GLP-1 RECEPTOR AGONISTS AND THEIR MEDICAL USE

[0001] This application claims the benefit under 35 U.S.C. §119(e) of U.S. Provisional Patent Application No. 63/566,857, filed March 18, 2024.

INCORPORATION BY REFERENCE OF MATERIAL SUBMITTED ELECTRONICALLY

[0002] Incorporated by reference in its entirety is a computer-readable nucleotide/amino acid sequence listing submitted concurrently herewith and identified as follows: 1.51 MB (XML) file named "10889-WO01-SEC_Sequence_Listing.xml"; created on March 13, 2025.

FIELD OF THE INVENTION

[0003] The present disclosure relates to improved Glucagon-like peptide-1 (GLP-1) receptor agonist polypeptides and molecules comprising these improved GLP-1 receptor agonist polypeptides, such as conjugate molecules comprising one or more GLP-1 receptor agonist polypeptides conjugated to an anti-gastric inhibitory peptide receptor (GIPR) antibody. The present disclosure is also directed to the use of these improved GLP-1 receptor agonist polypeptides and conjugate molecules comprising these polypeptides for treating or ameliorating a metabolic disorder, such as obesity and type 2 diabetes. These improved GLP-1 receptor agonist polypeptides and conjugate molecules comprising these polypeptides are also useful for treating or ameliorating obesity related conditions and type 2 diabetes related conditions.

BACKGROUND OF THE INVENTION

[0004] Glucose-dependent insulinotropic polypeptide (GIP) is a single 42-amino acid peptide secreted from K-cells in the small intestine (duodenum and jejunum). Human GIP is derived from the processing of proGIP, a 153-amino acid precursor that is encoded by a gene localized to chromosome 17q (Inagaki et al., Mol Endocrinol 1989; 3:1014-1021; Fehmann et al. Endocr Rev. 1995; 16:390-410). GIP was formerly called gastric inhibitory polypeptide.

[0005] GIP secretion is induced by food ingestion. GIP has a number of physiological effects in tissues, including promotion of fat storage in adipocytes and promotion of pancreatic islet β-cell function and glucose-dependent insulin secretion. GIP and glucagon like polypeptide-1 (GLP-1) are known insulinotropic factors ("incretins"). Intact GIP is rapidly degraded by DPPIV to an inactive form. The insulinotropic effect of GIP is lost in type 2 diabetic subjects while GLP-1's incretin effect remains intact (Nauck et al. *J. Clinc. Invest.* 1993; 91:301-307).

[0006] The GIP receptor (GIPR) is a member of the secretin-glucagon family of G-protein coupled receptors (GPCRs) having an extracellular N-terminus, seven transmembrane domains and an intracellular C-terminus. The N-terminal extracellular domains of this family of receptors are usually glycosylated and form the recognition and binding domain of the receptor. GIPR is highly expressed in a number of tissues, including the pancreas, gut, adipose tissue, heart, pituitary, adrenal cortex, and brain (Usdin et al., *Endocrinology* 1993, 133:2861-2870). Human GIPR comprises 466 amino acids and is encoded by a gene located on chromosome 19q13.3 (Gremlich et al., *Diabetes* 1995; 44:1202-8; Volz et al., *FEBS Lett.* 1995, 373:23-29). Studies have suggested that alternative mRNA splicing results in the production of GIP receptor variants of differing lengths in human, rat and mouse.

[0007] GIPR knockout mice ($GIPR^{-/-}$) are resistant to high fat diet-induced weight gain and have improved insulin sensitivity and lipid profiles (Yamada et al., Diabètes. 2006, 55:S86; Miyawaki et al. *Nature Med.* 2002, 8:738-742). In addition, a novel small molecule GIPR antagonist SKL-14959 prevents obesity and insulin resistance (*Diabetologia* 2008, 51:S373, 44th EASD Annual meeting poster).

[0008] Collectively, these links to obesity and insulin resistance imply GIPR inhibition is a useful approach for therapeutic intervention.

[0009] Glucagon-like peptide-1 is a 31-amino acid peptide derived from the proglucagon gene. It is secreted by intestinal L-cells and released in response to food ingestion to induce insulin secretion from pancreatic β–cells (Diabetes 2004, 53:S3, 205-214). In addition to the incretin effects, GLP-1 also decreases glucagon secretion, delays gastric emptying and reduces caloric intake (Diabetes Care, 2003, 26(10): 2929-2940). GLP-1 exerts its effects by activation of the GLP-1 receptor, which belongs to a class B G-protein-coupled receptor (Endocrinology 1993, 133(4):1907-10). The function of GLP-1 is limited by rapid degradation by the DPP-IV enzyme, resulting in a half-life of approximately 2 minutes. Recently, long-lasting GLP-1

receptor agonists (GLP-1 RAs) such as exenatide, liraglutide, dulaglutide have been developed and are now being used clinically to improve glycemic control in subjects with type 2 diabetes. Furthermore, GLP-1 receptor agonists also promote body weight reduction as well as reduction in blood pressure and plasma cholesterol levels in subjects (Bioorg. Med. Chem.Lett 2013, 23:4011-4018).

SUMMARY OF THE INVENTION

[0010] The present disclosure relates to improved GLP-1 receptor agonist polypeptides. The present disclosure also relates to molecules comprising these improved GLP-1 receptor agonist polypeptides, such as molecules comprising one or more GLP-1 receptor agonist polypeptides conjugated to an antagonist anti-gastric inhibitory peptide receptor (GIPR) antibody.

[0011] Accordingly, a first aspect of the present disclosure is directed to a human glucagon-like peptide 1 (GLP-1) receptor agonist polypeptide comprising the amino acid sequence of H[Aib]EGTFTSDYSSYLEEX_{17}AAX_{20}EFIX_{24}WL$X_{27}X_{28}$GGG (SEQ ID NO: 1575), wherein Aib at position 2 is α-amino-isobutyric acid (also referred to as 2-amino-isobutyric acid), X_{17} is Q, K, E, or R; X_{20} is K, R, Q, or homoarginine (hArg); X_{24} is A, E, Q, D, d-Ala, G, N, K, (1S,2S)-2-Aminocyclopentanecarboxylic acid (ACPC), (3S,4R)-4-Amino-3-pyrrolidinecarboxylic acid (APCA), T, S, or Y; X_{27} is V, K, Aib, N, S, T, Y, Q, or R; and X_{28} is K, E, R, Q, D, N, G, S, or T; and wherein the GLP-1 receptor agonist polypeptide does not comprise the amino acid sequence of H[Aib]EGTFTSDYSSYLEEQAAKEFIAWLVKGGG (SEQ ID NO: 1574).

[0012] In one embodiment, the GLP-1 receptor agonist polypeptide of the present disclosure comprises the amino acid sequence of H[Aib]EGTFTSDYSSYLEEX_{17}AAX_{20}EFIX_{24}WL$X_{27}X_{28}$GGG (SEQ ID NO: 1576), wherein X_{17} is Q or K; X_{20} is K or R; X_{24} is A, E, or Q; X_{27} is V or K; and X_{28} is K, E, or R, wherein the GLP-1 receptor agonist polypeptide does not comprise the amino acid sequence of H[Aib]EGTFTSDYSSYLEEQAAKEFIAWLVKGGG (SEQ ID NO: 1574).

[0013] In one embodiment, the GLP-1 receptor agonist polypeptide of the present disclosure comprises the amino acid sequence of

H[Aib]EGTFTSDYSSYLEEX_{17}AAREFIX_{24}WL$X_{27}X_{28}$GGG (SEQ ID NO: 1577) wherein X_{17} is Q or K; X_{24} is A, E, or Q; X_{27} is V or K; and X_{28} is K, E, or R.

[0014] In one embodiment, the GLP-1 receptor agonist polypeptide of the present disclosure comprises the amino acid sequence of H[Aib]EGTFTSDYSSYLEEX_{17}AAX_{20}EFIX_{24}WLKX_{28}GGG (SEQ ID NO: 1578), wherein X_{17} is Q or K; X_{20} is K or R; X_{24} is A, E, or Q; and X_{28} is K, E, or R.

[0015] In one embodiment, the GLP-1 receptor agonist polypeptide of the present disclosure comprises the amino acid sequence of any one of SEQ ID NO: 1579, SEQ ID NO: 1580, SEQ ID NO: 1581, SEQ ID NO: 1582, or SEQ ID NO: 1583 as provided herein.

[0016] In another aspect, the GLP-1 receptor agonist polypeptide of the present disclosure comprises 31 amino acids, comprises an amino acid sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 1580, and comprises an Aib at position 2; a tyrosine at position 10; a glutamic acid at positions 16, 24, and 28; an arginine at position 20; a lysine at positions 17 and 27; and a glycine at position 30.

[0017] In another aspect, the GLP-1 receptor agonist polypeptide of the present disclosure comprises 31 amino acids, comprises an amino acid sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 1579, and comprises an Aib at position 2; a tyrosine at position 10; a glutamic acid at positions 16 and 24; an arginine at position 20; a lysine at positions 27; and a glycine at position 30.

[0018] In another aspect, the GLP-1 receptor agonist polypeptide of the present disclosure comprises 31 amino acids, comprises an amino acid sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 1581, and comprises an Aib at position 2; a tyrosine at position 10; a glutamic acid at positions 16 and 24; an arginine at position 20; a lysine at positions 17, 27; and a glycine at position 30.

[0019] In another aspect, the GLP-1 receptor agonist polypeptide of the present disclosure comprises 31 amino acids, comprises an amino acid sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 1583, and comprises an Aib at position 2; a tyrosine at position 10; a glutamic acid at positions 16 and 28; an arginine at position 20; a lysine at positions 17, 27; a glutamine at position 24; and a glycine at position 30.

[0020] In another aspect, the GLP-1 receptor agonist polypeptide of the present disclosure comprises 31 amino acids, comprises an amino acid sequence having at least 90%

sequence identity to the amino acid sequence of SEQ ID NO: 1582, and comprises an Aib at position 2; a tyrosine at position 10; a glutamic acid at positions 16 and 24; an arginine at positions 20 and 28; a lysine at positions 27; and a glycine at position 30.

[0021] Another aspect of the present disclosure is directed to a molecule comprising a first human glucagon-like peptide 1 (GLP-1) receptor agonist polypeptide as described herein and a half-life extending moiety.

[0022] In one embodiment, the first GLP-1 receptor agonist polypeptide of the molecule comprises the amino acid sequence of H[Aib]EGTFTSDYSSYLEEX_{17}AAX_{20}EFIX_{24}WL$X_{27}X_{28}$GGG (SEQ ID NO: 1575), wherein X_{17} is Q, K, E, or R; X_{20} is K, R, Q, or homoarginine (hArg); X_{24} is A, E, Q, D, d-Ala, G, N, K, (1S,2S)-2-Aminocyclopentanecarboxylic acid (ACPC), (3S,4R)-4-Amino-3-pyrrolidinecarboxylic acid (APCA), T, S, or Y; X_{27} is V, K, Aib, N, S, T, Y, Q, or R; and X_{28} is K, E, R, Q, D, N, G, S, or T; and wherein the GLP-1 receptor agonist polypeptide does not comprise the amino acid sequence of SEQ ID NO: 1574.

[0023] In one embodiment, the first GLP-1 receptor agonist polypeptide of the molecule comprises the amino acid sequence of H[Aib]EGTFTSDYSSYLEEX_{17}AAX_{20}EFIX_{24}WL$X_{27}X_{28}$GGG (SEQ ID NO: 1576), wherein X_{17} is Q or K; X_{20} is K or R; X_{24} is A, E, or Q; X_{27} is V or K; and X_{28} is K, E, or R, wherein the GLP-1 receptor agonist polypeptide does not comprise the amino acid sequence of SEQ ID NO: 1574.

[0024] In one embodiment, the first GLP-1 receptor agonist polypeptide of the molecule comprises the amino acid sequence of H[Aib]EGTFTSDYSSYLEEX_{17}AAREFIX_{24}WL$X_{27}X_{28}$GGG (SEQ ID NO: 1577) wherein X_{17} is Q or K; X_{24} is A, E, or Q; X_{27} is V or K; and X_{28} is K, E, or R.

[0025] In one embodiment, the first GLP-1 receptor agonist polypeptide of the molecule comprises the amino acid sequence of H[Aib]EGTFTSDYSSYLEEX_{17}AAX_{20}EFIX_{24}WLKX_{28}GGG (SEQ ID NO: 1578), wherein X_{17} is Q or K; X_{20} is K or R; X_{24} is A, E, or Q; and X_{28} is K, E, or R.

[0026] In one embodiment, the first GLP-1 receptor agonist polypeptide of the molecule comprises the amino acid sequence of any one of SEQ ID NO: 1579, SEQ ID NO: 1580, SEQ ID NO: 1581, SEQ ID NO: 1582, or SEQ ID NO: 1583.

[0027] In one embodiment, the half-life extending moiety of the molecule is an antibody.

[0028] Another aspect of the present disclosure is directed to a conjugate molecule comprising a first human glucagon-like peptide 1 (GLP-1) receptor agonist polypeptide as described herein conjugated to an antagonist anti-glucose-dependent insulinotropic polypeptide receptor (GIPR) antibody.

[0029] In one embodiment, the conjugate molecule comprises a first GLP-1 receptor agonist polypeptide comprising an amino acid sequence of any one of SEQ ID NO: 1575–1583 conjugated to an antagonist anti-GIPR antibody. The anti-GIPR antibody of the conjugate molecule comprises a first cysteine conjugation site within a light chain or heavy chain of the antibody, and the first GLP-1 receptor agonist polypeptide is conjugated, at its C-terminus, to the first cysteine conjugation site of the anti-GIPR antibody. In one embodiment, the first cysteine conjugation site of the anti-GIPR antibody is at position 88 of the light chain, position 384 of the heavy chain, or position 487 of the heavy chain according to AHo numbering.

[0030] In one embodiment, the first GLP-1 receptor agonist polypeptide of the conjugate molecule is conjugated, at its C-terminus, to the first cysteine conjugation site of the anti-GIPR antibody via a first linker moiety. In one embodiment, the first linker moiety is a peptide linker and the peptide linker comprises the amino acid sequence of any one of SEQ ID NOs: 1585–1593. In one embodiment, the first linker moiety is a PEG linker.

[0031] In one embodiment, the conjugate molecule further comprises a second GLP-1 receptor agonist polypeptide. The second GLP-1 receptor agonist polypeptide is conjugated, at its C-terminus, to a second cysteine conjugation site of the anti-GIPR antibody.

[0032] In one embodiment, the second GLP-1 receptor agonist polypeptide comprises any of the GLP-1 receptor agonist polypeptides disclosed herein. In one embodiment, the second GLP-1 receptor agonist polypeptide comprises an amino acid sequence of any one of SEQ ID NO: 1575-1583. In one embodiment, the second GLP-1 receptor agonist polypeptide comprises the same amino acid sequence as the first GLP-1 receptor agonist polypeptide.

[0033] In one embodiment of this aspect of the disclosure, the second GLP-1 receptor agonist polypeptide of the conjugate molecule is conjugated, at its C-terminus, to the second cysteine conjugation site of the anti-GIPR antibody via a second linker moiety. In one embodiment, the second linker moiety is a peptide linker and the peptide linker comprises the amino acid sequence of any one of SEQ ID NOs: 1585–1593. In one embodiment, the second

peptide linker comprises the same amino acid sequence as the first peptide linker. In one embodiment, the second linker moiety is a PEG linker.

[0034] In one embodiment, the first and second conjugation sites of the anti-GIPR antibody of the conjugate molecule are at position 88 of each light chain, position 384 of each heavy chain, or position 487 of each heavy chain according to AHo numbering.

[0035] In one embodiment, the anti-GIPR antibody of the conjugate molecule comprises a CDRL1, a CDRL2, a CDRL3, a CDRH1, a CDRH2, and a CDRH3, wherein the CDRL1, the CDRL2, the CDRL3, the CDRH1, the CDRH2, and the CDRH3 comprise the amino acid sequences of SEQ ID NO: 702, SEQ ID NO: 859, SEQ ID NO: 1016, SEQ ID NO: 1173, SEQ ID NO: 1330, and SEQ ID NO: 1487, respectively.

[0036] In one embodiment, the anti-GIPR antibody of the conjugate molecule comprises a V_L and V_H comprising the amino acid sequence of SEQ ID NO: 74 and SEQ ID NO: 231, respectively.

[0037] In one embodiment, the anti-GIPR antibody of the conjugate molecule comprises a light chain and a heavy chain comprising the amino acid sequence of SEQ ID NO: 388 and SEQ ID NO: 545, respectively, with a cysteine substitution at position 88 of each light chain, position 384 of each heavy chain, or position 487 of each heavy chain according to AHo numbering.

[0038] Another aspect of the present disclosure is directed to a molecule, where the molecule comprises an antagonist anti-glucose-dependent insulinotropic polypeptide receptor (GIPR) antibody, wherein said antibody comprises: a first and second light chain, each light chain comprising a CDRL1, a CDRL2, and a CDRL3 of SEQ ID NO: 702, SEQ ID NO: 859, and SEQ ID NO: 1016, respectively, and a first and second heavy chain, each heavy chain comprising a CDRH1, a CDRH2, and a CDRH3 of SEQ ID NO: 1173, SEQ ID NO: 1330, and SEQ ID NO: 1487, respectively. The molecule further comprises a first and second GLP-1 receptor agonist polypeptide, wherein each GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1579; and a first and second peptide linker, wherein each peptide linker comprises the amino acid sequence of SEQ ID NO: 1592. The first GLP-1 receptor agonist polypeptide of the molecule is conjugated, at its C-terminus, via the first linker, to the first heavy chain of the anti-GIPR antibody at a cysteine residue at position 384 of the first heavy chain according to AHo numbering (which corresponds to position 275 of SEQ ID NO:

1571), and the second GLP-1 receptor agonist polypeptide is conjugated, at its C-terminus via the second linker, to the second heavy chain of the anti-GIPR antibody at a cysteine residue at position 384 of the second heavy chain according to AHo numbering (which corresponds to position 275 of SEQ ID NO: 1571). In one embodiment, each light chain of the antibody comprises a VL of SEQ ID NO: 74, and each heavy chain of the antibody comprises a VH of SEQ ID NO: 231. In one embodiment, each light chain of the antibody comprises the amino acid sequence of SEQ ID NO: 388, and each heavy chain of the antibody comprises the amino acid sequence of SEQ ID NO: 1571.

[0039] Another aspect of the present disclosure is directed to a molecule, where the molecule comprises an antagonist anti-glucose-dependent insulinotropic polypeptide receptor (GIPR) antibody, wherein said antibody comprises: a first and second light chain, each light chain comprising a CDRL1, a CDRL2, and a CDRL3 of SEQ ID NO: 702, SEQ ID NO: 859, and SEQ ID NO: 1016, respectively, and a first and second heavy chain, each heavy chain comprising a CDRH1, a CDRH2, and a CDRH3 of SEQ ID NO: 1173, SEQ ID NO: 1330, and SEQ ID NO: 1487, respectively. The molecule further comprises a first and second GLP-1 receptor agonist polypeptide, wherein each GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1580; and a first and second peptide linker, wherein each peptide linker comprises the amino acid sequence of SEQ ID NO: 1591. The first GLP-1 receptor agonist polypeptide of the molecule is conjugated, at its C-terminus via the first linker, to the first heavy chain of the anti-GIPR antibody at a cysteine residue at position 384 of the first heavy chain according to AHo numbering (which corresponds to position 275 of SEQ ID NO: 1571), and the second GLP-1 receptor agonist polypeptide is conjugated, at its C-terminus via the second linker, to the second heavy chain of the anti-GIPR antibody at a cysteine residue at position 384 of the second heavy chain according to AHo numbering (which corresponds to position 275 of SEQ ID NO: 1571). In one embodiment, each light chain of the antibody comprises a VL of SEQ ID NO: 74, and each heavy chain of the antibody comprises a VH of SEQ ID NO: 231. In one embodiment, each light chain of the antibody comprises the amino acid sequence of SEQ ID NO: 388, and each heavy chain of the antibody comprises the amino acid sequence of SEQ ID NO: 1571.

[0040] Another aspect of the present disclosure is directed to a molecule, where the molecule comprises an antagonist anti-glucose-dependent insulinotropic polypeptide receptor

(GIPR) antibody, wherein said antibody comprises: a first and second light chain, each light chain comprising a CDRL1, a CDRL2, and a CDRL3 of SEQ ID NO: 702, SEQ ID NO: 859, and SEQ ID NO: 1016, respectively, and a first and second heavy chain, each heavy chain comprising a CDRH1, a CDRH2, and a CDRH3 of SEQ ID NO: 1173, SEQ ID NO: 1330, and SEQ ID NO: 1487, respectively. The molecule further comprises a first and second GLP-1 receptor agonist polypeptide, wherein each GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1581; and a first and second peptide linker, wherein each peptide linker comprises the amino acid sequence of SEQ ID NO: 1586. The first GLP-1 receptor agonist polypeptide of the molecule is conjugated, at its C-terminus via the first linker, to the first heavy chain of the anti-GIPR antibody at a cysteine residue at position 384 of the first heavy chain according to AHo numbering (which corresponds to position 275 of SEQ ID NO: 1571), and the second GLP-1 receptor agonist polypeptide is conjugated, at its C-terminus via the second linker, to the second heavy chain of the anti-GIPR antibody at a cysteine residue at position 384 of the second heavy chain according to AHo numbering (which corresponds to position 275 of SEQ ID NO: 1571). In one embodiment, each light chain of the antibody comprises a VL of SEQ ID NO: 74, and each heavy chain of the antibody comprises a VH of SEQ ID NO: 231. In one embodiment, each light chain of the antibody comprises the amino acid sequence of SEQ ID NO: 388, and each heavy chain of the antibody comprises the amino acid sequence of SEQ ID NO: 1571.

[0041] Another aspect of the present disclosure is directed to a molecule, where the molecule comprises an antagonist anti-glucose-dependent insulinotropic polypeptide receptor (GIPR) antibody, wherein said antibody comprises: a first and second light chain, each light chain comprising a CDRL1, a CDRL2, and a CDRL3 of SEQ ID NO: 702, SEQ ID NO: 859, and SEQ ID NO: 1016, respectively, and a first and second heavy chain, each heavy chain comprising a CDRH1, a CDRH2, and a CDRH3 of SEQ ID NO: 1173, SEQ ID NO: 1330, and SEQ ID NO: 1487, respectively. The molecule further comprises a first and second GLP-1 receptor agonist polypeptide, wherein each GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1581; and a first and second peptide linker, wherein each peptide linker comprises the amino acid sequence of SEQ ID NO: 1585. The first GLP-1 receptor agonist polypeptide of the molecule is conjugated, at its C-terminus via the first linker, to the first heavy chain of the anti-GIPR antibody at a cysteine residue at position 384 of the first

heavy chain according to AHo numbering (which corresponds to position 275 of SEQ ID NO: 1571), and the second GLP-1 receptor agonist polypeptide is conjugated, at its C-terminus via the second linker, to the second heavy chain of the anti-GIPR antibody at a cysteine residue at position 384 of the second heavy chain according to AHo numbering (which corresponds to position 275 of SEQ ID NO: 1571). In one embodiment, each light chain of the antibody comprises a VL of SEQ ID NO: 74, and each heavy chain of the antibody comprises a VH of SEQ ID NO: 231. In one embodiment, each light chain of the antibody comprises the amino acid sequence of SEQ ID NO: 388, and each heavy chain of the antibody comprises the amino acid sequence of SEQ ID NO: 1571.

[0042] Another aspect of the present disclosure is directed to a pharmaceutical composition comprising a GLP-1 receptor agonist polypeptide as disclosed herein, or a GLP-1 receptor agonist polypeptide containing molecule as disclosed herein, and a pharmaceutically acceptable excipient.

[0043] Another aspect of the present disclosure is directed to a method of reducing body weight and/or food intake in a subject in need thereof. This method comprises administering, to the subject in need thereof, a GLP-1 receptor agonist polypeptide as disclosed herein, a GLP-1 receptor agonist polypeptide containing molecule as disclosed herein, or a pharmaceutical composition as disclosed herein.

[0044] Another aspect of the present disclosure is directed to a method of treating obesity or an obesity related condition in a subject in need thereof. This method comprises administering, to the subject in need thereof, a GLP-1 receptor agonist polypeptide as disclosed herein, a GLP-1 receptor agonist polypeptide containing molecule as disclosed herein, or a pharmaceutical composition as disclosed herein.

[0045] Another aspect of the present disclosure is directed to a method of treating type 2 diabetes or type 2 related condition in a subject in need thereof. This method comprises administering, to the subject in need thereof, a GLP-1 receptor agonist polypeptide as disclosed herein, a GLP-1 receptor agonist polypeptide containing molecule as disclosed herein, or a pharmaceutical composition as disclosed herein.

[0046] Described herein are novel GLP-1 receptor agonist polypeptides and molecules comprising an antagonist anti-GIPR antibody conjugated to one or more of the novel GLP-1 receptor agonist polypeptides. The GLP-receptor agonist polypeptides described herein

comprise one or more defined amino acid substitutions that enhance stability and/or efficacy of the agonist polypeptides and molecules containing the peptides.

BRIEF DESCRIPTION OF THE DRAWINGS

[0047] FIG. 1 shows the reaction scheme for the generation of an anti-GIPR antibody/GLP-1 receptor agonist conjugate molecule of the present disclosure.

[0048] FIG. 2 shows the structure of a GLP-1 receptor agonist polypeptide of the present disclosure covalently linked to a peptide linker. The GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1579. The C-terminal amino acid residue of the GLP-1 receptor agonist polypeptide is covalently linked to the N-terminal amino acid residue of the linker peptide of SEQ ID NO: 1592. The C-terminus of the polypeptide linker has been bromoacetylated (at the ε-amino group on the side chain of the lysine residue) to permit further conjugation to an anti-GIPR antibody via a bromoacetyl-thiol reaction with a thiol group of a cysteine residue.

[0049] FIG. 3 shows the structure of a GLP-1 receptor agonist polypeptide of the present disclosure covalently linked to a peptide linker. The GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1580. As shown, the C-terminal amino acid residue of the GLP-1 receptor agonist polypeptide is covalently linked to the α-amino group of the lysine residue of the linker peptide of SEQ ID NO: 1591. The N-terminus of the polypeptide linker has been bromoacetylated to permit further conjugation to an anti-GIPR antibody via a bromoacetyl-thiol reaction with a thiol group of a cysteine residue.

[0050] FIG. 4 shows the structure of a GLP-1 receptor agonist polypeptide of the present disclosure covalently linked to a peptide linker. The GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1581. As shown, the C-terminal amino acid residue of the GLP-1 receptor agonist polypeptide is covalently linked to the N-terminal amino acid residue of the linker peptide of SEQ ID NO: 1585. The C-terminal lysine residue of the polypeptide linker has been bromoacetylated (at the ε-amino group on the side chain of the lysine residue) to permit further conjugation to an anti-GIPR antibody via a bromoacetyl-thiol reaction with a thiol group of a cysteine residue

[0051] FIG. 5 shows the structure of a GLP-1 receptor agonist polypeptide of the present disclosure covalently linked to a peptide linker. The GLP-1 receptor agonist polypeptide

comprises the amino acid sequence of SEQ ID NO: 1581. As shown, the C-terminal amino acid residue of the GLP-1 receptor agonist polypeptide is covalently linked to the N-terminal amino acid residue of the linker peptide of SEQ ID NO: 1586. The C-terminal lysine residue of the polypeptide linker has been bromoacetylated (at the ε-amino group on the side chain of the lysine residue) to permit further conjugation to an anti-GIPR antibody via a bromoacetyl-thiol reaction with a thiol group of a cysteine residue

[0052] FIG. 6 shows the structure of a GLP-1 receptor agonist polypeptide of the present disclosure covalently linked to a peptide linker. The GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1581. As shown, the C-terminal amino acid residue of the GLP-1 receptor agonist polypeptide is covalently linked to the N-terminal amino acid residue of the linker peptide of SEQ ID NO: 1593. The C-terminal lysine residue of the polypeptide linker has been bromoacetylated (at the ε-amino group on the side chain of the lysine residue) to permit further conjugation to an anti-GIPR antibody via a bromoacetyl-thiol reaction with a thiol group of a cysteine residue.

[0053] FIG. 7 shows the structure of a GLP-1 receptor agonist polypeptide of the present disclosure covalently linked to a PEG linker. The GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1581. As shown, the C-terminal amino acid residue of the GLP-1 receptor agonist polypeptide is covalently linked to the PEG20 linker via the α-amino group of the lysine residue of the PEG20 linker. The PEG20 is covalently linked to the ε-amino group on the side chain of the lysine. The glycine residue at the opposing terminal end of the PEG linker has been bromoacetylated to permit further conjugation to an anti-GIPR antibody via a bromoacetyl-thiol reaction with a thiol group of a cysteine residue.

[0054] FIG. 8 shows the structure of a GLP-1 receptor agonist polypeptide of the present disclosure covalently linked to a PEG linker. The GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1582. As shown, the C-terminal amino acid residue of the GLP-1 receptor agonist polypeptide is covalently linked to the PEG20 linker via the α-amino group of the lysine residue of the PEG20 linker. The PEG20 is covalently linked to the ε-amino group on the side chain of the lysine. The glycine residue at the opposing terminal end of the PEG linker has been bromoacetylated to permit further conjugation to an anti-GIPR antibody via a bromoacetyl-thiol reaction with a thiol group of a cysteine residue.

[0055] FIG. 9 shows the structure of a GLP-1 receptor agonist polypeptide of the present disclosure covalently linked to a PEG linker. The GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1583. As shown, the C-terminal amino acid residue of the GLP-1 receptor agonist polypeptide is covalently linked to the PEG20 linker via the α-amino group of the lysine residue of the PEG20 linker. The PEG20 is covalently linked to the ε-amino group on the side chain of the lysine. The glycine residue at the opposing terminal end of the PEG linker has been bromoacetylated to permit further conjugation to an anti-GIPR antibody via a bromoacetyl-thiol reaction with a thiol group of a cysteine residue.

[0056] FIG. 10 shows body weight loss over a 12-day period in diet-induced obese C57BL6 mice administered, on day 0, a single dose of 0.5 mg/kg surrogate anti-GIPR/GLP-1 agonist conjugates, *i.e.*, reference conjugate molecule 1238 and conjugate molecule 62207 of the present disclosure, or vehicle (A52Su).

[0057] FIG. 11 shows body weight loss over an 18-day period in diet-induced obese C57BL6 mice administered, on day 0, a single dose of 0.5 mg/kg surrogate anti-GIPR/GLP-1 agonist conjugates, *i.e.*, reference conjugate molecule 1238 and conjugate molecule 65296 of the present disclosure, or vehicle (A52Su).

[0058] FIG. 12 shows body weight loss over an 18-day period in diet-induced obese C57BL6 mice administered, on day 0, a single dose of 0.5 mg/kg surrogate anti-GIPR/GLP-1 agonist conjugates, *i.e.*, reference conjugate molecule 1238 and conjugate molecules 69730 and 69850 of the present disclosure, or vehicle (A52Su).

