCCTCTGGATTCACTTTCAGTA ACGCCTGGATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGG AGTGGGTTGGCCGTATTAAAAGCAAAACTGATGGTGGGACAACAG ACTACACTGCACCCGTGAAAGGCAGATTCACCATCTCAAGAGATG ATTCAAAAAACACGCTGTATCTGCAAATGAATAGCCTGAAAGCCG AGGACACAGCCGTGTATTACTGTACCACAGATCGGACCGGGTATA GCATCAGCTGGTCTAGTTACTACTACTACTACGGTATGGACGTCTG GGGCCAAGGAACAACAGTTACCGTCTCTAGT	542
51B	HV-104	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTAAAGCCTGGG GGGTCCCTTAGACTCTCCTGTGCAGCCTCTGGATTCACTTTCAGTA ACGCCTGGATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGAGCTGG AGTGGGTTGGCCGTATTAAAAGCAAAACTGATGGTGGGACAACAG ACTACACTGCACCCGTGAAAGGCAGATTCACCATCTCAAGAGATG ATTCAAAAAACACGCTGTATCTGCAAATGAATAGCCTGAAAGCCG AGGACACAGCCGTGTATTACTGTACCACAGATCGGACCGGGTATA GCATCAGCTGGTCTAGTTACTACTACTACTACGGTATGGACGTCTG GGGCCAAGGAACAACAGTTACCGTCTCTAGT	543
52A, 52C, 52D, 54A, 54C, 55A, 55C, 59, 66	HV-105	CAGGTGCAGCTGGTGGAATCTGGGGGAGGCGTGGTCCAGCCTGGG AGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTA GCTTTGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGG AGTGGGTGGCAGTTATATCATTTGATGGAAGTATTAAGTATTCTGT AGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCAAA GAACACGCTGTTTCTGCAAATGAACAGCCTGCGAGCCGAGGACAC GGCTGTGTATTACTGTGCGAGAGATCGGCTCAATTACTATGATAGT AGTGGTTATTATCACTACAAATACTACGGTATGGCCGTCTGGGGCC AAGGGACAACAGTTACCGTCTCTAGT	544
52B, 54B, 55B	HV-106	CAGGTGCAGCTGGTGGAATCTGGGGGAGGCGTGGTCCAGCCTGGG AGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTA GCTTTGGCATGCACTGGGTCCGCCAGGCTCCAGGGAAGGAGCTGG AGTGGGTGGCAGTTATATCATTTGATGGAAGTATTAAGTATTCTGT AGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCAAA GAACACGCTGTTTCTGCAAATGAACAGCCTGCGAGCCGAGGACAC GGCTGTGTATTACTGTGCGAGAGATCGGCTCAATTACTATGATAGT AGTGGTTATTATCACTACAAATACTACGGTATGGCCGTCTGGGGCC AAGGGACAACAGTTACCGTCTCTAGT	545
53A, 53C, 56A, 56C	HV-107	CAGGTGCAGCTGGTGGAATCTGGGGGAGGCGTGGTCCAGCCTGGG AGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTA GCTTTGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGG AGTGGGTGGCAGTTATATCATTTGATGGAAGTATTAAGTATTCTGT AGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCAAA GAACACGCTGTTTCTGCAAATGAACAGCCTGCGAGCCGAGGACAC GGCTGTGTATTACTGTGCGAGAGATCGGCTCAATTACTATGAGAGT AGTGGTTATTATCACTACAAATACTACGGTATGGCCGTCTGGGGCC AAGGGACAACAGTTACCGTCTCTAGT	546
53B, 56B	HV-108	CAGGTGCAGCTGGTGGAATCTGGGGGAGGCGTGGTCCAGCCTGGG AGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTA GCTTTGGCATGCACTGGGTCCGCCAGGCTCCAGGGAAGGAGCTGG	547

Antibody ID	Designation	Nucleic Acid Sequence	SEQ ID NO:
		AGTGGGTGGCAGTTATATCATTTGATGGAAGTATTAAGTATTCTGT AGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCAAA GAACACGCTGTTTCTGCAAATGAACAGCCTGCGAGCCGAGGACAC GGCTGTGTATTACTGTGCGAGAGATCGGCTCAATTACTATGAGAGT AGTGGTTATTATCACTACAAATACTACGGTATGGCCGTCTGGGGCC AAGGGACAACAGTTACCGTCTCTAGT	
57A, 57C, 57D	HV-109	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGG AGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTA GCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGG AGTGGGTGGCAGTTATATGGTATGATGGAAGTAATAAATACTATG CAGACTCCGTGAAGGGCCGATTCATCATCTCCAGAGATAAATCCA AGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACA CGGCTGTGTATTACTGTGCGAGAGCGGGGGGTATAGCAGCAGCTG GCCTCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACAA CAGTTACCGTCTCTAGT	548
57B	HV-110	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGG AGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTA GCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGGAAGGAGCTGG AGTGGGTGGCAGTTATATGGTATGATGGAAGTAATAAATACTATG CAGACTCCGTGAAGGGCCGATTCATCATCTCCAGAGATAAATCCA AGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACA CGGCTGTGTATTACTGTGCGAGAGCGGGGGGTATAGCAGCAGCTG GCCTCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACAA CAGTTACCGTCTCTAGT	549
58A, 58C	HV-111	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGG AGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTA GCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGG AGTGGGTGGCAGTTATATGGTATGATGGAAGTAATAAATACTATG CAGAGTCCGTGAAGGGCCGATTCATCATCTCCAGAGATAAATCCA AGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACA CGGCTGTGTATTACTGTGCGAGAGCGGGGGGTATAGCAGCAGCTG GCCTCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACAA CAGTTACCGTCTCTAGT	550
58B	HV-112	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGG AGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTA GCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGGAAGGAGCTGG AGTGGGTGGCAGTTATATGGTATGATGGAAGTAATAAATACTATG CAGAGTCCGTGAAGGGCCGATTCATCATCTCCAGAGATAAATCCA AGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACA CGGCTGTGTATTACTGTGCGAGAGCGGGGGGTATAGCAGCAGCTG GCCTCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACAA CAGTTACCGTCTCTAGT	551
60	HV-113	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTAAAGCCTGGG GGGTCCCTTAGACTCTCCTGTGCAGCCTCTGGATTCACTTTCAGTA ACGCCTGGATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGG AGTGGGTTGGCCGTATTAAAAGCACAACTGATGGTGGGACAACAG ACTACGCTGCACCCGTGAAAGGCAGATTCACCATCTCAAGAGATG ATTCAAAAAACACGCTGTATCTGCAAATGAACAGCCTGAAAACCG AGGACACAGCCGTGTATTACTGTACCACAGATCGGACCGGATATA GCATCAGCTGGTCTAGTTACTACTACTACTACGGTATGGACGTCTG GGGCCAAGGGACCACGGTCACCGTCTCTAGT	552

Antibody ID	Designation	Nucleic Acid Sequence	SEQ ID NO:
61	HV-114	GAGGTGCAGCTATTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGG GAGTCCCTGAGACTCTCCTGTGCAGCCTCTGGGTTCACCTTTAGCA GCTATGCCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGG AGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTCGCACATACTACGC AGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAA GAACACGCTGTATCTGCAAATGAATAGCCTGAGAGCCGAGGACAC GGCCGTATATTACTGTGCGAAAGATCAAAGGGAGGTAGGGCCGTA TAGCAGTGGCTGGTACGACTACTACTACGGTATGGACGTCTGGGG CCAAGGGACCACGGTCACCGTCTCTAGT	553
62	HV-115	CAGGTGCAGTTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGG GCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCG GCTACTATATGCACTGGGTGCGACAGGCCCCTGGACAAGGGCTTG AGTGGATGGGATGGATCAACCCTAACAGTGGTGGCACAAACTATG CACAGAAGTTTCAGGGCAGGGTCACCATGACCAGGGACACGTCCA TCAGCACAGCCTACATGGAGCTGAGCAGGCTGAGATCTGACGACA CGGCCGTGTATTTCTGTGCGAGAGATCAAATGAGTATTATTATGCT TCGGGGAGTTTTTCCCCCTTACTATTACGGTATGGACGTCTGGGGC CAAGGGACCACGGTCACCGTCTCTAGT	554
63, 65, 68	HV-116	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGG AGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTA GCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGG AGTGGGTGGCAGTTATTTCATATGATGGAAGTCATGAATCCTATGC AGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACATTTCCAA GAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACAC GGCTGTGTATTTCTGTGCGAGAGAGAGGAAACGGGTTACGATGTC TACCTTATATTACTACTTCTACTACGGTATGGACGTCTGGGGCCAA GGGACCACGGTCACCGTCTCTAGT	555
64	HV-117	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTAAAGCCAGGG CGGTCCCTGAGACTCTCCTGTACAGCTTCTGGATTCACCTTTGGTG ATTATGCTATGAGCTGGTTCCGCCAGGCTCCAGGGAAGGGGCTGG AGTGGATAGGTTTCATTAGAAGCAGAGCTTATGGTGGGACACCAG AATACGCCGCGTCTGTGAAAGGCAGATTCACCATCTCAAGAGATG ATTCCAAAACCATCGCCTATCTGCAAATGAACAGCCTGAAAACCG AGGACACAGCCGTGTATTTCTGTGCTAGAGGACGGGGTATTGCAG CTCGTTGGGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCTA GT	556
67	HV-118	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGG GCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCG ACTACTATATGTACTGGGTGCGACAGGCCCCTGGACAAGGGCTTG AGTGGATGGGATGGATCAGCCCTAATAGTGGTGGCACAAACTATG CCCAGAAGTTTCAGGGCAGGGTCACCATGACCAGGGACACGTCTA TCAGCACAGCCTACATGGAGCTGAGTAGGCTGAGATCTGACGACA CGGCCGTGTATTACTGTGTGAGAGGAGGATATAGTGGCTACGCTG GGCTCTACTCCCACTACTACGGTATGGACGTCTGGGGCCAAGGGA CCACGGTCACCGTCTCTAGT	557
69	HV-119	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGG GGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATACACCTTCAGTA CCTATAGCATGAACTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGG AGTGGGTCTCATCCATTAGTAGTAGTAGTAGTTACAGATATTACGC AGACTCAGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAA GAACTCACTGTATCTGCAAATGAGTAGCCTGAGAGCCGAGGACAC	558

Antibody ID	Designation	Nucleic Acid Sequence	SEQ ID NO:
		GGCTGTGTATTACTGTGCGAGAGAAGGGGTGTCTGGCAGTTCGCC GTATAGCATCAGCTGGTACGACTACTATTACGGTATGGACGTCTGG GGCCAAGGGACCACGGTCACCGTCTCTAGT	
70	HV-120	GAGGTACAGCTGGTGGAGTCTGGGGGAGGCTTGGTAAAGCCTGGG GGGTCCCTTAGACTCTCCTGTGCAGCCTCTGGATTCACTTTCGGTA ACGCCTGGATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGG AGTGGGTTGGCCGTATTAAAAGCAAAACTGATGGTGGGACAACAG ACTACGCTGCACCCGTGAAAGGCAGATTCACCATCTCAAGAGATG ATTCAAAAAACACGCTGTATCTGCAAATGAACAGCCTGAAAACCG AGGACACAGCCGTGTATTACTGTACCACAGATCGGACCGGGTATA GCATCAGCTGGTCTAGTTACTACTACTACTACGGTATGGACGTCTG GGGCCAAGGGACCACGGTCACCGTCTCTAGT	559
71	HV-121	CAGGTGCAGCTGGTGGAATCTGGGGGAGGCGTGGTCCAGCCTGGG AGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTA GCTTTGGCATGCATTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGG AGTGGGTGGCAGTTATATCATTTGATGGAAGTATTAAGTACTCTGT AGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCAAA GAACACGCTGTTTCTGCAAATGAACAGCCTGCGAGCCGAGGACAC GGCTGTGTATTACTGTGCGAGAGATCGGCTCAATTACTATGATAGT AGTGGTTATTATCACTACAAATACTACGGTCTGGCCGTCTGGGGCC AAGGGACCACGGTCACCGTCTCTAGT	560

[0164] Isolated nucleic acids encoding anti-PAC1 receptor binding domains of the bispecific antigen binding proteins of the invention may comprise a nucleotide sequence that is at least 80% identical, at least 90% identical, at least 95% identical, or at least 98% identical to any of the nucleotide sequences listed in Table 11. In some embodiments, an isolated nucleic acid encoding an anti-PAC1 receptor light chain variable region comprises a sequence selected from SEQ ID NOs: 464 to 490. In related embodiments, an isolated nucleic acid encoding an anti-PAC1 receptor heavy chain variable region comprises a sequence selected from SEQ ID NOs: 491 to 516. Isolated nucleic acids encoding anti-CGRP receptor binding domains of the bispecific antigen binding proteins of the invention may comprise a nucleotide sequence that is at least 80% identical, at least 90% identical, at least 95% identical, or at least 98% identical to any of the nucleotide sequences listed in Table 12. In some embodiments, an isolated nucleic acid encoding an anti-CGRP receptor light chain variable region comprises a sequence selected from SEQ ID NOs: 517 to 539. In related embodiments, an isolated nucleic acid encoding an anti-CGRP receptor heavy chain variable region comprises a sequence selected from SEQ ID NOs: 540 to 560.

[0165] In embodiments in which the bispecific antigen binding protein of the invention is a heterodimeric antibody, the isolated nucleic acid encoding an anti-PAC1 receptor antibody light

chain may comprise a nucleotide sequence that is at least 80% identical, at least 90% identical, at least 95% identical, or at least 98% identical to any of the nucleotide sequences listed in Table 6A. In certain embodiments, the isolated nucleic acid encoding an anti-PAC1 receptor light chain of a heterodimeric antibody of the invention comprises a sequence selected from SEQ ID NOs: 222 to 232. In these and other embodiments, the isolated nucleic acid encoding an anti-PAC1 receptor antibody heavy chain may comprise a nucleotide sequence that is at least 80% identical, at least 90% identical, at least 95% identical, or at least 98% identical to any of the nucleotide sequences listed in Table 6B. In some embodiments, the isolated nucleic acid encoding an anti-PAC1 receptor heavy chain of a heterodimeric antibody of the invention comprises a sequence selected from SEQ ID NOs: 252 to 270.

[0166] In other embodiments in which the bispecific antigen binding protein of the invention is a heterodimeric antibody, the isolated nucleic acid encoding an anti-CGRP receptor antibody light chain may comprise a nucleotide sequence that is at least 80% identical, at least 90% identical, at least 95% identical, or at least 98% identical to any of the nucleotide sequences listed in Table 7A. In certain embodiments, the isolated nucleic acid encoding an anti-CGRP receptor light chain of a heterodimeric antibody of the invention comprises a sequence selected from SEQ ID NOs: 283 to 294. In these and other embodiments, the isolated nucleic acid encoding an anti-CGRP receptor antibody heavy chain may comprise a nucleotide sequence that is at least 80% identical, at least 90% identical, at least 95% identical, or at least 98% identical to any of the nucleotide sequences listed in Table 7B. In some embodiments, the isolated nucleic acid encoding an anti-CGRP receptor heavy chain of a heterodimeric antibody of the invention comprises a sequence selected from SEQ ID NOs: 317 to 338.

[0167] Nucleic acid sequences encoding the light chains and modified heavy chains (e.g., fusion proteins comprising a heavy chain and a scFv) of exemplary bispecific antigen binding proteins of the invention in the IgG-scFv format are listed in Table 13. In such embodiments, the isolated nucleic acid encoding the light chain of the IgG-scFv molecules may comprise a nucleotide sequence that is at least 80% identical, at least 90% identical, at least 95% identical, or at least 98% identical to any of the light chain nucleotide sequences listed in Table 13. For instance, in some embodiments, the isolated nucleic acid encoding the light chain of the IgG-scFv molecules comprises a sequence selected from SEQ ID NOs: 561 to 564. In related embodiments, the isolated nucleic acid encoding the modified heavy chain of the IgG-scFv molecules may

comprise a nucleotide sequence that is at least 80% identical, at least 90% identical, at least 95% identical, or at least 98% identical to any of the modified heavy chain nucleotide sequences listed in Table 13. In certain embodiments, the isolated nucleic acid encoding the modified heavy chain of the IgG-scFv molecules comprises a sequence selected from SEQ ID NOs: 565 to 594.

Table 13. Nucleic Acid Sequences of Exemplary Bispecific Antigen Binding Proteins in the IgG-scFv Format

IgG-scFv Molecule Designation	Light Chain Nucleic Acid Sequence	Modified Heavy Chain Nucleic Acid Sequence
Anti-PAC1 Receptor IgG x Anti-CGRP Receptor scFv		
iPS:386738	GATATCCAGCTCAC	CAAGTTCAGTTGGTGGAGTCTGGAGCCGAAGTAGTAAAGCC
	TCAATCGCCATCAT	AGGAGCTTCAGTGAAAGTCTCTTGTAAAGCAAGTGGATTCA
	TTCTCTCCGCTTCG	CGTTTAGCCGCTTTGCCATGCATTGGGTGCGGCAAGCTCCCG
	GTAGGCGACCGGG	GTCAGGGGTTGGAGTGGATGGGAGTTATTAGCTATGACGGG
	TCACGATCACATGC	GGCAATAAGTACTACGCCGAGTCTGTTAAGGGTCGGGTCAC
	AGGGCGTCGCAAA	AATGACACGGGACACCTCAACCAGTACACTCTATATGGAAC
	GCATTGGGAGGTCG	TGTCTAGCCTGAGATCCGAGGACACCGCTGTGTATTATTGCG
	TTGCATTGGTATCA	CTAGGGGGTACGATGTATTGACGGGTTATCCTGATTACTGGG
	GCAGAAACCCGGA	GGCAGGGGACACTCGTAACCGTCTCTAGTGCCTCCACCAAG
	AAGGCCCCGAAAC	GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC
	TTCTGATCAAATAC	TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA
	GCATCACAAAGCTT	CTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCT
	GAGCGGTGTGCCGT	GACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC
	CGCGCTTCTCCGGT	AGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAG
	TCCGGAAGCGGAA	CAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACA
	CGGAATTCACGCTT	AGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAA
	ACAATCTCCTCACT	ATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACC
	GCAGCCCGAGGATT	TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAA
	TCGCGACCTATTAC	ACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCA
	TGTCACCAGTCATC	CATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC
	CAGACTCCCGTTTA	AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGC
	CTTTTGGCCCTGGG	CAAGACAAAGCCGTGTGAGGAGCAGTACGGCAGCACGTACC
	ACCAAGGTGGACA	GTTGTGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA
	TTAAGCGTACGGTG	ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTC
	GCTGCACCATCTGT	CCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCA
	CTTCATCTTCCCGC	GCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG
	CATCTGATGAGCAG	AGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC
	TTGAAATCTGGAAC	AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAG
	TGCCTCTGTTGTGT	CAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCG
	GCCTGCTGAATAAC	TGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCA
	TTCTATCCCAGAGA	CCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCA
	GGCCAAAGTACAG	TGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCA
	TGGAAGGTGGATA	GAAGAGCCTAAGCTTGTCTCCGGGTGGTGGCGGATCGGGAG
	ACGCCCTCCAATCG	GTGGCGGATCCCAGGTGCAGCTGGTGGAATCTGGGGGAGGC
	GGTAACTCCCAGGA	GTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCC
	GAGTGTCACAGAG	TCTGGATTCACCTTCAGTAGCTTTGGCATGCACTGGGTCCGC
	CAGGACAGCAAGG	CAGGCTCCAGGCAAGTGTCTGGAGTGGGTGGCAGTTATATC
	ACAGCACCTACAGC	ATTTGATGGAAGTATTAAGTATTCTGTAGACTCCGTGAAGGG