[0059] FIG. 13 shows body weight loss over a 16-day period in diet-induced obese C57BL6 mice administered, on day 0, a single dose of 0.5 mg/kg surrogate anti-GIPR/GLP-1 agonist conjugates, *i.e.*, reference conjugate molecule 1238 and conjugate molecules 59112 and 59117 of the present disclosure, or vehicle (A52Su).

[0060] FIG. 14 shows body weight loss over a 20-day period in diet-induced obese C57BL6 mice administered, on day 0, a single dose of 0.5 mg/kg surrogate anti-GIPR/GLP-1 agonist conjugates, *i.e.*, reference conjugate molecule 1238 and conjugate molecule 65300 of the present disclosure, or vehicle (A52Su).

[0061] FIG. 15 shows body weight loss over a 24-day period in diet-induced obese C57BL6 mice administered, on day 0 and day 10, 0.5 mg/kg surrogate anti-GIPR/GLP-1 agonist

conjugates, *i.e.*, reference conjugate molecule 1238 and conjugate molecule 59112 of the present disclosure, or vehicle.

[0062] FIG. 16 shows body weight loss over a 24-day period in diet-induced obese C57BL6 mice administered, on day 0 and day 10, 0.5 mg/kg surrogate anti-GIPR/GLP-1 agonist conjugates, *i.e.*, reference conjugate molecule 1238 and conjugate molecules 62207, 65296, 65300 of the present disclosure, or vehicle.

[0063] FIG. 17 shows body weight loss over a 24-day period in diet-induced obese C57BL6 mice administered, on day 0 and day 10, 0.5 mg/kg surrogate anti-GIPR/GLP-1 agonist conjugates, *i.e.*, reference conjugate molecule 1238 and conjugate molecules 59117, 69730, 69850, 73313 of the present disclosure, or vehicle.

DETAILED DESCRIPTION OF THE INVENTION

[0064] The present disclosure relates to improved GLP-1 receptor agonists and molecules comprising the improved GLP-1 receptor agonists. The present disclosure further relates to the utility of these improved protein therapeutics for treating or ameliorating metabolic disorders, such as obesity, type 2 diabetes, elevated glucose levels, elevated insulin levels, non-alcoholic fatty liver disease, cardiovascular diseases, and diabetic nephropathy. Iand type 2 diabetes related conditions as described herein. The present disclosure also relates to the utility of these improved protein therapeutics for treating or ameliorating obesity related conditions and type 2 diabetes related conditions.

[0065] The section headings used herein are for organizational purposes only and are not to be construed as limiting the subject matter described.

[0066] Unless otherwise defined herein, scientific and technical terms used in connection with the present application shall have the meanings that are commonly understood by those of ordinary skill in the art. Further, unless otherwise required by context, singular terms shall include pluralities and plural terms shall include the singular.

[0067] Other than in the operating examples, or where otherwise indicated, all numbers expressing quantities of ingredients or reaction conditions used herein should be understood as modified in all instances by the term "about." The term "about" when used in connection with percentages means ±1%.

[0068] Following convention, as used herein "a" and "an" mean "one or more" unless specifically indicated otherwise.

[0069] As used herein, the terms "amino acid" and "residue" are interchangeable and, when used in the context of a peptide or polypeptide, refer to both naturally occurring and synthetic amino acids, as well as amino acid analogs, amino acid mimetics and non-naturally occurring amino acids that are chemically similar to the naturally occurring amino acids.

[0070] A "naturally occurring amino acid" is an amino acid that is encoded by the human genetic code, as well as those amino acids that are encoded by the genetic code that are modified after synthesis, e.g., hydroxyproline, γ-carboxyglutamate, and O-phosphoserine. An amino acid analog is a compound that has the same basic chemical structure as a naturally occurring amino acid, *i.e.*, an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, *e.g.*, homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs can have modified R groups (e.g., norleucine) or modified peptide backbones, but will retain the same basic chemical structure as a naturally occurring amino acid.

[0071] An "amino acid mimetic" is a chemical compound that has a structure that is different from the general chemical structure of an amino acid, but that functions in a manner similar to a naturally occurring amino acid. Examples include a methacryloyl or acryloyl derivative of an amide, β-, γ-, δ-imino acids (such as piperidine-4-carboxylic acid) and the like.

[0072] A "non-naturally occurring amino acid" is a compound that has the same basic chemical structure as a naturally occurring amino acid, but is not incorporated into a growing polypeptide chain by the translation complex. A non-naturally occurring amino acid also includes, but is not limited to, amino acids that occur by modification (e.g., posttranslational modifications) of a naturally encoded amino acid (including but not limited to, the 20 common amino acids) but are not themselves naturally incorporated into a growing polypeptide chain by the translation complex. A non-limiting list of examples of non-naturally occurring amino acids that can be inserted into a polypeptide sequence or substituted for a wild-type residue in polypeptide sequence include β-amino acids, homoamino acids, cyclic amino acids and amino acids with derivatized side chains. Examples include (in the L-form or D-form; abbreviated as in parentheses): citrulline (Cit), homocitrulline (hCit), Nα-methylcitrulline (NMeCit), Nα-methylhomocitrulline (Nα-MeHoCit), ornithine (Orn), Nα-Methylornithine (Nα-MeOrn or NMeOrn), sarcosine (Sar), homolysine (hLys or hK), homoarginine (hArg or hR),

homoglutamine (hQ), Nα-methylarginine (NMeR), Nα-methylleucine (Nα-MeL or NMeL), N-methylhomolysine (NMeHoK), Nα-methylglutamine (NMeQ), norleucine (Nle), norvaline (Nva), 1,2,3,4-tetrahydroisoquinoline (Tic), Octahydroindole-2-carboxylic acid (Oic), 3-(1-naphthyl)alanine (1-Nal), 3-(2-naphthyl)alanine (2-Nal), 1,2,3,4-tetrahydroisoquinoline (Tic), 2-indanylglycine (IgI), para-iodophenylalanine (pI-Phe), para-aminophenylalanine (4AmP or 4-Amino-Phe), 4-guanidino phenylalanine (Guf), glycyllysine (abbreviated "K(Nε-glycyl)" or "K(glycyl)" or "K(gly)"), nitrophenylalanine (nitrophe), aminophenylalanine (aminophe or Amino-Phe), benzylphenylalanine (benzylphe), γ-carboxyglutamic acid (γ-carboxyglu), hydroxyproline (hydroxypro), p-carboxyl-phenylalanine (Cpa), α-aminoadipic acid (Aad), Nα-methyl valine (NMeVal), N-α-methyl leucine (NMeLeu), Nα-methylnorleucine (NMeNle), cyclopentylglycine (Cpg), cyclohexylglycine (Chg), acetylarginine (acetylarg), α, β-diaminopropionoic acid (Dpr), α, γ-diaminobutyric acid (Dab), diaminopropionic acid (Dap), cyclohexylalanine (Cha), 4-methyl-phenylalanine (MePhe), β, β-diphenyl-alanine (BiPhA), aminobutyric acid (Abu), 4-phenyl-phenylalanine (or biphenylalanine; 4Bip), α-amino-isobutyric acid (Aib), beta-alanine, beta-aminopropionic acid, piperidinic acid, aminocaprioic acid, aminoheptanoic acid, aminopimelic acid, desmosine, diaminopimelic acid, N-ethylglycine, N-ethylaspargine, hydroxylysine, allo-hydroxylysine, isodesmosine, allo-isoleucine, N-methylglycine, N-methylisoleucine, N-methylvaline, 4-hydroxyproline (Hyp), γ-carboxyglutamate, ε-N,N,N-trimethyllysine, ε-N-acetyllysine, O-phosphoserine, N-acetylserine, N-formylmethionine, 3-methylhistidine, 5-hydroxylysine, ω-methylarginine, 4-Amino-O-Phthalic Acid (4APA), and other similar amino acids, and derivatized forms of any of those specifically listed.

[0073] As used herein, the term "polypeptide" refers to a polymer of amino acid residues. Polypeptides comprising between two and fifty amino acids may also be referred to as "peptides" herein. "Polypeptide" further encompasses an amino acid polymer in which one or more amino acid residue is an analog or mimetic of a corresponding naturally occurring amino acid, as well as naturally occurring amino acid polymers. The term can also encompass an amino acid polymer that has been modified, e.g., by the addition of carbohydrate residues to form a glycoprotein, or by the addition of a phosphate group to form a phosphorylated polypeptide. Polypeptides can be produced by a naturally-occurring and non-recombinant cell, or polypeptides can be produced by a genetically-engineered or recombinant cell, and comprise

molecules having the amino acid sequence of a native protein, or molecules having deletions from, additions to, and/or substitutions of one or more amino acids of a native sequence. Polypeptide can also be produced synthetically.

[0074] As used herein, a "variant" of a polypeptide comprises an amino acid sequence wherein one or more amino acid residues are inserted into, deleted from and/or substituted into the amino acid sequence relative to a reference polypeptide sequence.

[0075] As used herein, a "derivative" of a polypeptide is a polypeptide that has been chemically modified in some manner distinct from insertion, deletion, or substitution variants, such as, e.g., via conjugation to another chemical moiety.

[0076] A composition of the present invention that includes a GLP-1 receptor agonist polypeptide as described herein covalently linked, attached, or bound either directly or indirectly through a linker moiety, to an anti-GIPR antibody of the invention is referred to herein as a "conjugate", conjugate molecule", "conjugate protein", or "antibody conjugate".

[0077] As used herein, the term "linker moiety" refers to a biologically acceptable (i.e., safe and non-toxic) peptidyl or non-peptidyl organic group that is covalently bound to a first molecule (e.g., a first polypeptide) and covalently joins or conjugates the molecule to a second molecule (e.g., a second polypeptide). Where the linker moiety consists of a polypeptide or a polypeptide derivative (e.g., a polypeptide that has been chemically modified at one or both of the N-terminus and C-terminus to incorporate a functional group that permits conjugation to the first or second molecule), it may be referred to as a "linker polypeptide" herein. For example, in one embodiment, a linker polypeptide may comprise an acetylated terminus (e.g., when a thiol-bromoacetyl reaction is used to conjugate the derivatized terminus of the linker polypeptide to a cysteine residue of a polypeptide by forming a thioether linkage that comprises a sulfur atom of the cysteine residue).

[0078] The phrase "percent sequence identity," in the context of two or more polypeptide sequences, refers to the ratio of the number of identical amino acid residues between two or more aligned amino acid (polypeptide or protein) sequences over the aligned length of the sequences, expressed as a percentage. To calculate the percent sequence identity of two sequences, the sequences are aligned along their length. A sequence alignment algorithm, *e.g.*, BLAST (Myers et al., *J. Mol. Biol.* 215(3):403-10 (1990)), can be utilized to align two sequences to ensure the corresponding amino acids are positioned correctly against each other. The number of identical

amino acids at each position in the alignment is divided by the number of total number of aligned positions and multiplied by 100.

[0079] The terms "GIPR polypeptide" and "GIPR protein" are used interchangeably to refer to the naturally-occurring glucose-dependent insulinotropic polypeptide receptor protein that is expressed in a mammal, such as a human or a mouse, and includes naturally occurring alleles (e.g., naturally occurring allelic forms of human GIPR protein). For purposes of this disclosure, the term "GIPR polypeptide" can be used interchangeably to refer to any full-length GIPR polypeptide (UniProt Accession No. P48546-1), e.g., SEQ ID NO: 1572, which consists of 466 amino acid residues and which is encoded by the nucleotide sequence SEQ ID NO: 1573. The term also encompasses known isoforms of the GIPR protein (see e.g., UniProt Accession Nos. P48546-2 and P48546-3).

[0080] The term "GIPR polypeptide" also encompasses naturally occurring GIPR polypeptide variants. Such variants may include modifications to the naturally occurring GIPR sequence (SEQ ID NO: 1572) that include, but are not limited to, one or more amino acid substitutions, deletions, and/or insertions. A GIPR polypeptide encompasses an amino acid sequence that is at least about 85 percent identical to a naturally-occurring GIPR polypeptide (e.g., SEQ ID NO: 1572). In other embodiments, a GIPR polypeptide comprises an amino acid sequence that is at least about 90 percent, or about 95, 96, 97, 98, or 99 percent identical to a naturally-occurring GIPR polypeptide amino acid sequence (e.g., SEQ ID NO: 1572). Such GIPR polypeptides preferably, but need not, possess at least one activity of a wild-type GIPR polypeptide, such as the ability to bind GIP. The present invention also encompasses nucleic acid molecules encoding such GIPR polypeptide sequences.

[0081] The terms "GIP", "Gastric inhibitory polypeptide", "glucose-dependent insulinotropic peptide" and "GIP ligand" are used interchangeably and mean a naturally-occurring wild-type polypeptide expressed in a mammal, such as a human or a mouse, and includes naturally occurring alleles (e.g., naturally occurring allelic forms of human GIP protein). GIP is a natural ligand for GIPR. For purposes of this disclosure, the term "GIP" can be used interchangeably to refer to any mature GIP polypeptide.

[0082] As used herein, the term "antibody" refers to an intact immunoglobulin. An antibody comprises two full-length heavy chains and two full-length light chains. Antibodies

may be derived solely from a single source, or may be "chimeric," that is, different portions of the antibody may be derived from two different antibodies as described further below.

[0083] As used herein, the term "light chain" or "immunoglobulin light chain" refers to a polypeptide comprising, from amino terminus (N-terminus) to carboxyl terminus (C-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 a human kappa (κ) or human lambda (λ) constant domain.

[0084] As used herein, the term "heavy chain" or "immunoglobulin heavy chain" refers to a polypeptide comprising, from amino terminus (N-terminus) to carboxyl terminus (C-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. In accordance with the present disclosure, an antibody is of the IgG isotype. IgG has several subclasses, including, but not limited to IgG1, IgG2, IgG3, and IgG4.

[0085] Variable regions of immunoglobulin chains generally exhibit the same overall structure, comprising relatively conserved framework regions (FR) joined by three hypervariable regions, more often called "complementarity determining regions" or CDRs. The CDRs from the two chains of each heavy chain and light chain pair typically are aligned by the framework regions to form a structure that binds specifically to a specific epitope on the target antigen or protein. From N-terminus to C-terminus, naturally-occurring light and heavy chain variable regions of an antibody both typically conform with the following order of these elements: FR1, CDR1, FR2, CDR2, FR3, CDR3, and FR4. Numbering systems have been devised for assigning numbers to amino acids that occupy positions in each of these domains. Exemplary numbering systems are defined in Kabat Sequences of Proteins of Immunological Interest (1987 and 1991, NIH, Bethesda, MD), and Chothia & Lesk, J. Mol. Biol. 196:901-917 (1987); Chothia et al., Nature 342:878-883 (1989). Other numbering systems for identifying amino acids in immunoglobulin chains include IMGT® (the international ImMunoGeneTics information

system; Lefranc et al., Dev. Comp. Immunol. 29:185-203; 2005) and AHo (Honegger and Pluckthun, J. Mol. Biol. 309(3):657-670; 2001).

[0086] As used herein, an "antagonist anti-GIPR antibody" and "anti-GIPR antibody" refer to an intact immunoglobulin of the IgG isotype that partially or fully blocks, inhibits, or neutralizes a biological activity of the GIPR protein. Antagonist activity of the anti-GIPR antibody of the present disclosure is determined using the GIPR activity assay and GIPR binding assay defined herein.

[0087] As used herein, an "antibody fragment" is a portion (regardless of how that portion is obtained or synthesized) of an antibody that lacks at least some of the amino acids present in a full-length chain but which is capable of binding to the same antigen at the same epitope as the corresponding full-length antibody. Exemplary antibody fragments include, but are not limited to, Fab, Fab', and $F(ab')_2$ fragments.

[0088] As used herein, a "Fc domain" refers to the portion of an antibody comprising the second and third constant domains of the heavy chain (i.e., CH2 and CH3), and can optionally comprise the CH4 domain. The Fc domain may be an Fc domain 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. A "Fc-containing polypeptide" refers to a polypeptide comprising an Fc domain as defined herein.

[0089] As used herein, the terms "GLP-1 receptor agonist" and "GLP-1 receptor agonist polypeptide" are used interchangeably and refer to a molecule that mimics a biological activity of the naturally occurring glucagon-like peptide (GLP-1) molecule with respect to a GLP-1 receptor.

[0090] As used herein, the term "pharmaceutically acceptable" refers to a species or component that is generally safe, non-toxic, and neither biologically nor otherwise undesirable for use in a subject.

[0091] As used herein, the term "pharmaceutically acceptable excipient" refers to a broad range of ingredients that may be combined with a polypeptide or conjugate molecule disclosed herein to prepare a pharmaceutically acceptable composition or formulation. Excipients include,

for example, vehicles (e.g., solvents, dispersion media), coatings, isotonic and absorption delaying agents, diluents, colorants, glidants, disintegrants, flavoring agents, coatings, binders, sweeteners, lubricants, sorbents, and preservatives (e.g., antibacterial and antifungal agents).

[0092] As used herein, the term "therapeutically effective amount" refers to that amount of a polypeptide or conjugate molecule disclosed herein that elicits a desired biological or medical response in a cell, a tissue, a system, or a subject. The desired biological or medical response does not necessarily occur by administration of one dose, and may occur only after administration of a series of doses. Thus, a therapeutically effective amount may be administered in one or more administrations.

[0093] As used herein, the term "subject" or "subjects" refers to humans and other mammals. The term "mammal" as used herein includes, for example, humans, non-human primates, cattle, sheep, goats, pigs, horses, cats, dog, rabbits, rodents (e.g., rats or mice), and monkeys. Human subjects include neonates, infants, juveniles, adults, and geriatric subjects. In one embodiment, the subject is a human. In one embodiment, the subject is an adult human.

[0094] It should be understood that this invention is not limited to the particular methodology, protocols, and reagents, etc., described herein and as such may vary. The terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the disclosed, which is defined solely by the claims.

GLP-1 RECEPTOR AGONIST POLYPEPTIDES

[0095] The present disclosure is directed to GLP-1 receptor agonist polypeptides and molecules, *e.g.*, protein conjugates, comprising these GLP-1 receptor agonist polypeptides. These GLP-1 receptor agonist polypeptides, which are also referred to herein as GLP-1 receptor agonists and GLP-1R agonist polypeptides, encompass molecules that mimic one or more biological activities of the native human GLP-1 polypeptide with respect to its binding to the human GLP-1 receptor. In addition, these GLP-1 receptor agonist polypeptides possess one or more advantageous properties relative to the native GLP-1 protein and/or other GLP-1 receptor agonist polypeptides known in the art.

[0096] The native human GLP-1 polypeptide is produced from post-translational processing of proglucagon within intestinal cells. Proglucagon cleavage by PCSK1/PC1 generates a peptide comprising the proglucagon residues 71-108 or a C-terminally amidated form comprising residues 71-107 amide. Additional N-terminal truncation of this proglucagon

derived peptide fragment within the intestinal cells is required to form the active GLP-1 peptide. Thus, the active human GLP-1 peptide, which is referred to as GLP-1(7-37), comprises the amino acid sequence of HAEGTFTSDVSSYLEGQAAKEFIAWLVKGRG (SEQ ID NO: 1584). A C-terminally amidated version of this peptide is known as GLP-1(7-36)amide.

[0097] In one embodiment of the present disclosure, the GLP-1 receptor agonist polypeptide is an analog of the native human GLP-1(7-37) peptide, *i.e.*, an analog of the amino acid sequence of SEQ ID NO: 1584. As used herein, a "GLP-1 analog" refers to a molecule which possesses improved biological activity, e.g., improved stability or agonist potency, relative to the corresponding biological activity of GLP-1(7–37), when evaluated by the GLP-1 receptor agonist activity assay as described in Example 3 herein or using other art-known measures such as receptor binding assays or *in vivo* blood glucose assays as described, e.g., by Hargrove et al., *Regulatory Peptides*, 141:113-119 (2007), the disclosure of which is incorporated by reference herein. In one embodiment, a GLP-1 analog refers to a peptide comprising an amino acid sequence with at least 4, at least 5, at least 6, at least 7, at least 8, or at least 9 amino acid substitutions, insertions, deletions (or a combination of two or more of substitutions, insertions, deletions), when compared to the amino acid sequence of a GLP-1(7-37). In one embodiment, the GLP-1 analog of the present disclosure comprises an amino acid sequence with 5, 6, 7, 8, or 9 amino acid substitutions, insertions, deletions (or a combination of two or more of substitutions, insertions, deletions), when compared to the amino acid sequence of a GLP-1(7-37) (SEQ ID NO: 1584). In one embodiment, the GLP-1 analog of the present disclosure comprises an amino acid sequence with 5, 6, 7, 8, or 9 amino acid substitutions in the amino acid sequence of the GLP-1(7-37) polypeptide of SEQ ID NO: 1584. In one embodiment, these 5, 6, 7, 8, or 9 amino acid substitutions comprise a substitution at any 5 or more positions selected from A2, V10, G16, Q17, K20, A24, V27, K28, and R30 of the GLP-1(7-37) peptide of SEQ ID NO: 1584. In one embodiment, the GLP-1 analog comprises substitutions at A2, V10, G16, and R30, plus one or more additional amino acid substitutions at residues selected from Q17, K20, A24, V27, and K28 of SEQ ID NO: 1584. In one embodiment, the GLP-1 analog comprises substitutions at A2, V10, G16, and R30, plus two additional amino acid substitutions as residues selected from Q17, K20, A24, V27, and K28 of SEQ ID NO: 1584. In one embodiment, the GLP-1 analog comprises substitutions at A2, V10, G16, and R30, plus three additional amino acid substitutions as residues selected from Q17, K20, A24, V27, and K28 of SEQ ID NO: 1584.

In one embodiment, the GLP-1 analog comprises substitutions at A2, V10, G16, and R30, plus four additional amino acid substitutions as residues selected from Q17, K20, A24, V27, and K28 of SEQ ID NO: 1584. In one embodiment, the GLP-1 analog comprises substitutions at A2, V10, G16, R30, Q17, K20, A24, V27, and K28 of the GLP-1(7-37) peptide of SEQ ID NO: 1584. GLP-1 analogs of the present disclosure include any of the aforementioned analogs in an amidated form, acid form, pharmaceutically acceptable salt form, and any other physiologically active forms of the molecule.

[0098] In one embodiment, the GLP-1 receptor agonist polypeptide of the present disclosure comprises the amino acid sequence of H[Aib]EGTFTSDYSSYLEEX_{17}AAX_{20}EFIX_{24}WL$X_{27}X_{28}$GGG (SEQ ID NO: 1575), where Aib at position 2 is α-amino-isobutyric acid; X_{17} is selected from glutamine (Q), lysine (K), glutamic acid (E), or arginine (R), X_{20} is selected from K, R, Q, or homoarginine (hArg), X_{24} is selected from alanine (A), E, Q, aspartic acid (D), d-Ala, glycine (G), asparagine (N), K, (1S,2S)-2-Aminocyclopentanecarboxylic acid (ACPC), (3S,4R)-4-Amino-3-pyrrolidinecarboxylic acid (APCA), threonine (T), serine (S), or tyrosine (Y); X_{27} is selected from valine (V), K, α-amino-isobutyric acid (Aib), N, S, T, Y, Q, or R; and X_{28} is selected from K, E, R, Q, D, N, G, S, orT. In accordance with this, and all embodiments of the present disclosure, the GLP-1 receptor agonist of the present disclosure does not comprise the amino acid sequence of SEQ ID NO: 1574 (H[Aib]EGTFTSDYSSYLEEQAAKEFIAWLVKGGG).

[0099] In one embodiment, the GLP-1 receptor agonist polypeptide of the present disclosure comprises the amino acid sequence of H[Aib]EGTFTSDYSSYLEEX_{17}AAX_{20}EFIX_{24}WL$X_{27}X_{28}$GGG (SEQ ID NO: 1576), where X_{17} is Q or K; X_{20} is K or R; X_{24} is A, E, or Q; X_{27} is V or K; and X_{28} is K, E, or R. As noted above, the GLP-1 receptor agonist of the present disclosure does not comprise the amino acid sequence of SEQ ID NO: 1574.

[0100] In one embodiment, the GLP-1 receptor agonist polypeptide of the present disclosure comprises the amino acid sequence H[Aib]EGTFTSDYSSYLEEX_{17}AAREFIX_{24}WL$X_{27}X_{28}$GGG (SEQ ID NO: 1577), where X_{17} is Q or K; X_{24} is A, E, or Q; X_{27} is V or K; and X_{28} is K, E, or R. Alternatively, the GLP-1 receptor agonist of the present disclosure comprises the amino acid sequence of

(H[Aib]EGTFTSDYSSYLEEX$_{17}$AAX$_{20}$EFIX$_{24}$WLKX$_{28}$GGG (SEQ ID NO: 1578), where X$_{17}$ is Q or K; X$_{20}$ is K or R; X$_{24}$ is A, E, or Q; and X$_{28}$ is K, E, or R.

[0101] Non-limiting examples of GLP-1 receptor agonists of the present disclosure are presented in the Table 1 below. The description column of Table 1 provides the amino acid substitution (relative to GLP-1(7-37)) that are present at the identified position in the particular GLP-1 receptor agonist polypeptide sequence.

Table 1. GLP-1 Receptor Agonist Polypeptide Sequences

Description	**Sequence**	**SEQ ID NO:**
Aib2;Y10;E16;E24;R20;K27;G30	H[Aib]EGTFTSDYSSYLEEQAAREFIEWLKKGGG	1579
Aib2;Y10;E16;E24;E28;R20;K17;K27;G30	H[Aib]EGTFTSDYSSYLEEKAAREFIEWLKEGGG	1580
Aib2;Y10;E16;E24;R20;K17,K27;G30	H[Aib]EGTFTSDYSSYLEEKAAREFIEWLKKGGG	1581
Aib2;Y10;E16;E24;R20;R28;K27;G30	H[Aib]EGTFTSDYSSYLEEQAAREFIEWLKRGGG	1582
Aib2;Y10;E16;E28;K17;K27;R20;Q24;G30	H[Aib]EGTFTSDYSSYLEEKAAREFIQWLKEGGG	1583

Aib is α-amino-isobutyric acid

[0102] In one embodiment, the human glucagon-like peptide 1 (GLP-1) receptor agonist polypeptide of the present disclosure comprises 31 amino acids and comprises an amino acid sequence having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97% or at least 98% sequence identity to the amino acid sequence of SEQ ID NO: 1580. This GLP-1 receptor agonist polypeptide also comprises an α-amino-isobutyric acid (Aib) at position 2; a tyrosine at position 10; a glutamic acid at positions 16, 24, and 28; an arginine at position 20; a lysine at positions 17 and 27; and a glycine at position 30. In one embodiment, this GLP-1 receptor agonist polypeptide comprises an amino acid sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 1580. In one embodiment, this GLP-1 receptor agonist polypeptide comprises an amino acid sequence having at least 95% sequence identity to the amino acid sequence of SEQ ID NO: 1580. In one embodiment, this GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1580.

[0103] In one embodiment, the human glucagon-like peptide 1 (GLP-1) receptor agonist polypeptide of the present disclosure comprises 31 amino acids and comprises an amino acid

sequence having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97% or at least 98% sequence identity to the amino acid sequence of SEQ ID NO: 1579. This GLP-1 receptor agonist polypeptide also comprises an Aib at position 2; a tyrosine at position 10; a glutamic acid at positions 16 and 24; an arginine at position 20; a lysine at positions 27; and a glycine at position 30. In one embodiment, this GLP-1 receptor agonist polypeptide comprises an amino acid sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 1579. In one embodiment, this GLP-1 receptor agonist polypeptide comprises an amino acid sequence having at least 95% sequence identity to the amino acid sequence of SEQ ID NO: 1579. In one embodiment, this GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1579.

[0104] In one embodiment, the human glucagon-like peptide 1 (GLP-1) receptor agonist polypeptide of the present disclosure comprises 31 amino acids and comprises an amino acid sequence having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97% or at least 98% sequence identity to the amino acid sequence of SEQ ID NO: 1581. This GLP-1 receptor agonist polypeptide also comprises an Aib at position 2; a tyrosine at position 10; a glutamic acid at positions 16 and 24; an arginine at position 20; a lysine at positions 17, 27; and a glycine at position 30. In one embodiment, this GLP-1 receptor agonist polypeptide comprises an amino acid sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 1581. In one embodiment, this GLP-1 receptor agonist polypeptide comprises an amino acid sequence having at least 95% sequence identity to the amino acid sequence of SEQ ID NO: 1581. In one embodiment, this GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1581.

[0105] In one embodiment, the human glucagon-like peptide 1 (GLP-1) receptor agonist polypeptide of the present disclosure comprises 31 amino acids and comprises an amino acid sequence having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97% or at least 98% sequence identity to the amino acid sequence of SEQ ID NO: 1583. This GLP-1 receptor agonist polypeptide also comprises an Aib at position 2; a tyrosine at position 10; a glutamic acid at positions 16 and 28; an arginine at position 20; a lysine at positions 17, 27; a glutamine at position 24; and a glycine at position 30. In one embodiment, this GLP-1 receptor agonist polypeptide comprises an amino acid sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 1583. In one embodiment, this GLP-1 receptor agonist

polypeptide comprises an amino acid sequence having at least 95% sequence identity to the amino acid sequence of SEQ ID NO: 1583. In one embodiment, this GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1583.

[0106] In one embodiment, the human glucagon-like peptide 1 (GLP-1) receptor agonist polypeptide of the present disclosure comprises 31 amino acids and comprises an amino acid sequence having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97% or at least 98% sequence identity to the amino acid sequence of SEQ ID NO: 1582. This GLP-1 receptor agonist polypeptide also comprises an Aib at position 2; a tyrosine at position 10; a glutamic acid at positions 16 and 24; an arginine at positions 20 and 28; a lysine at positions 27; and a glycine at position 30. In one embodiment, this GLP-1 receptor agonist polypeptide comprises an amino acid sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 1582. In one embodiment, this GLP-1 receptor agonist polypeptide comprises an amino acid sequence having at least 95% sequence identity to the amino acid sequence of SEQ ID NO: 1582. In one embodiment, this GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1582.

[0107] In one embodiment, the GLP-1 receptor agonist consists of the amino acid sequence of SEQ ID NO: 1579. In one embodiment, the GLP-1 receptor agonist consists of the amino acid sequence of SEQ ID NO: 1580. In one embodiment, the GLP-1 receptor agonist consists of the amino acid sequence of SEQ ID NO: 1581. In one embodiment, the GLP-1 receptor agonist consists of the amino acid sequence of SEQ ID NO: 1582. In one embodiment, the GLP-1 receptor agonist consists of the amino acid sequence of SEQ ID NO: 1583.

[0108] In one embodiment, the GLP-1 receptor agonist agonizes the human GLP-1 receptor. In one embodiment, the GLP-1 receptor agonist polypeptide has an EC_{50} of less than or equal to 50 pM for agonizing the human GLP-1 receptor as measured using the GLP-1 receptor agonist activity assay described herein in Example 3. For example, the GLP-1 receptor agonist polypeptide has an EC_{50} of less than or equal to 45 pM, less than or equal to 40 pM, less than or equal to 35 pM, less than or equal to 30 pM, less than or equal to 25 pM, less than or equal to 20 pM, less than or equal to 15 pM. In one embodiment, the GLP-1 EC_{50} is measured in the GLP-1 receptor agonist activity assay described in Example 3 herein.

[0109] In one embodiment, the GLP-1 receptor agonist polypeptide has an EC_{50} of about 10 pM for agonizing the human GLP-1 receptor as measured using the GLP-1 receptor agonist

activity assay described herein in Example 3. In one embodiment, the GLP-1 receptor agonist polypeptide has an EC_{50} of about 15 pM, about 20 pM, about 25 pM, about 30 pM, about 35 pM, about 40 pM, about 45 pM, about 50 pM, about 55 pM, about 60 pM, about 65 pM, about 70 pM, about 75 pM for agonizing the human GLP-1 receptor as measured using the GLP-1 receptor agonist activity assay described herein in Example 3.

[0110] In one embodiment, the GLP-1 receptor agonists disclosed herein are chemically derivatized at one or more amino acid residues by known organic chemistry techniques. In accordance with this and all embodiments of the disclosure "chemical derivative" or "chemically derivatized" refers to a peptide (e.g., peptide linker as described herein), polypeptide (e.g., GLP-1 receptor agonist polypeptide), or other protein (e.g., anti-GIPR antibody as described herein) having one or more residues chemically derivatized by reaction of a functional side group. Such derivatized molecules include, for example, those molecules in which free amino groups have been derivatized to form amine hydrochlorides, p-toluene sulfonyl groups, carbobenzoxy groups, t-butyloxycarbonyl groups, chloroacetyl groups or formyl groups. Free carboxyl groups may be derivatized to form salts, methyl and ethyl esters or other types of esters or hydrazides. Free hydroxyl groups may be derivatized to form O-acyl or O-alkyl derivatives. The imidazole nitrogen of histidine may be derivatized to form N-im-benzylhistidine. Also included as chemical derivatives are those polypeptides which contain one or more naturally occurring amino acid derivatives of the twenty canonical amino acids, whether in L- or D-form. For example, 4-hydroxyproline may be substituted for proline; 5-hydroxylysine may be substituted for lysine; 3-methylhistidine may be substituted for histidine; homoserine may be substituted for serine; and ornithine may be substituted for lysine.

[0111] Useful derivatizations include, in one embodiment, those in which the amino terminal of the polypeptide is chemically blocked so that conjugation to an Fc-containing peptide or an antibody will be prevented from taking place at an N-terminal free amino group of the GLP-1 receptor agonist polypeptide. There may be other beneficial effects of such as modification, for example, a reduction in the polypeptide agonist's susceptibility to enzymatic proteolysis. The N-terminus can be acylated or modified to a substituted amine, or derivatized with another functional group, such as an aromatic moiety (e.g., an indole acid, benzyl (Bzl or Bn), dibenzyl (DiBzl or Bn2), or benzyloxycarbonyl (Cbz or Z)), N,N-dimethylglycine or creatine. For example, in one embodiment, an acyl moiety, such as, but not limited to, a formyl,

acetyl (Ac), propanoyl, butanyl, heptanyl, hexanoyl, octanoyl, or nonanoyl, are covalently linked to the N-terminal end of the peptide, which can prevent undesired side reactions during conjugation of the peptide to an Fc-containing peptide or antibody. Other exemplary N-terminal derivative groups include —NRR1 (other than —NH2), —NRC(O)R1, —NRC(O)OR1, —NRS(O)2R1, —NHC(O)NH1, succinimide, or benzyloxycarbonyl-NH— (Cbz-NH—), wherein R and R1 are each independently hydrogen or lower alkyl and wherein the phenyl ring may be substituted with 1 to 3 substituents selected from C1-C4 alkyl, C1-C4 alkoxy, chloro, and bromo.

[0112] In one embodiment, one or more individual amino acid residues of the GLP-1 receptor agonist polypeptide as described herein is derivatized. Various derivatizing agents are known to react specifically with selected sidechains or terminal residues, as described in detail below by way of example.

[0113] Lysinyl residues and amino terminal residues of the GLP-1 receptor agonist polypeptides described herein may be reacted with succinic or other carboxylic acid anhydrides, which reverse the charge of the lysinyl residues. Other suitable reagents for derivatizing alpha-amino-containing residues include imidoesters such as methyl picolinimidate; pyridoxal phosphate; pyridoxal; chloroborohydride; trinitrobenzenesulfonic acid; O-methylisourea; 2,4 pentanedione; and transaminase-catalyzed reaction with glyoxylate.

[0114] Arginyl residues may be modified by reaction with any one or combination of several conventional reagents, including phenylglyoxal, 2,3-butanedione, 1,2-cyclohexanedione, and ninhydrin. Derivatization of arginyl residues requires that the reaction be performed in alkaline conditions because of the high pKa of the guanidine functional group. Furthermore, these reagents may react with the groups of lysine as well as the arginine epsilon-amino group

[0115] Specific modification of tyrosyl residues has been studied extensively, with particular interest in introducing spectral labels into tyrosyl residues by reaction with aromatic diazonium compounds or tetranitromethane. Most commonly, N-acetylimidizole and tetranitromethane are used to form O-acetyl tyrosyl species and 3-nitro derivatives, respectively.

[0116] Carboxyl sidechain groups (aspartyl or glutamyl) of the GLP-1 receptor agonist polypeptides described herein may be selectively modified by reaction with carbodiimides (R′—N═C═N—R′) such as 1-cyclohexyl-3-(2-morpholinyl-(4-ethyl) carbodiimide or 1-ethyl-3-(4-azonia-4,4-dimethylpentyl) carbodiimide. Furthermore, aspartyl and glutamyl residues may be converted to asparaginyl and glutaminyl residues by reaction with ammonium ions.

[0117] Glutaminyl and asparaginyl residues may be deamidated to the corresponding glutamyl and aspartyl residues. Alternatively, these residues are deamidated under mildly acidic conditions.

[0118] Cysteinyl residues can be replaced by amino acid residues or other moieties either to eliminate disulfide bonding or, conversely, to stabilize cross-linking.

[0119] In one embodiment, one or more peptidyl [—C(O)NR—] linkages (bonds) between amino acid residues of the GLP-1 receptor agonist polypeptide are replaced by a non-peptidyl linkage. Exemplary non-peptidyl linkages are —CH2-carbamate [—CH2—OC(O)NR—], phosphonate, —CH2-sulfonamide [—CH2—S(O)2NR—], urea [—NHC(O)NH—], —CH2-secondary amine, and alkylated peptide [—C(O)NR6— wherein R6 is lower alkyl].

[0120] Other possible modifications to the GLP-1 receptor agonist polypeptide include hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, oxidation of the sulfur atom in Cys, methylation of the alpha-amino groups of lysine, arginine, and histidine side chains.

CONJUGATE MOLECULES COMPRISING THE GLP-1 RECEPTOR AGONIST POLYPEPTIDES

[0121] Another aspect of the present disclosure is directed to molecules comprising a GLP-1 receptor agonist polypeptide as described *supra*.

[0122] In one embodiment, the molecule comprises a first GLP-1 receptor agonist polypeptide, where the first GLP-1 receptor agonist polypeptide is conjugated to a half-life extending domain. The half-life extending domain may be conjugated directly or via a linker moiety to the GLP-1 receptor agonist polypeptide.

[0123] In one embodiment, the half-life extending domain is a polypeptide (e.g., an antibody, antibody fragment, or peptide) that alters the pharmacodynamics and pharmacokinetics of the GLP-1 receptor agonist polypeptide relative to the unconjugated polypeptide. For example, in one embodiment, a half-life extending domain extends elimination half-time relative to the unconjugated polypeptide. In addition, in one embodiment, a half-life extending domain alters one or more pharmacodynamic properties of the polypeptide, such as, e.g., tissue distribution, penetration, or diffusion.

[0124] In one embodiment, the half-life extending domain is a molecule that specifically binds to a circulating plasma protein.

[0125] In one embodiment, the half-life extending domain is a molecule that specifically binds to an albumin. In one embodiment, the half-life extending domain is a polypeptide (e.g., an antibody, antibody fragment, or peptide) that specifically binds to an albumin.

[0126] In one embodiment, the half-life extending domain is a molecule that specifically binds to human serum albumin (HSA). In one embodiment, the half-life extending domain is a polypeptide (e.g., an antibody, antibody fragment, or peptide) that specifically binds to HSA.

[0127] In one embodiment, the half-life extending domain is HSA or a variant thereof.

[0128] In one embodiment, the half-life extending domain is a molecule that specifically binds to the neonatal Fc receptor (FcRn). In one embodiment, the half-life extending domain is a polypeptide (e.g., an antibody, antibody fragment, or peptide) that specifically binds to FcRn.

[0129] In one embodiment, the half-life extending domain is an Fc domain.

[0130] In one embodiment, the half-life extending domain is an Fc-containing polypeptide. In one embodiment, the half-life extending domain is an antibody. In one embodiment, the half-life extending domain is an antibody fragment.

[0131] In one embodiment, the half-life extending domain is an antibody.

[0132] Another aspect of the disclosure is directed to a conjugate molecule comprising a GLP-1 receptor agonist polypeptide as disclosed herein and an antagonist anti-glucose-dependent insulinotropic polypeptide receptor (GIPR) antibody. In one embodiment, the conjugate molecule comprises a first GLP-1 receptor agonist polypeptide comprising the amino acid sequence of H[Aib]EGTFTSDYSSYLEEX_{17}AAX_{20}EFIX_{24}WL$X_{27}X_{28}$GGG (SEQ ID NO: 1575), wherein X_{17} is Q, K, E, or R; X_{20} is K, R, Q, or homoarginine (hArg); X_{24} is A, E, Q, D, d-Ala, G, N, K, (1S,2S)-2-Aminocyclopentanecarboxylic acid (ACPC), (3S,4R)-4-Amino-3-pyrrolidinecarboxylic acid (APCA), T, S, or Y; X_{27} is V, K, Aib, N, S, T, Y, Q, or R; and X_{28} is K, E, R, Q, D, N, G, S, or T, and wherein the GLP-1 receptor agonist polypeptide does not comprise the amino acid sequence of SEQ ID NO: 1574; and an antagonist anti-GIPR human antibody.

[0133] An exemplary molecule of the present disclosure comprises a first GLP-1 receptor agonist polypeptide conjugated to an antagonist anti-GIPR human antibody. This molecule is referred to herein as an "anti-GIPR antibody/GLP-1 receptor agonist conjugate molecule", a "conjugate molecule", or an "anti-GIPR/GLP-1 conjugate molecule". Exemplary antagonist anti-GIPR antibodies are disclosed *infra*.

[0134] According to this embodiment of the disclosure, the antagonist anti-GIPR antibody of this anti-GIPR/GLP-1 conjugate molecule comprises a first cysteine conjugation site within a light chain or a heavy chain of the anti-GIPR antibody. The first GLP-1 receptor agonist polypeptide of the molecule is conjugated, at its C-terminus, to the first cysteine conjugation site of the anti-GIPR antibody.

[0135] In one embodiment, this anti-GIPR/GLP-1 conjugate molecule further comprises a second GLP-1 receptor agonist polypeptide. The second GLP-1 receptor agonist polypeptide is conjugated, at its C-terminus, to a second cysteine conjugation site of the anti-GIPR antibody. The second cysteine conjugation site of the anti-GIPR antibody is also located within a light chain or heavy chain of the anti-GIPR antibody. Preferably the first and second cysteine conjugations sites of the anti-GIPR antibody are located at corresponding positions within each light chain or within each heavy chain.

[0136] In one embodiment, the first and second GLP-1 receptor agonist polypeptides of this conjugate molecule that are conjugated to the anti-GIPR antibody comprise the same amino acid sequence. In one embodiment, the first and second GLP-1 receptor agonist polypeptides of the conjugate molecule comprise different amino acid sequences.

[0137] In one embodiment, the first and/or second GLP-1 receptor agonist polypeptides of this anti-GIPR/GLP-1 receptor agonist conjugate molecule (or any conjugate molecule of the present disclosure) comprise the amino acid sequence of H[Aib]EGTFTSDYSSYLEEX_{17}AAX_{20}EFIX_{24}WL$X_{27}X_{28}$GGG (SEQ ID NO: 1575), where Aib at position 2 is α-amino-isobutyric acid; X_{17} is selected from glutamine (Q), lysine (K), glutamic acid (E), or arginine (R), X_{20} is selected from K, R, Q, or homoarginine (hArg), X_{24} is selected from alanine (A), E, Q, aspartic acid (D), d-Ala, glycine (G), asparagine (N), K, (1S,2S)-2-Aminocyclopentanecarboxylic acid (ACPC), (3S,4R)-4-Amino-3-pyrrolidinecarboxylic acid (APCA), threonine (T), serine (S), or tyrosine (Y); X_{27} is selected from valine (V), K, α-amino-isobutyric acid (Aib), N, S, T, Y, Q, R; and X_{28} is selected from K, E, R, Q, D, N, G, S, T. In accordance with this, and all embodiments of the present disclosure, the GLP-1 receptor agonist of the anti-GIPR/GLP-1 conjugate molecule of the present disclosure does not comprise the amino acid sequence of H[Aib]EGTFTSDYSSYLEEQAAKEFIAWLVKGGG (SEQ ID NO: 1574).

[0138] In one embodiment, incorporation of the amino acid substitutions at the identified positions, in particular at residues 17, 20, 24, 27, and 28 (SEQ ID NO: 1575), improves *in vivo* stability of the conjugate molecule. For example, the identified amino acid substitutions render the GLP-1 polypeptide resistant to *in vivo* clipping from the conjugate as measured by a high ratio (≥ 0.65) of intact to total GIPR-GLP-1 molecule $AUC_{0\text{-}t}$ (*see* Example 5). In one embodiment, the incorporation of the amino acid substitutions at the identified positions of the GLP-1 receptor agonist polypeptide, in particular at positions 17, 20, 24, 27, and 28**,** improves the potency of the conjugate molecule. For example, the identified amino acid substitutions render the conjugate molecule more therapeutically potent as measured by body weight loss following *in vivo* administration (*see* Example 4).

[0139] In one embodiment, the first and/or second GLP-1 receptor agonist polypeptides of the anti-GIPR/GLP-1 receptor agonist conjugate molecule comprises the amino acid sequence of H[Aib]EGTFTSDYSSYLEEX_{17}AAX_{20}EFIX_{24}WL$X_{27}X_{28}$GGG (SEQ ID NO: 1576), where X_{17} is Q or K; X_{20} is K or R; X_{24} is A, E, or Q; X_{27} is V or K; and X_{28} is K, E, or R. As noted above, the GLP-1 receptor agonist of the anti-GIPR antibody/GLP-1 receptor agonist conjugate molecule does not comprise the amino acid sequence of SEQ ID NO: 1574.

[0140] In one embodiment, the first and/or second GLP-1 receptor agonist polypeptides of the anti-GIPR/GLP-1 receptor agonist conjugate molecule comprises the amino acid sequence of H[Aib]EGTFTSDYSSYLEEX_{17}AAREFIX_{24}WL$X_{27}X_{28}$GGG (SEQ ID NO: 1577), where X_{17} is Q or K; X_{24} is A, E, or Q; X_{27} is V or K; and X_{28} is K, E, or R. Alternatively, the first and/or second GLP-1 receptor agonist of the anti-GIPR antibody/GLP-1 receptor agonist conjugate molecule comprises the amino acid sequence of H[Aib]EGTFTSDYSSYLEEX_{17}AAX_{20}EFIX_{24}WLKX_{28}GGG (SEQ ID NO: 1578), where X_{17} is Q or K; X_{20} is K or R; X_{24} is A, E, or Q; and X_{28} is K, E, or R.

[0141] In one embodiment, the first and/or second GLP-1 receptor agonist polypeptides of the conjugate molecule comprise 31 amino acids and comprise an amino acid sequence having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97% or at least 98% sequence identity to the amino acid sequence of SEQ ID NO: 1580. This GLP-1 receptor agonist polypeptide also comprises an Aib at position 2; a tyrosine at position 10; a glutamic acid at positions 16, 24, and 28; an arginine at position 20; a lysine at positions 17 and 27; and a glycine at position 30. In one embodiment, the first and/or second GLP-1 receptor agonist polypeptide

comprises an amino acid sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 1580. In one embodiment, the first and/or second GLP-1 receptor agonist polypeptide of the conjugate molecule comprises an amino acid sequence having at least 95% sequence identity to the amino acid sequence of SEQ ID NO: 1580. In one embodiment, the first and/or second GLP-1 receptor agonist of the anti-GIPR/GLP-1 conjugate molecule comprises the amino acid sequence of SEQ ID NO: 1580.

[0142] In one embodiment, the first and/or second GLP-1 receptor agonist polypeptides of the conjugate molecule comprise 31 amino acids and comprise an amino acid sequence having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97% or at least 98% sequence identity to the amino acid sequence of SEQ ID NO: 1579. This GLP-1 receptor agonist polypeptide also comprises an Aib at position 2; a tyrosine at position 10; a glutamic acid at positions 16 and 24; an arginine at position 20; a lysine at positions 27; and a glycine at position 30. In one embodiment, the first and/or second GLP-1 receptor agonist polypeptide comprises an amino acid sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 1579. In one embodiment, the first and/or second GLP-1 receptor agonist polypeptide comprises an amino acid sequence having at least 95% sequence identity to the amino acid sequence of SEQ ID NO: 1579. In one embodiment, the first and/or second GLP-1 receptor agonist of the anti-GIPR/GLP-1 conjugate molecule comprises the amino acid sequence of SEQ ID NO: 1579.

[0143] In one embodiment, the first and/or second GLP-1 receptor agonist polypeptides of the conjugate molecule comprise 31 amino acids and comprise an amino acid sequence having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97% or at least 98% sequence identity to the amino acid sequence of SEQ ID NO: 1581. The first and/or second GLP-1 receptor agonist polypeptide also comprises an Aib at position 2; a tyrosine at position 10; a glutamic acid at positions 16 and 24; an arginine at position 20; a lysine at positions 17, 27; and a glycine at position 30. In one embodiment, first and/or second GLP-1 receptor agonist polypeptide comprises an amino acid sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 1581. In one embodiment, the first and/or second GLP-1 receptor agonist polypeptide comprises an amino acid sequence having at least 95% sequence identity to the amino acid sequence of SEQ ID NO: 1581. In one embodiment, the first and/or

second GLP-1 receptor agonist of the anti-GIPR/GLP-1 conjugate molecule comprises the amino acid sequence of SEQ ID NO: 1581.

[0144] In one embodiment, the first and/or second GLP-1 receptor agonist polypeptides of the conjugate molecule comprise 31 amino acids and comprise an amino acid sequence having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97% or at least 98% sequence identity to the amino acid sequence of SEQ ID NO: 1583. This GLP-1 receptor agonist polypeptide also comprises an Aib at position 2; a tyrosine at position 10; a glutamic acid at positions 16 and 28; an arginine at position 20; a lysine at positions 17, 27; a glutamine at position 24; and a glycine at position 30. In one embodiment, the first and/or second GLP-1 receptor agonist polypeptide comprises an amino acid sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 1583. In one embodiment, the first and/or second GLP-1 receptor agonist polypeptide comprises an amino acid sequence having at least 95% sequence identity to the amino acid sequence of SEQ ID NO: 1583. In one embodiment, the first and/or second GLP-1 receptor agonist of the anti-GIPR/GLP-1 conjugate molecule comprises the amino acid sequence of SEQ ID NO: 1583.

[0145] In one embodiment, the first and/or second GLP-1 receptor agonist polypeptides of the conjugate molecule comprise 31 amino acids and comprise an amino acid sequence having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97% or at least 98% sequence identity to the amino acid sequence of SEQ ID NO:1582. This GLP-1 receptor agonist polypeptide also comprises an Aib at position 2; a tyrosine at position 10; a glutamic acid at positions 16 and 24; an arginine at positions 20 and 28; a lysine at positions 27; and a glycine at position 30. In one embodiment, the first and/or second GLP-1 receptor agonist polypeptide comprises an amino acid sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 1582. In one embodiment, the first and/or second GLP-1 receptor agonist polypeptide comprises an amino acid sequence having at least 95% sequence identity to the amino acid sequence of SEQ ID NO: 1582. In one embodiment, the first and/or second GLP-1 receptor agonist of the anti-GIPR/GLP-1 conjugate molecule comprises the amino acid sequence of SEQ ID NO: 1582.

[0146] In one embodiment, the first GLP-1 receptor agonist polypeptide of the conjugate molecule is directly conjugated, at its C-terminus, to the first cysteine conjugation site of the anti-GIPR antibody. In one embodiment, each of the first and second GLP-1 receptor agonist

polypeptides of the molecule is directly conjugated, at its C-terminus, to the first and second cysteine conjugations sites of the anti-GIPR antibody, respectively. The position of the first and second cysteine conjugation sites within the anti-GIPR antibody are described in more detail *infra*.

[0147] In one embodiment, the first GLP-1 receptor agonist polypeptide of the conjugate molecule is conjugated, at its C-terminus, to the first cysteine conjugation site of the anti-GIPR antibody via a linker moiety. In one embodiment, each of the first and second GLP-1 receptor agonist polypeptides of the conjugate molecule are conjugated, at their C-terminus, to the first and second cysteine conjugation sites of the anti-GIPR antibody, respectively, via first and second linker moieties, respectively.

[0148] In one embodiment a linker moiety couples the C-terminal end of a GLP-1 receptor agonist polypeptide to a conjugation site on an anti-GIPR antibody. The presence of any linker moiety in the GLP-1 receptor agonist conjugate molecules as described herein is optional. In one embodiment, the linker moiety serves primarily as a spacer to position, join, connect, or optimize presentation or position of the functional moieties of the molecule (e.g., the GLP-1 receptor agonist polypeptide and/or the anti-GIPR antibody). In another embodiment, a linker moiety is utilized to optimize pharmacological activity or stability of the GLP-1 receptor agonist containing molecules disclosed herein. In a preferred embodiment, the linker moiety of the anti-GIPR antibody/GLP-1 receptor agonist polypeptide conjugate molecule described herein contributes to the enhanced the stability of the molecule in terms of resistance to cleavage upon *in vivo* administration.

[0149] In one embodiment, the linker moiety is a peptide linker moiety. Peptide linkers are made up of amino acids that are typically linked together by peptide bonds and are a length of from 1 to about 40 amino acid residues, preferably, a length of from 10 to about 30 amino acid residues, and more preferably, a length of from 10 to about 20 amino acid residues. In some embodiments, the peptide linker may comprise amino acid residues where one or more of the amino acid residues are not linked via a peptide bond (i.e., The amino acid residues of the linker are chosen from among the twenty canonical amino acids. More preferably, the amino acid residues of the linker are chosen from among glycine, alanine, proline, asparagine, glutamine, and /or serine. Even more preferably, a peptidyl linker is made up of a majority of amino acids that are sterically unhindered, such as glycine, serine, and alanine linked by a peptide bond. It is

also desirable that, if present, the peptidyl linker is one that is not subject to rapid proteolytic turnover in circulation.

[0150] Exemplary linker moieties of the anti-GIPR antibody/GLP-1 receptor agonist conjugate molecules described herein include the linker peptide of SEQ ID NO: 1585, the linker peptide of SEQ ID NO: 1586, the linker peptide of SEQ ID NO: 1587, the linker peptide of SEQ ID NO: 1588, the linker peptide of SEQ ID NO: 1589, the linker peptide of SEQ ID NO: 1590, the linker peptide of SEQ ID NO: 1591, the linker peptide of SEQ ID NO: 1592, and the linker peptide of SEQ ID NO: 1593. Additional peptide linkers suitable for inclusion in the anti-GIPR antibody/GLP-1 receptor agonist conjugate molecules described herein are provided in Table 2 herein.

[0151] In one embodiment, the linkage between a GLP-1 receptor polypeptide and a peptide linker is a peptide bond between the C-terminal amino acid residue of the GLP-1 agonist polypeptide and N-terminal amino acid residue of the peptide linker. In one embodiment, the linkage between a GLP-1 receptor polypeptide and a peptide linker is an amide bond between the C-terminal amino acid residue of the GLP-1 agonist polypeptide and the side chain of a lysine residue (i.e., at the ε amino group of the lysine) on the peptide linker. In one embodiment, the linkage between a GLP-1 receptor polypeptide and a peptide linker is an amide bond between the C-terminal amino acid residue of the GLP-1 agonist polypeptide and the α amino group of a C-terminal lysine residue on the peptide linker.

[0152] In one embodiment, exemplary linker peptides comprise a sequence of amino acid residues coupled via standard peptide bonds (e.g., the peptide linkers of SEQ ID NOs: 1585-1587 and 1592-1654). In one embodiment, exemplary linker peptides comprise at least on non-standard peptide bond. In this embodiment, the linker peptide comprises a sequence of amino acid residues coupled via standard peptide bonds, where the C-terminal residue of this sequence is coupled, via an amide bond, to the epsilon amino group of a lysine residue. For example, the exemplary linker peptides of SEQ ID NOs: 1588-1591 comprise a non-standard amino acid linkage at the lysine residue. In particular, for the linker peptides of SEQ ID NOs: 1588 and 1590, the glutamine residue at position 15 of these peptides is linked via an amide bond to the epsilon amino group of the adjacent lysine. This unique linkage is represented in the linker peptide as provided in Table 2 by the lysine residue outside the parenthesis enclosing the remainder of the linker sequence. Similarly, for the linker peptides of SEQ ID NOs: 1589 and

1591, the serine residue at position 15 of these peptides is linked via an amide bond to the epsilon amino group of the adjacent lysine residue. The linkage between a GLP-1 receptor polypeptide and a peptide linker of SEQ ID NO: 1588, SEQ ID NO: 1589, SEQ ID NO: 1590, or SEQ ID NO: 1591 occurs via an amide bond between the C-terminal amino acid residue of the GLP-1 agonist polypeptide and the α amino group of the lysine residue of the linker. In these embodiments, the N-terminal amino acid residue of the linker peptide is coupled to the cysteine conjugation site on the anti-GIPR antibody residue. The N-terminal amino acid residue of the linker peptide may be modified, *e.g.*, bromoacetylated, to facility the coupling to the cysteine conjugation site on the anti-GIPR antibody.

[0153] In one embodiment, the molecule disclosed herein comprises a GLP-1 receptor agonist polypeptide of SEQ ID NO: 1579 covalently linked to the linker peptide of SEQ ID NO: 1585, the linker peptide of SEQ ID NO: 1586, the linker peptide of SEQ ID NO: 1587, the linker peptide of SEQ ID NO: 1588, the linker peptide of SEQ ID NO: 1589, the linker peptide of SEQ ID NO: 1590, the linker peptide of SEQ ID NO: 1591, the linker peptide of SEQ ID NO: 1592, or the linker peptide of SEQ ID NO: 1593. In one embodiment, the molecule disclosed herein comprises a GLP-1 receptor agonist polypeptide of SEQ ID NO: 1579, where the C-terminal amino acid residue of the polypeptide is covalently linked to the N-terminal amino acid residue of the linker peptide of SEQ ID NO: 1592 as depicted in FIG. 2. In one embodiment, the C-terminal lysine of the linker peptide is modified, *e.g.*,bromoacetylated, for coupling to the cysteine residue of the conjugation site on the anti-GIPR antibody.

[0154] In one embodiment, the molecule disclosed herein comprises a GLP-1 receptor agonist polypeptide of SEQ ID NO: 1580 covalently linked to the linker peptide of SEQ ID NO: 1585, the linker peptide of SEQ ID NO: 1586, the linker peptide of SEQ ID NO: 1587, the linker peptide of SEQ ID NO: 1588, the linker peptide of SEQ ID NO: 1589, the linker peptide of SEQ ID NO: 1590, the linker peptide of SEQ ID NO: 1591, the linker peptide of SEQ ID NO: 1592, or the linker peptide of SEQ ID NO: 1593. In one embodiment, the molecule disclosed herein comprises a GLP-1 receptor agonist polypeptide of SEQ ID NO: 1580, where the C-terminal amino acid residue of the polypeptide is covalently linked to the α-amino group of the lysine residue of the linker peptide of SEQ ID NO: 1591 as depicted in FIG. 3. As noted above, the adjacent serine residue of the linker, *i.e.*, the serine at position 15 of the linker peptide of SEQ ID NO: 1591, is linked via an amide bond to the epsilon amino group of the lysine residue as shown

in FIG. 3. In this embodiment, the N-terminal glycine residue of the linker peptide is modified, i.e., bromoacetylated, for coupling to the cysteine residue of the conjugation site on the anti-GIPR antibody.

[0155] In one embodiment, the molecule disclosed herein comprise a GLP-1 receptor agonist polypeptide of SEQ ID NO: 1581 covalently linked to the linker peptide of SEQ ID NO: 1585, the linker peptide of SEQ ID NO: 1586, the linker peptide of SEQ ID NO: 1587, the linker peptide of SEQ ID NO: 1588, the linker peptide of SEQ ID NO: 1589, the linker peptide of SEQ ID NO: 1590, the linker peptide of SEQ ID NO: 1591, the linker peptide of SEQ ID NO: 1592, or the linker peptide of SEQ ID NO: 1593. In one embodiment, the molecule disclosed here comprises a GLP-1 receptor agonist polypeptide of SEQ ID NO: 1581, where the C-terminal amino acid residue of the polypeptide is covalently linked to the N-terminal amino acid residue of the linker peptide of SEQ ID NO: 1585 as depicted in FIG. 4. In one embodiment, the C-terminal lysine of the linker peptide is modified, *e.g.*,bromoacetylated as shown in FIG. 4, for coupling to the cysteine residue of the conjugation site on the anti-GIPR antibody.

[0156] In one embodiment, the molecule disclosed here comprises a GLP-1 receptor agonist polypeptide of SEQ ID NO: 1581, where the C-terminal amino acid residue of the polypeptide is covalently linked to the N-terminal amino acid residue of the linker peptide of SEQ ID NO: 1586 as depicted in FIG. 5. In one embodiment, the C-terminal lysine of the linker peptide is modified, *e.g.*,bromoacetylated as shown in FIG. 5, for coupling to the cysteine residue of the conjugation site on the anti-GIPR antibody.

[0157] In one embodiment, the molecule disclosed here comprises a GLP-1 receptor agonist polypeptide of SEQ ID NO: 1581, where the C-terminal amino acid residue of the polypeptide is covalently linked to N-terminal amino acid residue of the linker peptide of SEQ ID NO: 1593 as depicted in FIG. 6. In one embodiment, the C-terminal lysine of the linker peptide is modified, *e.g.*,bromoacetylated on the sidechain, as shown in FIG. 6, for coupling to the cysteine residue of the conjugation site on the anti-GIPR antibody.

[0158] In one embodiment, the molecule disclosed herein comprise a GLP-1 receptor agonist polypeptide of SEQ ID NO: 1582 covalently linked to the linker peptide of SEQ ID NO: 1585, the linker peptide of SEQ ID NO: 1586, the linker peptide of SEQ ID NO: 1587, the linker peptide of SEQ ID NO: 1588, the linker peptide of SEQ ID NO: 1589, the linker peptide of SEQ

ID NO: 1590, the linker peptide of SEQ ID NO: 1591, the linker peptide of SEQ ID NO: 1592, or the linker peptide of SEQ ID NO: 1593.