IgG-scFv Molecule Designation	Light Chain Nucleic Acid Sequence	Modified Heavy Chain Nucleic Acid Sequence
	CTCAGCAGCACCCT GACGCTGAGCAAA GCAGACTACGAGA AACACAAAGTCTAC GCCTGCGAAGTCAC CCATCAGGGCCTGA GCTCGCCCGTCACA AAGAGCTTCAACA GGGGAGAGTGT (SEQ ID NO: 561)	CCGATTCACCATCTCCAGAGACAATTCAAAGAACACGCTGTT TCTGCAAATGAACAGCCTGCGAGCCGAGGACACGGCTGTGT ATTACTGTGCGAGAGATCGGCTCAATTACTATGATAGTAGTG GTTATTATCACTACAAATACTACGGTATGGCCGTCTGGGGCC AAGGGACAACAGTTACTGTCTCTAGTGGAGGCGGAGGATCT GGTGGCGGTGGTTCTGGCGGCGGAGGCTCCCAGTCTGTGTTG ACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGACAGAAGGT CACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATAA TTATGTATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCCAA ACTCCTCATTTATGACAATAATAAGCGACCCTCAGGGATTCC TGACCGATTCTCTGGCTCCAAGTCTGGCACGTCAACCACCCT GGGCATCACCGGACTCCAGACTGGGGACGAGGCCGATTATT ACTGCGGAACATGGGATAGCCGCCTGAGTGCTGTGGTTTTCG GCTGTGGGACCAAGCTGACCGTGCTA (SEQ ID NO: 565)
iPS:386764	SEQ ID NO: 561	CAAGTTCAGTTGGTGGAGTCTGGAGCCGAAGTAGTAAAGCC AGGAGCTTCAGTGAAAGTCTCTTGTAAAGCAAGTGGATTCA CGTTTAGCCGCTTTGCCATGCATTGGGTGCGGCAAGCTCCCG GTCAGGGGTTGGAGTGGATGGGAGTTATTAGCTATGACGGG GGCAATAAGTACTACGCCGAGTCTGTTAAGGGTCGGGTCAC AATGACACGGGACACCTCAACCAGTACACTCTATATGGAAC TGTCTAGCCTGAGATCCGAGGACACCGCTGTGTATTATTGCG CTAGGGGGTACGATGTATTGACGGGTTATCCTGATTACTGGG GGCAGGGGACACTCGTAACCGTCTCTAGTGCCTCCACCAAG GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCT GACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAG CAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACA AGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAA ATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACC TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAA ACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCA CATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGC CAAGACAAAGCCGTGTGAGGAGCAGTACGGCAGCACGTACC GTTGTGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTC CCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCA GCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG AGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAG CAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCG TGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCA CCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCA TGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCA GAAGAGCCTAAGCTTGTCTCCGGGTGGTGGCGGATCGGGAG GTGGCGGATCCCAGTCTGTGTTGACGCAGCCGCCCTCAGTGT CTGCGGCCCCAGGACAGAAGGTCACCATCTCCTGCTCTGGA AGCAGCTCCAACATTGGGAATAATTATGTATCCTGGTACCAG CAGCTCCCAGGAACAGCCCCCAAACTCCTCATTTATGACAAT AATAAGCGACCCTCAGGGATTCCTGACCGATTCTCTGGCTCC AAGTCTGGCACGTCAGCCACCCTGGGCATCACCGGACTCCA

IgG-scFv Molecule Designation	Light Chain Nucleic Acid Sequence	Modified Heavy Chain Nucleic Acid Sequence
		GACTGGGGACGAGGCCGATTATTACTGCGGAACATGGGATA GCCGCCTGAGTGCTGTGGTTTTCGGCGGAGGGACCAAGCTG ACCGTGCTTGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGG CGGCGGAGGCTCCCAGGTGCAGCTGGTGGAATCTGGGGGAG GCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAG CCTCTGGATTCACCTTCAGTAGCTTTGGCATGCACTGGGTCC GCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATA TCATTTGATGGAAGTATTAAGTATTCTGTAGACTCCGTGAAG GGCCGATTCACCATCTCCAGAGACAATTCAAAGAACACGCT GTTTCTGCAAATGAACAGCCTGCGAGCCGAGGACACGGCTG TGTATTACTGTGCGAGAGATCGGCTCAATTACTATGATAGTA GTGGTTATTATCACTACAAATACTACGGTATGGCCGTCTGGG GCCAAGGGACAACAGTTACTGTCTCTAGT (SEQ ID NO: 566)
iPS:386762	SEQ ID NO: 561	CAAGTTCAGTTGGTGGAGTCTGGAGCCGAAGTAGTAAAGCC AGGAGCTTCAGTGAAAGTCTCTTGTAAAGCAAGTGGATTCA CGTTTAGCCGCTTTGCCATGCATTGGGTGCGGCAAGCTCCCG GTCAGGGGTTGGAGTGGATGGGAGTTATTAGCTATGACGGG GGCAATAAGTACTACGCCGAGTCTGTTAAGGGTCGGGTCAC AATGACACGGGACACCTCAACCAGTACACTCTATATGGAAC TGTCTAGCCTGAGATCCGAGGACACCGCTGTGTATTATTGCG CTAGGGGGTACGATGTATTGACGGGTTATCCTGATTACTGGG GGCAGGGGACACTCGTAACCGTCTCTAGTGCCTCCACCAAG GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCT GACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAG CAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACA AGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAA ATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACC TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAA ACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCA CATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGC CAAGACAAAGCCGTGTGAGGAGCAGTACGGCAGCACGTACC GTTGTGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTC CCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCA GCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG AGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAG CAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCG TGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCA CCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCA TGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCA GAAGAGCCTAAGCTTGTCTCCGGGTGGTGGCGGATCGGGAG GTGGCGGATCCCAGTCTGTGTTGACGCAGCCGCCCTCAGTGT CTGCGGCCCCAGGACAGAAGGTCACCATCTCCTGCTCTGGA AGCAGCTCCAACATTGGGAATAATTATGTATCCTGGTACCAG CAGCTCCCAGGAACAGCCCCCAAACTCCTCATTTATGACAAT AATAAGCGACCCTCAGGGATTCCTGACCGATTCTCTGGCTCC AAGTCTGGCACGTCAGCCACCCTGGCCATCACCGGACTCCA GACTGGGGACGAGGCCGATTATTACTGCGGAACATGGGATA

IgG-scFv Molecule Designation	Light Chain Nucleic Acid Sequence	Modified Heavy Chain Nucleic Acid Sequence
		GCCGCCTGAGTGCTGTGGTTTTCGGCGGAGGGACCAAGCTG ACCGTGCTTGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGG CGGCGGAGGCTCCCAGGTGCAGCTGGTGGAATCTGGGGGAG GCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAG CCTCTGGATTCACCTTCAGTAGCTTTGGCATGCACTGGGTCC GCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATA TCATTTGATGGAAGTATTAAGTATTCTGTAGACTCCGTGAAG GGCCGATTCACCATCTCCAGAGACAATTCAAAGAACACGCT GTTTCTGCAAATGAACAGCCTGCGAGCCGAGGACACGGCTG TGTATTACTGTGCGAGAGATCGGCTCAATTACTATGATAGTA GTGGTTATTATCACTACAAATACTACGGTATGGCCGTCTGGG GCCAAGGGACAACAGTTACTGTCTCTAGT (SEQ ID NO: 567)
iPS:386760	SEQ ID NO: 561	CAAGTTCAGTTGGTGGAGTCTGGAGCCGAAGTAGTAAAGCC AGGAGCTTCAGTGAAAGTCTCTTGTAAAGCAAGTGGATTCA CGTTTAGCCGCTTTGCCATGCATTGGGTGCGGCAAGCTCCCG GTCAGGGGTTGGAGTGGATGGGAGTTATTAGCTATGACGGG GGCAATAAGTACTACGCCGAGTCTGTTAAGGGTCGGGTCAC AATGACACGGGACACCTCAACCAGTACACTCTATATGGAAC TGTCTAGCCTGAGATCCGAGGACACCGCTGTGTATTATTGCG CTAGGGGGTACGATGTATTGACGGGTTATCCTGATTACTGGG GGCAGGGGACACTCGTAACCGTCTCTAGTGCCTCCACCAAG GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCT GACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAG CAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACA AGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAA ATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACC TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAA ACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCA CATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGC CAAGACAAAGCCGTGTGAGGAGCAGTACGGCAGCACGTACC GTTGTGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTC CCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCA GCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG AGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAG CAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCG TGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCA CCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCA TGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCA GAAGAGCCTAAGCTTGTCTCCGGGTGGTGGCGGATCGGGAG GTGGCGGATCCCAGTCTGTGTTGACGCAGCCGCCCTCAGTGT CTGCGGCCCCAGGACAGAAGGTCACCATCTCCTGCTCTGGA AGCAGCTCCAACATTGGGAATAATTATGTATCCTGGTACCAG CAGCTCCCAGGAACAGCCCCCAAACTCCTCATTTATGACAAT AATAAGCGACCCTCAGGGATTCCTGACCGATTCTCTGGCTCC AAGTCTGGCACGTCAGCCACCCTGGGCATCACCGGACTCCA GACTGGGGACGAGGCCGATTATTACTGCGGAACATGGGATA GCCGCCTGAGTGCTGTGGTTTTCGGCGGAGGGACCAAGCTG

IgG-scFv Molecule Designation	Light Chain Nucleic Acid Sequence	Modified Heavy Chain Nucleic Acid Sequence
		ACCGTGCTTGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGG CGGCGGAGGCTCCCAGGTGCAGCTGGTGGAATCTGGGGGAG GCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAG CCTCTGGATTCACCTTCAGTAGCTTTGGCATGCACTGGGTCC GCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATA TCATTTGATGGAAGTATTAAGTATTCTGTAGACTCCGTGAAG GGCCGATTCACCATCTCCAGAGACAATTCAAAGAACACGCT GTTTCTGCAAATGAACAGCCTGCGAGCCGAGGACACGGCTG TGTATTACTGTGCGAGAGATCGGCTCAATTACTATGAAAGTA GTGGTTATTATCACTACAAATACTACGGTATGGCCGTCTGGG GCCAAGGGACAACAGTTACTGTCTCTAGT (SEQ ID NO: 568)
iPS:386758	SEQ ID NO: 561	CAAGTTCAGTTGGTGGAGTCTGGAGCCGAAGTAGTAAAGCC AGGAGCTTCAGTGAAAGTCTCTTGTAAAGCAAGTGGATTCA CGTTTAGCCGCTTTGCCATGCATTGGGTGCGGCAAGCTCCCG GTCAGGGGTTGGAGTGGATGGGAGTTATTAGCTATGACGGG GGCAATAAGTACTACGCCGAGTCTGTTAAGGGTCGGGTCAC AATGACACGGGACACCTCAACCAGTACACTCTATATGGAAC TGTCTAGCCTGAGATCCGAGGACACCGCTGTGTATTATTGCG CTAGGGGGTACGATGTATTGACGGGTTATCCTGATTACTGGG GGCAGGGGACACTCGTAACCGTCTCTAGTGCCTCCACCAAG GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCT GACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAG CAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACA AGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAA ATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACC TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAA ACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCA CATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGC CAAGACAAAGCCGTGTGAGGAGCAGTACGGCAGCACGTACC GTTGTGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTC CCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCA GCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG AGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAG CAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCG TGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCA CCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCA TGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCA GAAGAGCCTAAGCTTGTCTCCGGGTGGTGGCGGATCGGGAG GTGGCGGATCCCAGTCTGTGTTGACGCAGCCGCCCTCAGTGT CTGCGGCCCCAGGACAGAAGGTCACCATCTCCTGCTCTGGA AGCAGCTCCAACATTGGGAATAATTATGTATCCTGGTACCAG CAGCTCCCAGGAACAGCCCCCAAACTCCTCATTTATGACAAT AATAAGCGACCCTCAGGGATTCCTGACCGATTCTCTGGCTCC AAGTCTGGCACGTCAACCACCCTGGGCATCACCGGACTCCA GACTGGGGACGAGGCCGATTATTACTGCGGAACATGGGATA GCCGCCTGAGTGCTGTGGTTTTCGGCGGAGGGACCAAGCTG ACCGTGCTTGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGG

IgG-scFv Molecule Designation	Light Chain Nucleic Acid Sequence	Modified Heavy Chain Nucleic Acid Sequence
		CGGCGGAGGCTCCCAGGTGCAGCTGGTGGAATCTGGGGGAG GCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAG CCTCTGGATTCACCTTCAGTAGCTTTGGCATGCACTGGGTCC GCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATA TCATTTGATGGAAGTATTAAGTATTCTGTAGACTCCGTGAAG GGCCGATTCACCATCTCCAGAGACAATTCAAAGAACACGCT GTTTCTGCAAATGAACAGCCTGCGAGCCGAGGACACGGCTG TGTATTACTGTGCGAGAGATCGGCTCAATTACTATGAAAGTA GTGGTTATTATCACTACAAATACTACGGTATGGCCGTCTGGG GCCAAGGGACAACAGTTACTGTCTCTAGT (SEQ ID NO: 569)
iPS:386756	SEQ ID NO: 561	CAAGTTCAGTTGGTGGAGTCTGGAGCCGAAGTAGTAAAGCC AGGAGCTTCAGTGAAAGTCTCTTGTAAAGCAAGTGGATTCA CGTTTAGCCGCTTTGCCATGCATTGGGTGCGGCAAGCTCCCG GTCAGGGGTTGGAGTGGATGGGAGTTATTAGCTATGACGGG GGCAATAAGTACTACGCCGAGTCTGTTAAGGGTCGGGTCAC AATGACACGGGACACCTCAACCAGTACACTCTATATGGAAC TGTCTAGCCTGAGATCCGAGGACACCGCTGTGTATTATTGCG CTAGGGGGTACGATGTATTGACGGGTTATCCTGATTACTGGG GGCAGGGGACACTCGTAACCGTCTCTAGTGCCTCCACCAAG GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCT GACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAG CAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACA AGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAA ATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACC TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAA ACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCA CATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGC CAAGACAAAGCCGTGTGAGGAGCAGTACGGCAGCACGTACC GTTGTGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTC CCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCA GCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG AGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAG CAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCG TGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCA CCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCA TGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCA GAAGAGCCTAAGCTTGTCTCCGGGTGGTGGCGGATCGGGAG GTGGCGGATCCCAGTCTGTGTTGACGCAGCCGCCCTCAGTGT CTGCGGCCCCAGGACAGAAGGTCACCATCTCCTGCTCTGGA AGCAGCTCCAACATTGGGAATAATTATGTATCCTGGTACCAG CAGCTCCCAGGAACAGCCCCCAAACTCCTCATTTATGACAAT AATAAGCGACCCTCAGGGATTCCTGACCGATTCTCTGGCTCC AAGTCTGGCACGTCAACCACCCTGGGCATCACCGGACTCCA GACTGGGGACGAGGCCGATTATTACTGCGGAACATGGGATA GCCGCCTGAGTGCTGTGGTTTTCGGCGGAGGGACCAAGCTG ACCGTGCTTGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGG CGGCGGAGGCTCCCAGGTGCAGCTGGTGGAATCTGGGGGAG

IgG-scFv Molecule Designation	Light Chain Nucleic Acid Sequence	Modified Heavy Chain Nucleic Acid Sequence
		GCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAG CCTCTGGATTCACCTTCAGTAGCTTTGGCATGCACTGGGTCC GCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATA TCATTTGATGGAAGTATTAAGTATTCTGTAGACTCCGTGAAG GGCCGATTCACCATCTCCAGAGACAATTCAAAGAACACGCT GTTTCTGCAAATGAACAGCCTGCGAGCCGAGGACACGGCTG TGTATTACTGTGCGAGAGATCGGCTCAATTACTATGATAGTA GTGGTTATTATCACTACAAATACTACGGTATGGCCGTCTGGG GCCAAGGGACAACAGTTACTGTCTCTAGT (SEQ ID NO: 570)
iPS:386754	SEQ ID NO: 561	CAAGTTCAGTTGGTGGAGTCTGGAGCCGAAGTAGTAAAGCC AGGAGCTTCAGTGAAAGTCTCTTGTAAAGCAAGTGGATTCA CGTTTAGCCGCTTTGCCATGCATTGGGTGCGGCAAGCTCCCG GTCAGGGGTTGGAGTGGATGGGAGTTATTAGCTATGACGGG GGCAATAAGTACTACGCCGAGTCTGTTAAGGGTCGGGTCAC AATGACACGGGACACCTCAACCAGTACACTCTATATGGAAC TGTCTAGCCTGAGATCCGAGGACACCGCTGTGTATTATTGCG CTAGGGGGTACGATGTATTGACGGGTTATCCTGATTACTGGG GGCAGGGGACACTCGTAACCGTCTCTAGTGCCTCCACCAAG GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCT GACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAG CAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACA AGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAA ATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACC TGAACTCCTGGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAA ACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCA CATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGC CAAGACAAAGCCGTGTGAGGAGCAGTACGGCAGCACGTACC GTTGTGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTC CCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCA GCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG AGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAG CAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCG TGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCA CCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCA TGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCA GAAGAGCCTAAGCTTGTCTCCGGGTGGTGGCGGATCGGGAG GTGGCGGATCCCAGGTGCAGCTGGTGGAATCTGGGGGAGGC GTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCC TCTGGATTCACCTTCAGTAGCTTTGGCATGCACTGGGTCCGC CAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATC ATTTGATGGAAGTATTAAGTATTCTGTAGACTCCGTGAAGGG CCGATTCACCATCTCCAGAGACAATTCAAAGAACACGCTGTT TCTGCAAATGAACAGCCTGCGAGCCGAGGACACGGCTGTGT ATTACTGTGCGAGAGATCGGCTCAATTACTATGAAAGTAGT GGTTATTATCACTACAAATACTACGGTATGGCCGTCTGGGGC CAAGGGACAACAGTTACTGTCTCTAGTGGAGGCGGAGGATC TGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCCAGTCTGTGTT

IgG-scFv Molecule Designation	Light Chain Nucleic Acid Sequence	Modified Heavy Chain Nucleic Acid Sequence
		GACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGACAGAAGG TCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATA ATTATGTATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCCA AACTCCTCATTTATGACAATAATAAGCGACCCTCAGGGATTC CTGACCGATTCTCTGGCTCCAAGTCTGGCACGTCAACCACCC TGGGCATCACCGGACTCCAGACTGGGGACGAGGCCGATTAT TACTGCGGAACATGGGATAGCCGCCTGAGTGCTGTGGTTTTC GGCGGAGGGACCAAGCTGACCGTGCTA (SEQ ID NO: 571)
iPS:386752	SEQ ID NO: 561	CAAGTTCAGTTGGTGGAGTCTGGAGCCGAAGTAGTAAAGCC AGGAGCTTCAGTGAAAGTCTCTTGTAAAGCAAGTGGATTCA CGTTTAGCCGCTTTGCCATGCATTGGGTGCGGCAAGCTCCCG GTCAGGGGTTGGAGTGGATGGGAGTTATTAGCTATGACGGG GGCAATAAGTACTACGCCGAGTCTGTTAAGGGTCGGGTCAC AATGACACGGGACACCTCAACCAGTACACTCTATATGGAAC TGTCTAGCCTGAGATCCGAGGACACCGCTGTGTATTATTGCG CTAGGGGGTACGATGTATTGACGGGTTATCCTGATTACTGGG GGCAGGGGACACTCGTAACCGTCTCTAGTGCCTCCACCAAG GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCT GACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAG CAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACA AGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAA ATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACC TGAACTCCTGGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAA ACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCA CATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGC CAAGACAAAGCCGTGTGAGGAGCAGTACGGCAGCACGTACC GTTGTGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTC CCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCA GCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG AGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAG CAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCG TGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCA CCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCA TGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCA GAAGAGCCTAAGCTTGTCTCCGGGTGGTGGCGGATCGGGAG GTGGCGGATCCCAGGTGCAGCTGGTGGAATCTGGGGGAGGC GTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCC TCTGGATTCACCTTCAGTAGCTTTGGCATGCACTGGGTCCGC CAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATC ATTTGATGGAAGTATTAAGTATTCTGTAGACTCCGTGAAGGG CCGATTCACCATCTCCAGAGACAATTCAAAGAACACGCTGTT TCTGCAAATGAACAGCCTGCGAGCCGAGGACACGGCTGTGT ATTACTGTGCGAGAGATCGGCTCAATTACTATGATAGTAGTG GTTATTATCACTACAAATACTACGGTATGGCCGTCTGGGGCC AAGGGACAACAGTTACTGTCTCTAGTGGAGGCGGAGGATCT GGTGGCGGTGGTTCTGGCGGCGGAGGCTCCCAGTCTGTGTTG ACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGACAGAAGGT

IgG-scFv Molecule Designation	Light Chain Nucleic Acid Sequence	Modified Heavy Chain Nucleic Acid Sequence
		CACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATAA TTATGTATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCCAA ACTCCTCATTTATGACAATAATAAGCGACCCTCAGGGATTCC TGACCGATTCTCTGGCTCCAAGTCTGGCACGTCAGCCACCCT GGGCATCACCGGACTCCAGACTGGGGACGAGGCCGATTATT ACTGCGGAACATGGGATAGCCGCCTGAGTGCTGTGGTTTTCG GCGGAGGGACCAAGCTGACCGTGCTA (SEQ ID NO: 572)
iPS:386750	SEQ ID NO: 561	CAAGTTCAGTTGGTGGAGTCTGGAGCCGAAGTAGTAAAGCC AGGAGCTTCAGTGAAAGTCTCTTGTAAAGCAAGTGGATTCA CGTTTAGCCGCTTTGCCATGCATTGGGTGCGGCAAGCTCCCG GTCAGGGGTTGGAGTGGATGGGAGTTATTAGCTATGACGGG GGCAATAAGTACTACGCCGAGTCTGTTAAGGGTCGGGTCAC AATGACACGGGACACCTCAACCAGTACACTCTATATGGAAC TGTCTAGCCTGAGATCCGAGGACACCGCTGTGTATTATTGCG CTAGGGGGTACGATGTATTGACGGGTTATCCTGATTACTGGG GGCAGGGGACACTCGTAACCGTCTCTAGTGCCTCCACCAAG GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCT GACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAG CAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACA AGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAA ATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACC TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAA ACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCA CATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGC CAAGACAAAGCCGTGTGAGGAGCAGTACGGCAGCACGTACC GTTGTGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTC CCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCA GCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG AGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAG CAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCG TGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCA CCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCA TGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCA GAAGAGCCTAAGCTTGTCTCCGGGTGGTGGCGGATCGGGAG GTGGCGGATCCCAGGTGCAGCTGGTGGAATCTGGGGGAGGC GTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCC TCTGGATTCACCTTCAGTAGCTTTGGCATGCACTGGGTCCGC CAGGCTCCAGGCAAGTGTCTGGAGTGGGTGGCAGTTATATC ATTTGATGGAAGTATTAAGTATTCTGTAGACTCCGTGAAGGG CCGATTCACCATCTCCAGAGACAATTCAAAGAACACGCTGTT TCTGCAAATGAACAGCCTGCGAGCCGAGGACACGGCTGTGT ATTACTGTGCGAGAGATCGGCTCAATTACTATGATAGTAGTG GTTATTATCACTACAAATACTACGGTATGGCCGTCTGGGGCC AAGGGACAACAGTTACTGTCTCTAGTGGAGGCGGAGGATCT GGTGGCGGTGGTTCTGGCGGCGGAGGCTCCCAGTCTGTGTTG ACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGACAGAAGGT CACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATAA

IgG-scFv Molecule Designation	Light Chain Nucleic Acid Sequence	Modified Heavy Chain Nucleic Acid Sequence
		TTATGTATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCCAA ACTCCTCATTTATGACAATAATAAGCGACCCTCAGGGATTCC TGACCGATTCTCTGGCTCCAAGTCTGGCACGTCAGCCACCCT GGGCATCACCGGACTCCAGACTGGGGACGAGGCCGATTATT ACTGCGGAACATGGGATAGCCGCCTGAGTGCTGTGGTTTTCG GCTGTGGGACCAAGCTGACCGTGCTA (SEQ ID NO: 573)
iPS:386748	SEQ ID NO: 561	CAAGTTCAGTTGGTGGAGTCTGGAGCCGAAGTAGTAAAGCC AGGAGCTTCAGTGAAAGTCTCTTGTAAAGCAAGTGGATTCA CGTTTAGCCGCTTTGCCATGCATTGGGTGCGGCAAGCTCCCG GTCAGGGGTTGGAGTGGATGGGAGTTATTAGCTATGACGGG GGCAATAAGTACTACGCCGAGTCTGTTAAGGGTCGGGTCAC AATGACACGGGACACCTCAACCAGTACACTCTATATGGAAC TGTCTAGCCTGAGATCCGAGGACACCGCTGTGTATTATTGCG CTAGGGGGTACGATGTATTGACGGGTTATCCTGATTACTGGG GGCAGGGGACACTCGTAACCGTCTCTAGTGCCTCCACCAAG GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCT GACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAG CAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACA AGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAA ATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACC TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAA ACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCA CATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGC CAAGACAAAGCCGTGTGAGGAGCAGTACGGCAGCACGTACC GTTGTGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTC CCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCA GCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG AGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAG CAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCG TGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCA CCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCA TGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCA GAAGAGCCTAAGCTTGTCTCCGGGTGGTGGCGGATCGGGAG GTGGCGGATCCCAGGTGCAGCTGGTGGAATCTGGGGGAGGC GTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCC TCTGGATTCACCTTCAGTAGCTTTGGCATGCACTGGGTCCGC CAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATC ATTTGATGGAAGTATTAAGTATTCTGTAGACTCCGTGAAGGG CCGATTCACCATCTCCAGAGACAATTCAAAGAACACGCTGTT TCTGCAAATGAACAGCCTGCGAGCCGAGGACACGGCTGTGT ATTACTGTGCGAGAGATCGGCTCAATTACTATGAAAGTAGT GGTTATTATCACTACAAATACTACGGTATGGCCGTCTGGGGC CAAGGGACAACAGTTACTGTCTCTAGTGGAGGCGGAGGATC TGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCCAGTCTGTGTT GACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGACAGAAGG TCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATA ATTATGTATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCCA

IgG-scFv Molecule Designation	Light Chain Nucleic Acid Sequence	Modified Heavy Chain Nucleic Acid Sequence
		AACTCCTCATTTATGACAATAATAAGCGACCCTCAGGGATTC CTGACCGATTCTCTGGCTCCAAGTCTGGCACGTCAGCCACCC TGGGCATCACCGGACTCCAGACTGGGGACGAGGCCGATTAT TACTGCGGAACATGGGATAGCCGCCTGAGTGCTGTGGTTTTC GGCGGAGGGACCAAGCTGACCGTGCTA (SEQ ID NO: 574)
iPS:386746	SEQ ID NO: 561	CAAGTTCAGTTGGTGGAGTCTGGAGCCGAAGTAGTAAAGCC AGGAGCTTCAGTGAAAGTCTCTTGTAAAGCAAGTGGATTCA CGTTTAGCCGCTTTGCCATGCATTGGGTGCGGCAAGCTCCCG GTCAGGGGTTGGAGTGGATGGGAGTTATTAGCTATGACGGG GGCAATAAGTACTACGCCGAGTCTGTTAAGGGTCGGGTCAC AATGACACGGGACACCTCAACCAGTACACTCTATATGGAAC TGTCTAGCCTGAGATCCGAGGACACCGCTGTGTATTATTGCG CTAGGGGGTACGATGTATTGACGGGTTATCCTGATTACTGGG GGCAGGGGACACTCGTAACCGTCTCTAGTGCCTCCACCAAG GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCT GACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAG CAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACA AGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAA ATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACC TGAACTCCTGGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAA ACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCA CATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGC CAAGACAAAGCCGTGTGAGGAGCAGTACGGCAGCACGTACC GTTGTGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTC CCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCA GCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG AGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAG CAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCG TGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCA CCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCA TGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCA GAAGAGCCTAAGCTTGTCTCCGGGTGGTGGCGGATCGGGAG GTGGCGGATCCCAGGTGCAGCTGGTGGAATCTGGGGGAGGC GTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCC TCTGGATTCACCTTCAGTAGCTTTGGCATGCACTGGGTCCGC CAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATC ATTTGATGGAAGTATTAAGTATTCTGTAGACTCCGTGAAGGG CCGATTCACCATCTCCAGAGACAATTCAAAGAACACGCTGTT TCTGCAAATGAACAGCCTGCGAGCCGAGGACACGGCTGTGT ATTACTGTGCGAGAGATCGGCTCAATTACTATGATAGTAGTG GTTATTATCACTACAAATACTACGGTATGGCCGTCTGGGGCC AAGGGACAACAGTTACTGTCTCTAGTGGAGGCGGAGGATCT GGTGGCGGTGGTTCTGGCGGCGGAGGCTCCCAGTCTGTGTTG ACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGACAGAAGGT CACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATAA TTATGTATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCCAA ACTCCTCATTTATGACAATAATAAGCGACCCTCAGGGATTCC

IgG-scFv Molecule Designation	Light Chain Nucleic Acid Sequence	Modified Heavy Chain Nucleic Acid Sequence
		TGACCGATTCTCTGGCTCCAAGTCTGGCACGTCAGCCACCCT GGCCATCACCGGACTCCAGACTGGGGACGAGGCCGATTATT ACTGCGGAACATGGGATAGCCGCCTGAGTGCTGTGGTTTTCG GCGGAGGGACCAAGCTGACCGTGCTA (SEQ ID NO: 575)
iPS:386744	SEQ ID NO: 561	CAAGTTCAGTTGGTGGAGTCTGGAGCCGAAGTAGTAAAGCC AGGAGCTTCAGTGAAAGTCTCTTGTAAAGCAAGTGGATTCA CGTTTAGCCGCTTTGCCATGCATTGGGTGCGGCAAGCTCCCG GTCAGGGGTTGGAGTGGATGGGAGTTATTAGCTATGACGGG GGCAATAAGTACTACGCCGAGTCTGTTAAGGGTCGGGTCAC AATGACACGGGACACCTCAACCAGTACACTCTATATGGAAC TGTCTAGCCTGAGATCCGAGGACACCGCTGTGTATTATTGCG CTAGGGGGTACGATGTATTGACGGGTTATCCTGATTACTGGG GGCAGGGGACACTCGTAACCGTCTCTAGTGCCTCCACCAAG GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCT GACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAG CAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACA AGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAA ATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACC TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAA ACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCA CATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGC CAAGACAAAGCCGTGTGAGGAGCAGTACGGCAGCACGTACC GTTGTGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTC CCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCA GCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG AGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAG CAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCG TGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCA CCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCA TGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCA GAAGAGCCTAAGCTTGTCTCCGGGTGGTGGCGGATCGGGAG GTGGCGGATCCCAGGTGCAGCTGGTGGAATCTGGGGGAGGC GTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCC TCTGGATTCACCTTCAGTAGCTTTGGCATGCACTGGGTCCGC CAGGCTCCAGGCAAGTGTCTGGAGTGGGTGGCAGTTATATC ATTTGATGGAAGTATTAAGTATTCTGTAGACTCCGTGAAGGG CCGATTCACCATCTCCAGAGACAATTCAAAGAACACGCTGTT TCTGCAAATGAACAGCCTGCGAGCCGAGGACACGGCTGTGT ATTACTGTGCGAGAGATCGGCTCAATTACTATGATAGTAGTG GTTATTATCACTACAAATACTACGGTATGGCCGTCTGGGGCC AAGGGACAACAGTTACTGTCTCTAGTGGAGGCGGAGGATCT GGTGGCGGTGGTTCTGGCGGCGGAGGCTCCCAGTCTGTGTTG ACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGACAGAAGGT CACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATAA TTATGTATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCCAA ACTCCTCATTTATGACAATAATAAGCGACCCTCAGGGATTCC TGACCGATTCTCTGGCTCCAAGTCTGGCACGTCAGCCACCCT

IgG-scFv Molecule Designation	Light Chain Nucleic Acid Sequence	Modified Heavy Chain Nucleic Acid Sequence
		GGCCATCACCGGACTCCAGACTGGGGACGAGGCCGATTATT ACTGCGGAACATGGGATAGCCGCCTGAGTGCTGTGGTTTTCG GCTGTGGGACCAAGCTGACCGTGCTA (SEQ ID NO: 576)
iPS:386742	SEQ ID NO: 561	CAAGTTCAGTTGGTGGAGTCTGGAGCCGAAGTAGTAAAGCC AGGAGCTTCAGTGAAAGTCTCTTGTAAAGCAAGTGGATTCA CGTTTAGCCGCTTTGCCATGCATTGGGTGCGGCAAGCTCCCG GTCAGGGGTTGGAGTGGATGGGAGTTATTAGCTATGACGGG GGCAATAAGTACTACGCCGAGTCTGTTAAGGGTCGGGTCAC AATGACACGGGACACCTCAACCAGTACACTCTATATGGAAC TGTCTAGCCTGAGATCCGAGGACACCGCTGTGTATTATTGCG CTAGGGGGTACGATGTATTGACGGGTTATCCTGATTACTGGG GGCAGGGGACACTCGTAACCGTCTCTAGTGCCTCCACCAAG GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCT GACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAG CAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACA AGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAA ATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACC TGAACTCCTGGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAA ACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCA CATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGC CAAGACAAAGCCGTGTGAGGAGCAGTACGGCAGCACGTACC GTTGTGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTC CCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCA GCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG AGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAG CAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCG TGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCA CCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCA TGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCA GAAGAGCCTAAGCTTGTCTCCGGGTGGTGGCGGATCGGGAG GTGGCGGATCCCAGGTGCAGCTGGTGGAATCTGGGGGAGGC GTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCC TCTGGATTCACCTTCAGTAGCTTTGGCATGCACTGGGTCCGC CAGGCTCCAGGCAAGTGTCTGGAGTGGGTGGCAGTTATATC ATTTGATGGAAGTATTAAGTATTCTGTAGACTCCGTGAAGGG CCGATTCACCATCTCCAGAGACAATTCAAAGAACACGCTGTT TCTGCAAATGAACAGCCTGCGAGCCGAGGACACGGCTGTGT ATTACTGTGCGAGAGATCGGCTCAATTACTATGAAAGTAGT GGTTATTATCACTACAAATACTACGGTATGGCCGTCTGGGGC CAAGGGACAACAGTTACTGTCTCTAGTGGAGGCGGAGGATC TGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCCAGTCTGTGTT GACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGACAGAAGG TCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATA ATTATGTATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCCA AACTCCTCATTTATGACAATAATAAGCGACCCTCAGGGATTC CTGACCGATTCTCTGGCTCCAAGTCTGGCACGTCAGCCACCC TGGGCATCACCGGACTCCAGACTGGGGACGAGGCCGATTAT

IgG-scFv Molecule Designation	Light Chain Nucleic Acid Sequence	Modified Heavy Chain Nucleic Acid Sequence
		TACTGCGGAACATGGGATAGCCGCCTGAGTGCTGTGGTTTTC GGCTGTGGGACCAAGCTGACCGTGCTA (SEQ ID NO: 577)
iPS:386740	SEQ ID NO: 561	CAAGTTCAGTTGGTGGAGTCTGGAGCCGAAGTAGTAAAGCC AGGAGCTTCAGTGAAAGTCTCTTGTAAAGCAAGTGGATTCA CGTTTAGCCGCTTTGCCATGCATTGGGTGCGGCAAGCTCCCG GTCAGGGGTTGGAGTGGATGGGAGTTATTAGCTATGACGGG GGCAATAAGTACTACGCCGAGTCTGTTAAGGGTCGGGTCAC AATGACACGGGACACCTCAACCAGTACACTCTATATGGAAC TGTCTAGCCTGAGATCCGAGGACACCGCTGTGTATTATTGCG CTAGGGGGTACGATGTATTGACGGGTTATCCTGATTACTGGG GGCAGGGGACACTCGTAACCGTCTCTAGTGCCTCCACCAAG GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCT GACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAG CAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACA AGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAA ATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACC TGAACTCCTGGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAA ACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCA CATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGC CAAGACAAAGCCGTGTGAGGAGCAGTACGGCAGCACGTACC GTTGTGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTC CCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCA GCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG AGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAG CAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCG TGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCA CCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCA TGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCA GAAGAGCCTAAGCTTGTCTCCGGGTGGTGGCGGATCGGGAG GTGGCGGATCCCAGGTGCAGCTGGTGGAATCTGGGGGAGGC GTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCC TCTGGATTCACCTTCAGTAGCTTTGGCATGCACTGGGTCCGC CAGGCTCCAGGCAAGTGTCTGGAGTGGGTGGCAGTTATATC ATTTGATGGAAGTATTAAGTATTCTGTAGACTCCGTGAAGGG CCGATTCACCATCTCCAGAGACAATTCAAAGAACACGCTGTT TCTGCAAATGAACAGCCTGCGAGCCGAGGACACGGCTGTGT ATTACTGTGCGAGAGATCGGCTCAATTACTATGAAAGTAGT GGTTATTATCACTACAAATACTACGGTATGGCCGTCTGGGGC CAAGGGACAACAGTTACTGTCTCTAGTGGAGGCGGAGGATC TGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCCAGTCTGTGTT GACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGACAGAAGG TCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATA ATTATGTATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCCA AACTCCTCATTTATGACAATAATAAGCGACCCTCAGGGATTC CTGACCGATTCTCTGGCTCCAAGTCTGGCACGTCAACCACCC TGGGCATCACCGGACTCCAGACTGGGGACGAGGCCGATTAT TACTGCGGAACATGGGATAGCCGCCTGAGTGCTGTGGTTTTC

IgG-scFv Molecule Designation	Light Chain Nucleic Acid Sequence	Modified Heavy Chain Nucleic Acid Sequence
		GGCTGTGGGACCAAGCTGACCGTGCTA (SEQ ID NO: 578)
iPS:386736	SEQ ID NO: 561	CAAGTTCAGTTGGTGGAGTCTGGAGCCGAAGTAGTAAAGCC AGGAGCTTCAGTGAAAGTCTCTTGTAAAGCAAGTGGATTCA CGTTTAGCCGCTTTGCCATGCATTGGGTGCGGCAAGCTCCCG GTCAGGGGTTGGAGTGGATGGGAGTTATTAGCTATGACGGG GGCAATAAGTACTACGCCGAGTCTGTTAAGGGTCGGGTCAC AATGACACGGGACACCTCAACCAGTACACTCTATATGGAAC TGTCTAGCCTGAGATCCGAGGACACCGCTGTGTATTATTGCG CTAGGGGGTACGATGTATTGACGGGTTATCCTGATTACTGGG GGCAGGGGACACTCGTAACCGTCTCTAGTGCCTCCACCAAG GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCT GACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAG CAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACA AGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAA ATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACC TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAA ACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCA CATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGC CAAGACAAAGCCGTGTGAGGAGCAGTACGGCAGCACGTACC GTTGTGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTC CCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCA GCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG AGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAG CAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCG TGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCA CCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCA TGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCA GAAGAGCCTAAGCTTGTCTCCGGGTGGTGGCGGATCGGGAG GTGGCGGATCCCAGGTGCAGCTGGTGGAATCTGGGGGAGGC GTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCC TCTGGATTCACCTTCAGTAGCTTTGGCATGCACTGGGTCCGC CAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATC ATTTGATGGAAGTATTAAGTATTCTGTAGACTCCGTGAAGGG CCGATTCACCATCTCCAGAGACAATTCAAAGAACACGCTGTT TCTGCAAATGAACAGCCTGCGAGCCGAGGACACGGCTGTGT ATTACTGTGCGAGAGATCGGCTCAATTACTATGATAGTAGTG GTTATTATCACTACAAATACTACGGTATGGCCGTCTGGGGCC AAGGGACAACAGTTACTGTCTCTAGTGGAGGCGGAGGATCT GGTGGCGGTGGTTCTGGCGGCGGAGGCTCCCAGTCTGTGTTG ACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGACAGAAGGT CACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATAA TTATGTATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCCAA ACTCCTCATTTATGACAATAATAAGCGACCCTCAGGGATTCC TGACCGATTCTCTGGCTCCAAGTCTGGCACGTCAACCACCCT GGGCATCACCGGACTCCAGACTGGGGACGAGGCCGATTATT ACTGCGGAACATGGGATAGCCGCCTGAGTGCTGTGGTTTTCG GCGGAGGGACCAAGCTGACCGTGCTA (SEQ ID NO: 579)

IgG-scFv Molecule Designation	Light Chain Nucleic Acid Sequence	Modified Heavy Chain Nucleic Acid Sequence
Anti-CGRP Receptor IgG x Anti-PAC1 Receptor scFv		
iPS:386731	CAGTCTGTGTTGAC GCAGCCGCCCTCAG TGTCTGCGGCCCCA GGACAGAAGGTCA CCATCTCCTGCTCT GGAAGCAGCTCCA ACATTGGGAATAAT TATGTATCCTGGTA CCAGCAGCTCCCAG GAACAGCCCCCAA ACTCCTCATTTATG ACAATAATAAGCG ACCCTCAGGGATTC CTGACCGATTCTCT GGCTCCAAGTCTGG CACGTCAACCACCC TGGGCATCACCGGA CTCCAGACTGGGGA CGAGGCCGATTATT ACTGCGGAACATG GGATAGCCGCCTGA GTGCTGTGGTTTTC GGCGGAGGGACCA AGCTGACCGTCCTA GGTCAGCCCAAGG CCAACCCCACTGTC ACTCTGTTCCCGCC CTCCTCTGAGGAGC TCCAAGCCAACAA GGCCACACTAGTGT GTCTGATCAGTGAC TTCTACCCGGGAGC TGTGACAGTGGCCT GGAAGGCAGATGG CAGCCCCGTCAAGG CGGGAGTGGAGAC CACCAAACCCTCCA AACAGAGCAACAA CAAGTACGCGGCC AGCAGCTACCTGAG CCTGACGCCCGAGC AGTGGAAGTCCCAC AGAAGCTACAGCT GCCAGGTCACGCAT GAAGGGAGCACCG TGGAGAAGACAGT GGCCCCTACAGAAT GTTCA (SEQ ID NO: 562)	CAGGTGCAGCTGGTGGAATCTGGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCAC CTTCAGTAGCTTTGGCATGCACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCAGTTATATCATTTGATGGAA GTATTAAGTATTCTGTAGACTCCGTGAAGGGCCGATTCACCA TCTCCAGAGACAATTCAAAGAACACGCTGTTTCTGCAAATG AACAGCCTGCGAGCCGAGGACACGGCTGTGTATTACTGTGC GAGAGATCGGCTCAATTACTATGAAAGTAGTGGTTATTATCA CTACAAATACTACGGTATGGCCGTCTGGGGCCAAGGGACAA CAGTTACCGTCTCTAGTGCCTCCACCAAGGGCCCATCGGTCT TCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAG CGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCG GTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGT GCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTC CCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA CCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAAC ACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAA AACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGG GGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACA CCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGG TGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCC GTGTGAGGAGCAGTACGGCAGCACGTACCGTTGTGTCAGCG TCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCAT CGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAAC CACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACC AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTA TCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC CGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC GACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGAT GCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTAA GCTTGTCTCCGGGTGGTGGCGGATCGGGAGGTGGCGGATCC GATATCCAGCTCACTCAATCGCCATCATTTCTCTCCGCTTCG GTAGGCGACCGGGTCACGATCACATGCAGGGCGTCGCAAAG CATTGGGAGGTCGTTGCATTGGTATCAGCAGAAACCCGGAA AGGCCCCGAAACTTCTGATCAAATACGCATCACAAAGTTTG AGCGGTGTGCCGTCGCGCTTCTCCGGTTCCGGAAGCGGAAC GGAGTTCACGCTTACAATCTCCTCACTGCAGCCCGAGGATTT CGCGACCTATTACTGTCACCAGTCATCCAGACTCCCGTTTAC TTTTGGCCCTGGGACCAAGGTGGACATTAAGCGTGGAGGCG GAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCCAA GTTCAGTTGGTGGAGTCTGGAGCCGAAGTAGTAAAGCCAGG AGCTTCAGTGAAAGTCTCTTGTAAAGCAAGTGGATTCACGTT TAGCCGCTTTGCCATGCATTGGGTGCGGCAAGCTCCCGGTCA GGGGTTGGAGTGGATGGGAGTTATTAGCTATGACGGGGGCA ATAAGTACTACGCCGAGTCTGTTAAGGGTCGGGTCACAATG ACACGGGACACCTCAACCAGTACACTCTATATGGAACTGTCT AGCCTGAGATCCGAGGACACCGCTGTGTATTATTGCGCTAG GGGGTACGATGTATTGACGGGTTATCCTGATTACTGGGGGC AGGGGACACTCGTAACCGTGTCTTCA (SEQ ID NO: 580)

IgG-scFv Molecule Designation	Light Chain Nucleic Acid Sequence	Modified Heavy Chain Nucleic Acid Sequence
iPS:386725	SEQ ID NO: 562	CAGGTGCAGCTGGTGGAATCTGGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCAC CTTCAGTAGCTTTGGCATGCACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCAGTTATATCATTTGATGGAA GTATTAAGTATTCTGTAGACTCCGTGAAGGGCCGATTCACCA TCTCCAGAGACAATTCAAAGAACACGCTGTTTCTGCAAATG AACAGCCTGCGAGCCGAGGACACGGCTGTGTATTACTGTGC GAGAGATCGGCTCAATTACTATGATAGTAGTGGTTATTATCA CTACAAATACTACGGTATGGCCGTCTGGGGCCAAGGGACAA CAGTTACCGTCTCTAGTGCCTCCACCAAGGGCCCATCGGTCT TCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAG CGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCG GTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGT GCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTC CCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA CCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAAC ACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAA AACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGG GGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACA CCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGG TGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCC GTGTGAGGAGCAGTACGGCAGCACGTACCGTTGTGTCAGCG TCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCAT CGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAAC CACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACC AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTA TCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC CGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC GACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGAT GCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTAA GCTTGTCTCCGGGTGGTGGCGGATCGGGAGGTGGCGGATCC GATATCCAGCTCACTCAATCGCCATCATTTCTCTCCGCTTCG GTAGGCGACCGGGTCACGATCACATGCAGGGCGTCGCAAAG CATTGGGAGGTCGTTGCATTGGTATCAGCAGAAACCCGGAA AGGCCCCGAAACTTCTGATCAAATACGCATCACAAAGTTTG AGCGGTGTGCCGTCGCGCTTCTCCGGTTCCGGAAGCGGAAC GGAGTTCACGCTTACAATCTCCTCACTGCAGCCCGAGGATTT CGCGACCTATTACTGTCACCAGTCATCCAGACTCCCGTTTAC TTTTGGCCCTGGGACCAAGGTGGACATTAAGCGTGGAGGCG GAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCCAA GTTCAGTTGGTGGAGTCTGGAGCCGAAGTAGTAAAGCCAGG AGCTTCAGTGAAAGTCTCTTGTAAAGCAAGTGGATTCACGTT TAGCCGCTTTGCCATGCATTGGGTGCGGCAAGCTCCCGGTCA GGGGTTGGAGTGGATGGGAGTTATTAGCTATGACGGGGGCA ATAAGTACTACGCCGAGTCTGTTAAGGGTCGGGTCACAATG ACACGGGACACCTCAACCAGTACACTCTATATGGAACTGTCT AGCCTGAGATCCGAGGACACCGCTGTGTATTATTGCGCTAG GGGGTACGATGTATTGACGGGTTATCCTGATTACTGGGGGC AGGGGACACTCGTAACCGTGTCTTCA (SEQ ID NO: 581)
iPS:386717	SEQ ID NO: 562	CAGGTGCAGCTGGTGGAATCTGGGGGAGGCGTGGTCCAGCC

IgG-scFv Molecule Designation	Light Chain Nucleic Acid Sequence	Modified Heavy Chain Nucleic Acid Sequence
		TGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCAC CTTCAGTAGCTTTGGCATGCACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCAGTTATATCATTTGATGGAA GTATTAAGTATTCTGTAGACTCCGTGAAGGGCCGATTCACCA TCTCCAGAGACAATTCAAAGAACACGCTGTTTCTGCAAATG AACAGCCTGCGAGCCGAGGACACGGCTGTGTATTACTGTGC GAGAGATCGGCTCAATTACTATGAAAGTAGTGGTTATTATCA CTACAAATACTACGGTATGGCCGTCTGGGGCCAAGGGACAA CAGTTACCGTCTCTAGTGCCTCCACCAAGGGCCCATCGGTCT TCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAG CGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCG GTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGT GCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTC CCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA CCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAAC ACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAA AACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGG GGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACA CCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGG TGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCC GTGTGAGGAGCAGTACGGCAGCACGTACCGTTGTGTCAGCG TCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCAT CGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAAC CACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACC AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTA TCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC CGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC GACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGAT GCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTAA GCTTGTCTCCGGGTGGTGGCGGATCGGGAGGTGGCGGATCC CAAGTTCAGTTGGTGGAGTCTGGAGCCGAAGTAGTAAAGCC AGGAGCTTCAGTGAAAGTCTCTTGTAAAGCAAGTGGATTCA CGTTTAGCCGCTTTGCCATGCATTGGGTGCGGCAAGCTCCCG GTCAGGGGTTGGAGTGGATGGGAGTTATTAGCTATGACGGG GGCAATAAGTACTACGCCGAGTCTGTTAAGGGTCGGGTCAC AATGACACGGGACACCTCAACCAGTACACTCTATATGGAAC TGTCTAGCCTGAGATCCGAGGACACCGCTGTGTATTATTGCG CTAGGGGGTACGATGTATTGACGGGTTATCCTGATTACTGGG GGCAGGGGACACTCGTAACCGTCTCCTCAGGAGGCGGAGGA TCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCGATATCCA GCTCACTCAATCGCCATCATTTCTCTCCGCTTCGGTAGGCGA CCGGGTCACGATCACATGCAGGGCGTCGCAAAGCATTGGGA GGTCGTTGCATTGGTATCAGCAGAAACCCGGAAAGTGCCCG AAACTTCTGATCAAATACGCATCACAAAGTTTGAGCGGTGT GCCGTCGCGCTTCTCCGGTTCCGGAAGCGGAACGGAGTTCA CGCTTACAATCTCCTCACTGCAGCCCGAGGATTTCGCGACCT ATTACTGTCACCAGTCATCCAGACTCCCGTTTACTTTTGGCT GTGGGACCAAGGTGGACATTAAGCGT (SEQ ID NO: 582)
iPS:386715	SEQ ID NO: 562	CAGGTGCAGCTGGTGGAATCTGGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCAC

IgG-scFv Molecule Designation	Light Chain Nucleic Acid Sequence	Modified Heavy Chain Nucleic Acid Sequence
		CTTCAGTAGCTTTGGCATGCACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCAGTTATATCATTTGATGGAA GTATTAAGTATTCTGTAGACTCCGTGAAGGGCCGATTCACCA TCTCCAGAGACAATTCAAAGAACACGCTGTTTCTGCAAATG AACAGCCTGCGAGCCGAGGACACGGCTGTGTATTACTGTGC GAGAGATCGGCTCAATTACTATGATAGTAGTGGTTATTATCA CTACAAATACTACGGTATGGCCGTCTGGGGCCAAGGGACAA CAGTTACCGTCTCTAGTGCCTCCACCAAGGGCCCATCGGTCT TCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAG CGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCG GTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGT GCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTC CCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA CCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAAC ACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAA AACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGG GGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACA CCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGG TGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCC GTGTGAGGAGCAGTACGGCAGCACGTACCGTTGTGTCAGCG TCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCAT CGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAAC CACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACC AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTA TCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC CGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC GACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGAT GCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTAA GCTTGTCTCCGGGTGGTGGCGGATCGGGAGGTGGCGGATCC CAAGTTCAGTTGGTGGAGTCTGGAGCCGAAGTAGTAAAGCC AGGAGCTTCAGTGAAAGTCTCTTGTAAAGCAAGTGGATTCA CGTTTAGCCGCTTTGCCATGCATTGGGTGCGGCAAGCTCCCG GTCAGGGGTTGGAGTGGATGGGAGTTATTAGCTATGACGGG GGCAATAAGTACTACGCCGAGTCTGTTAAGGGTCGGGTCAC AATGACACGGGACACCTCAACCAGTACACTCTATATGGAAC TGTCTAGCCTGAGATCCGAGGACACCGCTGTGTATTATTGCG CTAGGGGGTACGATGTATTGACGGGTTATCCTGATTACTGGG GGCAGGGGACACTCGTAACCGTCTCCTCAGGAGGCGGAGGA TCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCGATATCCA GCTCACTCAATCGCCATCATTTCTCTCCGCTTCGGTAGGCGA CCGGGTCACGATCACATGCAGGGCGTCGCAAAGCATTGGGA GGTCGTTGCATTGGTATCAGCAGAAACCCGGAAAGTGCCCG AAACTTCTGATCAAATACGCATCACAAAGTTTGAGCGGTGT GCCGTCGCGCTTCTCCGGTTCCGGAAGCGGAACGGAGTTCA CGCTTACAATCTCCTCACTGCAGCCCGAGGATTTCGCGACCT ATTACTGTCACCAGTCATCCAGACTCCCGTTTACTTTTGGCT GTGGGACCAAGGTGGACATTAAGCGT (SEQ ID NO: 583)
iPS:386707	SEQ ID NO: 562	CAGGTGCAGCTGGTGGAATCTGGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCAC CTTCAGTAGCTTTGGCATGCACTGGGTCCGCCAGGCTCCAGG

IgG-scFv Molecule Designation	Light Chain Nucleic Acid Sequence	Modified Heavy Chain Nucleic Acid Sequence
		CAAGGGGCTGGAGTGGGTGGCAGTTATATCATTTGATGGAA GTATTAAGTATTCTGTAGACTCCGTGAAGGGCCGATTCACCA TCTCCAGAGACAATTCAAAGAACACGCTGTTTCTGCAAATG AACAGCCTGCGAGCCGAGGACACGGCTGTGTATTACTGTGC GAGAGATCGGCTCAATTACTATGAAAGTAGTGGTTATTATCA CTACAAATACTACGGTATGGCCGTCTGGGGCCAAGGGACAA CAGTTACCGTCTCTAGTGCCTCCACCAAGGGCCCATCGGTCT TCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAG CGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCG GTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGT GCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTC CCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA CCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAAC ACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAA AACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGG GGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACA CCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGG TGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCC GTGTGAGGAGCAGTACGGCAGCACGTACCGTTGTGTCAGCG TCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCAT CGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAAC CACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACC AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTA TCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC CGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC GACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGAT GCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTAA GCTTGTCTCCGGGTGGTGGCGGATCGGGAGGTGGCGGATCC CAAGTTCAGTTGGTGGAGTCTGGAGCCGAAGTAGTAAAGCC AGGAGCTTCAGTGAAAGTCTCTTGTAAAGCAAGTGGATTCA CGTTTAGCCGCTTTGCCATGCATTGGGTGCGGCAAGCTCCCG GTCAGGGGTTGGAGTGGATGGGAGTTATTAGCTATGACGGG GGCAATAAGTACTACGCCGAGTCTGTTAAGGGTCGGGTCAC AATGACACGGGACACCTCAACCAGTACACTCTATATGGAAC TGTCTAGCCTGAGATCCGAGGACACCGCTGTGTATTATTGCG CTAGGGGGTACGATGTATTGACGGGTTATCCTGATTACTGGG GGCAGGGGACACTCGTAACCGTCTCCTCAGGAGGCGGAGGA TCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCGATATCCA GCTCACTCAATCGCCATCATTTCTCTCCGCTTCGGTAGGCGA CCGGGTCACGATCACATGCAGGGCGTCGCAAAGCATTGGGA GGTCGTTGCATTGGTATCAGCAGAAACCCGGAAAGGCCCCG AAACTTCTGATCAAATACGCATCACAAAGTTTGAGCGGTGT GCCGTCGCGCTTCTCCGGTTCCGGAAGCGGAACGGAGTTCA CGCTTACAATCTCCTCACTGCAGCCCGAGGATTTCGCGACCT ATTACTGTCACCAGTCATCCAGACTCCCGTTTACTTTTGGCC CTGGGACCAAGGTGGACATTAAGCGT (SEQ ID NO: 584)
iPS:386705	SEQ ID NO: 562	CAGGTGCAGCTGGTGGAATCTGGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCAC CTTCAGTAGCTTTGGCATGCACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCAGTTATATCATTTGATGGAA

IgG-scFv Molecule Designation	Light Chain Nucleic Acid Sequence	Modified Heavy Chain Nucleic Acid Sequence
		GTATTAAGTATTCTGTAGACTCCGTGAAGGGCCGATTCACCA TCTCCAGAGACAATTCAAAGAACACGCTGTTTCTGCAAATG AACAGCCTGCGAGCCGAGGACACGGCTGTGTATTACTGTGC GAGAGATCGGCTCAATTACTATGATAGTAGTGGTTATTATCA CTACAAATACTACGGTATGGCCGTCTGGGGCCAAGGGACAA CAGTTACCGTCTCTAGTGCCTCCACCAAGGGCCCATCGGTCT TCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAG CGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCG GTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGT GCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTC CCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA CCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAAC ACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAA AACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGG GGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACA CCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGG TGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCC GTGTGAGGAGCAGTACGGCAGCACGTACCGTTGTGTCAGCG TCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCAT CGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAAC CACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACC AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTA TCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC CGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC GACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGAT GCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTAA GCTTGTCTCCGGGTGGTGGCGGATCGGGAGGTGGCGGATCC CAAGTTCAGTTGGTGGAGTCTGGAGCCGAAGTAGTAAAGCC AGGAGCTTCAGTGAAAGTCTCTTGTAAAGCAAGTGGATTCA CGTTTAGCCGCTTTGCCATGCATTGGGTGCGGCAAGCTCCCG GTCAGGGGTTGGAGTGGATGGGAGTTATTAGCTATGACGGG GGCAATAAGTACTACGCCGAGTCTGTTAAGGGTCGGGTCAC AATGACACGGGACACCTCAACCAGTACACTCTATATGGAAC TGTCTAGCCTGAGATCCGAGGACACCGCTGTGTATTATTGCG CTAGGGGGTACGATGTATTGACGGGTTATCCTGATTACTGGG GGCAGGGGACACTCGTAACCGTCTCCTCAGGAGGCGGAGGA TCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCGATATCCA GCTCACTCAATCGCCATCATTTCTCTCCGCTTCGGTAGGCGA CCGGGTCACGATCACATGCAGGGCGTCGCAAAGCATTGGGA GGTCGTTGCATTGGTATCAGCAGAAACCCGGAAAGGCCCCG AAACTTCTGATCAAATACGCATCACAAAGTTTGAGCGGTGT GCCGTCGCGCTTCTCCGGTTCCGGAAGCGGAACGGAGTTCA CGCTTACAATCTCCTCACTGCAGCCCGAGGATTTCGCGACCT ATTACTGTCACCAGTCATCCAGACTCCCGTTTACTTTTGGCC CTGGGACCAAGGTGGACATTAAGCGT (SEQ ID NO: 585)
iPS:386723	CAGTCTGTGTTGAC GCAGCCGCCCTCAG TGTCTGCGGCCCCA GGACAGAAGGTCA CCATCTCCTGCTCT	CAGGTGCAGCTGGTGGAATCTGGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCAC CTTCAGTAGCTTTGGCATGCACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCAGTTATATCATTTGATGGAA GTATTAAGTATTCTGTAGACTCCGTGAAGGGCCGATTCACCA

IgG-scFv Molecule Designation	Light Chain Nucleic Acid Sequence	Modified Heavy Chain Nucleic Acid Sequence
	GGAAGCAGCTCCA ACATTGGGAATAAT TATGTATCCTGGTA CCAGCAGCTCCCAG GAACAGCCCCCAA ACTCCTCATTTATG ACAATAATAAGCG ACCCTCAGGGATTC CTGACCGATTCTCT GGCTCCAAGTCTGG CACGTCAGCCACCC TGGGCATCACCGGA CTCCAGACTGGGGA CGAGGCCGATTATT ACTGCGGAACATG GGATAGCCGCCTGA GTGCTGTGGTTTTC GGCGGAGGGACCA AGCTGACCGTCCTA GGTCAGCCCAAGG CCAACCCCACTGTC ACTCTGTTCCCGCC CTCCTCTGAGGAGC TCCAAGCCAACAA GGCCACACTAGTGT GTCTGATCAGTGAC TTCTACCCGGGAGC TGTGACAGTGGCCT GGAAGGCAGATGG CAGCCCCGTCAAGG CGGGAGTGGAGAC CACCAAACCCTCCA AACAGAGCAACAA CAAGTACGCGGCC AGCAGCTACCTGAG CCTGACGCCCGAGC AGTGGAAGTCCCAC AGAAGCTACAGCT GCCAGGTCACGCAT GAAGGGAGCACCG TGGAGAAGACAGT GGCCCCTACAGAAT GTTCA (SEQ ID NO: 563)	TCTCCAGAGACAATTCAAAGAACACGCTGTTTCTGCAAATG AACAGCCTGCGAGCCGAGGACACGGCTGTGTATTACTGTGC GAGAGATCGGCTCAATTACTATGAAAGTAGTGGTTATTATCA CTACAAATACTACGGTATGGCCGTCTGGGGCCAAGGGACAA CAGTTACCGTCTCTAGTGCCTCCACCAAGGGCCCATCGGTCT TCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAG CGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCG GTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGT GCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTC CCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA CCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAAC ACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAA AACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGG GGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACA CCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGG TGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCC GTGTGAGGAGCAGTACGGCAGCACGTACCGTTGTGTCAGCG TCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCAT CGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAAC CACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACC AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTA TCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC CGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC GACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGAT GCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTAA GCTTGTCTCCGGGTGGTGGCGGATCGGGAGGTGGCGGATCC CAAGTTCAGTTGGTGGAGTCTGGAGCCGAAGTAGTAAAGCC AGGAGCTTCAGTGAAAGTCTCTTGTAAAGCAAGTGGATTCA CGTTTAGCCGCTTTGCCATGCATTGGGTGCGGCAAGCTCCCG GTCAGGGGTTGGAGTGGATGGGAGTTATTAGCTATGACGGG GGCAATAAGTACTACGCCGAGTCTGTTAAGGGTCGGGTCAC AATGACACGGGACACCTCAACCAGTACACTCTATATGGAAC TGTCTAGCCTGAGATCCGAGGACACCGCTGTGTATTATTGCG CTAGGGGGTACGATGTATTGACGGGTTATCCTGATTACTGGG GGCAGGGGACACTCGTAACCGTCTCCTCAGGAGGCGGAGGA TCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCGATATCCA GCTCACTCAATCGCCATCATTTCTCTCCGCTTCGGTAGGCGA CCGGGTCACGATCACATGCAGGGCGTCGCAAAGCATTGGGA GGTCGTTGCATTGGTATCAGCAGAAACCCGGAAAGTGCCCG AAACTTCTGATCAAATACGCATCACAAAGTTTGAGCGGTGT GCCGTCGCGCTTCTCCGGTTCCGGAAGCGGAACGGAGTTCA CGCTTACAATCTCCTCACTGCAGCCCGAGGATTTCGCGACCT ATTACTGTCACCAGTCATCCAGACTCCCGTTTACTTTTGGCT GTGGGACCAAGGTGGACATTAAGCGT (SEQ ID NO: 586)
iPS:386719	SEQ ID NO: 563	CAGGTGCAGCTGGTGGAATCTGGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCAC CTTCAGTAGCTTTGGCATGCACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCAGTTATATCATTTGATGGAA GTATTAAGTATTCTGTAGACTCCGTGAAGGGCCGATTCACCA TCTCCAGAGACAATTCAAAGAACACGCTGTTTCTGCAAATG