[0159] In one embodiment, the molecule disclosed herein comprise a GLP-1 receptor agonist polypeptide of SEQ ID NO: 1583 covalently linked to the linker peptide of SEQ ID NO: 1585, the linker peptide of SEQ ID NO: 1586, the linker peptide of SEQ ID NO: 1587, the linker peptide of SEQ ID NO: 1588, the linker peptide of SEQ ID NO: 1589, the linker peptide of SEQ ID NO: 1590, the linker peptide of SEQ ID NO: 1591, the linker peptide of SEQ ID NO: 1592, or the linker peptide of SEQ ID NO: 1593.

[0160] Other peptide linkers that are suitable for inclusion in the molecules as described herein are provided in Table 2.

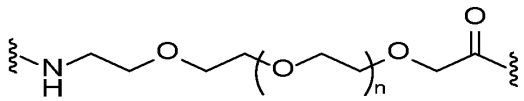
Table 2. Linker Peptide Sequences

Linker Sequence	**SEQ ID NO:**
GGQGGQGGQGGQGGQK	1585
GGGGQGGGGQGGGGQK	1586
SGGGGSGGGGSGGGGK	1587
GGQGGQGGQGGQGGQK	1588
GGSGGSGGSGGSGGSK	1589
GGGGQGGGGQGGGGQK	1590
GGGGSGGGGSGGGGSK	1591
GGSGGSGGSGGSGGSK	1592
GGGGSGGGGSGGGGSK	1593
GGGGS GGGGS PAPAP APAPA PASGG	1598
GSPAP APAPA PAPAP APAPA PASGG	1599
GGGGS GGGGS GGGGS GGGGS GGGGS	1600
GSPAP APAPA PAPAP APAPA PASG	1601
GSPAP APAPA PAPAG GGGSG GGGS	1602
GSPAP APAPA PASGG GG	1603
GSPAP APAPA PASGG	1604
GSPAP APAPA SGG	1605
GGGGS GGGGS GGGGS GGGGS	1606

Linker Sequence	SEQ ID NO:
GSGGG GSGGG GSGGG GSGGG G	1607
GGGGS GGGGS GGGGS	1608
GSGGG GSGGG GSGGG G	1609
GAKAA AEKAA AEKAA AEKAA AEA	1610
GAKAQ ADAKA QADAK AQADA KAQAD SGG	1611
GGGSG GGS	1612
GGGSG GGSGG GS	1613
GGGSG GGSGG GSGGG S	1614
GGGSG GGSGG GSGGG SGGGS	1615
GGGSG GGSGG GSGGG SGGGS GGGS	1616
GGGGS GGGGS	1617
GGGGS GGGGS GGGGS GGGGS GGGGS GGGGS	1618
GGG	1619
GGGG	1620
GGGGG	1621
GGGGG GG	1622
GGGGG K	1623
GGGGG KR	1624
GGGKG GGG	1625
GGGNG SGG	1626
GGGCG GGG	1627
GPNGG	1628
GGGGS	1629
GGEGG G	1630
GGEEE GGG	1631
GEEEG	1632
GEEE	1633
GGDGG G	1634
GGDDD GG	1635

Linker Sequence	SEQ ID NO:
GDDDG	1636
GDDD	1637
GGGGS DDSDE GSDGE DGGGG S	1638
WEWEW	1639
FEFEF	1640
EEEWW W	1641
EEEFF F	1642
WWEEE WW	1643
FFEEE FF	1644
GSGSA TGGSG STASS GSGSA TH	1645
HGSGS ATGGS GSTAS SGSGS AT	1646
AEAAA KEAAA KEAAA KAGG	1647
GSPAP APAPA PAPAP APAPA PASGG	1648
A PAPAP APAPA PAGGG GSGGG GSK	1649
A PAPAP APAPA PAPAP APAPA K	1650
G GGGSG GGGSG GGGSG GGGSK	1651
G GGGSG GGGSG GGGSK	1652
G GSAPA PAPAP APAPA PAPAP APSGK	1653
GG GGSGG GGSGG GGSK	1654

[0161] In one embodiment, the linker moiety, if present, is a non-peptidyl linker moiety. One non-limiting example class of suitable non-peptidyl linkers is polyethylene glycol (PEG) linkers, such as, e.g.,



wherein n is such that the linker has a molecular weight of about 100 Daltons (Da) to about 5000 Da, preferably about 100 Da to about 500 Da. Additional non-peptidyl linker moieties that are suitable for incorporation into the GLP-1 agonist polypeptide containing molecules are disclosed

infra. In one embodiment, the PEG linker is a PEG20 linker comprising K-(G-PEG20), K-(PEG20) or (G-PEG20)-K.

[0162] In one embodiment, the molecule disclosed herein comprise a GLP-1 receptor agonist polypeptide of SEQ ID NO: 1581 covalently linked to the α-amino group of the lysine residue of the PEG20 linker (G-PEG20)-K as shown in FIG. 7. At the opposite end of the PEG20 molecule is a bromoacetylated glycine residue that facilitates conjugation to the cysteine conjugation site on the anti-GIPR antibody.

[0163] In one embodiment, the molecule disclosed herein comprise a GLP-1 receptor agonist polypeptide of SEQ ID NO: 1582 covalently linked to the α-amino group of the lysine residue of the PEG20 linker (G-PEG20)-K as shown in FIG. 8. At the opposite end of the PEG20 molecule is a bromoacetylated glycine residue that facilitates conjugation to the cysteine conjugation site on the anti-GIPR antibody.

[0164] In one embodiment, the molecule disclosed herein comprise a GLP-1 receptor agonist polypeptide of SEQ ID NO: 1583 covalently linked to the α-amino group of the lysine residue of the PEG20 linker (G-PEG20)-K as shown in FIG. 9. At the opposite end of the PEG20 molecule is a bromoacetylated glycine residue that facilitates conjugation to the cysteine conjugation site on the anti-GIPR antibody.

[0165] Additional non-peptidyl linker moieties that are suitable for incorporation into the GLP-1 agonist polypeptide containing molecules include alkyl linkers such as -NH-$(CH_2)_s$-C(O), wherein s = 2-20. These alkyl linkers may further be substituted by any non-sterically hindering group such as lower alkyl (e.g., C_1-C_6) lower acyl, halogen (e.g., Cl, Br), CN, NH_2, phenyl, etc.

[0166] Other suitable non-peptidyl linkers comprise a rigid polyheterocyclic core of controlled length. Such linkers may be chemically differentiated on either end to accommodate orthogonal coupling chemistries (i.e., azide "click", amide coupling, thioether formation by alkylation with maleimide or haloacetamide, oxime formation, reductive amination, etc.).

[0167] Non-peptidyl linkers can be synthesized by conventional organic chemistry reactions.

[0168] The above is merely illustrative and not an exhaustive treatment of the kinds of non-peptidyl linkers that can optionally be employed in accordance with the present disclosure.

[0169] In one embodiment, the antagonist anti-GIPR antibodies of the conjugate molecules disclosed herein comprise at least one conjugation site. In one embodiment, the anti-

GIPR antibodies of the conjugate molecule disclosed herein comprise at least two conjugation sites (e.g., a first and second conjugation site). The one or more conjugation sites of the anti-GIPR antibody are amenable to conjugation of the GLP-1 receptor agonist polypeptides as disclosed herein by a defined conjugation chemistry through the side chain of an amino acid residue at the conjugation site. GLP-1 receptor agonist polypeptides can be conjugated or coupled to the selected conjugation site of the anti-GIPR antibody through an assortment of different conjugation chemistries known in the art. For example, in one embodiment, a maleimide-activated conjugation partner targeting an accessible cysteine thiol on the anti-GIPR antibody can be used. In one embodiment, conjugation or coupling chemistries targeting the side chains of either canonical or non-canonical, e.g., unnatural, amino acids in the anti-GIPR antibody sequence can be used.

[0170] Chemistries for chemoselective conjugation of the anti-GIPR antibody to the GLP-1 receptor agonist polypeptide include, but are not limited to, copper(I)-catalyzed azide–alkyne [3+2] dipolar cycloadditions, Staudinger ligation, other acyl transfers processes, oximations, hydrazone bonding formation, and other suitable organic chemistry reactions such as cross-couplings using water-soluble palladium catalysts (see e.g., Bong et al., *Organic Letters* 3(16):2509-11 (2001); Dibowski et al., *Angew. Chem. Int. Ed.* 37(4):476-78 (1998); DeVasher et al., *J. Org. Chem.* 69:7919-27 (2004); Shaugnessy et al., *J.Org. Chem,* 68, 6767-6774 (2003); Prescher et al., *Nature Chemical Biology* 1(1); 13-21 (2005)).

[0171] In one embodiment, conjugation (or covalent binding) to the anti-GIPR antibody is through the side chain of an amino acid residue at the conjugation site, for example, but not limited to, a cysteinyl residue. The amino acid residue, for example, a cysteinyl residue, at the internal conjugation site that is selected can be one that occupies the same amino acid residue position in a native Fc domain sequence, or the amino acid residue can be engineered into the Fc domain sequence by substitution or insertion.

[0172] Non-limiting examples of unnatural amino acid residues that can be useful as a conjugation site include: azido-containing amino acid residues, e.g., azidohomoalanine, p-azido-phenylalanine; keto-containing amino acid residues, e.g., p-acetyl-phenylalanine; alkyne-containing amino acid residues, e.g., p-ethynylphenylalanine, homopropargylglycine, p-(prop-2-ynyl)-tyrosine; alkene-containing amino acid residues e.g., homoallylglycine; aryl halide-

containing amino acid residues e.g. p-iodophenylalanine, p-bromophenylalanine; and 1,2-aminothiol containing amino acid residues.

[0173] Non-canonical amino acid residues (e.g., unnatural amino acid residues) can be incorporated into an anti-GIPR antibody by amino acid substitution or insertion. Non-canonical amino acid residues can be incorporated into the antibody by chemical peptide synthesis rather than by synthesis in biological systems, such as recombinantly expressing cells, or alternatively the skilled artisan can employ known techniques of protein engineering that use recombinantly expressing cells (see, e.g., Link et al., *Current Opinion in Biotechnology*, 14(6):603-609 (2003); U.S. Patent No. 7,045,337 to Schultz).

[0174] Any of the exposed amino acid residues on the anti-GIPR antibody can be potentially useful conjugation sites. Such sites may naturally contain cysteine or another reactive amino acid for site-selective coupling. Other sites can be mutated to a cysteine or another reactive amino acid for site-selective coupling. In some embodiments, the conjugation site is located within the light chain constant region (CL), heavy chain constant region 1 (CH1), CH2 or CH3 region of the anti-GIPR antibody.

[0175] In one embodiment, the anti-GIPR antibody comprises a cysteine amino acid at one or more conjugation site(s). In one embodiment, the one or more conjugation site(s) is located within the CL, CH1, CH2 or CH3 region of the anti-GIPR antibody. In one embodiment, the one or more conjugation site(s) are at positions independently selected from the group consisting of 88 (e.g., D88) of the light chain, 384 (e.g., E384) of the heavy chain, and 487 (e.g., T487) of the heavy chain, according to AHo numbering. For sake of clarity position 88 of the light chain according to Aho number corresponds to position 70 according to Kabat Numbering. Position 88 of the light chain according to AHo number corresponds to position 70 in the reference light chain antibody sequence of SEQ ID NO: 455 (light chain of anti-GIPR antibody 5G12.006). Position 88 of the light chain according to AHo number corresponds to position 70 in the reference light chain antibody sequence of SEQ ID NO: 388 (light chain of anti-GIPR antibody 2G10.006).

[0176] Position 384 of the heavy chain according to AHo numbering is another suitable conjugation site within the anti-GIPR antibody. Position 384 of the heavy chain according to AHo numbering corresponds to position 272 according to EU Numbering. Position 384 of the heavy chain according to AHo numbering corresponds to position 276 in the reference heavy

chain antibody sequence of SEQ ID NO: 612 (heavy chain of anti-GIPR antibody 5G12.006) and to position 275 in the reference heavy chain antibody sequence of SEQ ID NO: 545 (heavy chain of anti-GIPR antibody 2G10.006).

[0177] Position 487 of the heavy chain according to AHo numbering is another suitable conjugation site within the anti-GIPR antibody. Position 487 of the antibody heavy chain according to AHo numbering corresponds to position 359 according to EU numbering. Position 487 according to AHo numbering also corresponds to position 363 in the reference heavy chain antibody sequence of SEQ ID NO: 612 (heavy chain of anti-GIPR antibody 5G12.006) and position 362 in the reference heavy chain antibody sequence of SEQ ID NO: 545 (heavy chain of anti-GIPR antibody 2G10.006).

[0178] Exemplary antibodies that bind and antagonize GIPR, including human GIPR (hGIPR), for inclusion in the conjugate molecules as described herein are provided *infra* and disclosed in U.S. Patent No. 10,294,303, which is hereby incorporated by reference in its entirety.

[0179] In one embodiment, the antagonist anti-GIPR antibody of the conjugate molecule binds to the extracellular portion of human GIPR. In one embodiment, antagonist anti-GIPR antibody inhibits binding of GIP to the extracellular portion of human GIPR. In one embodiment, the human GIPR has the amino acid sequence of SEQ ID NO: 1572.

[0180] In one embodiment, the antagonist anti-GIPR antibody of the conjugate molecule binds to the N-terminal extracellular domain of human GIPR. In one embodiment, the antagonist anti-GIPR antibody inhibits binding of GIP to the N-terminal extracellular domain of human GIPR. In one embodiment, the human GIPR has the amino acid sequence of SEQ ID NO: 1572.

[0181] In one embodiment, the antagonist anti-GIPR antibody of the conjugate molecule binds to one or more amino acids at positions 1-139 of human GIPR. In one embodiment, the antagonist anti-GIPR antibody inhibits binding of GIP to the amino acids at positions 1-139 of human GIPR. In one embodiment, the human GIPR has the amino acid sequence of SEQ ID NO: 1572.

[0182] In one embodiment, the antagonist anti-GIPR antibody of the conjugate molecule of the present disclosure prevents or reduces binding of GIP to GIPR, where the level of prevention or reduction can be measured, for example, by a GIPR binding assay (e.g., a radioactive- or fluorescence-labeled GIP ligand binding study). A GIPR binding assay can be an

assay using FMAT or FACS that measures fluorescence-labeled GIP binding to GIPR expressing cells, and the antagonistic activity of an anti-GIPR antibody is measured by its ability to displace fluorescence-labeled GIP binding to GIPR expressing cells. Alternatively, a GIPR binding assay can measure radioactive-labeled GIP binding to GIPR expressing cells, and the antagonist activity of an anti-GIPR antibody is measured by its ability to displace radioactive labeled GIP binding to GIPR expressing cells (*see e.g., Biochimica et Biophysica Acta* (2001) 1547:143-155). The reduction in GIP binding can be at least 10%, 25%, 50%, 100% or more relative treatment with a non-GIPR control antibody under comparable conditions.

[0183] In one embodiment, the antagonist anti-GIPR antibody of the conjugate molecule of the present disclosure prevents or reduces binding of GIP to GIPR, where the level of prevention or reduction is measured using a GIPR activity assay that measures GIP binding protein activity in a cellular setting. In one embodiment, the GIPR activity assay is a cAMP assay in GIPR expressing cells, in which GIP induces cAMP signal, and the antagonist activity of an anti-GIPR antibody is measured in the presence/absence of GIP ligand, in which IC50/EC50 and degree of inhibition/activation can be obtained (*see e.g.*, Gault et al., *Biochem. Biophys. Res. Commun.* (2002) 290:1420–1426). In another embodiment, the GIPR activity assay is an insulin secretion assay in pancreatic beta cells. GIP induces glucose-dependent insulin secretion, and the antagonist activity of an anti-GIPR antibody is measured in the presence/absence of GIP ligand and the IC50/EC50 and degree of GIP inhibition can be obtained (*see e.g.*, Gault et al., *Biochem. Biophys. Res. Commun.* (2002) 290:1420–1426).

[0184] The prevention or reduction of GIP binding to GIPR achieved using the anti-GIPR antibody-GLP-1 conjugate molecule of the present disclosure results in one or more of the following pharmacodynamic effects following *in vivo* administration: an increase in glucose tolerance; an increase in insulin sensitivity; a decrease in body weight or a reduction in body weight gain; a decrease in fat mass or a decrease in inflammation in fat tissue; a decrease in circulating cholesterol levels; a decrease in circulating triglyceride levels; a decrease in liver steatosis or reduction of the liver triglyceride level; a decrease one or more liver enzymes, e.g., aspartate aminotransferase (AST), alanine aminotransferase (ALT), and/or alkaline phosphatase (ALP) levels. Methods for assaying and determining the preceding characteristics are known in the art and disclosed in U.S. Patent No. 10,294,303, which is hereby incorporated by reference in its entirety.

[0185] In one embodiment, the antagonist anti-GIPR antibodies disclosed herein are characterized by their binding affinity for GIPR. In one embodiment, the anti-GIPR antibodies disclosed herein that are suitable for conjugation to a GLP-1 receptor agonist disclosed herein binds human GIPR with an equilibrium dissociation constant (KD) of ≤200 nM, a KD of ≤150 nM, a KD of ≤100 nM, a KD of ≤50 nM, a KD of ≤10 nM, a KD of ≤5 nM, a KD of ≤2 nM, or a KD of ≤1 nM, e.g., as measured via a surface plasma resonance or kinetic exclusion assay technique. In one embodiment, the anti-GIPR antibody has a KD for human GIPR of 1 nM, 2 nM, 3 nM, 4 nM, 5 nM, 6 nM, 7 nM, 8 nM, 9 nM, 10 nM, 15 nM, 20 nM, 25 nM, 30 nM, 35 nM, 40 nM, 45 nM, 50 nM, 55 nM, 60 nM, 65 nM, 70 nM, 75 nM, 80 nM, 85 nM, 90 nM, 95 nM, 100 nM, 110 nM, 120 nM, 130 nM, 140 nM, 150 nM, 160 nM, 170 nM, 180 nM, 190 nM, 200 nM, 210 nM, 220 nM, 230 nM, 240 nM, 250 nM, 260 nM, 270 nM, 280 nM, 290 nM, 300 nM, 310 nM, 320 nM, 330 nM, 340 nM, 350 nM, 360 nM, 370 nM, 380 nM, 390 nM, 400 nM, 410 nM, 420 nM, 430 nM, 440 nM, 450 nM, 460 nM, 470 nM, 480 nM, 490 nM, or 500 nM.

[0186] In one embodiment, the antagonist anti-GIPR antibodies disclosed herein have a slow dissociation rate or off-rate. For example, in one embodiment, the antagonist anti-GIPR antibody has a kd (off-rate) of $1x\ 10^{-2}\ s^{-1}$, or $1x\ 10^{-3}\ s^{-1}$, or $1x\ 10^{-4}\ s^{-1}$, or $1x\ 10^{-5}\ s^{-1}$.

[0187] In one embodiment, the antagonist anti-GIPR antibody is a monoclonal antibody, a recombinant antibody, a human antibody, or a multi-specific antibody. In one embodiment, the anti-GIPR antibody is a monoclonal antibody. In one embodiment, the anti-GIPR antibody is a recombinant antibody. In one embodiment, the anti-GIPR antibody is a human antibody.

[0188] As defined herein, the antagonist anti-GIPR antibody is of the IgG isotype. In one embodiment, the antagonist anti-GIPR antibody is of the IgG1-, IgG2- IgG3- or IgG4-subclass. In one embodiment, the antibody is of the IgG1-, IgG2-, or IgG4- subclass. In one embodiment, the antibody is of the IgG1- or IgG2- subclass. In one embodiment, the antibody is of the IgG1- subclass.

[0189] Non-limiting examples of anti-GIPR antibodies of the IgG1 subclass are summarized in Table 3. In one embodiment, the anti-GIPR antibody is an antibody with the CDR, variable domain, and light and heavy chain sequences as specified in one of the rows of Table 3.

[0190] SEQ ID NOs have been assigned to variable light chain, variable heavy chain, light chain, heavy chain, CDRL1, CDRL2, CDRL3, CDRH1, CDRH2, and CDRH3 sequences of

the exemplary antagonist anti-GIPR antibodies provided in Tables 3-11. These antibodies can be identified by SEQ ID NO, but also by construct name (e.g., 2C2.005) or identifier number (e.g., iPS:336175). The anti-GIPR antibodies identified in Tables 3-11 below can be grouped into families based on construct name. For example, the "4B1 family" includes the constructs 4B1, 4B1.010, 4B1.011, 4B1.012, 4B1.013, 4B1.014, 4B1.015, and 4B1.016.

[0191] The various light chain and heavy chain variable regions provided herein are depicted in Tables 4 and 5, respectively. Each of these variable regions may be attached to a heavy or light chain constant regions to form a complete antibody heavy and light chain, respectively. Furthermore, each of the so generated heavy and light chain sequences may be combined to form a complete antibody structure.

Table 3. Anti-GIPR Antibody Amino Acid Sequences

Identifier	Construct	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
iPS:336175	2C2.005	1	158	315	472	629	786	943	1100	1257	1414
iPS:335914	4B1	2	159	316	473	630	787	944	1101	1258	1415
iPS:335938	6H1	3	160	317	474	631	788	945	1102	1259	1416
iPS:335941	2F11	4	161	318	475	632	789	946	1103	1260	1417
iPS:335970	5C2	5	162	319	476	633	790	947	1104	1261	1418
iPS:335978	13H12	6	163	320	477	634	791	948	1105	1262	1419
iPS:335986	11C1	7	164	321	478	635	792	949	1106	1263	1420
iPS:335994	12H11	8	165	322	479	636	793	950	1107	1264	1421
iPS:336024	18E3	9	166	323	480	637	794	951	1108	1265	1422
iPS:336041	2G10_LC1	10	167	324	481	638	795	952	1109	1266	1423
iPS:336077	4H9.004	11	168	325	482	639	796	953	1110	1267	1424
iPS:336088	6A5.004	12	169	326	483	640	797	954	1111	1268	1425
iPS:336099	17H11.004	13	170	327	484	641	798	955	1112	1269	1426
iPS:359621	17H11.004.001	14	171	328	485	642	799	956	1113	1270	1427
iPS:359781	4H9.004.001	15	172	329	486	643	800	957	1114	1271	1428
iPS:360929	4H9.004.002	16	173	330	487	644	801	958	1115	1272	1429
iPS:360936	4H9.004.003	17	174	331	488	645	802	959	1116	1273	1430
iPS:360943	4H9.004.004	18	175	332	489	646	803	960	1117	1274	1431
iPS:360949	4H9.004.005	19	176	333	490	647	804	961	1118	1275	1432
iPS:359761	4H9.004.006	20	177	334	491	648	805	962	1119	1276	1433
iPS:360955	4B1.010	21	178	335	492	649	806	963	1120	1277	1434
iPS:360962	4B1.011	22	179	336	493	650	807	964	1121	1278	1435
iPS:360968	4B1.012	23	180	337	494	651	808	965	1122	1279	1436
iPS:360974	4B1.013	24	181	338	495	652	809	966	1123	1280	1437
iPS:360978	4B1.014	25	182	339	496	653	810	967	1124	1281	1438
iPS:359785	4B1.015	26	183	340	497	654	811	968	1125	1282	1439
iPS:360982	4B1.016	27	184	341	498	655	812	969	1126	1283	1440
iPS:335922	18F2	28	185	342	499	656	813	970	1127	1284	1441
iPS:360986	18F2.002	29	186	343	500	657	814	971	1128	1285	1442
iPS:360995	18F2.003	30	187	344	501	658	815	972	1129	1286	1443
iPS:360999	18F2.004	31	188	345	502	659	816	973	1130	1287	1444
iPS:361005	18F2.005	32	189	346	503	660	817	974	1131	1288	1445
iPS:361009	18F2.006	33	190	347	504	661	818	975	1132	1289	1446

Table 3. Anti-GIPR Antibody Amino Acid Sequences

Identifier	Construct	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
iPS:361013	18F2.007	34	191	348	505	662	819	976	1133	1290	1447
iPS:361017	18F2.008	35	192	349	506	663	820	977	1134	1291	1448
iPS:361021	18F2.009	36	193	350	507	664	821	978	1135	1292	1449
iPS:361028	18F2.010	37	194	351	508	665	822	979	1136	1293	1450
iPS:360535	18F2.011	38	195	352	509	666	823	980	1137	1294	1451
iPS:361035	18F2.012	39	196	353	510	667	824	981	1138	1295	1452
iPS:359940	2F11.002	40	197	354	511	668	825	982	1139	1296	1453
iPS:361039	2F11.003	41	198	355	512	669	826	983	1140	1297	1454
iPS:361043	2F11.004	42	199	356	513	670	827	984	1141	1298	1455
iPS:361049	2F11.005	43	200	357	514	671	828	985	1142	1299	1456
iPS:361055	2F11.006	44	201	358	515	672	829	986	1143	1300	1457
iPS:361059	2F11.007	45	202	359	516	673	830	987	1144	1301	1458
iPS:361063	2F11.008	46	203	360	517	674	831	988	1145	1302	1459
iPS:359949	2F11.009	47	204	361	518	675	832	989	1146	1303	1460
iPS:359956	2F11.010	48	205	362	519	676	833	990	1147	1304	1461
iPS:359865	6H1.002	49	206	363	520	677	834	991	1148	1305	1462
iPS:359869	6H1.003	50	207	364	521	678	835	992	1149	1306	1463
iPS:359873	6H1.004	51	208	365	522	679	836	993	1150	1307	1464
iPS:359877	6H1.005	52	209	366	523	680	837	994	1151	1308	1465
iPS:361067	6H1.006	53	210	367	524	681	838	995	1152	1309	1466
iPS:361071	6H1.007	54	211	368	525	682	839	996	1153	1310	1467
iPS:361075	6H1.008	55	212	369	526	683	840	997	1154	1311	1468
iPS:361079	6A5.004.001	56	213	370	527	684	841	998	1155	1312	1469
iPS:361085	6A5.004.002	57	214	371	528	685	842	999	1156	1313	1470
iPS:361091	6A5.004.003	58	215	372	529	686	843	1000	1157	1314	1471
iPS:361095	6A5.004.004	59	216	373	530	687	844	1001	1158	1315	1472
iPS:361101	6A5.004.005	60	217	374	531	688	845	1002	1159	1316	1473
iPS:361105	6A5.004.006	61	218	375	532	689	846	1003	1160	1317	1474
iPS:361109	6A5.004.007	62	219	376	533	690	847	1004	1161	1318	1475
iPS:361113	6A5.004.008	63	220	377	534	691	848	1005	1162	1319	1476
iPS:361120	6A5.004.009	64	221	378	535	692	849	1006	1163	1320	1477
iPS:359896	6A5.004.010	65	222	379	536	693	850	1007	1164	1321	1478
iPS:359890	6A5.004.011	66	223	380	537	694	851	1008	1165	1322	1479

Table 3. Anti-GIPR Antibody Amino Acid Sequences

Identifier	Construct	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
iPS:359567	2A11.002	67	224	381	538	695	852	1009	1166	1323	1480
iPS:335965	2A11.003	68	225	382	539	696	853	1010	1167	1324	1481
iPS:361158	2A11.004	69	226	383	540	697	854	1011	1168	1325	1482
iPS:361165	2A11.005	70	227	384	541	698	855	1012	1169	1326	1483
iPS:361172	2G10_LC1.003	71	228	385	542	699	856	1013	1170	1327	1484
iPS:361178	2G10_LC1.004	72	229	386	543	700	857	1014	1171	1328	1485
iPS:361185	2G10_LC1.005	73	230	387	544	701	858	1015	1172	1329	1486
iPS:361192	2G10_LC1.006	74	231	388	545	702	859	1016	1173	1330	1487
iPS:359609	2G10_LC1.007	75	232	389	546	703	860	1017	1174	1331	1488
iPS:359615	2G10_LC1.008	76	233	390	547	704	861	1018	1175	1332	1489
iPS:361196	2G10_LC1.009	77	234	391	548	705	862	1019	1176	1333	1490
iPS:361202	2G10_LC1.010	78	235	392	549	706	863	1020	1177	1334	1491
iPS:359644	18E3.002	79	236	393	550	707	864	1021	1178	1335	1492
iPS:361206	18E3.003	80	237	394	551	708	865	1022	1179	1336	1493
iPS:359628	18E3.004	81	238	395	552	709	866	1023	1180	1337	1494
iPS:359637	18E3.005	82	239	396	553	710	867	1024	1181	1338	1495
iPS:361210	18E3.006	83	240	397	554	711	868	1025	1182	1339	1496
iPS:361214	18E3.007	84	241	398	555	712	869	1026	1183	1340	1497
iPS:361218	18E3.008	85	242	399	556	713	870	1027	1184	1341	1498
iPS:361222	5C2.006	86	243	400	557	714	871	1028	1185	1342	1499
iPS:361229	5C2.007	87	244	401	558	715	872	1029	1186	1343	1500
iPS:361236	5C2.008	88	245	402	559	716	873	1030	1187	1344	1501
iPS:359685	5C2.009	89	246	403	560	717	874	1031	1188	1345	1502
iPS:361240	5C2.010	90	247	404	561	718	875	1032	1189	1346	1503
iPS:361247	5C2.011	91	248	405	562	719	876	1033	1190	1347	1504
iPS:361254	5C2.012	92	249	406	563	720	877	1034	1191	1348	1505
iPS:361261	5C2.013	93	250	407	564	721	878	1035	1192	1349	1506
iPS:361268	5C2.014	94	251	408	565	722	879	1036	1193	1350	1507
iPS:359669	5C2.015	95	252	409	566	723	880	1037	1194	1351	1508
iPS:359678	5C2.016	96	253	410	567	724	881	1038	1195	1352	1509
iPS:361275	11C1.002	97	254	411	568	725	882	1039	1196	1353	1510
iPS:361282	11C1.003	98	255	412	569	726	883	1040	1197	1354	1511
iPS:361289	11C1.004	99	256	413	570	727	884	1041	1198	1355	1512