IgG-scFv Molecule Designation	Light Chain Nucleic Acid Sequence	Modified Heavy Chain Nucleic Acid Sequence
		AACAGCCTGCGAGCCGAGGACACGGCTGTGTATTACTGTGC GAGAGATCGGCTCAATTACTATGATAGTAGTGGTTATTATCA CTACAAATACTACGGTATGGCCGTCTGGGGCCAAGGGACAA CAGTTACCGTCTCTAGTGCCTCCACCAAGGGCCCATCGGTCT TCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAG CGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCG GTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGT GCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTC CCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA CCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAAC ACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAA AACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGG GGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACA CCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGG TGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCC GTGTGAGGAGCAGTACGGCAGCACGTACCGTTGTGTCAGCG TCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCAT CGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAAC CACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACC AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTA TCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC CGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC GACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGAT GCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTAA GCTTGTCTCCGGGTGGTGGCGGATCGGGAGGTGGCGGATCC CAAGTTCAGTTGGTGGAGTCTGGAGCCGAAGTAGTAAAGCC AGGAGCTTCAGTGAAAGTCTCTTGTAAAGCAAGTGGATTCA CGTTTAGCCGCTTTGCCATGCATTGGGTGCGGCAAGCTCCCG GTCAGGGGTTGGAGTGGATGGGAGTTATTAGCTATGACGGG GGCAATAAGTACTACGCCGAGTCTGTTAAGGGTCGGGTCAC AATGACACGGGACACCTCAACCAGTACACTCTATATGGAAC TGTCTAGCCTGAGATCCGAGGACACCGCTGTGTATTATTGCG CTAGGGGGTACGATGTATTGACGGGTTATCCTGATTACTGGG GGCAGGGGACACTCGTAACCGTCTCCTCAGGAGGCGGAGGA TCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCGATATCCA GCTCACTCAATCGCCATCATTTCTCTCCGCTTCGGTAGGCGA CCGGGTCACGATCACATGCAGGGCGTCGCAAAGCATTGGGA GGTCGTTGCATTGGTATCAGCAGAAACCCGGAAAGTGCCCG AAACTTCTGATCAAATACGCATCACAAAGTTTGAGCGGTGT GCCGTCGCGCTTCTCCGGTTCCGGAAGCGGAACGGAGTTCA CGCTTACAATCTCCTCACTGCAGCCCGAGGATTTCGCGACCT ATTACTGTCACCAGTCATCCAGACTCCCGTTTACTTTTGGCT GTGGGACCAAGGTGGACATTAAGCGT (SEQ ID NO: 587)
iPS:386713	SEQ ID NO: 563	CAGGTGCAGCTGGTGGAATCTGGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCAC CTTCAGTAGCTTTGGCATGCACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCAGTTATATCATTTGATGGAA GTATTAAGTATTCTGTAGACTCCGTGAAGGGCCGATTCACCA TCTCCAGAGACAATTCAAAGAACACGCTGTTTCTGCAAATG AACAGCCTGCGAGCCGAGGACACGGCTGTGTATTACTGTGC

IgG-scFv Molecule Designation	Light Chain Nucleic Acid Sequence	Modified Heavy Chain Nucleic Acid Sequence
		GAGAGATCGGCTCAATTACTATGAAAGTAGTGGTTATTATCA CTACAAATACTACGGTATGGCCGTCTGGGGCCAAGGGACAA CAGTTACCGTCTCTAGTGCCTCCACCAAGGGCCCATCGGTCT TCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAG CGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCG GTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGT GCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTC CCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA CCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAAC ACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAA AACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGG GGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACA CCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGG TGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCC GTGTGAGGAGCAGTACGGCAGCACGTACCGTTGTGTCAGCG TCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCAT CGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAAC CACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACC AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTA TCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC CGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC GACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGAT GCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTAA GCTTGTCTCCGGGTGGTGGCGGATCGGGAGGTGGCGGATCC CAAGTTCAGTTGGTGGAGTCTGGAGCCGAAGTAGTAAAGCC AGGAGCTTCAGTGAAAGTCTCTTGTAAAGCAAGTGGATTCA CGTTTAGCCGCTTTGCCATGCATTGGGTGCGGCAAGCTCCCG GTCAGGGGTTGGAGTGGATGGGAGTTATTAGCTATGACGGG GGCAATAAGTACTACGCCGAGTCTGTTAAGGGTCGGGTCAC AATGACACGGGACACCTCAACCAGTACACTCTATATGGAAC TGTCTAGCCTGAGATCCGAGGACACCGCTGTGTATTATTGCG CTAGGGGGTACGATGTATTGACGGGTTATCCTGATTACTGGG GGCAGGGGACACTCGTAACCGTCTCCTCAGGAGGCGGAGGA TCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCGATATCCA GCTCACTCAATCGCCATCATTTCTCTCCGCTTCGGTAGGCGA CCGGGTCACGATCACATGCAGGGCGTCGCAAAGCATTGGGA GGTCGTTGCATTGGTATCAGCAGAAACCCGGAAAGGCCCCG AAACTTCTGATCAAATACGCATCACAAAGTTTGAGCGGTGT GCCGTCGCGCTTCTCCGGTTCCGGAAGCGGAACGGAGTTCA CGCTTACAATCTCCTCACTGCAGCCCGAGGATTTCGCGACCT ATTACTGTCACCAGTCATCCAGACTCCCGTTTACTTTTGGCC CTGGGACCAAGGTGGACATTAAGCGT (SEQ ID NO: 588)
iPS:386709	SEQ ID NO: 563	CAGGTGCAGCTGGTGGAATCTGGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCAC CTTCAGTAGCTTTGGCATGCACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCAGTTATATCATTTGATGGAA GTATTAAGTATTCTGTAGACTCCGTGAAGGGCCGATTCACCA TCTCCAGAGACAATTCAAAGAACACGCTGTTTCTGCAAATG AACAGCCTGCGAGCCGAGGACACGGCTGTGTATTACTGTGC GAGAGATCGGCTCAATTACTATGATAGTAGTGGTTATTATCA

IgG-scFv Molecule Designation	Light Chain Nucleic Acid Sequence	Modified Heavy Chain Nucleic Acid Sequence
		CTACAAATACTACGGTATGGCCGTCTGGGGCCAAGGGACAA CAGTTACCGTCTCTAGTGCCTCCACCAAGGGCCCATCGGTCT TCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAG CGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCG GTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGT GCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTC CCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA CCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAAC ACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAA AACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGG GGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACA CCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGG TGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCC GTGTGAGGAGCAGTACGGCAGCACGTACCGTTGTGTCAGCG TCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCAT CGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAAC CACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACC AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTA TCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC CGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC GACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGAT GCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTAA GCTTGTCTCCGGGTGGTGGCGGATCGGGAGGTGGCGGATCC CAAGTTCAGTTGGTGGAGTCTGGAGCCGAAGTAGTAAAGCC AGGAGCTTCAGTGAAAGTCTCTTGTAAAGCAAGTGGATTCA CGTTTAGCCGCTTTGCCATGCATTGGGTGCGGCAAGCTCCCG GTCAGGGGTTGGAGTGGATGGGAGTTATTAGCTATGACGGG GGCAATAAGTACTACGCCGAGTCTGTTAAGGGTCGGGTCAC AATGACACGGGACACCTCAACCAGTACACTCTATATGGAAC TGTCTAGCCTGAGATCCGAGGACACCGCTGTGTATTATTGCG CTAGGGGGTACGATGTATTGACGGGTTATCCTGATTACTGGG GGCAGGGGACACTCGTAACCGTCTCCTCAGGAGGCGGAGGA TCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCGATATCCA GCTCACTCAATCGCCATCATTTCTCTCCGCTTCGGTAGGCGA CCGGGTCACGATCACATGCAGGGCGTCGCAAAGCATTGGGA GGTCGTTGCATTGGTATCAGCAGAAACCCGGAAAGGCCCCG AAACTTCTGATCAAATACGCATCACAAAGTTTGAGCGGTGT GCCGTCGCGCTTCTCCGGTTCCGGAAGCGGAACGGAGTTCA CGCTTACAATCTCCTCACTGCAGCCCGAGGATTTCGCGACCT ATTACTGTCACCAGTCATCCAGACTCCCGTTTACTTTTGGCC CTGGGACCAAGGTGGACATTAAGCGT (SEQ ID NO: 589)
iPS:386727	SEQ ID NO: 563	CAGGTGCAGCTGGTGGAATCTGGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCAC CTTCAGTAGCTTTGGCATGCACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCAGTTATATCATTTGATGGAA GTATTAAGTATTCTGTAGACTCCGTGAAGGGCCGATTCACCA TCTCCAGAGACAATTCAAAGAACACGCTGTTTCTGCAAATG AACAGCCTGCGAGCCGAGGACACGGCTGTGTATTACTGTGC GAGAGATCGGCTCAATTACTATGATAGTAGTGGTTATTATCA CTACAAATACTACGGTATGGCCGTCTGGGGCCAAGGGACAA

IgG-scFv Molecule Designation	Light Chain Nucleic Acid Sequence	Modified Heavy Chain Nucleic Acid Sequence
		CAGTTACCGTCTCTAGTGCCTCCACCAAGGGCCCATCGGTCT TCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAG CGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCG GTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGT GCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTC CCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA CCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAAC ACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAA AACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGG GGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACA CCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGG TGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCC GTGTGAGGAGCAGTACGGCAGCACGTACCGTTGTGTCAGCG TCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCAT CGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAAC CACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACC AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTA TCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC CGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC GACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGAT GCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTAA GCTTGTCTCCGGGTGGTGGCGGATCGGGAGGTGGCGGATCC GATATCCAGCTCACTCAATCGCCATCATTTCTCTCCGCTTCG GTAGGCGACCGGGTCACGATCACATGCAGGGCGTCGCAAAG CATTGGGAGGTCGTTGCATTGGTATCAGCAGAAACCCGGAA AGGCCCCGAAACTTCTGATCAAATACGCATCACAAAGTTTG AGCGGTGTGCCGTCGCGCTTCTCCGGTTCCGGAAGCGGAAC GGAGTTCACGCTTACAATCTCCTCACTGCAGCCCGAGGATTT CGCGACCTATTACTGTCACCAGTCATCCAGACTCCCGTTTAC TTTTGGCCCTGGGACCAAGGTGGACATTAAGCGTGGAGGCG GAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCCAA GTTCAGTTGGTGGAGTCTGGAGCCGAAGTAGTAAAGCCAGG AGCTTCAGTGAAAGTCTCTTGTAAAGCAAGTGGATTCACGTT TAGCCGCTTTGCCATGCATTGGGTGCGGCAAGCTCCCGGTCA GGGGTTGGAGTGGATGGGAGTTATTAGCTATGACGGGGGCA ATAAGTACTACGCCGAGTCTGTTAAGGGTCGGGTCACAATG ACACGGGACACCTCAACCAGTACACTCTATATGGAACTGTCT AGCCTGAGATCCGAGGACACCGCTGTGTATTATTGCGCTAG GGGGTACGATGTATTGACGGGTTATCCTGATTACTGGGGGC AGGGGACACTCGTAACCGTGTCTTCA (SEQ ID NO: 590)
iPS:386721	CAGTCTGTGTTGAC GCAGCCGCCCTCAG TGTCTGCGGCCCCA GGACAGAAGGTCA CCATCTCCTGCTCT GGAAGCAGCTCCA ACATTGGGAATAAT TATGTATCCTGGTA CCAGCAGCTCCCAG GAACAGCCCCCAA	CAGGTGCAGCTGGTGGAATCTGGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCAC CTTCAGTAGCTTTGGCATGCACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCAGTTATATCATTTGATGGAA GTATTAAGTATTCTGTAGACTCCGTGAAGGGCCGATTCACCA TCTCCAGAGACAATTCAAAGAACACGCTGTTTCTGCAAATG AACAGCCTGCGAGCCGAGGACACGGCTGTGTATTACTGTGC GAGAGATCGGCTCAATTACTATGATAGTAGTGGTTATTATCA CTACAAATACTACGGTATGGCCGTCTGGGGCCAAGGGACAA CAGTTACCGTCTCTAGTGCCTCCACCAAGGGCCCATCGGTCT

IgG-scFv Molecule Designation	Light Chain Nucleic Acid Sequence	Modified Heavy Chain Nucleic Acid Sequence
	ACTCCTCATTTATG ACAATAATAAGCG ACCCTCAGGGATTC CTGACCGATTCTCT GGCTCCAAGTCTGG CACGTCAGCCACCC TGGCCATCACCGGA CTCCAGACTGGGGA CGAGGCCGATTATT ACTGCGGAACATG GGATAGCCGCCTGA GTGCTGTGGTTTTC GGCGGAGGGACCA AGCTGACCGTCCTA GGTCAGCCCAAGG CCAACCCCACTGTC ACTCTGTTCCCGCC CTCCTCTGAGGAGC TCCAAGCCAACAA GGCCACACTAGTGT GTCTGATCAGTGAC TTCTACCCGGGAGC TGTGACAGTGGCCT GGAAGGCAGATGG CAGCCCCGTCAAGG CGGGAGTGGAGAC CACCAAACCCTCCA AACAGAGCAACAA CAAGTACGCGGCC AGCAGCTACCTGAG CCTGACGCCCGAGC AGTGGAAGTCCCAC AGAAGCTACAGCT GCCAGGTCACGCAT GAAGGGAGCACCG TGGAGAAGACAGT GGCCCCTACAGAAT GTTCA (SEQ ID NO: 564)	TCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAG CGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCG GTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGT GCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTC CCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA CCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAAC ACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAA AACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGG GGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACA CCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGG TGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCC GTGTGAGGAGCAGTACGGCAGCACGTACCGTTGTGTCAGCG TCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCAT CGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAAC CACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACC AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTA TCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC CGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC GACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGAT GCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTAA GCTTGTCTCCGGGTGGTGGCGGATCGGGAGGTGGCGGATCC CAAGTTCAGTTGGTGGAGTCTGGAGCCGAAGTAGTAAAGCC AGGAGCTTCAGTGAAAGTCTCTTGTAAAGCAAGTGGATTCA CGTTTAGCCGCTTTGCCATGCATTGGGTGCGGCAAGCTCCCG GTCAGGGGTTGGAGTGGATGGGAGTTATTAGCTATGACGGG GGCAATAAGTACTACGCCGAGTCTGTTAAGGGTCGGGTCAC AATGACACGGGACACCTCAACCAGTACACTCTATATGGAAC TGTCTAGCCTGAGATCCGAGGACACCGCTGTGTATTATTGCG CTAGGGGGTACGATGTATTGACGGGTTATCCTGATTACTGGG GGCAGGGGACACTCGTAACCGTCTCCTCAGGAGGCGGAGGA TCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCGATATCCA GCTCACTCAATCGCCATCATTTCTCTCCGCTTCGGTAGGCGA CCGGGTCACGATCACATGCAGGGCGTCGCAAAGCATTGGGA GGTCGTTGCATTGGTATCAGCAGAAACCCGGAAAGTGCCCG AAACTTCTGATCAAATACGCATCACAAAGTTTGAGCGGTGT GCCGTCGCGCTTCTCCGGTTCCGGAAGCGGAACGGAGTTCA CGCTTACAATCTCCTCACTGCAGCCCGAGGATTTCGCGACCT ATTACTGTCACCAGTCATCCAGACTCCCGTTTACTTTTGGCT GTGGGACCAAGGTGGACATTAAGCGT (SEQ ID NO: 591)
iPS:386711	SEQ ID NO: 564	CAGGTGCAGCTGGTGGAATCTGGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCAC CTTCAGTAGCTTTGGCATGCACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCAGTTATATCATTTGATGGAA GTATTAAGTATTCTGTAGACTCCGTGAAGGGCCGATTCACCA TCTCCAGAGACAATTCAAAGAACACGCTGTTTCTGCAAATG AACAGCCTGCGAGCCGAGGACACGGCTGTGTATTACTGTGC GAGAGATCGGCTCAATTACTATGATAGTAGTGGTTATTATCA CTACAAATACTACGGTATGGCCGTCTGGGGCCAAGGGACAA CAGTTACCGTCTCTAGTGCCTCCACCAAGGGCCCATCGGTCT TCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAG

IgG-scFv Molecule Designation	Light Chain Nucleic Acid Sequence	Modified Heavy Chain Nucleic Acid Sequence
		CGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCG GTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGT GCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTC CCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA CCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAAC ACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAA AACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGG GGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACA CCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGG TGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCC GTGTGAGGAGCAGTACGGCAGCACGTACCGTTGTGTCAGCG TCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCAT CGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAAC CACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACC AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTA TCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC CGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC GACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGAT GCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTAA GCTTGTCTCCGGGTGGTGGCGGATCGGGAGGTGGCGGATCC CAAGTTCAGTTGGTGGAGTCTGGAGCCGAAGTAGTAAAGCC AGGAGCTTCAGTGAAAGTCTCTTGTAAAGCAAGTGGATTCA CGTTTAGCCGCTTTGCCATGCATTGGGTGCGGCAAGCTCCCG GTCAGGGGTTGGAGTGGATGGGAGTTATTAGCTATGACGGG GGCAATAAGTACTACGCCGAGTCTGTTAAGGGTCGGGTCAC AATGACACGGGACACCTCAACCAGTACACTCTATATGGAAC TGTCTAGCCTGAGATCCGAGGACACCGCTGTGTATTATTGCG CTAGGGGGTACGATGTATTGACGGGTTATCCTGATTACTGGG GGCAGGGGACACTCGTAACCGTCTCCTCAGGAGGCGGAGGA TCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCGATATCCA GCTCACTCAATCGCCATCATTTCTCTCCGCTTCGGTAGGCGA CCGGGTCACGATCACATGCAGGGCGTCGCAAAGCATTGGGA GGTCGTTGCATTGGTATCAGCAGAAACCCGGAAAGGCCCCG AAACTTCTGATCAAATACGCATCACAAAGTTTGAGCGGTGT GCCGTCGCGCTTCTCCGGTTCCGGAAGCGGAACGGAGTTCA CGCTTACAATCTCCTCACTGCAGCCCGAGGATTTCGCGACCT ATTACTGTCACCAGTCATCCAGACTCCCGTTTACTTTTGGCC CTGGGACCAAGGTGGACATTAAGCGT (SEQ ID NO: 592)
iPS:386733	SEQ ID NO: 564	CAGGTGCAGCTGGTGGAATCTGGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCAC CTTCAGTAGCTTTGGCATGCACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCAGTTATATCATTTGATGGAA GTATTAAGTATTCTGTAGACTCCGTGAAGGGCCGATTCACCA TCTCCAGAGACAATTCAAAGAACACGCTGTTTCTGCAAATG AACAGCCTGCGAGCCGAGGACACGGCTGTGTATTACTGTGC GAGAGATCGGCTCAATTACTATGAAAGTAGTGGTTATTATCA CTACAAATACTACGGTATGGCCGTCTGGGGCCAAGGGACAA CAGTTACCGTCTCTAGTGCCTCCACCAAGGGCCCATCGGTCT TCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAG CGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCG

IgG-scFv Molecule Designation	Light Chain Nucleic Acid Sequence	Modified Heavy Chain Nucleic Acid Sequence
		GTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGT GCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTC CCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA CCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAAC ACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAA AACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGG GGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACA CCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGG TGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCC GTGTGAGGAGCAGTACGGCAGCACGTACCGTTGTGTCAGCG TCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCAT CGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAAC CACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACC AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTA TCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC CGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC GACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGAT GCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTAA GCTTGTCTCCGGGTGGTGGCGGATCGGGAGGTGGCGGATCC GATATCCAGCTCACTCAATCGCCATCATTTCTCTCCGCTTCG GTAGGCGACCGGGTCACGATCACATGCAGGGCGTCGCAAAG CATTGGGAGGTCGTTGCATTGGTATCAGCAGAAACCCGGAA AGGCCCCGAAACTTCTGATCAAATACGCATCACAAAGTTTG AGCGGTGTGCCGTCGCGCTTCTCCGGTTCCGGAAGCGGAAC GGAGTTCACGCTTACAATCTCCTCACTGCAGCCCGAGGATTT CGCGACCTATTACTGTCACCAGTCATCCAGACTCCCGTTTAC TTTTGGCCCTGGGACCAAGGTGGACATTAAGCGTGGAGGCG GAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCCAA GTTCAGTTGGTGGAGTCTGGAGCCGAAGTAGTAAAGCCAGG AGCTTCAGTGAAAGTCTCTTGTAAAGCAAGTGGATTCACGTT TAGCCGCTTTGCCATGCATTGGGTGCGGCAAGCTCCCGGTCA GGGGTTGGAGTGGATGGGAGTTATTAGCTATGACGGGGGCA ATAAGTACTACGCCGAGTCTGTTAAGGGTCGGGTCACAATG ACACGGGACACCTCAACCAGTACACTCTATATGGAACTGTCT AGCCTGAGATCCGAGGACACCGCTGTGTATTATTGCGCTAG GGGGTACGATGTATTGACGGGTTATCCTGATTACTGGGGGC AGGGGACACTCGTAACCGTGTCTTCA (SEQ ID NO: 593)
iPS:386729	SEQ ID NO: 564	CAGGTGCAGCTGGTGGAATCTGGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCAC CTTCAGTAGCTTTGGCATGCACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCAGTTATATCATTTGATGGAA GTATTAAGTATTCTGTAGACTCCGTGAAGGGCCGATTCACCA TCTCCAGAGACAATTCAAAGAACACGCTGTTTCTGCAAATG AACAGCCTGCGAGCCGAGGACACGGCTGTGTATTACTGTGC GAGAGATCGGCTCAATTACTATGATAGTAGTGGTTATTATCA CTACAAATACTACGGTATGGCCGTCTGGGGCCAAGGGACAA CAGTTACCGTCTCTAGTGCCTCCACCAAGGGCCCATCGGTCT TCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAG CGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCG GTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGT

IgG-scFv Molecule Designation	Light Chain Nucleic Acid Sequence	Modified Heavy Chain Nucleic Acid Sequence
		GCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTC CCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA CCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAAC ACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAA AACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGG GGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACA CCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGG TGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCC GTGTGAGGAGCAGTACGGCAGCACGTACCGTTGTGTCAGCG TCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCAT CGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAAC CACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACC AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTA TCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC CGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC GACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGAT GCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTAA GCTTGTCTCCGGGTGGTGGCGGATCGGGAGGTGGCGGATCC GATATCCAGCTCACTCAATCGCCATCATTTCTCTCCGCTTCG GTAGGCGACCGGGTCACGATCACATGCAGGGCGTCGCAAAG CATTGGGAGGTCGTTGCATTGGTATCAGCAGAAACCCGGAA AGGCCCCGAAACTTCTGATCAAATACGCATCACAAAGTTTG AGCGGTGTGCCGTCGCGCTTCTCCGGTTCCGGAAGCGGAAC GGAGTTCACGCTTACAATCTCCTCACTGCAGCCCGAGGATTT CGCGACCTATTACTGTCACCAGTCATCCAGACTCCCGTTTAC TTTTGGCCCTGGGACCAAGGTGGACATTAAGCGTGGAGGCG GAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCCAA GTTCAGTTGGTGGAGTCTGGAGCCGAAGTAGTAAAGCCAGG AGCTTCAGTGAAAGTCTCTTGTAAAGCAAGTGGATTCACGTT TAGCCGCTTTGCCATGCATTGGGTGCGGCAAGCTCCCGGTCA GGGGTTGGAGTGGATGGGAGTTATTAGCTATGACGGGGGCA ATAAGTACTACGCCGAGTCTGTTAAGGGTCGGGTCACAATG ACACGGGACACCTCAACCAGTACACTCTATATGGAACTGTCT AGCCTGAGATCCGAGGACACCGCTGTGTATTATTGCGCTAG GGGGTACGATGTATTGACGGGTTATCCTGATTACTGGGGGC AGGGGACACTCGTAACCGTGTCTTCA (SEQ ID NO: 594)

[0168] Nucleic acid sequences encoding the three components (e.g., light chains, modified heavy chains, and second polypeptides comprising the other half of the carboxyl-terminal Fab domains) of exemplary bispecific antigen binding proteins of the invention in the IgG-Fab format are listed in Table 14. In such embodiments, the isolated nucleic acid encoding the light chain of the IgG-Fab molecules may comprise a nucleotide sequence that is at least 80% identical, at least 90% identical, at least 95% identical, or at least 98% identical to any of the light chain nucleotide sequences listed in Table 14. For instance, in some embodiments, the isolated nucleic acid

encoding the light chain of the IgG-Fab molecules comprises a sequence selected from SEQ ID NOs: 225, 287, 595, and 596. In related embodiments, the isolated nucleic acid encoding the modified heavy chain of the IgG-Fab molecules may comprise a nucleotide sequence that is at least 80% identical, at least 90% identical, at least 95% identical, or at least 98% identical to any of the modified heavy chain nucleotide sequences listed in Table 14. In certain embodiments, the isolated nucleic acid encoding the modified heavy chain of the IgG-Fab molecules comprises a sequence selected from SEQ ID NOs: 597 to 620. In these and other embodiments, the isolated nucleic acid encoding the second polypeptide of the IgG-Fab molecules, which comprises the other half of the carboxyl-terminal Fab domain (e.g. a Fd fragment or second light chain), may comprise a nucleotide sequence that is at least 80% identical, at least 90% identical, at least 95% identical, or at least 98% identical to any of the second polypeptide nucleotide sequences listed in Table 14. In some embodiments, the isolated nucleic acid encoding the second polypeptide of the IgG-Fab molecules comprises a sequence selected from SEQ ID NOs: 621 to 632.

Table 14. Nucleic Acid Sequences of Exemplary Bispecific Antigen Binding Proteins in the IgG-Fab Format

IgG-Fab Molecule Designation	Light Chain Nucleic Acid Sequence	Modified Heavy Chain Nucleic Acid Sequence	Second Polypeptide Nucleic Acid Sequence
Anti-PAC1 Receptor IgG x Anti-CGRP Receptor Fab			
iPS:392513	GATATCCAG CTCACTCAA TCGCCATCA TTTCTCTCCG CTTCGGTAG GCGACCGGG TCACGATCA CATGCAGGG CGTCGCAAA GCATTGGGA GGTCGTTGC ATTGGTATC AGCAGAAAC CCGGAAAGG CCCCGAAAC TTCTGATCA AATACGCAT CACAAAGCT TGAGCGGTG TGCCGTCGC GCTTCTCCG GTTCCGGAA	CAAGTTCAGTTGGTGGAGTCTGGAGCCGAAGTAG TAAAGCCAGGAGCTTCAGTGAAAGTCTCTTGTAA AGCAAGTGGATTCACGTTTAGCCGCTTTGCCATGC ATTGGGTGCGGCAAGCTCCCGGTCAGGGGTTGGA GTGGATGGGAGTTATTAGCTATGACGGGGGCAAT AAGTACTACGCCGAGTCTGTTAAGGGTCGGGTCA CAATGACACGGGACACCTCAACCAGTACACTCTA TATGGAACTGTCTAGCCTGAGATCCGAGGACACC GCTGTGTATTATTGCGCTAGGGGGTACGATGTATT GACGGGTTATCCTGATTACTGGGGGCAGGGGACA CTCGTAACCGTCTCTAGTGCCTCCACCAAGGGCCC ATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCA CCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGT CAAGGACTACTTCCCCGAACCGGTGACGGTGTCG TGGAACTCAGGCGCCCTGACCAGCGGCGTGCACA CCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTAC TCCCTCAAAAGCGTGGTGACCGTGCCCTCCAGCA GCTTGGGCACCCAGACCTACATCTGCAACGTGAA TCACAAGCCCAGCAACACCAAGGTGGACAAGAA AGTTGAGCCCAAATCTTGTGACAAAACTCACACA TGCCCACCGTGCCCAGCACCTGAACTCCTGGGGG GACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG	CAGGTGCAGCTG GTGGAATCTGGG GGAGGCGTGGTC CAGCCTGGGAGG TCCCTGAGACTCT CCTGTGCAGCCTC TGGATTCACCTTC AGTAGCTTTGGC ATGCACTGGGTC CGCCAGGCTCCA GGCAAGGGGCTG GAGTGGGTGGCA GTTATATCATTTG ATGGAAGTATTA AGTATTCTGTAGA CTCCGTGAAGGG CCGATTCACCATC TCCAGAGACAAT TCAAAGAACACG CTGTTTCTGCAAA TGAACAGCCTGC GAGCCGAGGACA

IgG-Fab Molecule Designation	Light Chain Nucleic Acid Sequence	Modified Heavy Chain Nucleic Acid Sequence	Second Polypeptide Nucleic Acid Sequence
	GCGGAACGG AATTCACGC TTACAATCT CCTCACTGC AGCCCGAGG ATTTCGCGA CCTATTACT GTCACCAGT CATCCAGAC TCCCGTTTAC TTTTGGCCCT GGGACCAAG GTGGACATT AAGCGTACG GTGGCTGCA CCATCTGTCT TCATCTTCCC GCCATCTGA TGAGCAGTT GAAATCTGG AACTGCCTC TGTTGTGTG CCTGCTGAA TAACTTCTAT CCCAGAGAG GCCAAAGTA CAGTGGAAG GTGGATAAC GCCCTCCAA TCGGGTAAC TCCCAGGAG AGTGTCACA GAGCAGGAC AGCAAGGAC AGCACCTAC AGCCTCGAG AGCACCCTG ACGCTGAGC AAAGCAGAC TACGAGAAA CACAAAGTC TACGCCTGC GAAGTCACC CATCAGGGC CTGAGCTCG CCCGTCACA AAGAGCTTC AACAGGGGA GAGTGT (SEQ ID NO: 225)	GACACCCTCATGATCTCCCGGACCCCTGAGGTCA CATGCGTGGTGGTGGACGTGAGCCACGAAGACCC TGAGGTCAAGTTCAACTGGTACGTGGACGGCGTG GAGGTGCATAATGCCAAGACAAAGCCGTGTGAGG AGCAGTACGGCAGCACGTACCGTTGTGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGGC AAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC TCCCAGCCCCCATCGAGAAAACCATCTCCAAAGC CAAAGGGCAGCCCCGAGAACCACAGGTGTACACC CTGCCCCCATCCCGGGAGGAGATGACCAAGAACC AGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTA TCCCAGCGACATCGCCGTGGAGTGGGAGAGCAAT GGGCAGCCGGAGAACAACTACAAGACCACGCCTC CCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTAT AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCATG AGGCTCTGCACAACCACTACACGCAGAAGAGCCT AAGCTTGTCTCCGGGTGGTGGCGGATCGGGAGGT GGCGGATCCCAGTCTGTGTTGACGCAGCCGCCCT CAGTGTCTGCGGCCCCAGGACAGAAGGTCACCAT CTCCTGCTCTGGAAGCAGCTCCAACATTGGGAAT AATTATGTATCCTGGTACCAGCAGCTCCCAGGAA CAGCCCCCAAACTCCTCATTTATGACAATAATAA GCGACCCTCAGGGATTCCTGACCGATTCTCTGGCT CCAAGTCTGGCACGTCAACCACCCTGGGCATCAC CGGACTCCAGACTGGGGACGAGGCCGATTATTAC TGCGGAACATGGGATAGCCGCCTGAGTGCTGTGG TTTTCGGCGGAGGGACCAAGCTGACCGTCCTAGC TAGTACAAAGGGCCCCTCCGTCTTTCCACTCGCAC CCAGTTCAAAGTCCACTTCTGGAGGCACTGCGGC CTTGGGCTGTTTGGTGAAAGACTACTTCCCAGAG CCAGTGACAGTCTCTTGGAATAGCGGAGCACTGA CCAGCGGTGTGCATACCTTTCCAGCTGTGCTGCAG AGCAGCGGCCTCTACTCACTGAAGAGTGTCGTCA CCGTTCCCTCTTCCAGCCTCGGCACTCAAACTTAC ATCTGCAACGTGAATCATAAGCCATCTAACACCA AGGTAGACAAGAAAGTC (SEQ ID NO: 597)	CGGCTGTGTATTA CTGTGCGAGAGA TCGGCTCAATTAC TATGATAGTAGT GGTTATTATCACT ACAAATACTACG GTATGGCCGTCTG GGGCCAAGGAAC AACAGTTACCGT CTCTAGTGGTCAG CCCAAGGCCAAC CCCACTGTCACTC TGTTCCCGCCCTC CTCTGAGGAGCT CCAAGCCAACAA GGCCACACTAGT GTGTCTGATCAGT GACTTCTACCCGG GAGCTGTGACAG TGGCCTGGAAGG CAGATGGCAGCC CCGTCAAGGCGG GAGTGGAGACCA CCAAACCCTCCA AACAGAGCAACA ACAAGTACGCGG CCGAAAGCTACC TGAGCCTGACGC CCGAGCAGTGGA AGTCCCACAGAA GCTACAGCTGCC AGGTCACGCATG AAGGGAGCACCG TGGAGAAGACAG TGGCCCCTACAG AATGTTCA (SEQ ID NO: 621)
iPS:392514	SEQ ID NO: 225	CAAGTTCAGTTGGTGGAGTCTGGAGCCGAAGTAG TAAAGCCAGGAGCTTCAGTGAAAGTCTCTTGTAA	CAGGTGCAGCTG GTGGAATCTGGG

IgG-Fab Molecule Designation	Light Chain Nucleic Acid Sequence	Modified Heavy Chain Nucleic Acid Sequence	Second Polypeptide Nucleic Acid Sequence
		AGCAAGTGGATTCACGTTTAGCCGCTTTGCCATGC	GGAGGCGTGGTC
		ATTGGGTGCGGCAAGCTCCCGGTCAGGGGTTGGA	CAGCCTGGGAGG
		GTGGATGGGAGTTATTAGCTATGACGGGGGCAAT	TCCCTGAGACTCT
		AAGTACTACGCCGAGTCTGTTAAGGGTCGGGTCA	CCTGTGCAGCCTC
		CAATGACACGGGACACCTCAACCAGTACACTCTA	TGGATTCACCTTC
		TATGGAACTGTCTAGCCTGAGATCCGAGGACACC	AGTAGCTTTGGC
		GCTGTGTATTATTGCGCTAGGGGGTACGATGTATT	ATGCACTGGGTC
		GACGGGTTATCCTGATTACTGGGGGCAGGGGACA	CGCGAGGCTCCA
		CTCGTAACCGTCTCTAGTGCCTCCACCAAGGGCCC	GGCAAGGGGCTG
		ATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCA	GAGTGGGTGGCA
		CCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGT	GTTATATCATTTG
		CAAGGACTACTTCCCCGAACCGGTGACGGTGTCG	ATGGAAGTATTA
		TGGAACTCAGGCGCCCTGACCAGCGGCGTGCACA	AGTATTCTGTAGA
		CCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTAC	CTCCGTGAAGGG
		TCCCTCAAAAGCGTGGTGACCGTGCCCTCCAGCA	CCGATTCACCATC
		GCTTGGGCACCCAGACCTACATCTGCAACGTGAA	TCCAGAGACAAT
		TCACAAGCCCAGCAACACCAAGGTGGACAAGAA	TCAAAGAACACG
		AGTTGAGCCCAAATCTTGTGACAAAACTCACACA	CTGTTTCTGCAAA
		TGCCCACCGTGCCCAGCACCTGAACTCCTGGGGG	TGAACAGCCTGC
		GACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG	GAGCCGAGGACA
		GACACCCTCATGATCTCCCGGACCCCTGAGGTCA	CGGCTGTGTATTA
		CATGCGTGGTGGTGGACGTGAGCCACGAAGACCC	CTGTGCGAGAGA
		TGAGGTCAAGTTCAACTGGTACGTGGACGGCGTG	TCGGCTCAATTAC
		GAGGTGCATAATGCCAAGACAAAGCCGTGTGAGG	TATGATAGTAGT
		AGCAGTACGGCAGCACGTACCGTTGTGTCAGCGT	GGTTATTATCACT
		CCTCACCGTCCTGCACCAGGACTGGCTGAATGGC	ACAAATACTACG
		AAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC	GTATGGCCGTCTG
		TCCCAGCCCCCATCGAGAAAACCATCTCCAAAGC	GGGCCAAGGAAC
		CAAAGGGCAGCCCCGAGAACCACAGGTGTACACC	AACAGTTACCGT
		CTGCCCCCATCCCGGGAGGAGATGACCAAGAACC	CTCTAGTGGTCAG
		AGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTA	CCCAAGGCCAAC
		TCCCAGCGACATCGCCGTGGAGTGGGAGAGCAAT	CCCACTGTCACTC
		GGGCAGCCGGAGAACAACTACAAGACCACGCCTC	TGTTCCCGCCCTC
		CCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTAT	CTCTGAGGAGCT
		AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG	CCAAGCCAACAA
		CAGGGGAACGTCTTCTCATGCTCCGTGATGCATG	GGCCACACTAGT
		AGGCTCTGCACAACCACTACACGCAGAAGAGCCT	GTGTCTGATCAGT
		AAGCTTGTCTCCGGGTGGTGGCGGATCGGGAGGT	GACTTCTACCCGG
		GGCGGATCCCAGTCTGTGTTGACGCAGCCGCCCT	GAGCTGTGACAG
		CAGTGTCTGCGGCCCCAGGACAGAAGGTCACCAT	TGGCCTGGAAGG
		CTCCTGCTCTGGAAGCAGCTCCAACATTGGGAAT	CAGATGGCAGCC
		AATTATGTATCCTGGTACCAGAAGCTCCCAGGAA	CCGTCAAGGCGG
		CAGCCCCCAAACTCCTCATTTATGACAATAATAA	GAGTGGAGACCA
		GCGACCCTCAGGGATTCCTGACCGATTCTCTGGCT	CCAAACCCTCCA
		CCAAGTCTGGCACGTCAACCACCCTGGGCATCAC	AACAGAGCAACA
		CGGACTCCAGACTGGGGACGAGGCCGATTATTAC	ACAAGTACGCGG
		TGCGGAACATGGGATAGCCGCCTGAGTGCTGTGG	CCGAAAGCTACC
		TTTTCGGCGGAGGGACCAAGCTGACCGTCCTAGC	TGAGCCTGACGC
		TAGTACAAAGGGCCCCTCCGTCTTTCCACTCGCAC	CCGAGCAGTGGA
		CCAGTTCAAAGTCCACTTCTGGAGGCACTGCGGC	AGTCCCACAGAA
		CTTGGGCTGTTTGGTGAAAGACTACTTCCCAGAG	GCTACAGCTGCC
		CCAGTGACAGTCTCTTGGAATAGCGGAGCACTGA	AGGTCACGCATG
		CCAGCGGTGTGCATACCTTTCCAGCTGTGCTGCAG	AAGGGAGCACCG

IgG-Fab Molecule Designation	Light Chain Nucleic Acid Sequence	Modified Heavy Chain Nucleic Acid Sequence	Second Polypeptide Nucleic Acid Sequence
		AGCAGCGGCCTCTACTCACTGAAGAGTGTCGTCA CCGTTCCCTCTTCCAGCCTCGGCACTCAAACTTAC ATCTGCAACGTGAATCATAAGCCATCTAACACCA AGGTAGACAAGAAAGTC (SEQ ID NO: 598)	TGGAGAAGACAG TGGCCCCTACAG AATGTTCA (SEQ ID NO: 622)
iPS:392475	SEQ ID NO: 225	CAAGTTCAGTTGGTGGAGTCTGGAGCCGAAGTAG TAAAGCCAGGAGCTTCAGTGAAAGTCTCTTGTAA AGCAAGTGGATTCACGTTTAGCCGCTTTGCCATGC ATTGGGTGCGGCAAGCTCCCGGTCAGGGGTTGGA GTGGATGGGAGTTATTAGCTATGACGGGGGCAAT AAGTACTACGCCGAGTCTGTTAAGGGTCGGGTCA CAATGACACGGGACACCTCAACCAGTACACTCTA TATGGAACTGTCTAGCCTGAGATCCGAGGACACC GCTGTGTATTATTGCGCTAGGGGGTACGATGTATT GACGGGTTATCCTGATTACTGGGGGCAGGGGACA CTCGTAACCGTCTCTAGTGCCTCCACCAAGGGCCC ATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCA CCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGT CAAGGACTACTTCCCCGAACCGGTGACGGTGTCG TGGAACTCAGGCGCCCTGACCAGCGGCGTGCACA CCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTAC TCCCTCAAAAGCGTGGTGACCGTGCCCTCCAGCA GCTTGGGCACCCAGACCTACATCTGCAACGTGAA TCACAAGCCCAGCAACACCAAGGTGGACAAGAA AGTTGAGCCCAAATCTTGTGACAAAACTCACACA TGCCCACCGTGCCCAGCACCTGAACTCCTGGGGG GACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG GACACCCTCATGATCTCCCGGACCCCTGAGGTCA CATGCGTGGTGGTGGACGTGAGCCACGAAGACCC TGAGGTCAAGTTCAACTGGTACGTGGACGGCGTG GAGGTGCATAATGCCAAGACAAAGCCGTGTGAGG AGCAGTACGGCAGCACGTACCGTTGTGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGGC AAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC TCCCAGCCCCCATCGAGAAAACCATCTCCAAAGC CAAAGGGCAGCCCCGAGAACCACAGGTGTACACC CTGCCCCCATCCCGGGAGGAGATGACCAAGAACC AGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTA TCCCAGCGACATCGCCGTGGAGTGGGAGAGCAAT GGGCAGCCGGAGAACAACTACAAGACCACGCCTC CCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTAT AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCATG AGGCTCTGCACAACCACTACACGCAGAAGAGCCT AAGCTTGTCTCCGGGTGGTGGCGGATCGGGAGGT GGCGGATCCCAGTCTGTGTTGACGCAGCCGCCCT CAGTGTCTGCGGCCCCAGGACAGAAGGTCACCAT CTCCTGCTCTGGAAGCAGCTCCAACATTGGGAAT AATTATGTATCCTGGTACCAGCAGCTCCCAGGAA CAGCCCCCAAACTCCTCATTTATGACAATAATAA GCGACCCTCAGGGATTCCTGACCGATTCTCTGGCT CCAAGTCTGGCACGTCAACCACCCTGGGCATCAC CGGACTCCAGACTGGGGACGAGGCCGATTATTAC TGCGGAACATGGGATAGCCGCCTGAGTGCTGTGG	CAGGTGCAGCTG GTGGAATCTGGG GGAGGCGTGGTC CAGCCTGGGAGG TCCCTGAGACTCT CCTGTGCAGCCTC TGGATTCACCTTC AGTAGCTTTGGC ATGCACTGGGTC CGCCAGGCTCCA GGCAAGGGGCTG GAGTGGGTGGCA GTTATATCATTTG ATGGAAGTATTA AGTATTCTGTAGA CTCCGTGAAGGG CCGATTCACCATC TCCAGAGACAAT TCAAAGAACACG CTGTTTCTGCAAA TGAACAGCCTGC GAGCCGAGGACA CGGCTGTGTATTA CTGTGCGAGAGA TCGGCTCAATTAC TATGAAAGTAGT GGTTATTATCACT ACAAATACTACG GTATGGCCGTCTG GGGCCAAGGAAC AACAGTTACCGT CTCTAGTGGTCAG CCCAAGGCCAAC CCCACTGTCACTC TGTTCCCGCCCTC CTCTGAGGAGCT CCAAGCCAACAA GGCCACACTAGT GTGTCTGATCAGT GACTTCTACCCGG GAGCTGTGACAG TGGCCTGGAAGG CAGATGGCAGCC CCGTCAAGGCGG GAGTGGAGACCA CCAAACCCTCCA AACAGAGCAACA ACAAGTACGCGG CCGAAAGCTACC

IgG-Fab Molecule Designation	Light Chain Nucleic Acid Sequence	Modified Heavy Chain Nucleic Acid Sequence	Second Polypeptide Nucleic Acid Sequence
		TTTTCGGCGGAGGGACCAAGCTGACCGTCCTAGC TAGTACAAAGGGCCCCTCCGTCTTTCCACTCGCAC CCAGTTCAAAGTCCACTTCTGGAGGCACTGCGGC CTTGGGCTGTTTGGTGAAAGACTACTTCCCAGAG CCAGTGACAGTCTCTTGGAATAGCGGAGCACTGA CCAGCGGTGTGCATACCTTTCCAGCTGTGCTGCAG AGCAGCGGCCTCTACTCACTGAAGAGTGTCGTCA CCGTTCCCTCTTCCAGCCTCGGCACTCAAACTTAC ATCTGCAACGTGAATCATAAGCCATCTAACACCA AGGTAGACAAGAAAGTC (SEQ ID NO: 599)	TGAGCCTGACGC CCGAGCAGTGGA AGTCCCACAGAA GCTACAGCTGCC AGGTCACGCATG AAGGGAGCACCG TGGAGAAGACAG TGGCCCCTACAG AATGTTCA (SEQ ID NO: 623)
iPS:392519	SEQ ID NO: 225	CAAGTTCAGTTGGTGGAGTCTGGAGCCGAAGTAG TAAAGCCAGGAGCTTCAGTGAAAGTCTCTTGTAA AGCAAGTGGATTCACGTTTAGCCGCTTTGCCATGC ATTGGGTGCGGCAAGCTCCCGGTCAGGGGTTGGA GTGGATGGGAGTTATTAGCTATGACGGGGGCAAT AAGTACTACGCCGAGTCTGTTAAGGGTCGGGTCA CAATGACACGGGACACCTCAACCAGTACACTCTA TATGGAACTGTCTAGCCTGAGATCCGAGGACACC GCTGTGTATTATTGCGCTAGGGGGTACGATGTATT GACGGGTTATCCTGATTACTGGGGGCAGGGGACA CTCGTAACCGTCTCTAGTGCCTCCACCAAGGGCCC ATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCA CCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGT CAAGGACTACTTCCCCGAACCGGTGACGGTGTCG TGGAACTCAGGCGCCCTGACCAGCGGCGTGCACA CCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTAC TCCCTCAAAAGCGTGGTGACCGTGCCCTCCAGCA GCTTGGGCACCCAGACCTACATCTGCAACGTGAA TCACAAGCCCAGCAACACCAAGGTGGACAAGAA AGTTGAGCCCAAATCTTGTGACAAAACTCACACA TGCCCACCGTGCCCAGCACCTGAACTCCTGGGGG GACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG GACACCCTCATGATCTCCCGGACCCCTGAGGTCA CATGCGTGGTGGTGGACGTGAGCCACGAAGACCC TGAGGTCAAGTTCAACTGGTACGTGGACGGCGTG GAGGTGCATAATGCCAAGACAAAGCCGTGTGAGG AGCAGTACGGCAGCACGTACCGTTGTGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGGC AAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC TCCCAGCCCCCATCGAGAAAACCATCTCCAAAGC CAAAGGGCAGCCCCGAGAACCACAGGTGTACACC CTGCCCCCATCCCGGGAGGAGATGACCAAGAACC AGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTA TCCCAGCGACATCGCCGTGGAGTGGGAGAGCAAT GGGCAGCCGGAGAACAACTACAAGACCACGCCTC CCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTAT AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCATG AGGCTCTGCACAACCACTACACGCAGAAGAGCCT AAGCTTGTCTCCGGGTGGTGGCGGATCGGGAGGT GGCGGATCCCAGTCTGTGTTGACGCAGCCGCCCT CAGTGTCTGCGGCCCCAGGACAGAAGGTCACCAT CTCCTGCTCTGGAAGCAGCTCCAACATTGGGAAT	CAGGTGCAGCTG GTGGAATCTGGG GGAGGCGTGGTC CAGCCTGGGAGG TCCCTGAGACTCT CCTGTGCAGCCTC TGGATTCACCTTC AGTAGCTTTGGC ATGCACTGGGTC CGCGAGGCTCCA GGCAAGGGGCTG GAGTGGGTGGCA GTTATATCATTTG ATGGAAGTATTA AGTATTCTGTAGA CTCCGTGAAGGG CCGATTCACCATC TCCAGAGACAAT TCAAAGAACACG CTGTTTCTGCAAA TGAACAGCCTGC GAGCCGAGGACA CGGCTGTGTATTA CTGTGCGAGAGA TCGGCTCAATTAC TATGAAAGTAGT GGTTATTATCACT ACAAATACTACG GTATGGCCGTCTG GGGCCAAGGAAC AACAGTTACCGT CTCTAGTGGTCAG CCCAAGGCCAAC CCCACTGTCACTC TGTTCCCGCCCTC CTCTGAGGAGCT CCAAGCCAACAA GGCCACACTAGT GTGTCTGATCAGT GACTTCTACCCGG GAGCTGTGACAG TGGCCTGGAAGG CAGATGGCAGCC

IgG-Fab Molecule Designation	Light Chain Nucleic Acid Sequence	Modified Heavy Chain Nucleic Acid Sequence	Second Polypeptide Nucleic Acid Sequence
		AATTATGTATCCTGGTACCAGAAGCTCCCAGGAA CAGCCCCCAAACTCCTCATTTATGACAATAATAA GCGACCCTCAGGGATTCCTGACCGATTCTCTGGCT CCAAGTCTGGCACGTCAACCACCCTGGGCATCAC CGGACTCCAGACTGGGGACGAGGCCGATTATTAC TGCGGAACATGGGATAGCCGCCTGAGTGCTGTGG TTTTCGGCGGAGGGACCAAGCTGACCGTCCTAGC TAGTACAAAGGGCCCCTCCGTCTTTCCACTCGCAC CCAGTTCAAAGTCCACTTCTGGAGGCACTGCGGC CTTGGGCTGTTTGGTGAAAGACTACTTCCCAGAG CCAGTGACAGTCTCTTGGAATAGCGGAGCACTGA CCAGCGGTGTGCATACCTTTCCAGCTGTGCTGCAG AGCAGCGGCCTCTACTCACTGAAGAGTGTCGTCA CCGTTCCCTCTTCCAGCCTCGGCACTCAAACTTAC ATCTGCAACGTGAATCATAAGCCATCTAACACCA AGGTAGACAAGAAAGTC (SEQ ID NO: 600)	CCGTCAAGGCGG GAGTGGAGACCA CCAAACCCTCCA AACAGAGCAACA ACAAGTACGCGG CCGAAAGCTACC TGAGCCTGACGC CCGAGCAGTGGA AGTCCCACAGAA GCTACAGCTGCC AGGTCACGCATG AAGGGAGCACCG TGGAGAAGACAG TGGCCCCTACAG AATGTTCA (SEQ ID NO: 624)
iPS:392515	SEQ ID NO: 225	CAAGTTCAGTTGGTGGAGTCTGGAGCCGAAGTAG TAAAGCCAGGAGCTTCAGTGAAAGTCTCTTGTAA AGCAAGTGGATTCACGTTTAGCCGCTTTGCCATGC ATTGGGTGCGGCAAGCTCCCGGTCAGGGGTTGGA GTGGATGGGAGTTATTAGCTATGACGGGGGCAAT AAGTACTACGCCGAGTCTGTTAAGGGTCGGGTCA CAATGACACGGGACACCTCAACCAGTACACTCTA TATGGAACTGTCTAGCCTGAGATCCGAGGACACC GCTGTGTATTATTGCGCTAGGGGGTACGATGTATT GACGGGTTATCCTGATTACTGGGGGCAGGGGACA CTCGTAACCGTCTCTAGTGCCTCCACCAAGGGCCC ATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCA CCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGT CAAGGACTACTTCCCCGAACCGGTGACGGTGTCG TGGAACTCAGGCGCCCTGACCAGCGGCGTGCACA CCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTAC TCCCTCAAAAGCGTGGTGACCGTGCCCTCCAGCA GCTTGGGCACCCAGACCTACATCTGCAACGTGAA TCACAAGCCCAGCAACACCAAGGTGGACAAGAA AGTTGAGCCCAAATCTTGTGACAAAACTCACACA TGCCCACCGTGCCCAGCACCTGAACTCCTGGGGG GACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG GACACCCTCATGATCTCCCGGACCCCTGAGGTCA CATGCGTGGTGGTGGACGTGAGCCACGAAGACCC TGAGGTCAAGTTCAACTGGTACGTGGACGGCGTG GAGGTGCATAATGCCAAGACAAAGCCGTGTGAGG AGCAGTACGGCAGCACGTACCGTTGTGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGGC AAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC TCCCAGCCCCCATCGAGAAAACCATCTCCAAAGC CAAAGGGCAGCCCCGAGAACCACAGGTGTACACC CTGCCCCCATCCCGGGAGGAGATGACCAAGAACC AGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTA TCCCAGCGACATCGCCGTGGAGTGGGAGAGCAAT GGGCAGCCGGAGAACAACTACAAGACCACGCCTC CCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTAT AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG	CAGGTGCAGCTG GTGGAATCTGGG GGAGGCGTGGTC CAGCCTGGGAGG TCCCTGAGACTCT CCTGTGCAGCCTC TGGATTCACCTTC AGTAGCTTTGGC ATGCACTGGGTC CGCCAGGCTCCA GGCAAGGGGCTG GAGTGGGTGGCA GTTATATCATTTG ATGGAAGTATTA AGTATTCTGTAGA CTCCGTGAAGGG CCGATTCACCATC TCCAGAGACAAT TCAAAGAACACG CTGTTTCTGCAAA TGAACAGCCTGC GAGCCGAGGACA CGGCTGTGTATTA CTGTGCGAGAGA TCGGCTCAATTAC TATGATAGTAGT GGTTATTATCACT ACAAATACTACG GTATGGCCGTCTG GGGCCAAGGAAC AACAGTTACCGT CTCTAGTGCCTCC ACCAAGGGCCCA TCGGTCTTCCCCC TGGCACCCTCCTC CAAGAGCACCTC TGGGGGCACAGC

IgG-Fab Molecule Designation	Light Chain Nucleic Acid Sequence	Modified Heavy Chain Nucleic Acid Sequence	Second Polypeptide Nucleic Acid Sequence
		CAGGGGAACGTCTTCTCATGCTCCGTGATGCATG AGGCTCTGCACAACCACTACACGCAGAAGAGCCT AAGCTTGTCTCCGGGTGGTGGCGGATCGGGAGGT GGCGGATCCCAGTCTGTGTTGACGCAGCCGCCCT CAGTGTCTGCGGCCCCAGGACAGAAGGTCACCAT CTCCTGCTCTGGAAGCAGCTCCAACATTGGGAAT AATTATGTATCCTGGTACCAGCAGCTCCCAGGAA CAGCCCCCAAACTCCTCATTTATGACAATAATAA GCGACCCTCAGGGATTCCTGACCGATTCTCTGGCT CCAAGTCTGGCACGTCAACCACCCTGGGCATCAC CGGACTCCAGACTGGGGACGAGGCCGATTATTAC TGCGGAACATGGGATAGCCGCCTGAGTGCTGTGG TTTTCGGCGGAGGGACCAAGCTGACCGTCCTAGG TCAGCCCAAGGCCAACCCCACTGTCACTCTGTTCC CGCCCTCCTCTGAGGAGCTCCAAGCCAACAAGGC CACACTAGTGTGTCTGATCAGTGACTTCTACCCGG GAGCTGTGACAGTGGCCTGGAAGGCAGATGGCAG CCCCGTCAAGGCGGGAGTGGAGACCACCAAACCC TCCAAACAGAGCAACAACAAGTACGCGGCCAAG AGCTACCTGAGCCTGACGCCCGAGCAGTGGAAGT CCCACAGAAGCTACAGCTGCCAGGTCACGCATGA AGGGAGCACCGTGGAGAAGACAGTGGCCCCTAC AGAATGTTCA (SEQ ID NO: 601)	GGCCCTGGGCTG CCTGGTCAAGGA CTACTTCCCCGAA CCGGTGACGGTG TCGTGGAACTCA GGCGCCCTGACC AGCGGCGTGCAC ACCTTCCCGGCTG TCCTACAGTCCTC AGGACTCTACTCC CTCGAAAGCGTG GTGACCGTGCCCT CCAGCAGCTTGG GCACCCAGACCT ACATCTGCAACG TGAATCACAAGC CCAGCAACACCA AGGTGGACAAGA AAGTT (SEQ ID NO: 625)
iPS:392516	SEQ ID NO: 225	CAAGTTCAGTTGGTGGAGTCTGGAGCCGAAGTAG TAAAGCCAGGAGCTTCAGTGAAAGTCTCTTGTAA AGCAAGTGGATTCACGTTTAGCCGCTTTGCCATGC ATTGGGTGCGGCAAGCTCCCGGTCAGGGGTTGGA GTGGATGGGAGTTATTAGCTATGACGGGGGCAAT AAGTACTACGCCGAGTCTGTTAAGGGTCGGGTCA CAATGACACGGGACACCTCAACCAGTACACTCTA TATGGAACTGTCTAGCCTGAGATCCGAGGACACC GCTGTGTATTATTGCGCTAGGGGGTACGATGTATT GACGGGTTATCCTGATTACTGGGGGCAGGGGACA CTCGTAACCGTCTCTAGTGCCTCCACCAAGGGCCC ATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCA CCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGT CAAGGACTACTTCCCCGAACCGGTGACGGTGTCG TGGAACTCAGGCGCCCTGACCAGCGGCGTGCACA CCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTAC TCCCTCAAAAGCGTGGTGACCGTGCCCTCCAGCA GCTTGGGCACCCAGACCTACATCTGCAACGTGAA TCACAAGCCCAGCAACACCAAGGTGGACAAGAA AGTTGAGCCCAAATCTTGTGACAAAACTCACACA TGCCCACCGTGCCCAGCACCTGAACTCCTGGGGG GACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG GACACCCTCATGATCTCCCGGACCCCTGAGGTCA CATGCGTGGTGGTGGACGTGAGCCACGAAGACCC TGAGGTCAAGTTCAACTGGTACGTGGACGGCGTG GAGGTGCATAATGCCAAGACAAAGCCGTGTGAGG AGCAGTACGGCAGCACGTACCGTTGTGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGGC AAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC TCCCAGCCCCCATCGAGAAAACCATCTCCAAAGC	CAGGTGCAGCTG GTGGAATCTGGG GGAGGCGTGGTC CAGCCTGGGAGG TCCCTGAGACTCT CCTGTGCAGCCTC TGGATTCACCTTC AGTAGCTTTGGC ATGCACTGGGTC CGCGAGGCTCCA GGCAAGGGGCTG GAGTGGGTGGCA GTTATATCATTTG ATGGAAGTATTA AGTATTCTGTAGA CTCCGTGAAGGG CCGATTCACCATC TCCAGAGACAAT TCAAAGAACACG CTGTTTCTGCAAA TGAACAGCCTGC GAGCCGAGGACA CGGCTGTGTATTA CTGTGCGAGAGA TCGGCTCAATTAC TATGATAGTAGT GGTTATTATCACT ACAAATACTACG GTATGGCCGTCTG GGGCCAAGGAAC

IgG-Fab Molecule Designation	Light Chain Nucleic Acid Sequence	Modified Heavy Chain Nucleic Acid Sequence	Second Polypeptide Nucleic Acid Sequence
		CAAAGGGCAGCCCCGAGAACCACAGGTGTACACC CTGCCCCCATCCCGGGAGGAGATGACCAAGAACC AGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTA TCCCAGCGACATCGCCGTGGAGTGGGAGAGCAAT GGGCAGCCGGAGAACAACTACAAGACCACGCCTC CCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTAT AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCATG AGGCTCTGCACAACCACTACACGCAGAAGAGCCT AAGCTTGTCTCCGGGTGGTGGCGGATCGGGAGGT GGCGGATCCCAGTCTGTGTTGACGCAGCCGCCCT CAGTGTCTGCGGCCCCAGGACAGAAGGTCACCAT CTCCTGCTCTGGAAGCAGCTCCAACATTGGGAAT AATTATGTATCCTGGTACCAGAAGCTCCCAGGAA CAGCCCCCAAACTCCTCATTTATGACAATAATAA GCGACCCTCAGGGATTCCTGACCGATTCTCTGGCT CCAAGTCTGGCACGTCAACCACCCTGGGCATCAC CGGACTCCAGACTGGGGACGAGGCCGATTATTAC TGCGGAACATGGGATAGCCGCCTGAGTGCTGTGG TTTTCGGCGGAGGGACCAAGCTGACCGTCCTAGG TCAGCCCAAGGCCAACCCCACTGTCACTCTGTTCC CGCCCTCCTCTGAGGAGCTCCAAGCCAACAAGGC CACACTAGTGTGTCTGATCAGTGACTTCTACCCGG GAGCTGTGACAGTGGCCTGGAAGGCAGATGGCAG CCCCGTCAAGGCGGGAGTGGAGACCACCAAACCC TCCAAACAGAGCAACAACAAGTACGCGGCCAAG AGCTACCTGAGCCTGACGCCCGAGCAGTGGAAGT CCCACAGAAGCTACAGCTGCCAGGTCACGCATGA AGGGAGCACCGTGGAGAAGACAGTGGCCCCTAC AGAATGTTCA (SEQ ID NO: 602)	AACAGTTACCGT CTCTAGTGCCTCC ACCAAGGGCCCA TCGGTCTTCCCCC TGGCACCCTCCTC CAAGAGCACCTC TGGGGGCACAGC GGCCCTGGGCTG CCTGGTCAAGGA CTACTTCCCCGAA CCGGTGACGGTG TCGTGGAACTCA GGCGCCCTGACC AGCGGCGTGCAC ACCTTCCCGGCTG TCCTACAGTCCTC AGGACTCTACTCC CTCGAAAGCGTG GTGACCGTGCCCT CCAGCAGCTTGG GCACCCAGACCT ACATCTGCAACG TGAATCACAAGC CCAGCAACACCA AGGTGGACAAGA AAGTT (SEQ ID NO: 626)
iPS:392521	SEQ ID NO: 225	CAAGTTCAGTTGGTGGAGTCTGGAGCCGAAGTAG TAAAGCCAGGAGCTTCAGTGAAAGTCTCTTGTAA AGCAAGTGGATTCACGTTTAGCCGCTTTGCCATGC ATTGGGTGCGGCAAGCTCCCGGTCAGGGGTTGGA GTGGATGGGAGTTATTAGCTATGACGGGGGCAAT AAGTACTACGCCGAGTCTGTTAAGGGTCGGGTCA CAATGACACGGGACACCTCAACCAGTACACTCTA TATGGAACTGTCTAGCCTGAGATCCGAGGACACC GCTGTGTATTATTGCGCTAGGGGGTACGATGTATT GACGGGTTATCCTGATTACTGGGGGCAGGGGACA CTCGTAACCGTCTCTAGTGCCTCCACCAAGGGCCC ATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCA CCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGT CAAGGACTACTTCCCCGAACCGGTGACGGTGTCG TGGAACTCAGGCGCCCTGACCAGCGGCGTGCACA CCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTAC TCCCTCAAAAGCGTGGTGACCGTGCCCTCCAGCA GCTTGGGCACCCAGACCTACATCTGCAACGTGAA TCACAAGCCCAGCAACACCAAGGTGGACAAGAA AGTTGAGCCCAAATCTTGTGACAAAACTCACACA TGCCCACCGTGCCCAGCACCTGAACTCCTGGGGG GACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG GACACCCTCATGATCTCCCGGACCCCTGAGGTCA	CAGGTGCAGCTG GTGGAATCTGGG GGAGGCGTGGTC CAGCCTGGGAGG TCCCTGAGACTCT CCTGTGCAGCCTC TGGATTCACCTTC AGTAGCTTTGGC ATGCACTGGGTC CGCGAGGCTCCA GGCAAGGGGCTG GAGTGGGTGGCA GTTATATCATTTG ATGGAAGTATTA AGTATTCTGTAGA CTCCGTGAAGGG CCGATTCACCATC TCCAGAGACAAT TCAAAGAACACG CTGTTTCTGCAAA TGAACAGCCTGC GAGCCGAGGACA CGGCTGTGTATTA

DEMANDE OU BREVET VOLUMINEUX

LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVET COMPREND PLUS D'UN TOME.