Table 3. Anti-GIPR Antibody Amino Acid Sequences

Identifier	Construct	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
iPS:359712	11C1.005	100	257	414	571	728	885	1042	1199	1356	1513
iPS:361293	11C1.006	101	258	415	572	729	886	1043	1200	1357	1514
iPS:361297	11C1.007	102	259	416	573	730	887	1044	1201	1358	1515
iPS:361301	11C1.008	103	260	417	574	731	888	1045	1202	1359	1516
iPS:359703	11C1.009	104	261	418	575	732	889	1046	1203	1360	1517
iPS:361305	11C1.010	105	262	419	576	733	890	1047	1204	1361	1518
iPS:361312	13H12.002	106	263	420	577	734	891	1048	1205	1362	1519
iPS:359744	13H12.003	107	264	421	578	735	892	1049	1206	1363	1520
iPS:361319	13H12.004	108	265	422	579	736	893	1050	1207	1364	1521
iPS:359737	13H12.005	109	266	423	580	737	894	1051	1208	1365	1522
iPS:361326	13H12.006	110	267	424	581	738	895	1052	1209	1366	1523
iPS:361330	12H11.002	111	268	425	582	739	896	1053	1210	1367	1524
iPS:361337	12H11.003	112	269	426	583	740	897	1054	1211	1368	1525
iPS:361344	12H11.004	113	270	427	584	741	898	1055	1212	1369	1526
iPS:361351	12H11.005	114	271	428	585	742	899	1056	1213	1370	1527
iPS:361358	12H11.006	115	272	429	586	743	900	1057	1214	1371	1528
iPS:361365	12H11.007	116	273	430	587	744	901	1058	1215	1372	1529
iPS:361372	12H11.008	117	274	431	588	745	902	1059	1216	1373	1530
iPS:361379	12H11.009	118	275	432	589	746	903	1060	1217	1374	1531
iPS:361383	12H11.010	119	276	433	590	747	904	1061	1218	1375	1532
iPS:361387	12H11.011	120	277	434	591	748	905	1062	1219	1376	1533
iPS:361391	12H11.012	121	278	435	592	749	906	1063	1220	1377	1534
iPS:361395	12H11.013	122	279	436	593	750	907	1064	1221	1378	1535
iPS:361402	12H11.014	123	280	437	594	751	908	1065	1222	1379	1536
iPS:361406	2C2.005.001	124	281	438	595	752	909	1066	1223	1380	1537
iPS:361412	2C2.005.002	125	282	439	596	753	910	1067	1224	1381	1538
iPS:361418	2C2.005.003	126	283	440	597	754	911	1068	1225	1382	1539
iPS:361424	2C2.005.004	127	284	441	598	755	912	1069	1226	1383	1540
iPS:361430	2C2.005.005	128	285	442	599	756	913	1070	1227	1384	1541
iPS:361436	2C2.005.006	129	286	443	600	757	914	1071	1228	1385	1542
iPS:361442	2C2.005.007	130	287	444	601	758	915	1072	1229	1386	1543
iPS:361448	2C2.005.008	131	288	445	602	759	916	1073	1230	1387	1544
iPS:361454	2C2.005.009	132	289	446	603	760	917	1074	1231	1388	1545

Table 3. Anti-GIPR Antibody Amino Acid Sequences											
Identifier	**Construct**	**VL**	**VH**	**LC**	**HC**	**CDRL1**	**CDRL2**	**CDRL3**	**CDRH1**	**CDRH2**	**CDRH3**
iPS:361460	2C2.005.010	133	290	447	604	761	918	1075	1232	1389	1546
iPS:361466	2C2.005.011	134	291	448	605	762	919	1076	1233	1390	1547
iPS:361472	2C2.005.012	135	292	449	606	763	920	1077	1234	1391	1548
iPS:361478	2C2.005.013	136	293	450	607	764	921	1078	1235	1392	1549
iPS:361485	2C2.005.014	137	294	451	608	765	922	1079	1236	1393	1550
iPS:361845	18F2.013	138	295	452	609	766	923	1080	1237	1394	1551
iPS:361851	6H1.009	139	296	453	610	767	924	1081	1238	1395	1552
iPS:361855	2C2.005.015	140	297	454	611	768	925	1082	1239	1396	1553
iPS:336067	5G12.006	141	298	455	612	769	926	1083	1240	1397	1554
iPS:336169	17B11.002	142	299	456	613	770	927	1084	1241	1398	1555
iPS:361127	5G12.006.001	143	300	457	614	771	928	1085	1242	1399	1556
iPS:361136	5G12.006.002	144	301	458	615	772	929	1086	1243	1400	1557
iPS:361140	5G12.006.003	145	302	459	616	773	930	1087	1244	1401	1558
iPS:359919	5G12.006.004	146	303	460	617	774	931	1088	1245	1402	1559
iPS:361144	5G12.006.005	147	304	461	618	775	932	1089	1246	1403	1560
iPS:361151	5G12.006.006	148	305	462	619	776	933	1090	1247	1404	1561
iPS:361491	17B11.002.001	149	306	463	620	777	934	1091	1248	1405	1562
iPS:361499	17B11.002.002	150	307	464	621	778	935	1092	1249	1406	1563
iPS:361503	17B11.002.003	151	308	465	622	779	936	1093	1250	1407	1564
iPS:361507	17B11.002.004	152	309	466	623	780	937	1094	1251	1408	1565
iPS:361514	17B11.002.005	153	310	467	624	781	938	1095	1252	1409	1566
iPS:360582	17B11.002.006	154	311	468	625	782	939	1096	1253	1410	1567
iPS:361518	17B11.002.007	155	312	469	626	783	940	1097	1254	1411	1568
iPS:360570	17B11.002.008	156	313	470	627	784	941	1098	1255	1412	1569
iPS:362051	5G12.005.001	157	314	471	628	785	942	1099	1256	1413	1570

Table 4. Variable Light (VL) Region Amino Acid Sequences of Exemplary Anti-GIPR Antibodies

Identifier	**Construct**	**VL**	**SEQ ID NO:**
iPS:336175	2C2.005	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQHLPGTAPKLLIYTNNQRPS GVPDRFSGSKSGTSASLAISGLQSEDEADYFCATFDDSLNGPVFGGGTKLTVLG	1

Identifier	Construct	VL	SEQ ID NO:
iPS:335914	4B1	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKRLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	2
iPS:335938	6H1	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKRLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	3
iPS:335941	2F11	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLET GVPSRFSGSGSGTDFSFTISSLQPEDIATYYCQQYDILLTFGGGTKVEIKR	4
iPS:335970	5C2	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYIAWYQQQPGHPPKLLIYW ASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQGTKVEI KR	5
iPS:335978	13H12	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYIAWYQQKPGHPPKLLIYW ASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQGTKVEI KR	6
iPS:335986	11C1	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIY WTSTRDSGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTK VEIKR	7
iPS:335994	12H11	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIY WTSTRDSGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTK VEIKR	8
iPS:336024	18E3	EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAWYQQKPGQAPRLLIYGASSRAT GIPDRFSGSGSGTDFTLTISRQEPDDFAVYYCQQYGSSPLTFGGGTKVEIKR	9
iPS:336041	2G10_LC1	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGAATRA TGIPARVSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPLTFGGGTKVEIKR	10
iPS:336077	4H9.004	DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGWYQQKPGKAPKRLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFVTYYCLQHNSYPFTFGPGTKVDVKR	11
iPS:336088	6A5.004	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNWYQQKPGKAPKLLIYDASNLEP GVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQYDDLFTFGPGTKVDIKR	12
iPS:336099	17H11.004	DIQMTQSPSSVSASVGDRVTITCRASQGLIIWLAWYQQKPGKAPKLLIYAASSLQS GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQTNSFPPTFGQGTKVEIKR	13
iPS:359621	17H11.004.001	DIQMTQSPSSVSASVGDRVTITCRASQGLIIWLAWYQQKPGKAPKLLIYAASSLQS GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQTNSFPPTFGQGTKVEIKR	14
iPS:359781	4H9.004.001	DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGWYQQKPGKAPKLLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFVTYYCLQHNSYPFTFGQGTKVDVKR	15

Identifier	Construct	VL	SEQ ID NO:
iPS:360929	4H9.004.002	DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGWYQQKPGKAPKLLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFVTYYCLQHNSYPFTFGQGTKVDVKR	16
iPS:360936	4H9.004.003	DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGWYQQKPGKAPKLLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFVTYYCLQHNSYPFTFGQGTKVDVKR	17
iPS:360943	4H9.004.004	DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGWYQQKPGKAPKLLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFVTYYCLQHNSYPFTFGPGTKVDVKR	18
iPS:360949	4H9.004.005	DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGWYQQKPGKAPKRLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFVTYYCLQHNSYPFTFGQGTKVDVKR	19
iPS:359761	4H9.004.006	DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGWYQQKPGKAPKLLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFVTYYCLQHNSYPFTFGQGTKVDVKR	20
iPS:360955	4B1.010	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKLLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIKR	21
iPS:360962	4B1.011	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKRLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIKR	22
iPS:360968	4B1.012	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKLLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	23
iPS:360974	4B1.013	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKLLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIKR	24
iPS:360978	4B1.014	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKLLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIKR	25
iPS:359785	4B1.015	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKLLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIKR	26
iPS:360982	4B1.016	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKLLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIKR	27
iPS:335922	18F2	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGWYHQKPGKAPKRLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	28
iPS:360986	18F2.002	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGWYQQKPGKAPKLLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	29
iPS:360995	18F2.003	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGWYQQKPGKAPKLLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	30

Identifier	Construct	VL	SEQ ID NO:
iPS:360999	18F2.004	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGWYHQKPGKAPKLLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	31
iPS:361005	18F2.005	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGWYQQKPGKAPKRLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	32
iPS:361009	18F2.006	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGWYQQKPGKAPKRLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	33
iPS:361013	18F2.007	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGWYHQKPGKAPKLLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	34
iPS:361017	18F2.008	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGWYHQKPGKAPKRLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	35
iPS:361021	18F2.009	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGWYQQKPGKAPKLLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	36
iPS:361028	18F2.010	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGWYQQKPGKAPKLLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	37
iPS:360535	18F2.011	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGWYQQKPGKAPKLLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIKR	38
iPS:361035	18F2.012	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGWYQQKPGKAPKLLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	39
iPS:359940	2F11.002	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLET GVPSRFSGSGSGTDFSLTISSLQPEDFATYYCQQYDILLTFGGGTKVEIKR	40
iPS:361039	2F11.003	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLET GVPSRFSGSGSGTDFSLTISSLQPEDFATYYCQQYDILLTFGGGTKVEIKR	41
iPS:361043	2F11.004	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLET GVPSRFSGSGSGTDFSLTISSLQPEDIATYYCQQYDILLTFGGGTKVEIKR	42
iPS:361049	2F11.005	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLET GVPSRFSGSGSGTDFSFTISSLQPEDFATYYCQQYDILLTFGGGTKVEIKR	43
iPS:361055	2F11.006	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLET GVPSRFSGSGSGTDFSLTISSLQPEDIATYYCQQYDILLTFGGGTKVEIKR	44
iPS:361059	2F11.007	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLET GVPSRFSGSGSGTDFSFTISSLQPEDFATYYCQQYDILLTFGGGTKVEIKR	45

Identifier	Construct	VL	SEQ ID NO:
iPS:361063	2F11.008	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLET GVPSRFSGSGSGTDFSFTISSLQPEDIATYYCQQYDILLTFGGGTKVEIKR	46
iPS:359949	2F11.009	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLET GVPSRFSGSGSGTDFSLTISSLQPEDFATYYCQQYDILLTFGGGTKVEIKR	47
iPS:359956	2F11.010	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLET GVPSRFSGSGSGTDFSLTISSLQPEDFATYYCQQYDILLTFGGGTKVEIKR	48
iPS:359865	6H1.002	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKRLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	49
iPS:359869	6H1.003	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKRLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	50
iPS:359873	6H1.004	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKLLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIKR	51
iPS:359877	6H1.005	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKLLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIKR	52
iPS:361067	6H1.006	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKLLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	53
iPS:361071	6H1.007	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKLLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	54
iPS:361075	6H1.008	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKLLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	55
iPS:361079	6A5.004.001	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNWYQQKPGKAPKLLIYDASNLEP GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYDDLFTFGPGTKVDIKR	56
iPS:361085	6A5.004.002	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNWYQQKPGKAPKLLIYDASNLEP GVPSRFSGSGSGTDFTLTISSLQPEDIATYYCQQYDDLFTFGPGTKVDIKR	57
iPS:361091	6A5.004.003	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNWYQQKPGKAPKLLIYDASNLEP GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYDDLFTFGPGTKVDIKR	58
iPS:361095	6A5.004.004	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNWYQQKPGKAPKLLIYDASNLEP GVPSRFSGSGSGTDFTFTISSLQPEDFATYYCQQYDDLFTFGPGTKVDIKR	59
iPS:361101	6A5.004.005	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNWYQQKPGKAPKLLIYDASNLEP GVPSRFSGSGSGTDFTLTISSLQPEDIATYYCQQYDDLFTFGPGTKVDIKR	60

Identifier	Construct	VL	SEQ ID NO:
iPS:361105	6A5.004.006	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNWYQQKPGKAPKLLIYDASNLEP GVPSRFSGSGSGTDFTFTISSLQPEDFATYYCQQYDDLFTFGPGTKVDIKR	61
iPS:361109	6A5.004.007	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNWYQQKPGKAPKLLIYDASNLEP GVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQYDDLFTFGPGTKVDIKR	62
iPS:361113	6A5.004.008	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNWYQQKPGKAPKLLIYDASNLEP GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYDDLFTFGPGTKVDIKR	63
iPS:361120	6A5.004.009	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNWYQQKPGKAPKLLIYDASNLEP GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYDDLFTFGPGTKVDIKR	64
iPS:359896	6A5.004.010	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNWYQQKPGKAPKLLIYDASNLEP GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYDDLFTFGQGTKVDIKR	65
iPS:359890	6A5.004.011	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNWYQQKPGKAPKLLIYDASNLEP GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYDDLFTFGQGTKVDIKR	66
iPS:359567	2A11.002	EIVLTQSPGTLSLSPGERATLSCRASQIFTSTYLAWYQQKPGQAPRLLIYGASSRAT GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPRFGQGTRLEIKR	67
iPS:335965	2A11.003	EIVLTQSPGTLSLSPGERATLSCRASQIFTSTYLAWYQQKPGQAPRLLIYGASSRAT GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPRFGQGTRLEIKR	68
iPS:361158	2A11.004	EIVLTQSPGTLSLSPGERATLSCRASQIFTSTYLAWYQQKPGQAPRLLIYGASSRAT GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPRFGQGTRLEIKR	69
iPS:361165	2A11.005	EIVLTQSPGTLSLSPGERATLSCRASQIFTSTYLAWYQQKPGQAPRLLIYGASSRAT GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPRFGQGTRLEIKR	70
iPS:361172	2G10_LC1.003	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGAATRA TGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPLTFGGGTKVEIKR	71
iPS:361178	2G10_LC1.004	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGAATRA TGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPLTFGGGTKVEIKR	72
iPS:361185	2G10_LC1.005	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGAATRA TGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPLTFGGGTKVEIKR	73
iPS:361192	2G10_LC1.006	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGAATRA TGIPARVSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPLTFGGGTKVEIKR	74
iPS:359609	2G10_LC1.007	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGAATRA TGIPARFSGSGSGTEFTLTISSLEPEDFAVYYCQQYNNFPLTFGGGTKVEIKR	75

Identifier	Construct	VL	SEQ ID NO:
iPS:359615	2G10_LC1.008	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGAATRA TGIPARFSGSGSGTEFTLTISSLEPEDFAVYYCQQYNNYPLTFGGGTKVEIKR	76
iPS:361196	2G10_LC1.009	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGAATRA TGIPARFSGSGSGTEFTLTISSLEPEDFAVYYCQQYNNWPLTFGGGTKVEIKR	77
iPS:361202	2G10_LC1.010	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGAATRA TGIPARFSGSGSGTEFTLTISSLEPEDFAVYYCQQYNNWPLTFGGGTKVEIKR	78
iPS:359644	18E3.002	EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAWYQQKPGQAPRLLIYGASSRAT GIPDRFSGSGSGTDFTLTISRLEPDDFAVYYCQQYGSSPLTFGGGTKVEIKR	79
iPS:361206	18E3.003	EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAWYQQKPGQAPRLLIYGASSRAT GIPDRFSGSGSGTDFTLTISRQEPDDFAVYYCQQYGSSPLTFGGGTKVEIKR	80
iPS:359628	18E3.004	EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAWYQQKPGQAPRLLIYGASSRAT GIPDRFSGSGSGTDFTLTISRLEPDDFAVYYCQQYGSSPLTFGGGTKVEIKR	81
iPS:359637	18E3.005	EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAWYQQKPGQAPRLLIYGASSRAT GIPDRFSGSGSGTDFTLTISRLEPDDFAVYYCQQYGSSPLTFGGGTKVEIKR	82
iPS:361210	18E3.006	EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAWYQQKPGQAPRLLIYGASSRAT GIPDRFSGSGSGTDFTLTISRLEPDDFAVYYCQQYGSSPLTFGGGTKVEIKR	83
iPS:361214	18E3.007	EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAWYQQKPGQAPRLLIYGASSRAT GIPDRFSGSGSGTDFTLTISRQEPDDFAVYYCQQYGSSPLTFGGGTKVEIKR	84
iPS:361218	18E3.008	EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAWYQQKPGQAPRLLIYGASSRAT GIPDRFSGSGSGTDFTLTISRQEPDDFAVYYCQQYGSSPLTFGGGTKVEIKR	85
iPS:361222	5C2.006	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYIAWYQQQPGHPPKLLIYW ASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQGTKVEI KR	86
iPS:361229	5C2.007	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYIAWYQQQPGHPPKLLIYW ASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQGTKVEI KR	87
iPS:361236	5C2.008	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYIAWYQQQPGHPPKLLIYW ASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQGTKVEI KR	88
iPS:359685	5C2.009	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYIAWYQQQPGHPPKLLIYW ASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQGTKVEI KR	89

Identifier	Construct	VL	SEQ ID NO:
iPS:361240	5C2.010	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYIAWYQQQPGHPPKLLIYW ASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQGTKVEI KR	90
iPS:361247	5C2.011	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYIAWYQQQPGHPPKLLIYW ASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQGTKVEI KR	91
iPS:361254	5C2.012	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYIAWYQQQPGHPPKLLIYW ASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQGTKVEI KR	92
iPS:361261	5C2.013	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYIAWYQQQPGHPPKLLIYW ASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQGTKVEI KR	93
iPS:361268	5C2.014	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYIAWYQQQPGHPPKLLIYW ASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQGTKVEI KR	94
iPS:359669	5C2.015	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYIAWYQQKPGQPPKLLIYW ASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQGTKVEI KR	95
iPS:359678	5C2.016	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYIAWYQQKPGQPPKLLIYW ASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQGTKVEI KR	96
iPS:361275	11C1.002	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIY WTSTRESGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTKV EIKR	97
iPS:361282	11C1.003	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIY WTSTRESGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTKV EIKR	98
iPS:361289	11C1.004	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIY WTSTRDSGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTK VEIKR	99
iPS:359712	11C1.005	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIY WTSTRESGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTKV EIKR	100

Identifier	Construct	VL	SEQ ID NO:
iPS:361293	11C1.006	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIY WTSTRESGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTKV EIKR	101
iPS:361297	11C1.007	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIY WTSTRDSGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTK VEIKR	102
iPS:361301	11C1.008	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIY WTSTRDSGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTK VEIKR	103
iPS:359703	11C1.009	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPKLLIY WTSTRESGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTKV EIKR	104
iPS:361305	11C1.010	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIY WTSTRESGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTKV EIKR	105
iPS:361312	13H12.002	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYIAWYQQKPGHPPKLLIYW ASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQGTKVEI KR	106
iPS:359744	13H12.003	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYIAWYQQKPGHPPKLLIYW ASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQGTKVEI KR	107
iPS:361319	13H12.004	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYIAWYQQKPGHPPKLLIYW ASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQGTKVEI KR	108
iPS:359737	13H12.005	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYIAWYQQKPGQPPKLLIYW ASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQGTKVEI KR	109
iPS:361326	13H12.006	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYIAWYQQKPGQPPKLLIYW ASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQGTKVEI KR	110
iPS:361330	12H11.002	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIY WTSTRDSGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTK VEIKR	111

Identifier	Construct	VL	SEQ ID NO:
iPS:361337	12H11.003	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIY WTSTRDSGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTK VEIKR	112
iPS:361344	12H11.004	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIY WTSTRDSGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTK VEIKR	113
iPS:361351	12H11.005	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIY WTSTRDSGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTK VEIKR	114
iPS:361358	12H11.006	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIY WTSTRDSGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTK VEIKR	115
iPS:361365	12H11.007	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIY WTSTRDSGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTK VEIKR	116
iPS:361372	12H11.008	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIY WTSTRDSGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTK VEIKR	117
iPS:361379	12H11.009	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIY WTSTRESGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTKV EIKR	118
iPS:361383	12H11.010	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIY WTSTRESGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTKV EIKR	119
iPS:361387	12H11.011	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIY WTSTRESGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTKV EIKR	120
iPS:361391	12H11.012	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIY WTSTRESGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTKV EIKR	121
iPS:361395	12H11.013	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPKLLIY WTSTRDSGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTK VEIKR	122

Identifier	Construct	VL	SEQ ID NO:
iPS:361402	12H11.014	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPKLLIY WTSTRESGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTKV EIKR	123
iPS:361406	2C2.005.001	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSQTVNWYQHLPGTAPKLLIYTNNQRPS GVPDRFSGSKSGTSASLAISGLQSEDEADYFCATFDESLSGPVFGGGTKLTVLG	124
iPS:361412	2C2.005.002	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSQTVNWYQHLPGTAPKLLIYTNNQRPS GVPDRFSGSKSGTSASLAISGLQSEDEADYFCATFDESLQGPVFGGGTKLTVLG	125
iPS:361418	2C2.005.003	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVNWYQHLPGTAPKLLIYTNNQRPS GVPDRFSGSKSGTSASLAISGLQSEDEADYFCATFDESLSGPVFGGGTKLTVLG	126
iPS:361424	2C2.005.004	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVNWYQHLPGTAPKLLIYTNNQRPS GVPDRFSGSKSGTSASLAISGLQSEDEADYFCATFDESLQGPVFGGGTKLTVLG	127
iPS:361430	2C2.005.005	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSQTVNWYQHLPGTAPKLLIYTNNQRPS GVPDRFSGSKSGTSASLAISGLQSEDEADYFCATFDDSLNGPVFGGGTKLTVLG	128
iPS:361436	2C2.005.006	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVNWYQHLPGTAPKLLIYTNNQRPS GVPDRFSGSKSGTSASLAISGLQSEDEADYFCATFDDSLNGPVFGGGTKLTVLG	129
iPS:361442	2C2.005.007	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQHLPGTAPKLLIYTNNQRPS GVPDRFSGSKSGTSASLAISGLQSEDEADYFCATFDESLNGPVFGGGTKLTVLG	130
iPS:361448	2C2.005.008	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQHLPGTAPKLLIYTNNQRPS GVPDRFSGSKSGTSASLAISGLQSEDEADYFCATFDDSLQGPVFGGGTKLTVLG	131
iPS:361454	2C2.005.009	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQHLPGTAPKLLIYTNNQRPS GVPDRFSGSKSGTSASLAISGLQSEDEADYFCATFDDSLSGPVFGGGTKLTVLG	132
iPS:361460	2C2.005.010	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQHLPGTAPKLLIYTNNQRPS GVPDRFSGSKSGTSASLAISGLQSEDEADYFCATFDDSLNAPVFGGGTKLTVLG	133
iPS:361466	2C2.005.011	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQHLPGTAPKLLIYTNNQRPS GVPDRFSGSKSGTSASLAISGLQSEDEADYFCATFDSSLNGPVFGGGTKLTVLG	134
iPS:361472	2C2.005.012	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVNWYQHLPGTAPKLLIYTNNQRPS GVPDRFSGSKSGTSASLAISGLQSEDEADYFCATFDSSLNAPVFGGGTKLTVLG	135
iPS:361478	2C2.005.013	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVNWYQHLPGTAPKLLIYTNNQRPS GVPDRFSGSKSGTSASLAISGLQSEDEADYFCATFDSSLNAPVFGGGTKLTVLG	136
iPS:361485	2C2.005.014	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSQTVNWYQHLPGTAPKLLIYTNNQRPS GVPDRFSGSKSGTSASLAISGLQSEDEADYFCATFDESLSGPVFGGGTKLTVLG	137

Identifier	Construct	VL	SEQ ID NO:
iPS:361845	18F2.013	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGWYQQKPGKAPKRLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIKR	138
iPS:361851	6H1.009	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKRLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIKR	139
iPS:361855	2C2.005.015	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQQLPGTAPKLLIYTNNQRPS GVPDRFSGSKSGTSASLAISGLQSEDEADYFCATFDSSLSGPVFGGGTKLTVLG	140
iPS:336067	5G12.006	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWYQQKPGKAPELLIYVASSLQSG VPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTLISFGQGTKLEITR	141
iPS:336169	17B11.002	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYEQFPGTAPKLLIYDNNKRP SGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAVVFGGGTKLTVLG	142
iPS:361127	5G12.006.001	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWYQQKPGKAPELLIYVASSLQSG VPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTLISFGQGTKLEIKR	143
iPS:361136	5G12.006.002	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWYQQKPGKAPELLIYVASSLQSG VPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTLISFGQGTKLEIKR	144
iPS:361140	5G12.006.003	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWYQQKPGKAPELLIYVASSLQSG VPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTLISFGQGTKLEITR	145
iPS:359919	5G12.006.004	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWYQQKPGKAPKLLIYVASSLQSG VPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTLISFGQGTKLEIKR	146
iPS:361144	5G12.006.005	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWYQQKPGKAPELLIYVASSLQSG VPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTLISFGQGTKLEIKR	147
iPS:361151	5G12.006.006	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWYQQKPGKAPELLIYVASSLQSG VPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTLISFGQGTKLEIKR	148
iPS:361491	17B11.002.001	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRP SGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAVVFGGGTKLTVLG	149
iPS:361499	17B11.002.002	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRP SGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAVVFGGGTKLTVLG	150
iPS:361503	17B11.002.003	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYEQFPGTAPKLLIYDNNKRP SGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAVVFGGGTKLTVLG	151
iPS:361507	17B11.002.004	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRP SGIPDRFSGSKSGTSATLAITGLQTGDEADYYCGTFESSLSAVVFGGGTKLTVLG	152

Identifier	Construct	VL	SEQ ID NO:
iPS:361514	17B11.002.005	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRP SGIPDRFSGSKSGTSATLAITGLQTGDEADYYCGTWDSSLSAVVFGGGTKLTVLG	153
iPS:360582	17B11.002.006	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRP SGIPDRFSGSKSGTSATLAITGLQTGDEADYYCGTWDSSLSAVVFGGGTKLTVLG	154
iPS:361518	17B11.002.007	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRP SGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAVVFGGGTKLTVLG	155
iPS:360570	17B11.002.008	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRP SGIPDRFSGSKSGTSATLAITGLQTGDEADYYCGTFESSLSAVVFGGGTKLTVLG	156
iPS:362051	5G12.005.001	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWYQQKPGKAPKLLIYVASSLQSG VPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTLLSFGQGTKLEIKR	157

Table 5. Variable Heavy (VH) Region Amino Acid Sequences of Exemplary Anti-GIPR Antibodies

Identifier	Construct	VH	SEQ ID NO:
iPS:336175	2C2.005	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWIN PNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGGDYVWGT YRPHYYYGMDVWGQGTTVTVSS	158
iPS:335914	4B1	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DGSNENYADSVKGRFTISRDNSKNTLYLHMNSLRVADTAVYYCARDGTIFGVVL GDYWGQGTLVTVSS	159
iPS:335938	6H1	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAVIWY DGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGTIFGVLLG DYWGQGTLVTVSS	160
iPS:335941	2F11	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWY DGSNKYYADSVKGRFTISSDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLD YWGQGTLVTVSS	161
iPS:335970	5C2	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWINP DSGGTDYSQRFQGRFTMTRDTSISTAYMELNRLRSDDTAVYYCAREATIFGMVIV PFDYWGQGTLVTVSS	162
iPS:335978	13H12	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWINP DSGGTDYSQRFQGRFTMTRDTSISTAYMELSRLRSDDTAVYYCAREATIFGMVIVP FDYWGQGTLVTVSS	163

Identifier	Construct	VH	SEQ ID NO:
iPS:335986	11C1	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLVWMGWISP NSGDTSYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYFCTREATIFGMLIVP FDYWGQGTLVTVSS	164
iPS:335994	12H11	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWISPN NGDTNYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYYCTREATIFGMLIVP FDYWGQGTLVTVSS	165
iPS:336024	18E3	QVQLQESGPGLVKPSQTLSLTCTVSGDSISSGGYYWSWIRQHPGKGLEWIGYIYYS GSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFGVVMGGG MDVWGQGTTVTVSS	166
iPS:336041	2G10_LC1	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGEGLEWVAAIWF DGSDKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQAIFGVVP DYWGQGTLVTVSS	167
iPS:336077	4H9.004	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAVIWY DGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGTIFGVLLG DYWGQGTLVTVSS	168
iPS:336088	6A5.004	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQPPGKGLEWVAAIWYD GNNKYYADSVKGRFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLEY LGQGTLVTVSS	169
iPS:336099	17H11.004	QVQLQESGPGLVKPSETLSLTCTVSQGSISSYYWSWIRQPAGKGLEWIGRIYTSGST NYNPSLKSRVTMSIDTSKNQFSLKLNSVTAADTAVYYCARDVAVAGFDYWGQGT LVTVSS	170
iPS:359621	17H11.004.001	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPAGKGLEWIGRIYTSGST NYNPSLKSRVTMSIDTSKNQFSLKLNSVTAADTAVYYCARDVAVAGFDYWGQGT LVTVSS	171
iPS:359781	4H9.004.001	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAVIWY DASNKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGTIFGVLL GDYWGQGTLVTVSS	172
iPS:360929	4H9.004.002	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAVIWY DASNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGTIFGVLLG DYWGQGTLVTVSS	173
iPS:360936	4H9.004.003	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAVIWY DGSNKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGTIFGVLL GDYWGQGTLVTVSS	174

Identifier	Construct	VH	SEQ ID NO:
iPS:360943	4H9.004.004	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAVIWY DASNKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGTIFGVLL GDYWGQGTLVTVSS	175
iPS:360949	4H9.004.005	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAVIWY DASNKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGTIFGVLL GDYWGQGTLVTVSS	176
iPS:359761	4H9.004.006	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAVIWY DASNKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVLL GDYWGQGTLVTVSS	177
iPS:360955	4B1.010	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DASNENYADAVKGRFTISRDNSKNTLYLQMNSLRVADTAVYYCARDGTIFGVVL GDYWGQGTLVTVSS	178
iPS:360962	4B1.011	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DASNENYADAVKGRFTISRDNSKNTLYLQMNSLRVADTAVYYCARDGTIFGVVL GDYWGQGTLVTVSS	179
iPS:360968	4B1.012	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DASNENYADAVKGRFTISRDNSKNTLYLQMNSLRVADTAVYYCARDGTIFGVVL GDYWGQGTLVTVSS	180
iPS:360974	4B1.013	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DASNENYADSVKGRFTISRDNSKNTLYLHMNSLRVADTAVYYCARDGTIFGVVL GDYWGQGTLVTVSS	181
iPS:360978	4B1.014	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DGSNENYADAVKGRFTISRDNSKNTLYLHMNSLRVADTAVYYCARDGTIFGVVL GDYWGQGTLVTVSS	182
iPS:359785	4B1.015	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DASNENYADAVKGRFTISRDNSKNTLYLQMNSLRVEDTAVYYCARDRTIFGVVL GDYWGQGTLVTVSS	183
iPS:360982	4B1.016	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DASNENYADAVKGRFTISRDNSKNTLYLQMNSLRVEDTAVYYCARDGTIFGVVL GDYWGQGTLVTVSS	184
iPS:335922	18F2	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DGSNENYADSVKGRFTISRDNSKNTLYLHMNSLRAADTAVYYCARDGTIFGVVL GDYWGQGTLVTVSS	185