CECI EST LE TOME 1 DE 2
CONTENANT LES PAGES 1 À 212

NOTE : Pour les tomes additionels, veuillez contacter le Bureau canadien des brevets

JUMBO APPLICATIONS/PATENTS

THIS SECTION OF THE APPLICATION/PATENT CONTAINS MORE THAN ONE VOLUME

THIS IS VOLUME 1 OF 2
CONTAINING PAGES 1 TO 212

NOTE: For additional volumes, please contact the Canadian Patent Office

NOM DU FICHIER / FILE NAME :

NOTE POUR LE TOME / VOLUME NOTE:

CLAIMS

What is claimed:

1. A bispecific antibody comprising a first light chain (LC1) and a first heavy chain (HC1) from a first antibody that specifically binds to human calcitonin gene-related peptide (CGRP) receptor and a second light chain (LC2) and second heavy chain (HC2) from a second antibody that specifically binds to human pituitary adenylate cyclase-activating polypeptide type 1 (PAC1) receptor, wherein the bispecific antibody inhibits activation of human CGRP receptor and human PAC1 receptor.

2. The bispecific antibody of claim 1, wherein the first antibody and the second antibody are humanized or human antibodies.

3. The bispecific antibody of claim 1 or 2, wherein the antibody comprises a constant region from an IgG1, IgG2, IgG3, or IgG4 immunoglobulin.

4. The bispecific antibody of claim 3, wherein the constant region comprises human IgG1 or IgG2 immunoglobulin CH2 and CH3 domains.

5. The bispecific antibody of claim 3, wherein the antibody comprises a constant region from a human IgG1 immunoglobulin with a N297G mutation according to the EU numbering system.

6. The bispecific antibody of any one of claims 3 to 5, wherein the constant region further comprises R292C and V302C mutations according to the EU numbering system.

7. The bispecific antibody of any one of claims 1 to 6, wherein HC1 or HC2 comprises at least one substitution to replace lysine at position 370, 392, and/or 409 according to the EU numbering system with a negatively-charged amino acid.

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8. The bispecific antibody of any one of claims 1 to 6, wherein HC1 or HC2 comprises at least one amino acid substitution to replace:

(a) an aspartic acid at position 356 and/or 399 according to the EU numbering system with a positively-charged amino acid; or

(b) a glutamic acid at position 356 and/or 357 according to the EU numbering system with a positively-charged amino acid.

9. The bispecific antibody of any one of claims 1 to 8, wherein the HC1 comprises at least one amino acid substitution at position 44 according to the Kabat numbering system and/or position 183 according to the EU numbering system to introduce a charged amino acid and LC1 comprises at least one amino acid substitution at position 100 and/or position 176 according to the Kabat numbering system to introduce a charged amino acid, wherein the charged amino acid introduced into HC1 has the opposite charge of the amino acid introduced into LC1.

10. The bispecific antibody of claim 9, wherein the amino acid substitution in HC1 is G44E and/or S183E, and the amino acid substitution in LC1 is G100K and/or S176K.

11. The bispecific antibody of any one of claims 1 to 10, wherein HC2 comprises at least one amino acid substitution at position 44 according to the Kabat numbering system and/or position 183 according to the EU numbering system to introduce a charged amino acid and LC2 comprises at least one amino acid substitution at position 100 and/or position 176 according to the Kabat numbering system to introduce a charged amino acid, wherein the charged amino acid introduced into HC2 has the opposite charge of the amino acid introduced into LC2.

12. The bispecific antibody of claim 11, wherein the amino acid substitution in HC2 is G44K and/or S183K, and the amino acid substitution in LC2 is G100E and/or S176E.

13. A pharmaceutical composition comprising the bispecific antibody of any one of claims 1 to 12, and a pharmaceutically acceptable diluent, excipient or carrier.

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14. Use of the bispecific antibody of any one of claims 1 to 12 in the preparation of a medicament for treating headache in a patient in need thereof.

15. The use of claim 14, wherein the headache is cluster headache.

16. The use of claim 14, wherein the headache is migraine headache.

17. The use of claim 16, wherein the migraine is episodic migraine.

18. The use of claim 16, wherein the migraine is chronic migraine.

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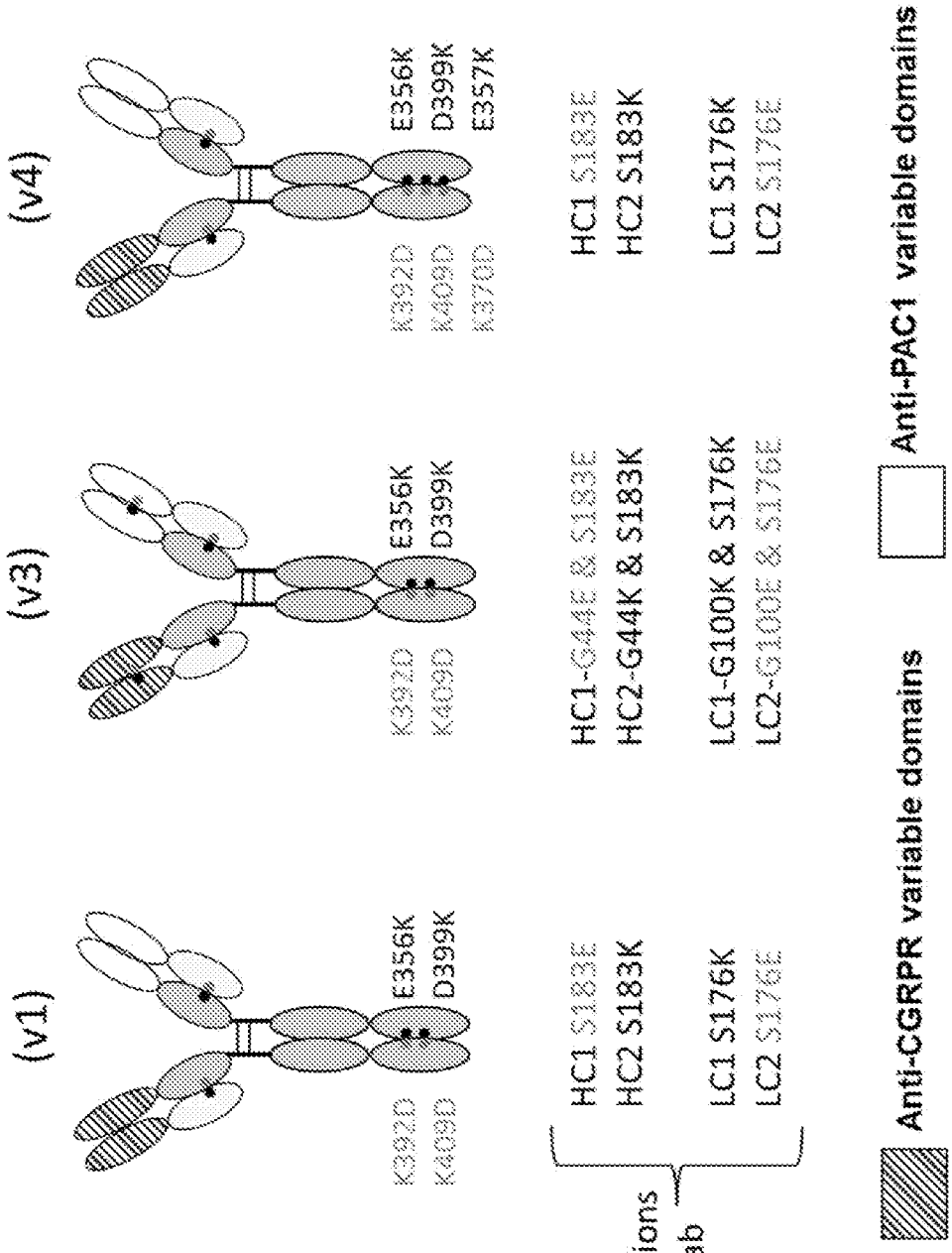
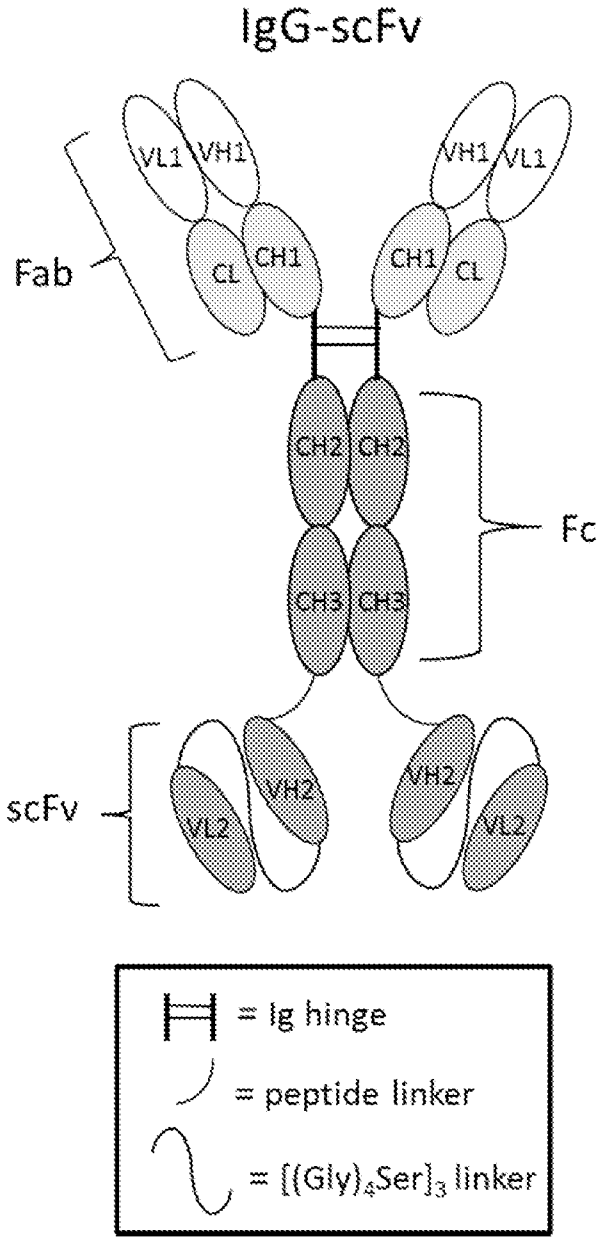

(v1)
(v3)
(v4)
E356K
D399K
K392D
K409D
E357K
K370D
Mutations in Fab
HC1 S183E
HC2 S183K
LC1 S176K
LC2 S176E
HC1-G44E & S183E
HC2-G44K & S183K
LC1-G100K & S176K
LC2-G100E & S176E
Anti-CGRPR variable domains
Anti-PAC1 variable domains

FIG. 1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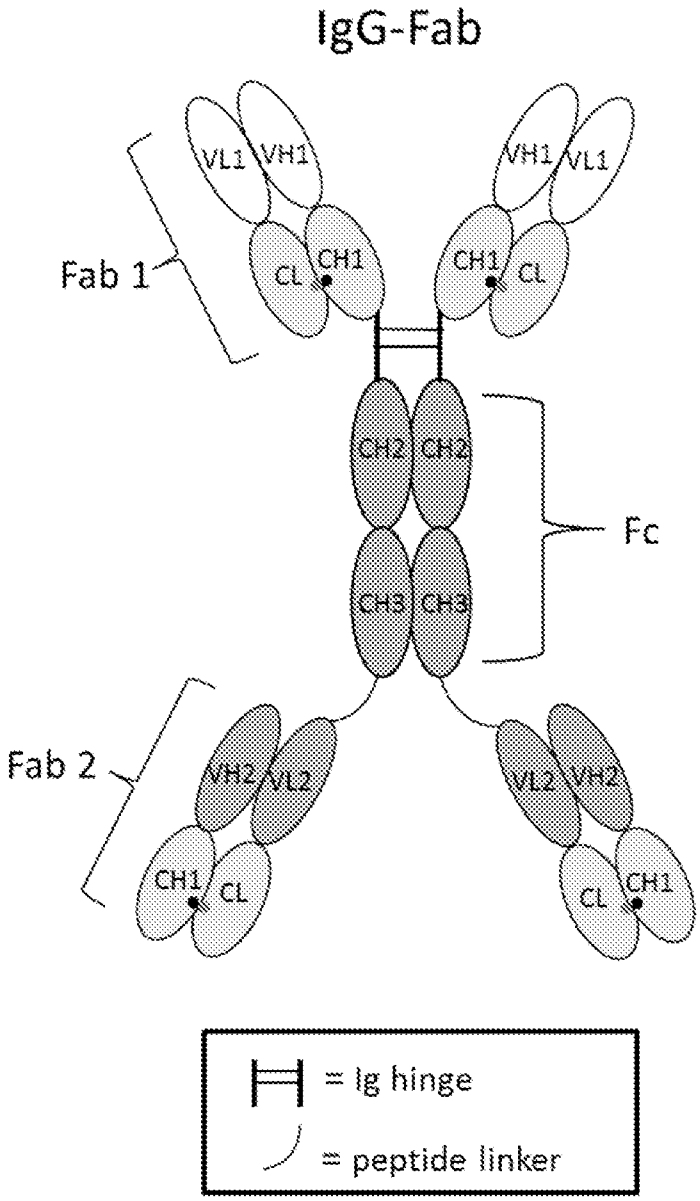
VH1
VH1
VL1
Fab
CL
CH1
CH1
CL
CH2
CH2
Fc
CH3
CH3
scFv
VH2
VH2
VL2
VL2
= Ig hinge
= peptide linker
= [(Gly)4Ser]3 linker

FIG. 2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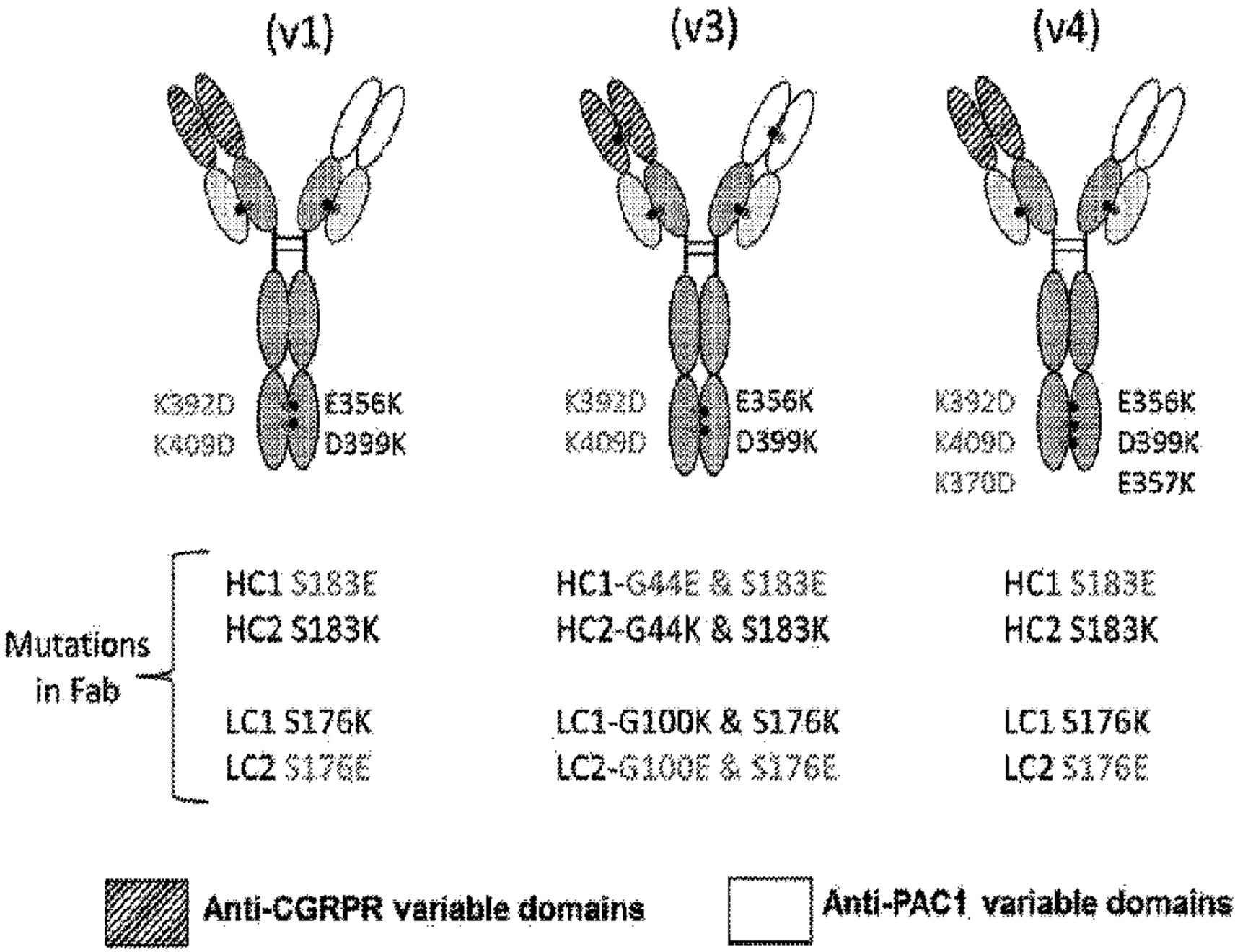
VL1
VH1
VH1
VL1
Fab 1
CL
CH1
CH1
CL
CH2
CH2
Fc
CH3
CH3
Fab 2
VH2
VL2
VL2
VH2
CH1
CL
CL
CH1
= Ig hinge
= peptide linker

FIG. 3


(v1)
(v3)
(v4)
K392D
K409D
E356K
D399K
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K409D
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E356K
D399K
E357K
Mutations in Fab
HC1 S183E
HC2 S183K
LC1 S176K
LC2 S176E
HC1-G44E & S183E
HC2-G44K & S183K
LC1-G100K & S176K
LC2-G100E & S176E
HC1 S183E
HC2 S183K
LC1 S176K
LC2 S176E
Anti-CGRPR variable domains
Anti-PAC1 variable domains