Identifier	Construct	VH	SEQ ID NO:
iPS:360986	18F2.002	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DASNENYADAVKGRFTISRDNSKNTLYLQMNSLRAADTAVYYCARDGTIFGVVL GDYWGQGTLVTVSS	186
iPS:360995	18F2.003	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DASNENYADAVKGRFTISRDNSKNTLYLHMNSLRAADTAVYYCARDGTIFGVVL GDYWGQGTLVTVSS	187
iPS:360999	18F2.004	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DASNENYADAVKGRFTISRDNSKNTLYLQMNSLRAADTAVYYCARDGTIFGVVL GDYWGQGTLVTVSS	188
iPS:361005	18F2.005	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DASNENYADAVKGRFTISRDNSKNTLYLQMNSLRAADTAVYYCARDGTIFGVVL GDYWGQGTLVTVSS	189
iPS:361009	18F2.006	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DASNENYADAVKGRFTISRDNSKNTLYLHMNSLRAADTAVYYCARDGTIFGVVL GDYWGQGTLVTVSS	190
iPS:361013	18F2.007	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DASNENYADAVKGRFTISRDNSKNTLYLHMNSLRAADTAVYYCARDGTIFGVVL GDYWGQGTLVTVSS	191
iPS:361017	18F2.008	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DASNENYADAVKGRFTISRDNSKNTLYLQMNSLRAADTAVYYCARDGTIFGVVL GDYWGQGTLVTVSS	192
iPS:361021	18F2.009	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DGSNENYADAVKGRFTISRDNSKNTLYLQMNSLRAADTAVYYCARDGTIFGVVL GDYWGQGTLVTVSS	193
iPS:361028	18F2.010	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DASNENYADSVKGRFTISRDNSKNTLYLQMNSLRAADTAVYYCARDGTIFGVVL GDYWGQGTLVTVSS	194
iPS:360535	18F2.011	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DASNENYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVL GDYWGQGTLVTVSS	195
iPS:361035	18F2.012	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DASNENYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGTIFGVVL GDYWGQGTLVTVSS	196

Identifier	Construct	VH	SEQ ID NO:
iPS:359940	2F11.002	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWY DASNKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVL DYWGQGTLVTVSS	197
iPS:361039	2F11.003	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWY DASNKYYADAVKGRFTISSDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVL DYWGQGTLVTVSS	198
iPS:361043	2F11.004	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWY DASNKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVL DYWGQGTLVTVSS	199
iPS:361049	2F11.005	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWY DASNKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVL DYWGQGTLVTVSS	200
iPS:361055	2F11.006	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWY DASNKYYADAVKGRFTISSDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVL DYWGQGTLVTVSS	201
iPS:361059	2F11.007	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWY DASNKYYADAVKGRFTISSDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVL DYWGQGTLVTVSS	202
iPS:361063	2F11.008	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWY DASNKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVL DYWGQGTLVTVSS	203
iPS:359949	2F11.009	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWY DASNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLD YWGQGTLVTVSS	204
iPS:359956	2F11.010	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWY DGSNKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVL DYWGQGTLVTVSS	205
iPS:359865	6H1.002	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAVIWY DASNKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGTIFGVLL GDYWGQGTLVTVSS	206
iPS:359869	6H1.003	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAVIWY DASNKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVLL GDYWGQGTLVTVSS	207

Identifier	Construct	VH	SEQ ID NO:
iPS:359873	6H1.004	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAVIWY DASNKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGTIFGVLL GDYWGQGTLVTVSS	208
iPS:359877	6H1.005	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAVIWY DASNKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVLL GDYWGQGTLVTVSS	209
iPS:361067	6H1.006	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAVIWY DGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGTIFGVLLG DYWGQGTLVTVSS	210
iPS:361071	6H1.007	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAVIWY DASNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGTIFGVLLG DYWGQGTLVTVSS	211
iPS:361075	6H1.008	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAVIWY DGSNKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGTIFGVLL GDYWGQGTLVTVSS	212
iPS:361079	6A5.004.001	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQPPGKGLEWVAAIWYD ANNKYYADAVKGRFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLE YWGQGTLVTVSS	213
iPS:361085	6A5.004.002	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQPPGKGLEWVAAIWYD ANNKYYADAVKGRFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLE YWGQGTLVTVSS	214
iPS:361091	6A5.004.003	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQPPGKGLEWVAAIWYD ANNKYYADAVKGRFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLE YLGQGTLVTVSS	215
iPS:361095	6A5.004.004	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQPPGKGLEWVAAIWYD ANNKYYADAVKGRFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLE YWGQGTLVTVSS	216
iPS:361101	6A5.004.005	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQPPGKGLEWVAAIWYD ANNKYYADAVKGRFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLE YLGQGTLVTVSS	217
iPS:361105	6A5.004.006	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQPPGKGLEWVAAIWYD ANNKYYADAVKGRFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLE YLGQGTLVTVSS	218

Identifier	Construct	VH	SEQ ID NO:
iPS:361109	6A5.004.007	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQPPGKGLEWVAAIWYD ANNKYYADAVKGRFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLE YWGQGTLVTVSS	219
iPS:361113	6A5.004.008	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQPPGKGLEWVAAIWYD GNNKYYADAVKGRFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLE YWGQGTLVTVSS	220
iPS:361120	6A5.004.009	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQPPGKGLEWVAAIWYD ANNKYYADSVKGRFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLEY WGQGTLVTVSS	221
iPS:359896	6A5.004.010	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQPPGKGLEWVAAIWYD ANNKYYADAVKGRFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLE YWGQGTLVTVSS	222
iPS:359890	6A5.004.011	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQPPGKGLEWVAAIWYD ANNKYYADAVKGRFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLE YLGQGTLVTVSS	223
iPS:359567	2A11.002	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQAPGKGLEWVAVIWY DASNKYYEDAVKGRFTISRDNSKNTLFLQVNSLRAEDTAVYYCARGITIFGHGFEY WGQGTLVTVSS	224
iPS:335965	2A11.003	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQAPGKGLEWVAVIWY DGSNKYYEDSVKGRFTISRDNSKNTLFLQVNSLRAEDTAVYYCARGITIFGHGFEY WGQGTLVTVSS	225
iPS:361158	2A11.004	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQAPGKGLEWVAVIWY DGSNKYYEDAVKGRFTISRDNSKNTLFLQVNSLRAEDTAVYYCARGITIFGHGFEY WGQGTLVTVSS	226
iPS:361165	2A11.005	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQAPGKGLEWVAVIWY DASNKYYEDSVKGRFTISRDNSKNTLFLQVNSLRAEDTAVYYCARGITIFGHGFEY WGQGTLVTVSS	227
iPS:361172	2G10_LC1.003	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGEGLEWVAAIWF DASDKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQAIFGVVP DYWGQGTLVTVSS	228
iPS:361178	2G10_LC1.004	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGEGLEWVAAIWF DASDKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQAIFGVVP DYWGQGTLVTVSS	229

Identifier	Construct	VH	SEQ ID NO:
iPS:361185	2G10_LC1.005	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGEGLEWVAAIWF DGSDKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQAIFGVVP DYWGQGTLVTVSS	230
iPS:361192	2G10_LC1.006	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGEGLEWVAAIWF DASDKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQAIFGVVP DYWGQGTLVTVSS	231
iPS:359609	2G10_LC1.007	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVAAIWF DASDKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQAIFGVVP DYWGQGTLVTVSS	232
iPS:359615	2G10_LC1.008	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVAAIWF DASDKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQAIFGVVP DYWGQGTLVTVSS	233
iPS:361196	2G10_LC1.009	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGEGLEWVAAIWF DASDKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQAIFGVVP DYWGQGTLVTVSS	234
iPS:361202	2G10_LC1.010	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVAAIWF DASDKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQAIFGVVP DYWGQGTLVTVSS	235
iPS:359644	18E3.002	QVQLQESGPGLVKPSETLSLTCTVSGDSISSGGYYWSWIRQPPGKGLEWIGYIYYS GSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFGVVMGGG MDVWGQGTTVTVSS	236
iPS:361206	18E3.003	QVQLQESGPGLVKPSETLSLTCTVSGDSISSGGYYWSWIRQPPGKGLEWIGYIYYS GSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFGVVMGGG MDVWGQGTTVTVSS	237
iPS:359628	18E3.004	QVQLQESGPGLVKPSQTLSLTCTVSGDSISSGGYYWSWIRQPPGKGLEWIGYIYYS GSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFGVVMGGG MDVWGQGTTVTVSS	238
iPS:359637	18E3.005	QVQLQESGPGLVKPSETLSLTCTVSGDSISSGGYYWSWIRQHPGKGLEWIGYIYYS GSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFGVVMGGG MDVWGQGTTVTVSS	239
iPS:361210	18E3.006	QVQLQESGPGLVKPSQTLSLTCTVSGDSISSGGYYWSWIRQHPGKGLEWIGYIYYS GSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFGVVMGGG MDVWGQGTTVTVSS	240

Identifier	Construct	VH	SEQ ID NO:
iPS:361214	18E3.007	QVQLQESGPGLVKPSETLSLTCTVSGDSISSGGYYWSWIRQHPGKGLEWIGYIYYS GSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFGVVMGGG MDVWGQGTTVTVSS	241
iPS:361218	18E3.008	QVQLQESGPGLVKPSQTLSLTCTVSGDSISSGGYYWSWIRQPPGKGLEWIGYIYYS GSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFGVVMGGG MDVWGQGTTVTVSS	242
iPS:361222	5C2.006	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWINP ESGGTDYSQRFQGRVTMTRDTSISTAYMELNRLRSDDTAVYYCAREATIFGMVIV PFDYWGQGTLVTVSS	243
iPS:361229	5C2.007	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWINP ESGGTDYSQRFQGRFTMTRDTSISTAYMELNRLRSDDTAVYYCAREATIFGMVIVP FDYWGQGTLVTVSS	244
iPS:361236	5C2.008	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWINP DAGGTDYSQRFQGRVTMTRDTSISTAYMELNRLRSDDTAVYYCAREATIFGMVIV PFDYWGQGTLVTVSS	245
iPS:359685	5C2.009	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWINP DAGGTDYSQRFQGRFTMTRDTSISTAYMELNRLRSDDTAVYYCAREATIFGMVIV PFDYWGQGTLVTVSS	246
iPS:361240	5C2.010	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWINP DSGGTDYSQRFQGRVTMTRDTSISTAYMELNRLRSDDTAVYYCAREATIFGMVIV PFDYWGQGTLVTVSS	247
iPS:361247	5C2.011	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWINP DSGGTDYSQRFQGRFTMTRDTSISTAYMELNRLRSDDTAVYYCAREATIFGMVIV PFDYWGQGTLVTVSS	248
iPS:361254	5C2.012	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWINP DSGGTDYSQRFQGRVTMTRDTSISTAYMELNRLRSDDTAVYYCAREATIFGMVIV PFDYWGQGTLVTVSS	249
iPS:361261	5C2.013	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWINP DAGGTDYSQRFQGRFTMTRDTSISTAYMELNRLRSDDTAVYYCAREATIFGMVIV PFDYWGQGTLVTVSS	250
iPS:361268	5C2.014	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWINP DAGGTDYSQRFQGRVTMTRDTSISTAYMELNRLRSDDTAVYYCAREATIFGMVIV PFDYWGQGTLVTVSS	251

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iPS:359669	5C2.015	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWINP DAGGTDYSQRFQGRVTMTRDTSISTAYMELNSLRSDDTAVYYCAREATIFGMVIV PFDYWGQGTLVTVSS	252
iPS:359678	5C2.016	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWINP ESGGTDYSQRFQGRVTMTRDTSISTAYMELNSLRSDDTAVYYCAREATIFGMVIVP FDYWGQGTLVTVSS	253
iPS:361275	11C1.002	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLVWMGWISP NSGETSYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYFCAREATIFGMLIVP FDYWGQGTLVTVSS	254
iPS:361282	11C1.003	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLVWMGWISP NSGDTSYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYFCAREATIFGMLIVP FDYWGQGTLVTVSS	255
iPS:361289	11C1.004	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLVWMGWISP NSGETSYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYFCAREATIFGMLIVP FDYWGQGTLVTVSS	256
iPS:359712	11C1.005	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLVWMGWISP NSGETSYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYFCTREATIFGMLIVP FDYWGQGTLVTVSS	257
iPS:361293	11C1.006	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLVWMGWISP NSGDTSYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYFCTREATIFGMLIVP FDYWGQGTLVTVSS	258
iPS:361297	11C1.007	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLVWMGWISP NSGETSYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYFCTREATIFGMLIVP FDYWGQGTLVTVSS	259
iPS:361301	11C1.008	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLVWMGWISP NSGDTSYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYFCAREATIFGMLIVP FDYWGQGTLVTVSS	260
iPS:359703	11C1.009	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWISP NSGETSYAQKFQDRVTMTRDTSISTAYMELSSLRSDDTAVYFCAREATIFGMLIVP FDYWGQGTLVTVSS	261
iPS:361305	11C1.010	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWISP NSGETSYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYFCAREATIFGMLIVP FDYWGQGTLVTVSS	262

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iPS:361312	13H12.002	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWINP ESGGTDYSQRFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCAREATIFGMVIVP FDYWGQGTLVTVSS	263
iPS:359744	13H12.003	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWINP ESGGTDYSQRFQGRFTMTRDTSISTAYMELSRLRSDDTAVYYCAREATIFGMVIVP FDYWGQGTLVTVSS	264
iPS:361319	13H12.004	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWINP DSGGTDYSQRFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCAREATIFGMVIV PFDYWGQGTLVTVSS	265
iPS:359737	13H12.005	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWINP ESGGTDYSQRFQGRVTMTRDTSISTAYMELSSLRSDDTAVYYCAREATIFGMVIVP FDYWGQGTLVTVSS	266
iPS:361326	13H12.006	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWINP ESGGTDYSQRFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCAREATIFGMVIVP FDYWGQGTLVTVSS	267
iPS:361330	12H11.002	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWISPN QGETNYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYYCAREATIFGMLIVP FDYWGQGTLVTVSS	268
iPS:361337	12H11.003	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWISPN QGDTNYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYYCAREATIFGMLIVP FDYWGQGTLVTVSS	269
iPS:361344	12H11.004	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWISPN QGETNYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYYCTREATIFGMLIVPF DYWGQGTLVTVSS	270
iPS:361351	12H11.005	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWISPN NGETNYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYYCAREATIFGMLIVP FDYWGQGTLVTVSS	271
iPS:361358	12H11.006	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWISPN NGDTNYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYYCAREATIFGMLIVP FDYWGQGTLVTVSS	272
iPS:361365	12H11.007	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWISPN QGDTNYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYYCTREATIFGMLIVP FDYWGQGTLVTVSS	273

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iPS:361372	12H11.008	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWISPN NGETNYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYYCTREATIFGMLIVPF DYWGQGTLVTVSS	274
iPS:361379	12H11.009	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWISPN QGETNYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYYCAREATIFGMLIVP FDYWGQGTLVTVSS	275
iPS:361383	12H11.010	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWISPN NGDTNYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYYCAREATIFGMLIVP FDYWGQGTLVTVSS	276
iPS:361387	12H11.011	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWISPN QGDTNYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYYCAREATIFGMLIVP FDYWGQGTLVTVSS	277
iPS:361391	12H11.012	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWISPN NGETNYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYYCAREATIFGMLIVP FDYWGQGTLVTVSS	278
iPS:361395	12H11.013	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWISP NQGETNYAQKFQDRVTMTRDTSISTAYMELSSLRSDDTAVYYCAREATIFGMLIV PFDYWGQGTLVTVSS	279
iPS:361402	12H11.014	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWISP NQGETNYAQKFQDRVTMTRDTSISTAYMELSSLRSDDTAVYYCAREATIFGMLIV PFDYWGQGTLVTVSS	280
iPS:361406	2C2.005.001	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWIN PNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGGDYVWGT YRPHYYYGMDVWGQGTTVTVSS	281
iPS:361412	2C2.005.002	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWIN PNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGGDYVWGT YRPHYYYGMDVWGQGTTVTVSS	282
iPS:361418	2C2.005.003	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWIN PNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGGDYVWGT YRPHYYYGMDVWGQGTTVTVSS	283
iPS:361424	2C2.005.004	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWIN PNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGGDYVWGT YRPHYYYGMDVWGQGTTVTVSS	284

Identifier	Construct	VH	SEQ ID NO:
iPS:361430	2C2.005.005	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWIN PNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGGDYVWGT YRPHYYYGMDVWGQGTTVTVSS	285
iPS:361436	2C2.005.006	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWIN PNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGGDYVWGT YRPHYYYGMDVWGQGTTVTVSS	286
iPS:361442	2C2.005.007	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWIN PNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGGDYVWGT YRPHYYYGMDVWGQGTTVTVSS	287
iPS:361448	2C2.005.008	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWIN PNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGGDYVWGT YRPHYYYGMDVWGQGTTVTVSS	288
iPS:361454	2C2.005.009	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWIN PNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGGDYVWGT YRPHYYYGMDVWGQGTTVTVSS	289
iPS:361460	2C2.005.010	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWIN PNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGGDYVWGT YRPHYYYGMDVWGQGTTVTVSS	290
iPS:361466	2C2.005.011	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWIN PNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGGDYVWGT YRPHYYYGMDVWGQGTTVTVSS	291
iPS:361472	2C2.005.012	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWIN PNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGGDYVWGT YRPHYYYGMDVWGQGTTVTVSS	292
iPS:361478	2C2.005.013	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWIN PNSGGTNYAQKFQGRVTMTRDTSISTAYMELSSLRSDDTAVYYCARGGDYVFGT YRPHYYYGMDVWGQGTTVTVSS	293
iPS:361485	2C2.005.014	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWIN PNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGGDYVFGT YRPHYYYGMDVWGQGTTVTVSS	294
iPS:361845	18F2.013	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DASNENYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVL GDYWGQGTLVTVSS	295

Identifier	Construct	VH	SEQ ID NO:
iPS:361851	6H1.009	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAVIWY DASNKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVLL GDYWGQGTLVTVSS	296
iPS:361855	2C2.005.015	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWIN PNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGGDYVWGT YRPHYYYGMDVWGQGTTVTVSS	297
iPS:336067	5G12.006	QVQLVESGGGVVQPGRSLRLSCTASGFTFSSYGIHWVRQAPGKGLEWVAVIWYD GSNKFHADSVKGRFTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKVAGMPEAF EIWGQGTKVTVSS	298
iPS:336169	17B11.002	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN PNSGNTGYAQKFQGRVTMTRDTSISTAYMELSSLRSQDTAVYYCARGGDYVWGS YRPYYYYYGMDVWGQGTTVTVSS	299
iPS:361127	5G12.006.001	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGIHWVRQAPGKGLEWVAVIWYD ASNKFHADAVKGRFTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKVAGMPEAF EIWGQGTKVTVSS	300
iPS:361136	5G12.006.002	QVQLVESGGGVVQPGRSLRLSCTASGFTFSSYGIHWVRQAPGKGLEWVAVIWYD ASNKFHADAVKGRFTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKVAGMPEAF EIWGQGTKVTVSS	301
iPS:361140	5G12.006.003	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGIHWVRQAPGKGLEWVAVIWYD ASNKFHADAVKGRFTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKVAGMPEAF EIWGQGTKVTVSS	302
iPS:359919	5G12.006.004	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGIHWVRQAPGKGLEWVAVIWYD ASNKFHADAVKGRFTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKVAGMPEAF EIWGQGTLVTVSS	303
iPS:361144	5G12.006.005	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGIHWVRQAPGKGLEWVAVIWYD ASNKFHADSVKGRFTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKVAGMPEAF EIWGQGTKVTVSS	304
iPS:361151	5G12.006.006	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGIHWVRQAPGKGLEWVAVIWYD GSNKFHADAVKGRFTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKVAGMPEAF EIWGQGTKVTVSS	305
iPS:361491	17B11.002.001	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN PNSGGTGYAQKFQGRVTMTRDTSISTAYMELSSLRSQDTAVYYCARGGDYVWGS YRPYYYYYGMDVWGQGTTVTVSS	306

Identifier	Construct	VH	SEQ ID NO:
iPS:361499	17B11.002.002	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN PNSGNTGYAQKFQGRVTMTRDTSISTAYMELSSLRSQDTAVYYCARGGDYVWGS YRPYYYYYGMDVWGQGTTVTVSS	307
iPS:361503	17B11.002.003	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN PNSGGTGYAQKFQGRVTMTRDTSISTAYMELSSLRSQDTAVYYCARGGDYVWGS YRPYYYYYGMDVWGQGTTVTVSS	308
iPS:361507	17B11.002.004	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQAPGQGLEWMGWMN PNSGGTGYAQKFQGRVTMTRDTSISTAYMELSSLRSDDTAVYYCARGGDYVWGS YRPYYYYYGMDVWGQGTTVTVSS	309
iPS:361514	17B11.002.005	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN PNSGGTGYAQKFQGRVTMTRDTSISTAYMELSSLRSQDTAVYYCARGGDYVWGS YRPYYYYYGMDVWGQGTTVTVSS	310
iPS:360582	17B11.002.006	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQAPGQGLEWMGWMN PNSGNTGYAQKFQGRVTMTRDTSISTAYMELSSLRSDDTAVYYCARGGDYVWGS YRPYYYYYGMDVWGQGTTVTVSS	311
iPS:361518	17B11.002.007	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN PNSGGTGYAQKFQGRVTMTRDTSISTAYMELSSLRSQDTAVYYCARGGDYVFGS YRPYYYYYGMDVWGQGTTVTVSS	312
iPS:360570	17B11.002.008	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQAPGQGLEWMGWMN PNSGGTGYAQKFQGRVTMTRDTSISTAYMELSSLRSDDTAVYYCARGGDYVFGS YRPYYYYYGMDVWGQGTTVTVSS	313
iPS:362051	5G12.005.001	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGIHWVRQAPGKGLEWVAVIWYD ASNKFHADAVKGRFTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKVAGMPEAF EIWGQGTLVTVSS	314

Table 6. CDRL1, CDRL2, and CDRL3 Amino Acid Sequences of Exemplary Anti-GIPR Antibodies

Identifier	Construct	CDRL1	CDRL2	CDRL3
iPS:336175	2C2.005	SGSSSNIGSNTVN SEQ ID NO: 629	TNNQRPS SEQ ID NO: 786	ATFDDSLNGPV SEQ ID NO: 943
iPS:335914	4B1	RASQDIRDYLG SEQ ID NO: 630	GASSLQS SEQ ID NO: 787	LQHNNYPFT SEQ ID NO: 944
iPS:335938	6H1	RASQDIRDYLG SEQ ID NO: 631	GASSLQS SEQ ID NO: 788	LQHNNYPFT SEQ ID NO: 945
iPS:335941	2F11	QASQDISNYLN SEQ ID NO: 632	DASNLET SEQ ID NO: 789	QQYDILLT SEQ ID NO: 946
iPS:335970	5C2	KSSQSVLSSSNNKNYIA SEQ ID NO: 633	WASTRES SEQ ID NO: 790	QQYYSTPWT SEQ ID NO: 947
iPS:335978	13H12	KSSQSVLSSSNNKNYIA SEQ ID NO: 634	WASTRES SEQ ID NO: 791	QQYYSTPWT SEQ ID NO: 948
iPS:335986	11C1	KSSQSVLSSSNNKNYLA SEQ ID NO: 635	WTSTRDS SEQ ID NO: 792	QQYYRTPWT SEQ ID NO: 949
iPS:335994	12H11	KSSQSVLSSSNNKNYLA SEQ ID NO: 636	WTSTRDS SEQ ID NO: 793	QQYYRTPWT SEQ ID NO: 950
iPS:336024	18E3	RASQSISYSYLA SEQ ID NO: 637	GASSRAT SEQ ID NO: 794	QQYGSSPLT SEQ ID NO: 951
iPS:336041	2G10_LC1	RASQSVSSNLA SEQ ID NO: 638	GAATRAT SEQ ID NO: 795	QQYNNWPLT SEQ ID NO: 952
iPS:336077	4H9.004	RASQGIRNELG SEQ ID NO: 639	GASSLQS SEQ ID NO: 796	LQHNSYPFT SEQ ID NO: 953
iPS:336088	6A5.004	QASQDITNYLN SEQ ID NO: 640	DASNLEP SEQ ID NO: 797	QQYDDLFT SEQ ID NO: 954
iPS:336099	17H11.004	RASQGLIIWLA SEQ ID NO: 641	AASSLQS SEQ ID NO: 798	QQTNSFPPT SEQ ID NO: 955
iPS:359621	17H11.004.001	RASQGLIIWLA SEQ ID NO: 642	AASSLQS SEQ ID NO: 799	QQTNSFPPT SEQ ID NO: 956
iPS:359781	4H9.004.001	RASQGIRNELG SEQ ID NO: 643	GASSLQS SEQ ID NO: 800	LQHNSYPFT SEQ ID NO: 957

Identifier	Construct	CDRL1	CDRL2	CDRL3
iPS:360929	4H9.004.002	RASQGIRNELG SEQ ID NO: 644	GASSLQS SEQ ID NO: 801	LQHNSYPFT SEQ ID NO: 958
iPS:360936	4H9.004.003	RASQGIRNELG SEQ ID NO: 645	GASSLQS SEQ ID NO: 802	LQHNSYPFT SEQ ID NO: 959
iPS:360943	4H9.004.004	RASQGIRNELG SEQ ID NO: 646	GASSLQS SEQ ID NO: 803	LQHNSYPFT SEQ ID NO: 960
iPS:360949	4H9.004.005	RASQGIRNELG SEQ ID NO: 647	GASSLQS SEQ ID NO: 804	LQHNSYPFT SEQ ID NO: 961
iPS:359761	4H9.004.006	RASQGIRNELG SEQ ID NO: 648	GASSLQS SEQ ID NO: 805	LQHNSYPFT SEQ ID NO: 962
iPS:360955	4B1.010	RASQDIRDYLG SEQ ID NO: 649	GASSLQS SEQ ID NO: 806	LQHNNYPFT SEQ ID NO: 963
iPS:360962	4B1.011	RASQDIRDYLG SEQ ID NO: 650	GASSLQS SEQ ID NO: 807	LQHNNYPFT SEQ ID NO: 964
iPS:360968	4B1.012	RASQDIRDYLG SEQ ID NO: 651	GASSLQS SEQ ID NO: 808	LQHNNYPFT SEQ ID NO: 965
iPS:360974	4B1.013	RASQDIRDYLG SEQ ID NO: 652	GASSLQS SEQ ID NO: 809	LQHNNYPFT SEQ ID NO: 966
iPS:360978	4B1.014	RASQDIRDYLG SEQ ID NO: 653	GASSLQS SEQ ID NO: 810	LQHNNYPFT SEQ ID NO: 967
iPS:359785	4B1.015	RASQDIRDYLG SEQ ID NO: 654	GASSLQS SEQ ID NO: 811	LQHNNYPFT SEQ ID NO: 968
iPS:360982	4B1.016	RASQDIRDYLG SEQ ID NO: 655	GASSLQS SEQ ID NO: 812	LQHNNYPFT SEQ ID NO: 969
iPS:335922	18F2	RASQDLRNYLG SEQ ID NO: 656	GASSLQS SEQ ID NO: 813	LQHNNYPFT SEQ ID NO: 970
iPS:360986	18F2.002	RASQDLRNYLG SEQ ID NO: 657	GASSLQS SEQ ID NO: 814	LQHNNYPFT SEQ ID NO: 971

Identifier	Construct	CDRL1	CDRL2	CDRL3
iPS:360995	18F2.003	RASQDLRNYLG SEQ ID NO: 658	GASSLQS SEQ ID NO: 815	LQHNNYPFT SEQ ID NO: 972
iPS:360999	18F2.004	RASQDLRNYLG SEQ ID NO: 659	GASSLQS SEQ ID NO: 816	LQHNNYPFT SEQ ID NO: 973
iPS:361005	18F2.005	RASQDLRNYLG SEQ ID NO: 660	GASSLQS SEQ ID NO: 817	LQHNNYPFT SEQ ID NO: 974
iPS:361009	18F2.006	RASQDLRNYLG SEQ ID NO: 661	GASSLQS SEQ ID NO: 818	LQHNNYPFT SEQ ID NO: 975
iPS:361013	18F2.007	RASQDLRNYLG SEQ ID NO: 662	GASSLQS SEQ ID NO: 819	LQHNNYPFT SEQ ID NO: 976
iPS:361017	18F2.008	RASQDLRNYLG SEQ ID NO: 663	GASSLQS SEQ ID NO: 820	LQHNNYPFT SEQ ID NO: 977
iPS:361021	18F2.009	RASQDLRNYLG SEQ ID NO: 664	GASSLQS SEQ ID NO: 821	LQHNNYPFT SEQ ID NO: 978
iPS:361028	18F2.010	RASQDLRNYLG SEQ ID NO: 665	GASSLQS SEQ ID NO: 822	LQHNNYPFT SEQ ID NO: 979
iPS:360535	18F2.011	RASQDLRNYLG SEQ ID NO: 666	GASSLQS SEQ ID NO: 823	LQHNNYPFT SEQ ID NO: 980
iPS:361035	18F2.012	RASQDLRNYLG SEQ ID NO: 667	GASSLQS SEQ ID NO: 824	LQHNNYPFT SEQ ID NO: 981
iPS:359940	2F11.002	QASQDISNYLN SEQ ID NO: 668	DASNLET SEQ ID NO: 825	QQYDILLT SEQ ID NO: 982
iPS:361039	2F11.003	QASQDISNYLN SEQ ID NO: 669	DASNLET SEQ ID NO: 826	QQYDILLT SEQ ID NO: 983
iPS:361043	2F11.004	QASQDISNYLN SEQ ID NO: 670	DASNLET SEQ ID NO: 827	QQYDILLT SEQ ID NO: 984
iPS:361049	2F11.005	QASQDISNYLN SEQ ID NO: 671	DASNLET SEQ ID NO: 828	QQYDILLT SEQ ID NO: 985

Identifier	Construct	CDRL1	CDRL2	CDRL3
iPS:361055	2F11.006	QASQDISNYLN SEQ ID NO: 672	DASNLET SEQ ID NO: 829	QQYDILLT SEQ ID NO: 986
iPS:361059	2F11.007	QASQDISNYLN SEQ ID NO: 673	DASNLET SEQ ID NO: 830	QQYDILLT SEQ ID NO: 987
iPS:361063	2F11.008	QASQDISNYLN SEQ ID NO: 674	DASNLET SEQ ID NO: 831	QQYDILLT SEQ ID NO: 988
iPS:359949	2F11.009	QASQDISNYLN SEQ ID NO: 675	DASNLET SEQ ID NO: 832	QQYDILLT SEQ ID NO: 989
iPS:359956	2F11.010	QASQDISNYLN SEQ ID NO: 676	DASNLET SEQ ID NO: 833	QQYDILLT SEQ ID NO: 990
iPS:359865	6H1.002	RASQDIRDYLG SEQ ID NO: 677	GASSLQS SEQ ID NO: 834	LQHNNYPFT SEQ ID NO: 991
iPS:359869	6H1.003	RASQDIRDYLG SEQ ID NO: 678	GASSLQS SEQ ID NO: 835	LQHNNYPFT SEQ ID NO: 992
iPS:359873	6H1.004	RASQDIRDYLG SEQ ID NO: 679	GASSLQS SEQ ID NO: 836	LQHNNYPFT SEQ ID NO: 993
iPS:359877	6H1.005	RASQDIRDYLG SEQ ID NO: 680	GASSLQS SEQ ID NO: 837	LQHNNYPFT SEQ ID NO: 994
iPS:361067	6H1.006	RASQDIRDYLG SEQ ID NO: 681	GASSLQS SEQ ID NO: 838	LQHNNYPFT SEQ ID NO: 995
iPS:361071	6H1.007	RASQDIRDYLG SEQ ID NO: 682	GASSLQS SEQ ID NO: 839	LQHNNYPFT SEQ ID NO: 996
iPS:361075	6H1.008	RASQDIRDYLG SEQ ID NO: 683	GASSLQS SEQ ID NO: 840	LQHNNYPFT SEQ ID NO: 997
iPS:361079	6A5.004.001	QASQDITNYLN SEQ ID NO: 684	DASNLEP SEQ ID NO: 841	QQYDDLFT SEQ ID NO: 998
iPS:361085	6A5.004.002	QASQDITNYLN SEQ ID NO: 685	DASNLEP SEQ ID NO: 842	QQYDDLFT SEQ ID NO: 999

Identifier	Construct	CDRL1	CDRL2	CDRL3
iPS:361091	6A5.004.003	QASQDITNYLN SEQ ID NO: 686	DASNLEP SEQ ID NO: 843	QQYDDLFT SEQ ID NO: 1000
iPS:361095	6A5.004.004	QASQDITNYLN SEQ ID NO: 687	DASNLEP SEQ ID NO: 844	QQYDDLFT SEQ ID NO: 1001
iPS:361101	6A5.004.005	QASQDITNYLN SEQ ID NO: 688	DASNLEP SEQ ID NO: 845	QQYDDLFT SEQ ID NO: 1002
iPS:361105	6A5.004.006	QASQDITNYLN SEQ ID NO: 689	DASNLEP SEQ ID NO: 846	QQYDDLFT SEQ ID NO: 1003
iPS:361109	6A5.004.007	QASQDITNYLN SEQ ID NO: 690	DASNLEP SEQ ID NO: 847	QQYDDLFT SEQ ID NO: 1004
iPS:361113	6A5.004.008	QASQDITNYLN SEQ ID NO: 691	DASNLEP SEQ ID NO: 848	QQYDDLFT SEQ ID NO: 1005
iPS:361120	6A5.004.009	QASQDITNYLN SEQ ID NO: 692	DASNLEP SEQ ID NO: 849	QQYDDLFT SEQ ID NO: 1006
iPS:359896	6A5.004.010	QASQDITNYLN SEQ ID NO: 693	DASNLEP SEQ ID NO: 850	QQYDDLFT SEQ ID NO: 1007
iPS:359890	6A5.004.011	QASQDITNYLN SEQ ID NO: 694	DASNLEP SEQ ID NO: 851	QQYDDLFT SEQ ID NO: 1008
iPS:359567	2A11.002	RASQIFTSTYLA SEQ ID NO: 695	GASSRAT SEQ ID NO: 852	QQYGSSPR SEQ ID NO: 1009
iPS:335965	2A11.003	RASQIFTSTYLA SEQ ID NO: 696	GASSRAT SEQ ID NO: 853	QQYGSSPR SEQ ID NO: 1010
iPS:361158	2A11.004	RASQIFTSTYLA SEQ ID NO: 697	GASSRAT SEQ ID NO: 854	QQYGSSPR SEQ ID NO: 1011
iPS:361165	2A11.005	RASQIFTSTYLA SEQ ID NO: 698	GASSRAT SEQ ID NO: 855	QQYGSSPR SEQ ID NO: 1012
iPS:361172	2G10_LC1.003	RASQSVSSNLA SEQ ID NO: 699	GAATRAT SEQ ID NO: 856	QQYNNWPLT SEQ ID NO: 1013

Identifier	Construct	CDRL1	CDRL2	CDRL3
iPS:361178	2G10_LC1.004	RASQSVSSNLA SEQ ID NO: 700	GAATRAT SEQ ID NO: 857	QQYNNWPLT SEQ ID NO: 1014
iPS:361185	2G10_LC1.005	RASQSVSSNLA SEQ ID NO: 701	GAATRAT SEQ ID NO: 858	QQYNNWPLT SEQ ID NO: 1015
iPS:361192	2G10_LC1.006	RASQSVSSNLA SEQ ID NO: 702	GAATRAT SEQ ID NO: 859	QQYNNWPLT SEQ ID NO: 1016
iPS:359609	2G10_LC1.007	RASQSVSSNLA SEQ ID NO: 703	GAATRAT SEQ ID NO: 860	QQYNNFPLT SEQ ID NO: 1017
iPS:359615	2G10_LC1.008	RASQSVSSNLA SEQ ID NO: 704	GAATRAT SEQ ID NO: 861	QQYNNYPLT SEQ ID NO: 1018
iPS:361196	2G10_LC1.009	RASQSVSSNLA SEQ ID NO: 705	GAATRAT SEQ ID NO: 862	QQYNNWPLT SEQ ID NO: 1019
iPS:361202	2G10_LC1.010	RASQSVSSNLA SEQ ID NO: 706	GAATRAT SEQ ID NO: 863	QQYNNWPLT SEQ ID NO: 1020
iPS:359644	18E3.002	RASQSISYSYLA SEQ ID NO: 707	GASSRAT SEQ ID NO: 864	QQYGSSPLT SEQ ID NO: 1021
iPS:361206	18E3.003	RASQSISYSYLA SEQ ID NO: 708	GASSRAT SEQ ID NO: 865	QQYGSSPLT SEQ ID NO: 1022
iPS:359628	18E3.004	RASQSISYSYLA SEQ ID NO: 709	GASSRAT SEQ ID NO: 866	QQYGSSPLT SEQ ID NO: 1023
iPS:359637	18E3.005	RASQSISYSYLA SEQ ID NO: 710	GASSRAT SEQ ID NO: 867	QQYGSSPLT SEQ ID NO: 1024
iPS:361210	18E3.006	RASQSISYSYLA SEQ ID NO: 711	GASSRAT SEQ ID NO: 868	QQYGSSPLT SEQ ID NO: 1025
iPS:361214	18E3.007	RASQSISYSYLA SEQ ID NO: 712	GASSRAT SEQ ID NO: 869	QQYGSSPLT SEQ ID NO: 1026
iPS:361218	18E3.008	RASQSISYSYLA SEQ ID NO: 713	GASSRAT SEQ ID NO: 870	QQYGSSPLT SEQ ID NO: 1027

Identifier	Construct	CDRL1	CDRL2	CDRL3
iPS:361222	5C2.006	KSSQSVLSSSNNKNYIA SEQ ID NO: 714	WASTRES SEQ ID NO: 871	QQYYSTPWT SEQ ID NO: 1028
iPS:361229	5C2.007	KSSQSVLSSSNNKNYIA SEQ ID NO: 715	WASTRES SEQ ID NO: 872	QQYYSTPWT SEQ ID NO: 1029
iPS:361236	5C2.008	KSSQSVLSSSNNKNYIA SEQ ID NO: 716	WASTRES SEQ ID NO: 873	QQYYSTPWT SEQ ID NO: 1030
iPS:359685	5C2.009	KSSQSVLSSSNNKNYIA SEQ ID NO: 717	WASTRES SEQ ID NO: 874	QQYYSTPWT SEQ ID NO: 1031
iPS:361240	5C2.010	KSSQSVLSSSNNKNYIA SEQ ID NO: 718	WASTRES SEQ ID NO: 875	QQYYSTPWT SEQ ID NO: 1032
iPS:361247	5C2.011	KSSQSVLSSSNNKNYIA SEQ ID NO: 719	WASTRES SEQ ID NO: 876	QQYYSTPWT SEQ ID NO: 1033
iPS:361254	5C2.012	KSSQSVLSSSNNKNYIA SEQ ID NO: 720	WASTRES SEQ ID NO: 877	QQYYSTPWT SEQ ID NO: 1034
iPS:361261	5C2.013	KSSQSVLSSSNNKNYIA SEQ ID NO: 721	WASTRES SEQ ID NO: 878	QQYYSTPWT SEQ ID NO: 1035
iPS:361268	5C2.014	KSSQSVLSSSNNKNYIA SEQ ID NO: 722	WASTRES SEQ ID NO: 879	QQYYSTPWT SEQ ID NO: 1036
iPS:359669	5C2.015	KSSQSVLSSSNNKNYIA SEQ ID NO: 723	WASTRES SEQ ID NO: 880	QQYYSTPWT SEQ ID NO: 1037
iPS:359678	5C2.016	KSSQSVLSSSNNKNYIA SEQ ID NO: 724	WASTRES SEQ ID NO: 881	QQYYSTPWT SEQ ID NO: 1038
iPS:361275	11C1.002	KSSQSVLSSSNNKNYLA SEQ ID NO: 725	WTSTRES SEQ ID NO: 882	QQYYRTPWT SEQ ID NO: 1039
iPS:361282	11C1.003	KSSQSVLSSSNNKNYLA SEQ ID NO: 726	WTSTRES SEQ ID NO: 883	QQYYRTPWT SEQ ID NO: 1040
iPS:361289	11C1.004	KSSQSVLSSSNNKNYLA SEQ ID NO: 727	WTSTRDS SEQ ID NO: 884	QQYYRTPWT SEQ ID NO: 1041

Identifier	Construct	CDRL1	CDRL2	CDRL3
iPS:359712	11C1.005	KSSQSVLSSSNNKNYLA SEQ ID NO: 728	WTSTRES SEQ ID NO: 885	QQYYRTPWT SEQ ID NO: 1042
iPS:361293	11C1.006	KSSQSVLSSSNNKNYLA SEQ ID NO: 729	WTSTRES SEQ ID NO: 886	QQYYRTPWT SEQ ID NO: 1043
iPS:361297	11C1.007	KSSQSVLSSSNNKNYLA SEQ ID NO: 730	WTSTRDS SEQ ID NO: 887	QQYYRTPWT SEQ ID NO: 1044
iPS:361301	11C1.008	KSSQSVLSSSNNKNYLA SEQ ID NO: 731	WTSTRDS SEQ ID NO: 888	QQYYRTPWT SEQ ID NO: 1045
iPS:359703	11C1.009	KSSQSVLSSSNNKNYLA SEQ ID NO: 732	WTSTRES SEQ ID NO: 889	QQYYRTPWT SEQ ID NO: 1046
iPS:361305	11C1.010	KSSQSVLSSSNNKNYLA SEQ ID NO: 733	WTSTRES SEQ ID NO: 890	QQYYRTPWT SEQ ID NO: 1047
iPS:361312	13H12.002	KSSQSVLSSSNNKNYIA SEQ ID NO: 734	WASTRES SEQ ID NO: 891	QQYYSTPWT SEQ ID NO: 1048
iPS:359744	13H12.003	KSSQSVLSSSNNKNYIA SEQ ID NO: 735	WASTRES SEQ ID NO: 892	QQYYSTPWT SEQ ID NO: 1049
iPS:361319	13H12.004	KSSQSVLSSSNNKNYIA SEQ ID NO: 736	WASTRES SEQ ID NO: 893	QQYYSTPWT SEQ ID NO: 1050
iPS:359737	13H12.005	KSSQSVLSSSNNKNYIA SEQ ID NO: 737	WASTRES SEQ ID NO: 894	QQYYSTPWT SEQ ID NO: 1051
iPS:361326	13H12.006	KSSQSVLSSSNNKNYIA SEQ ID NO: 738	WASTRES SEQ ID NO: 895	QQYYSTPWT SEQ ID NO: 1052
iPS:361330	12H11.002	KSSQSVLSSSNNKNYLA SEQ ID NO: 739	WTSTRDS SEQ ID NO: 896	QQYYRTPWT SEQ ID NO: 1053
iPS:361337	12H11.003	KSSQSVLSSSNNKNYLA SEQ ID NO: 740	WTSTRDS SEQ ID NO: 897	QQYYRTPWT SEQ ID NO: 1054
iPS:361344	12H11.004	KSSQSVLSSSNNKNYLA SEQ ID NO: 741	WTSTRDS SEQ ID NO: 898	QQYYRTPWT SEQ ID NO: 1055

Identifier	Construct	CDRL1	CDRL2	CDRL3
iPS:361351	12H11.005	KSSQSVLSSSNNKNYLA SEQ ID NO: 742	WTSTRDS SEQ ID NO: 899	QQYYRTPWT SEQ ID NO: 1056
iPS:361358	12H11.006	KSSQSVLSSSNNKNYLA SEQ ID NO: 743	WTSTRDS SEQ ID NO: 900	QQYYRTPWT SEQ ID NO: 1057
iPS:361365	12H11.007	KSSQSVLSSSNNKNYLA SEQ ID NO: 744	WTSTRDS SEQ ID NO: 901	QQYYRTPWT SEQ ID NO: 1058
iPS:361372	12H11.008	KSSQSVLSSSNNKNYLA SEQ ID NO: 745	WTSTRDS SEQ ID NO: 902	QQYYRTPWT SEQ ID NO: 1059
iPS:361379	12H11.009	KSSQSVLSSSNNKNYLA SEQ ID NO: 746	WTSTRES SEQ ID NO: 903	QQYYRTPWT SEQ ID NO: 1060
iPS:361383	12H11.010	KSSQSVLSSSNNKNYLA SEQ ID NO: 747	WTSTRES SEQ ID NO: 904	QQYYRTPWT SEQ ID NO: 1061
iPS:361387	12H11.011	KSSQSVLSSSNNKNYLA SEQ ID NO: 748	WTSTRES SEQ ID NO: 905	QQYYRTPWT SEQ ID NO: 1062
iPS:361391	12H11.012	KSSQSVLSSSNNKNYLA SEQ ID NO: 749	WTSTRES SEQ ID NO: 906	QQYYRTPWT SEQ ID NO: 1063
iPS:361395	12H11.013	KSSQSVLSSSNNKNYLA SEQ ID NO: 750	WTSTRDS SEQ ID NO: 907	QQYYRTPWT SEQ ID NO: 1064
iPS:361402	12H11.014	KSSQSVLSSSNNKNYLA SEQ ID NO: 751	WTSTRES SEQ ID NO: 908	QQYYRTPWT SEQ ID NO: 1065
iPS:361406	2C2.005.001	SGSSSNIGSQTVN SEQ ID NO: 752	TNNQRPS SEQ ID NO: 909	ATFDESLSGPV SEQ ID NO: 1066
iPS:361412	2C2.005.002	SGSSSNIGSQTVN SEQ ID NO: 753	TNNQRPS SEQ ID NO: 910	ATFDESLQGPV SEQ ID NO: 1067
iPS:361418	2C2.005.003	SGSSSNIGSNYVN SEQ ID NO: 754	TNNQRPS SEQ ID NO: 911	ATFDESLSGPV SEQ ID NO: 1068
iPS:361424	2C2.005.004	SGSSSNIGSNYVN SEQ ID NO: 755	TNNQRPS SEQ ID NO: 912	ATFDESLQGPV SEQ ID NO: 1069

Identifier	Construct	CDRL1	CDRL2	CDRL3
iPS:361430	2C2.005.005	SGSSSNIGSQTVN SEQ ID NO: 756	TNNQRPS SEQ ID NO: 913	ATFDDSLNGPV SEQ ID NO: 1070
iPS:361436	2C2.005.006	SGSSSNIGSNYVN SEQ ID NO: 757	TNNQRPS SEQ ID NO: 914	ATFDDSLNGPV SEQ ID NO: 1071
iPS:361442	2C2.005.007	SGSSSNIGSNTVN SEQ ID NO: 758	TNNQRPS SEQ ID NO: 915	ATFDESLNGPV SEQ ID NO: 1072
iPS:361448	2C2.005.008	SGSSSNIGSNTVN SEQ ID NO: 759	TNNQRPS SEQ ID NO: 916	ATFDDSLQGPV SEQ ID NO: 1073
iPS:361454	2C2.005.009	SGSSSNIGSNTVN SEQ ID NO: 760	TNNQRPS SEQ ID NO: 917	ATFDDSLSGPV SEQ ID NO: 1074
iPS:361460	2C2.005.010	SGSSSNIGSNTVN SEQ ID NO: 761	TNNQRPS SEQ ID NO: 918	ATFDDSLNAPV SEQ ID NO: 1075
iPS:361466	2C2.005.011	SGSSSNIGSNTVN SEQ ID NO: 762	TNNQRPS SEQ ID NO: 919	ATFDSSLNGPV SEQ ID NO: 1076
iPS:361472	2C2.005.012	SGSSSNIGSNYVN SEQ ID NO: 763	TNNQRPS SEQ ID NO: 920	ATFDSSLNAPV SEQ ID NO: 1077
iPS:361478	2C2.005.013	SGSSSNIGSNYVN SEQ ID NO: 764	TNNQRPS SEQ ID NO: 921	ATFDSSLNAPV SEQ ID NO: 1078
iPS:361485	2C2.005.014	SGSSSNIGSQTVN SEQ ID NO: 765	TNNQRPS SEQ ID NO: 922	ATFDESLSGPV SEQ ID NO: 1079
iPS:361845	18F2.013	RASQDLRNYLG SEQ ID NO: 766	GASSLQS SEQ ID NO: 923	LQHNNYPFT SEQ ID NO: 1080
iPS:361851	6H1.009	RASQDIRDYLG SEQ ID NO: 767	GASSLQS SEQ ID NO: 924	LQHNNYPFT SEQ ID NO: 1081
iPS:361855	2C2.005.015	SGSSSNIGSNTVN SEQ ID NO: 768	TNNQRPS SEQ ID NO: 925	ATFDSSLSGPV SEQ ID NO: 1082
iPS:336067	5G12.006	RASQTISRFLN SEQ ID NO: 769	VASSLQS SEQ ID NO: 926	QQSYSTLIS SEQ ID NO: 1083

Identifier	Construct	CDRL1	CDRL2	CDRL3
iPS:336169	17B11.002	SGSSSNIGNNYVS SEQ ID NO: 770	DNNKRPS SEQ ID NO: 927	GTWDSSLSAVV SEQ ID NO: 1084
iPS:361127	5G12.006.001	RASQTISRFLN SEQ ID NO: 771	VASSLQS SEQ ID NO: 928	QQSYSTLIS SEQ ID NO: 1085
iPS:361136	5G12.006.002	RASQTISRFLN SEQ ID NO: 772	VASSLQS SEQ ID NO: 929	QQSYSTLIS SEQ ID NO: 1086
iPS:361140	5G12.006.003	RASQTISRFLN SEQ ID NO: 773	VASSLQS SEQ ID NO: 930	QQSYSTLIS SEQ ID NO: 1087
iPS:359919	5G12.006.004	RASQTISRFLN SEQ ID NO: 774	VASSLQS SEQ ID NO: 931	QQSYSTLIS SEQ ID NO: 1088
iPS:361144	5G12.006.005	RASQTISRFLN SEQ ID NO: 775	VASSLQS SEQ ID NO: 932	QQSYSTLIS SEQ ID NO: 1089
iPS:361151	5G12.006.006	RASQTISRFLN SEQ ID NO: 776	VASSLQS SEQ ID NO: 933	QQSYSTLIS SEQ ID NO: 1090
iPS:361491	17B11.002.001	SGSSSNIGNNYVS SEQ ID NO: 777	DNNKRPS SEQ ID NO: 934	GTWDSSLSAVV SEQ ID NO: 1091
iPS:361499	17B11.002.002	SGSSSNIGNNYVS SEQ ID NO: 778	DNNKRPS SEQ ID NO: 935	GTWDSSLSAVV SEQ ID NO: 1092
iPS:361503	17B11.002.003	SGSSSNIGNNYVS SEQ ID NO: 779	DNNKRPS SEQ ID NO: 936	GTWDSSLSAVV SEQ ID NO: 1093
iPS:361507	17B11.002.004	SGSSSNIGNNYVS SEQ ID NO: 780	DNNKRPS SEQ ID NO: 937	GTFESSLSAVV SEQ ID NO: 1094
iPS:361514	17B11.002.005	SGSSSNIGNNYVS SEQ ID NO: 781	DNNKRPS SEQ ID NO: 938	GTWDSSLSAVV SEQ ID NO: 1095
iPS:360582	17B11.002.006	SGSSSNIGNNYVS SEQ ID NO: 782	DNNKRPS SEQ ID NO: 939	GTWDSSLSAVV SEQ ID NO: 1096
iPS:361518	17B11.002.007	SGSSSNIGNNYVS SEQ ID NO: 783	DNNKRPS SEQ ID NO: 940	GTWDSSLSAVV SEQ ID NO: 1097

Identifier	Construct	CDRL1	CDRL2	CDRL3
iPS:360570	17B11.002.008	SGSSSNIGNNYVS SEQ ID NO: 784	DNNKRPS SEQ ID NO: 941	GTFESSLSAVV SEQ ID NO: 1098
iPS:362051	5G12.005.001	RASQTISRFLN SEQ ID NO: 785	VASSLQS SEQ ID NO: 942	QQSYSTLLS SEQ ID NO: 1099

Table 7. CDRH1, CDRH2, and CDRH3 Amino Acid Sequences of Exemplary Anti-GIPR Antibodies

Identifier	Construct	CDRH1	CDRH2	CDRH3
iPS:336175	2C2.005	GYYMH SEQ ID NO: 1100	WINPNSGGTNYAQKFQG SEQ ID NO: 1257	GGDYVWGTYRPHYYYGMDV SEQ ID NO: 1414
iPS:335914	4B1	NFGMH SEQ ID NO: 1101	VIWYDGSNENYADSVKG SEQ ID NO: 1258	DGTIFGVVLGDY SEQ ID NO: 1415
iPS:335938	6H1	YFGMH SEQ ID NO: 1102	VIWYDGSNKYYADSVKG SEQ ID NO: 1259	DGTIFGVLLGDY SEQ ID NO: 1416
iPS:335941	2F11	SYGMH SEQ ID NO: 1103	VIWYDGSNKYYADSVKG SEQ ID NO: 1260	DRTIFGVVLDY SEQ ID NO: 1417
iPS:335970	5C2	GYYIH SEQ ID NO: 1104	WINPDSGGTDYSQRFQG SEQ ID NO: 1261	EATIFGMVIVPFDY SEQ ID NO: 1418
iPS:335978	13H12	GYYIH SEQ ID NO: 1105	WINPDSGGTDYSQRFQG SEQ ID NO: 1262	EATIFGMVIVPFDY SEQ ID NO: 1419
iPS:335986	11C1	GYYIH SEQ ID NO: 1106	WISPNSGDTSYAQKFQD SEQ ID NO: 1263	EATIFGMLIVPFDY SEQ ID NO: 1420
iPS:335994	12H11	GYYIH SEQ ID NO: 1107	WISPNNGDTNYAQKFQD SEQ ID NO: 1264	EATIFGMLIVPFDY SEQ ID NO: 1421
iPS:336024	18E3	SGGYYWS SEQ ID NO: 1108	YIYYSGSTYYNPSLKS SEQ ID NO: 1265	DRITIFGVVMGGGMDV SEQ ID NO: 1422
iPS:336041	2G10_LC1	NYGMH SEQ ID NO: 1109	AIWFDGSDKYYADSVKG SEQ ID NO: 1266	DQAIFGVVPDY SEQ ID NO: 1423
iPS:336077	4H9.004	YFGMH SEQ ID NO: 1110	VIWYDGSNKYYADSVKG SEQ ID NO: 1267	DGTIFGVLLGDY SEQ ID NO: 1424
iPS:336088	6A5.004	SYGMH SEQ ID NO: 1111	AIWYDGNNKYYADSVKG SEQ ID NO: 1268	DRTIFGVVLEY SEQ ID NO: 1425
iPS:336099	17H11.004	SYYWS	RIYTSGSTNYNPSLKS	DVAVAGFDY

Identifier	Construct	CDRH1	CDRH2	CDRH3
		SEQ ID NO: 1112	SEQ ID NO: 1269	SEQ ID NO: 1426
iPS:359621	17H11.004.001	SYYWS SEQ ID NO: 1113	RIYTSGSTNYNPSLKS SEQ ID NO: 1270	DVAVAGFDY SEQ ID NO: 1427
iPS:359781	4H9.004.001	YFGMH SEQ ID NO: 1114	VIWYDASNKYYADAVKG SEQ ID NO: 1271	DGTIFGVLLGDY SEQ ID NO: 1428
iPS:360929	4H9.004.002	YFGMH SEQ ID NO: 1115	VIWYDASNKYYADSVKG SEQ ID NO: 1272	DGTIFGVLLGDY SEQ ID NO: 1429
iPS:360936	4H9.004.003	YFGMH SEQ ID NO: 1116	VIWYDGSNKYYADAVKG SEQ ID NO: 1273	DGTIFGVLLGDY SEQ ID NO: 1430
iPS:360943	4H9.004.004	YFGMH SEQ ID NO: 1117	VIWYDASNKYYADAVKG SEQ ID NO: 1274	DGTIFGVLLGDY SEQ ID NO: 1431
iPS:360949	4H9.004.005	YFGMH SEQ ID NO: 1118	VIWYDASNKYYADAVKG SEQ ID NO: 1275	DGTIFGVLLGDY SEQ ID NO: 1432
iPS:359761	4H9.004.006	YFGMH SEQ ID NO: 1119	VIWYDASNKYYADAVKG SEQ ID NO: 1276	DRTIFGVLLGDY SEQ ID NO: 1433
iPS:360955	4B1.010	NFGMH SEQ ID NO: 1120	VIWYDASNENYADAVKG SEQ ID NO: 1277	DGTIFGVVLGDY SEQ ID NO: 1434
iPS:360962	4B1.011	NFGMH SEQ ID NO: 1121	VIWYDASNENYADAVKG SEQ ID NO: 1278	DGTIFGVVLGDY SEQ ID NO: 1435
iPS:360968	4B1.012	NFGMH SEQ ID NO: 1122	VIWYDASNENYADAVKG SEQ ID NO: 1279	DGTIFGVVLGDY SEQ ID NO: 1436
iPS:360974	4B1.013	NFGMH SEQ ID NO: 1123	VIWYDASNENYADSVKG SEQ ID NO: 1280	DGTIFGVVLGDY SEQ ID NO: 1437
iPS:360978	4B1.014	NFGMH SEQ ID NO: 1124	VIWYDGSNENYADAVKG SEQ ID NO: 1281	DGTIFGVVLGDY SEQ ID NO: 1438
iPS:359785	4B1.015	NFGMH SEQ ID NO: 1125	VIWYDASNENYADAVKG SEQ ID NO: 1282	DRTIFGVVLGDY SEQ ID NO: 1439
iPS:360982	4B1.016	NFGMH SEQ ID NO: 1126	VIWYDASNENYADAVKG SEQ ID NO: 1283	DGTIFGVVLGDY SEQ ID NO: 1440
iPS:335922	18F2	NFGMH SEQ ID NO: 1127	VIWYDGSNENYADSVKG SEQ ID NO: 1284	DGTIFGVVLGDY SEQ ID NO: 1441
iPS:360986	18F2.002	NFGMH SEQ ID NO: 1128	VIWYDASNENYADAVKG SEQ ID NO: 1285	DGTIFGVVLGDY SEQ ID NO: 1442

Identifier	Construct	CDRH1	CDRH2	CDRH3
iPS:360995	18F2.003	NFGMH SEQ ID NO: 1129	VIWYDASNENYADAVKG SEQ ID NO: 1286	DGTIFGVVLGDY SEQ ID NO: 1443
iPS:360999	18F2.004	NFGMH SEQ ID NO: 1130	VIWYDASNENYADAVKG SEQ ID NO: 1287	DGTIFGVVLGDY SEQ ID NO: 1444
iPS:361005	18F2.005	NFGMH SEQ ID NO: 1131	VIWYDASNENYADAVKG SEQ ID NO: 1288	DGTIFGVVLGDY SEQ ID NO: 1445
iPS:361009	18F2.006	NFGMH SEQ ID NO: 1132	VIWYDASNENYADAVKG SEQ ID NO: 1289	DGTIFGVVLGDY SEQ ID NO: 1446
iPS:361013	18F2.007	NFGMH SEQ ID NO: 1133	VIWYDASNENYADAVKG SEQ ID NO: 1290	DGTIFGVVLGDY SEQ ID NO: 1447
iPS:361017	18F2.008	NFGMH SEQ ID NO: 1134	VIWYDASNENYADAVKG SEQ ID NO: 1291	DGTIFGVVLGDY SEQ ID NO: 1448
iPS:361021	18F2.009	NFGMH SEQ ID NO: 1135	VIWYDGSNENYADAVKG SEQ ID NO: 1292	DGTIFGVVLGDY SEQ ID NO: 1449
iPS:361028	18F2.010	NFGMH SEQ ID NO: 1136	VIWYDASNENYADSVKG SEQ ID NO: 1293	DGTIFGVVLGDY SEQ ID NO: 1450
iPS:360535	18F2.011	NFGMH SEQ ID NO: 1137	VIWYDASNENYADAVKG SEQ ID NO: 1294	DRTIFGVVLGDY SEQ ID NO: 1451
iPS:361035	18F2.012	NFGMH SEQ ID NO: 1138	VIWYDASNENYADAVKG SEQ ID NO: 1295	DGTIFGVVLGDY SEQ ID NO: 1452
iPS:359940	2F11.002	SYGMH SEQ ID NO: 1139	VIWYDASNKYYADAVKG SEQ ID NO: 1296	DRTIFGVVLDY SEQ ID NO: 1453
iPS:361039	2F11.003	SYGMH SEQ ID NO: 1140	VIWYDASNKYYADAVKG SEQ ID NO: 1297	DRTIFGVVLDY SEQ ID NO: 1454
iPS:361043	2F11.004	SYGMH SEQ ID NO: 1141	VIWYDASNKYYADAVKG SEQ ID NO: 1298	DRTIFGVVLDY SEQ ID NO: 1455
iPS:361049	2F11.005	SYGMH SEQ ID NO: 1142	VIWYDASNKYYADAVKG SEQ ID NO: 1299	DRTIFGVVLDY SEQ ID NO: 1456
iPS:361055	2F11.006	SYGMH SEQ ID NO: 1143	VIWYDASNKYYADAVKG SEQ ID NO: 1300	DRTIFGVVLDY SEQ ID NO: 1457
iPS:361059	2F11.007	SYGMH SEQ ID NO: 1144	VIWYDASNKYYADAVKG SEQ ID NO: 1301	DRTIFGVVLDY SEQ ID NO: 1458
iPS:361063	2F11.008	SYGMH SEQ ID NO: 1145	VIWYDASNKYYADAVKG SEQ ID NO: 1302	DRTIFGVVLDY SEQ ID NO: 1459

Identifier	Construct	CDRH1	CDRH2	CDRH3
iPS:359949	2F11.009	SYGMH SEQ ID NO: 1146	VIWYDASNKYYADSVKG SEQ ID NO: 1303	DRTIFGVVLDY SEQ ID NO: 1460
iPS:359956	2F11.010	SYGMH SEQ ID NO: 1147	VIWYDGSNKYYADAVKG SEQ ID NO: 1304	DRTIFGVVLDY SEQ ID NO: 1461
iPS:359865	6H1.002	YFGMH SEQ ID NO: 1148	VIWYDASNKYYADAVKG SEQ ID NO: 1305	DGTIFGVLLGDY SEQ ID NO: 1462
iPS:359869	6H1.003	YFGMH SEQ ID NO: 1149	VIWYDASNKYYADAVKG SEQ ID NO: 1306	DRTIFGVLLGDY SEQ ID NO: 1463
iPS:359873	6H1.004	YFGMH SEQ ID NO: 1150	VIWYDASNKYYADAVKG SEQ ID NO: 1307	DGTIFGVLLGDY SEQ ID NO: 1464
iPS:359877	6H1.005	YFGMH SEQ ID NO: 1151	VIWYDASNKYYADAVKG SEQ ID NO: 1308	DRTIFGVLLGDY SEQ ID NO: 1465
iPS:361067	6H1.006	YFGMH SEQ ID NO: 1152	VIWYDGSNKYYADSVKG SEQ ID NO: 1309	DGTIFGVLLGDY SEQ ID NO: 1466
iPS:361071	6H1.007	YFGMH SEQ ID NO: 1153	VIWYDASNKYYADSVKG SEQ ID NO: 1310	DGTIFGVLLGDY SEQ ID NO: 1467
iPS:361075	6H1.008	YFGMH SEQ ID NO: 1154	VIWYDGSNKYYADAVKG SEQ ID NO: 1311	DGTIFGVLLGDY SEQ ID NO: 1468
iPS:361079	6A5.004.001	SYGMH SEQ ID NO: 1155	AIWYDANNKYYADAVKG SEQ ID NO: 1312	DRTIFGVVLEY SEQ ID NO: 1469
iPS:361085	6A5.004.002	SYGMH SEQ ID NO: 1156	AIWYDANNKYYADAVKG SEQ ID NO: 1313	DRTIFGVVLEY SEQ ID NO: 1470
iPS:361091	6A5.004.003	SYGMH SEQ ID NO: 1157	AIWYDANNKYYADAVKG SEQ ID NO: 1314	DRTIFGVVLEY SEQ ID NO: 1471
iPS:361095	6A5.004.004	SYGMH SEQ ID NO: 1158	AIWYDANNKYYADAVKG SEQ ID NO: 1315	DRTIFGVVLEY SEQ ID NO: 1472
iPS:361101	6A5.004.005	SYGMH SEQ ID NO: 1159	AIWYDANNKYYADAVKG SEQ ID NO: 1316	DRTIFGVVLEY SEQ ID NO: 1473
iPS:361105	6A5.004.006	SYGMH SEQ ID NO: 1160	AIWYDANNKYYADAVKG SEQ ID NO: 1317	DRTIFGVVLEY SEQ ID NO: 1474
iPS:361109	6A5.004.007	SYGMH SEQ ID NO: 1161	AIWYDANNKYYADAVKG SEQ ID NO: 1318	DRTIFGVVLEY SEQ ID NO: 1475
iPS:361113	6A5.004.008	SYGMH SEQ ID NO: 1162	AIWYDGNNKYYADAVKG SEQ ID NO: 1319	DRTIFGVVLEY SEQ ID NO: 1476

Identifier	Construct	CDRH1	CDRH2	CDRH3
iPS:361120	6A5.004.009	SYGMH SEQ ID NO: 1163	AIWYDANNKYYADSVKG SEQ ID NO: 1320	DRTIFGVVLEY SEQ ID NO: 1477
iPS:359896	6A5.004.010	SYGMH SEQ ID NO: 1164	AIWYDANNKYYADAVKG SEQ ID NO: 1321	DRTIFGVVLEY SEQ ID NO: 1478
iPS:359890	6A5.004.011	SYGMH SEQ ID NO: 1165	AIWYDANNKYYADAVKG SEQ ID NO: 1322	DRTIFGVVLEY SEQ ID NO: 1479
iPS:359567	2A11.002	SYGMH SEQ ID NO: 1166	VIWYDASNKYYEDAVKG SEQ ID NO: 1323	GITIFGHGFEY SEQ ID NO: 1480
iPS:335965	2A11.003	SYGMH SEQ ID NO: 1167	VIWYDGSNKYYEDSVKG SEQ ID NO: 1324	GITIFGHGFEY SEQ ID NO: 1481
iPS:361158	2A11.004	SYGMH SEQ ID NO: 1168	VIWYDGSNKYYEDAVKG SEQ ID NO: 1325	GITIFGHGFEY SEQ ID NO: 1482
iPS:361165	2A11.005	SYGMH SEQ ID NO: 1169	VIWYDASNKYYEDSVKG SEQ ID NO: 1326	GITIFGHGFEY SEQ ID NO: 1483
iPS:361172	2G10_LC1.003	NYGMH SEQ ID NO: 1170	AIWFDASDKYYADAVKG SEQ ID NO: 1327	DQAIFGVVPDY SEQ ID NO: 1484
iPS:361178	2G10_LC1.004	NYGMH SEQ ID NO: 1171	AIWFDASDKYYADSVKG SEQ ID NO: 1328	DQAIFGVVPDY SEQ ID NO: 1485
iPS:361185	2G10_LC1.005	NYGMH SEQ ID NO: 1172	AIWFDGSDKYYADAVKG SEQ ID NO: 1329	DQAIFGVVPDY SEQ ID NO: 1486
iPS:361192	2G10_LC1.006	NYGMH SEQ ID NO: 1173	AIWFDASDKYYADAVKG SEQ ID NO: 1330	DQAIFGVVPDY SEQ ID NO: 1487
iPS:359609	2G10_LC1.007	NYGMH SEQ ID NO: 1174	AIWFDASDKYYADAVKG SEQ ID NO: 1331	DQAIFGVVPDY SEQ ID NO: 1488
iPS:359615	2G10_LC1.008	NYGMH SEQ ID NO: 1175	AIWFDASDKYYADAVKG SEQ ID NO: 1332	DQAIFGVVPDY SEQ ID NO: 1489
iPS:361196	2G10_LC1.009	NYGMH SEQ ID NO: 1176	AIWFDASDKYYADAVKG SEQ ID NO: 1333	DQAIFGVVPDY SEQ ID NO: 1490
iPS:361202	2G10_LC1.010	NYGMH SEQ ID NO: 1177	AIWFDASDKYYADAVKG SEQ ID NO: 1334	DQAIFGVVPDY SEQ ID NO: 1491
iPS:359644	18E3.002	SGGYYWS SEQ ID NO: 1178	YIYYSGSTYYNPSLKS SEQ ID NO: 1335	DRITIFGVVMGGGMDV SEQ ID NO: 1492
iPS:361206	18E3.003	SGGYYWS SEQ ID NO: 1179	YIYYSGSTYYNPSLKS SEQ ID NO: 1336	DRITIFGVVMGGGMDV SEQ ID NO: 1493

Identifier	Construct	CDRH1	CDRH2	CDRH3
iPS:359628	18E3.004	SGGYYWS SEQ ID NO: 1180	YIYYSGSTYYNPSLKS SEQ ID NO: 1337	DRITIFGVVMGGGMDV SEQ ID NO: 1494
iPS:359637	18E3.005	SGGYYWS SEQ ID NO: 1181	YIYYSGSTYYNPSLKS SEQ ID NO: 1338	DRITIFGVVMGGGMDV SEQ ID NO: 1495
iPS:361210	18E3.006	SGGYYWS SEQ ID NO: 1182	YIYYSGSTYYNPSLKS SEQ ID NO: 1339	DRITIFGVVMGGGMDV SEQ ID NO: 1496
iPS:361214	18E3.007	SGGYYWS SEQ ID NO: 1183	YIYYSGSTYYNPSLKS SEQ ID NO: 1340	DRITIFGVVMGGGMDV SEQ ID NO: 1497
iPS:361218	18E3.008	SGGYYWS SEQ ID NO: 1184	YIYYSGSTYYNPSLKS SEQ ID NO: 1341	DRITIFGVVMGGGMDV SEQ ID NO: 1498
iPS:361222	5C2.006	GYYIH SEQ ID NO: 1185	WINPESGGTDYSQRFQG SEQ ID NO: 1342	EATIFGMVIVPFDY SEQ ID NO: 1499
iPS:361229	5C2.007	GYYIH SEQ ID NO: 1186	WINPESGGTDYSQRFQG SEQ ID NO: 1343	EATIFGMVIVPFDY SEQ ID NO: 1500
iPS:361236	5C2.008	GYYIH SEQ ID NO: 1187	WINPDAGGTDYSQRFQG SEQ ID NO: 1344	EATIFGMVIVPFDY SEQ ID NO: 1501
iPS:359685	5C2.009	GYYIH SEQ ID NO: 1188	WINPDAGGTDYSQRFQG SEQ ID NO: 1345	EATIFGMVIVPFDY SEQ ID NO: 1502
iPS:361240	5C2.010	GYYIH SEQ ID NO: 1189	WINPDSGGTDYSQRFQG SEQ ID NO: 1346	EATIFGMVIVPFDY SEQ ID NO: 1503
iPS:361247	5C2.011	GYYIH SEQ ID NO: 1190	WINPDSGGTDYSQRFQG SEQ ID NO: 1347	EATIFGMVIVPFDY SEQ ID NO: 1504
iPS:361254	5C2.012	GYYIH SEQ ID NO: 1191	WINPDSGGTDYSQRFQG SEQ ID NO: 1348	EATIFGMVIVPFDY SEQ ID NO: 1505
iPS:361261	5C2.013	GYYIH SEQ ID NO: 1192	WINPDAGGTDYSQRFQG SEQ ID NO: 1349	EATIFGMVIVPFDY SEQ ID NO: 1506
iPS:361268	5C2.014	GYYIH SEQ ID NO: 1193	WINPDAGGTDYSQRFQG SEQ ID NO: 1350	EATIFGMVIVPFDY SEQ ID NO: 1507
iPS:359669	5C2.015	GYYIH SEQ ID NO: 1194	WINPDAGGTDYSQRFQG SEQ ID NO: 1351	EATIFGMVIVPFDY SEQ ID NO: 1508
iPS:359678	5C2.016	GYYIH SEQ ID NO: 1195	WINPESGGTDYSQRFQG SEQ ID NO: 1352	EATIFGMVIVPFDY SEQ ID NO: 1509
iPS:361275	11C1.002	GYYIH SEQ ID NO: 1196	WISPNSGETSYAQKFQD SEQ ID NO: 1353	EATIFGMLIVPFDY SEQ ID NO: 1510

Identifier	Construct	CDRH1	CDRH2	CDRH3
iPS:361282	11C1.003	GYYIH SEQ ID NO: 1197	WISPNSGDTSYAQKFQD SEQ ID NO: 1354	EATIFGMLIVPFDY SEQ ID NO: 1511
iPS:361289	11C1.004	GYYIH SEQ ID NO: 1198	WISPNSGETSYAQKFQD SEQ ID NO: 1355	EATIFGMLIVPFDY SEQ ID NO: 1512
iPS:359712	11C1.005	GYYIH SEQ ID NO: 1199	WISPNSGETSYAQKFQD SEQ ID NO: 1356	EATIFGMLIVPFDY SEQ ID NO: 1513
iPS:361293	11C1.006	GYYIH SEQ ID NO: 1200	WISPNSGDTSYAQKFQD SEQ ID NO: 1357	EATIFGMLIVPFDY SEQ ID NO: 1514
iPS:361297	11C1.007	GYYIH SEQ ID NO: 1201	WISPNSGETSYAQKFQD SEQ ID NO: 1358	EATIFGMLIVPFDY SEQ ID NO: 1515
iPS:361301	11C1.008	GYYIH SEQ ID NO: 1202	WISPNSGDTSYAQKFQD SEQ ID NO: 1359	EATIFGMLIVPFDY SEQ ID NO: 1516
iPS:359703	11C1.009	GYYIH SEQ ID NO: 1203	WISPNSGETSYAQKFQD SEQ ID NO: 1360	EATIFGMLIVPFDY SEQ ID NO: 1517
iPS:361305	11C1.010	GYYIH SEQ ID NO: 1204	WISPNSGETSYAQKFQD SEQ ID NO: 1361	EATIFGMLIVPFDY SEQ ID NO: 1518
iPS:361312	13H12.002	GYYIH SEQ ID NO: 1205	WINPESGGTDYSQRFQG SEQ ID NO: 1362	EATIFGMVIVPFDY SEQ ID NO: 1519
iPS:359744	13H12.003	GYYIH SEQ ID NO: 1206	WINPESGGTDYSQRFQG SEQ ID NO: 1363	EATIFGMVIVPFDY SEQ ID NO: 1520
iPS:361319	13H12.004	GYYIH SEQ ID NO: 1207	WINPDSGGTDYSQRFQG SEQ ID NO: 1364	EATIFGMVIVPFDY SEQ ID NO: 1521
iPS:359737	13H12.005	GYYIH SEQ ID NO: 1208	WINPESGGTDYSQRFQG SEQ ID NO: 1365	EATIFGMVIVPFDY SEQ ID NO: 1522
iPS:361326	13H12.006	GYYIH SEQ ID NO: 1209	WINPESGGTDYSQRFQG SEQ ID NO: 1366	EATIFGMVIVPFDY SEQ ID NO: 1523
iPS:361330	12H11.002	GYYIH SEQ ID NO: 1210	WISPNQGETNYAQKFQD SEQ ID NO: 1367	EATIFGMLIVPFDY SEQ ID NO: 1524
iPS:361337	12H11.003	GYYIH SEQ ID NO: 1211	WISPNQGDTNYAQKFQD SEQ ID NO: 1368	EATIFGMLIVPFDY SEQ ID NO: 1525
iPS:361344	12H11.004	GYYIH SEQ ID NO: 1212	WISPNQGETNYAQKFQD SEQ ID NO: 1369	EATIFGMLIVPFDY SEQ ID NO: 1526
iPS:361351	12H11.005	GYYIH SEQ ID NO: 1213	WISPNNGETNYAQKFQD SEQ ID NO: 1370	EATIFGMLIVPFDY SEQ ID NO: 1527

Identifier	Construct	CDRH1	CDRH2	CDRH3
iPS:361358	12H11.006	GYYIH SEQ ID NO: 1214	WISPNNGDTNYAQKFQD SEQ ID NO: 1371	EATIFGMLIVPFDY SEQ ID NO: 1528
iPS:361365	12H11.007	GYYIH SEQ ID NO: 1215	WISPNQGDTNYAQKFQD SEQ ID NO: 1372	EATIFGMLIVPFDY SEQ ID NO: 1529
iPS:361372	12H11.008	GYYIH SEQ ID NO: 1216	WISPNNGETNYAQKFQD SEQ ID NO: 1373	EATIFGMLIVPFDY SEQ ID NO: 1530
iPS:361379	12H11.009	GYYIH SEQ ID NO: 1217	WISPNQGETNYAQKFQD SEQ ID NO: 1374	EATIFGMLIVPFDY SEQ ID NO: 1531
iPS:361383	12H11.010	GYYIH SEQ ID NO: 1218	WISPNNGDTNYAQKFQD SEQ ID NO: 1375	EATIFGMLIVPFDY SEQ ID NO: 1532
iPS:361387	12H11.011	GYYIH SEQ ID NO: 1219	WISPNQGDTNYAQKFQD SEQ ID NO: 1376	EATIFGMLIVPFDY SEQ ID NO: 1533
iPS:361391	12H11.012	GYYIH SEQ ID NO: 1220	WISPNNGETNYAQKFQD SEQ ID NO: 1377	EATIFGMLIVPFDY SEQ ID NO: 1534
iPS:361395	12H11.013	GYYIH SEQ ID NO: 1221	WISPNQGETNYAQKFQD SEQ ID NO: 1378	EATIFGMLIVPFDY SEQ ID NO: 1535
iPS:361402	12H11.014	GYYIH SEQ ID NO: 1222	WISPNQGETNYAQKFQD SEQ ID NO: 1379	EATIFGMLIVPFDY SEQ ID NO: 1536
iPS:361406	2C2.005.001	GYYMH SEQ ID NO: 1223	WINPNSGGTNYAQKFQG SEQ ID NO: 1380	GGDYVWGTYRPHYYYGMDV SEQ ID NO: 1537
iPS:361412	2C2.005.002	GYYMH SEQ ID NO: 1224	WINPNSGGTNYAQKFQG SEQ ID NO: 1381	GGDYVWGTYRPHYYYGMDV SEQ ID NO: 1538
iPS:361418	2C2.005.003	GYYMH SEQ ID NO: 1225	WINPNSGGTNYAQKFQG SEQ ID NO: 1382	GGDYVWGTYRPHYYYGMDV SEQ ID NO: 1539
iPS:361424	2C2.005.004	GYYMH SEQ ID NO: 1226	WINPNSGGTNYAQKFQG SEQ ID NO: 1383	GGDYVWGTYRPHYYYGMDV SEQ ID NO: 1540
iPS:361430	2C2.005.005	GYYMH SEQ ID NO: 1227	WINPNSGGTNYAQKFQG SEQ ID NO: 1384	GGDYVWGTYRPHYYYGMDV SEQ ID NO: 1541
iPS:361436	2C2.005.006	GYYMH SEQ ID NO: 1228	WINPNSGGTNYAQKFQG SEQ ID NO: 1385	GGDYVWGTYRPHYYYGMDV SEQ ID NO: 1542
iPS:361442	2C2.005.007	GYYMH SEQ ID NO: 1229	WINPNSGGTNYAQKFQG SEQ ID NO: 1386	GGDYVWGTYRPHYYYGMDV SEQ ID NO: 1543
iPS:361448	2C2.005.008	GYYMH SEQ ID NO: 1230	WINPNSGGTNYAQKFQG SEQ ID NO: 1387	GGDYVWGTYRPHYYYGMDV SEQ ID NO: 1544

Identifier	Construct	CDRH1	CDRH2	CDRH3
iPS:361454	2C2.005.009	GYYMH SEQ ID NO: 1231	WINPNSGGTNYAQKFQG SEQ ID NO: 1388	GGDYVWGTYRPHYYYGMDV SEQ ID NO: 1545
iPS:361460	2C2.005.010	GYYMH SEQ ID NO: 1232	WINPNSGGTNYAQKFQG SEQ ID NO: 1389	GGDYVWGTYRPHYYYGMDV SEQ ID NO: 1546
iPS:361466	2C2.005.011	GYYMH SEQ ID NO: 1233	WINPNSGGTNYAQKFQG SEQ ID NO: 1390	GGDYVWGTYRPHYYYGMDV SEQ ID NO: 1547
iPS:361472	2C2.005.012	GYYMH SEQ ID NO: 1234	WINPNSGGTNYAQKFQG SEQ ID NO: 1391	GGDYVWGTYRPHYYYGMDV SEQ ID NO: 1548
iPS:361478	2C2.005.013	GYYMH SEQ ID NO: 1235	WINPNSGGTNYAQKFQG SEQ ID NO: 1392	GGDYVFGTYRPHYYYGMDV SEQ ID NO: 1549
iPS:361485	2C2.005.014	GYYMH SEQ ID NO: 1236	WINPNSGGTNYAQKFQG SEQ ID NO: 1393	GGDYVFGTYRPHYYYGMDV SEQ ID NO: 1550
iPS:361845	18F2.013	NFGMH SEQ ID NO: 1237	VIWYDASNENYADAVKG SEQ ID NO: 1394	DRTIFGVVLGDY SEQ ID NO: 1551
iPS:361851	6H1.009	YFGMH SEQ ID NO: 1238	VIWYDASNKYYADAVKG SEQ ID NO: 1395	DRTIFGVLLGDY SEQ ID NO: 1552
iPS:361855	2C2.005.015	GYYMH SEQ ID NO: 1239	WINPNSGGTNYAQKFQG SEQ ID NO: 1396	GGDYVWGTYRPHYYYGMDV SEQ ID NO: 1553
iPS:336067	5G12.006	SYGIH SEQ ID NO: 1240	VIWYDGSNKFHADSVKG SEQ ID NO: 1397	GKVAGMPEAFEI SEQ ID NO: 1554
iPS:336169	17B11.002	SYDIN SEQ ID NO: 1241	WMNPNSGNTGYAQKFQG SEQ ID NO: 1398	GGDYVWGSYRPYYYYYGMDV SEQ ID NO: 1555
iPS:361127	5G12.006.001	SYGIH SEQ ID NO: 1242	VIWYDASNKFHADAVKG SEQ ID NO: 1399	GKVAGMPEAFEI SEQ ID NO: 1556
iPS:361136	5G12.006.002	SYGIH SEQ ID NO: 1243	VIWYDASNKFHADAVKG SEQ ID NO: 1400	GKVAGMPEAFEI SEQ ID NO: 1557
iPS:361140	5G12.006.003	SYGIH SEQ ID NO: 1244	VIWYDASNKFHADAVKG SEQ ID NO: 1401	GKVAGMPEAFEI SEQ ID NO: 1558
iPS:359919	5G12.006.004	SYGIH SEQ ID NO: 1245	VIWYDASNKFHADAVKG SEQ ID NO: 1402	GKVAGMPEAFEI SEQ ID NO: 1559
iPS:361144	5G12.006.005	SYGIH SEQ ID NO: 1246	VIWYDASNKFHADSVKG SEQ ID NO: 1403	GKVAGMPEAFEI SEQ ID NO: 1560
iPS:361151	5G12.006.006	SYGIH SEQ ID NO: 1247	VIWYDGSNKFHADAVKG SEQ ID NO: 1404	GKVAGMPEAFEI SEQ ID NO: 1561

Identifier	Construct	CDRH1	CDRH2	CDRH3
iPS:361491	17B11.002.001	SYDIN SEQ ID NO: 1248	WMNPNSGGTGYAQKFQG SEQ ID NO: 1405	GGDYVWGSYRPYYYYYGMDV SEQ ID NO: 1562
iPS:361499	17B11.002.002	SYDIN SEQ ID NO: 1249	WMNPNSGNTGYAQKFQG SEQ ID NO: 1406	GGDYVWGSYRPYYYYYGMDV SEQ ID NO: 1563
iPS:361503	17B11.002.003	SYDIN SEQ ID NO: 1250	WMNPNSGGTGYAQKFQG SEQ ID NO: 1407	GGDYVWGSYRPYYYYYGMDV SEQ ID NO: 1564
iPS:361507	17B11.002.004	SYDIN SEQ ID NO: 1251	WMNPNSGGTGYAQKFQG SEQ ID NO: 1408	GGDYVWGSYRPYYYYYGMDV SEQ ID NO: 1565
iPS:361514	17B11.002.005	SYDIN SEQ ID NO: 1252	WMNPNSGGTGYAQKFQG SEQ ID NO: 1409	GGDYVWGSYRPYYYYYGMDV SEQ ID NO: 1566
iPS:360582	17B11.002.006	SYDIN SEQ ID NO: 1253	WMNPNSGNTGYAQKFQG SEQ ID NO: 1410	GGDYVWGSYRPYYYYYGMDV SEQ ID NO: 1567
iPS:361518	17B11.002.007	SYDIN SEQ ID NO: 1254	WMNPNSGGTGYAQKFQG SEQ ID NO: 1411	GGDYVFGSYRPYYYYYGMDV SEQ ID NO: 1568
iPS:360570	17B11.002.008	SYDIN SEQ ID NO: 1255	WMNPNSGGTGYAQKFQG SEQ ID NO: 1412	GGDYVFGSYRPYYYYYGMDV SEQ ID NO: 1569
iPS:362051	5G12.005.001	SYGIH SEQ ID NO: 1256	VIWYDASNKFHADAVKG SEQ ID NO: 1413	GKVAGMPEAFEI SEQ ID NO: 1570

Table 8. Light Chain (LC) Amino Acid Sequences of Exemplary Anti-GIPR Antibodies

Identifier	Construct	LC	SEQ ID NO:
iPS:336175	2C2.005	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQHLPGTAPKLLIYTNNQRPS GVPDRFSGSKSGTSASLAISGLQSEDEADYFCATFDDSLNGPVFGGGTKLTVLGQP KAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPS KQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	315
iPS:335914	4B1	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKRLIYGASSLQSG VPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	316

Identifier	Construct	LC	SEQ ID NO:
iPS:335938	6H1	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKRLIYGASSLQSG VPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	317
iPS:335941	2F11	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLET GVPSRFSGSGSGTDFSFTISSLQPEDIATYYCQQYDILLTFGGGTKVEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	318
iPS:335970	5C2	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYIAWYQQPGHPPKLLIYW ASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	319
iPS:335978	13H12	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYIAWYQQKPGHPPKLLIYW ASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	320
iPS:335986	11C1	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIYW TSTRDSGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	321
iPS:335994	12H11	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIYW TSTRDSGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	322
iPS:336024	18E3	EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAWYQQKPGQAPRLLIYGASSRAT GIPDRFSGSGSGTDFTLTISRQEPDDFAVYYCQQYGSSPLTFGGGTKVEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	323
iPS:336041	2G10_LC1	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGAATRAT GIPARVSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPLTFGGGTKVEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	324
iPS:336077	4H9.004	DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGWYQQKPGKAPKRLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFVTYYCLQHNSYPFTFGPGTKVDVKRTVAAP	325

Identifier	Construct	LC	SEQ ID NO:
		SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	
iPS:336088	6A5.004	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNWYQQKPGKAPKLLIYDASNLEP GVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQYDDLFTFGPGTKVDIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	326
iPS:336099	17H11.004	DIQMTQSPSSVSASVGDRVTITCRASQGLIIWLAWYQQKPGKAPKLLIYAASSLQS GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQTNSFPPTFGQGTKVEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	327
iPS:359621	17H11.004.001	DIQMTQSPSSVSASVGDRVTITCRASQGLIIWLAWYQQKPGKAPKLLIYAASSLQS GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQTNSFPPTFGQGTKVEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	328
iPS:359781	4H9.004.001	DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGWYQQKPGKAPKLLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFVTYYCLQHNSYPFTFGQGTKVDVKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	329
iPS:360929	4H9.004.002	DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGWYQQKPGKAPKLLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFVTYYCLQHNSYPFTFGQGTKVDVKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	330
iPS:360936	4H9.004.003	DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGWYQQKPGKAPKLLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFVTYYCLQHNSYPFTFGQGTKVDVKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	331
iPS:360943	4H9.004.004	DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGWYQQKPGKAPKLLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFVTYYCLQHNSYPFTFGPGTKVDVKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	332
iPS:360949	4H9.004.005	DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGWYQQKPGKAPKRLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFVTYYCLQHNSYPFTFGQGTKVDVKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	333

Identifier	Construct	LC	SEQ ID NO:
iPS:359761	4H9.004.006	DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGWYQQKPGKAPKLLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFVTYYCLQHNSYPFTFGQGTKVDVKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	334
iPS:360955	4B1.010	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKLLIYGASSLQSG VPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	335
iPS:360962	4B1.011	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKRLIYGASSLQSG VPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	336
iPS:360968	4B1.012	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKLLIYGASSLQSG VPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	337
iPS:360974	4B1.013	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKLLIYGASSLQSG VPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	338
iPS:360978	4B1.014	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKLLIYGASSLQSG VPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	339
iPS:359785	4B1.015	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKLLIYGASSLQSG VPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	340
iPS:360982	4B1.016	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKLLIYGASSLQSG VPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	341
iPS:335922	18F2	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGWYHQKPGKAPKRLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKRTVAAP	342

Identifier	Construct	LC	SEQ ID NO:
		SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	
iPS:360986	18F2.002	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGWYQQKPGKAPKLLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	343
iPS:360995	18F2.003	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGWYQQKPGKAPKLLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	344
iPS:360999	18F2.004	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGWYHQKPGKAPKLLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	345
iPS:361005	18F2.005	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGWYQQKPGKAPKRLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	346
iPS:361009	18F2.006	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGWYQQKPGKAPKRLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	347
iPS:361013	18F2.007	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGWYHQKPGKAPKLLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	348
iPS:361017	18F2.008	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGWYHQKPGKAPKRLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	349
iPS:361021	18F2.009	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGWYQQKPGKAPKLLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	350

Identifier	Construct	LC	SEQ ID NO:
iPS:361028	18F2.010	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGWYQQKPGKAPKLLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	351
iPS:360535	18F2.011	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGWYQQKPGKAPKLLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	352
iPS:361035	18F2.012	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGWYQQKPGKAPKLLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	353
iPS:359940	2F11.002	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLET GVPSRFSGSGSGTDFSLTISSLQPEDFATYYCQQYDILLTFGGGTKVEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	354
iPS:361039	2F11.003	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLET GVPSRFSGSGSGTDFSLTISSLQPEDFATYYCQQYDILLTFGGGTKVEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	355
iPS:361043	2F11.004	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLET GVPSRFSGSGSGTDFSLTISSLQPEDIATYYCQQYDILLTFGGGTKVEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	356
iPS:361049	2F11.005	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLET GVPSRFSGSGSGTDFSFTISSLQPEDFATYYCQQYDILLTFGGGTKVEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	357
iPS:361055	2F11.006	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLET GVPSRFSGSGSGTDFSLTISSLQPEDIATYYCQQYDILLTFGGGTKVEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	358
iPS:361059	2F11.007	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLET GVPSRFSGSGSGTDFSFTISSLQPEDFATYYCQQYDILLTFGGGTKVEIKRTVAAPSV	359

Identifier	Construct	LC	SEQ ID NO:
		FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	
iPS:361063	2F11.008	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLET GVPSRFSGSGSGTDFSFTISSLQPEDIATYYCQQYDILLTFGGGTKVEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	360
iPS:359949	2F11.009	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLET GVPSRFSGSGSGTDFSLTISSLQPEDFATYYCQQYDILLTFGGGTKVEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	361
iPS:359956	2F11.010	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLET GVPSRFSGSGSGTDFSLTISSLQPEDFATYYCQQYDILLTFGGGTKVEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	362
iPS:359865	6H1.002	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKRLIYGASSLQSG VPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	363
iPS:359869	6H1.003	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKRLIYGASSLQSG VPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	364
iPS:359873	6H1.004	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKLLIYGASSLQSG VPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	365
iPS:359877	6H1.005	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKLLIYGASSLQSG VPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	366
iPS:361067	6H1.006	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKLLIYGASSLQSG VPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	367

Identifier	Construct	LC	SEQ ID NO:
iPS:361071	6H1.007	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKLLIYGASSLQSG VPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	368
iPS:361075	6H1.008	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKLLIYGASSLQSG VPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	369
iPS:361079	6A5.004.001	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNWYQQKPGKAPKLLIYDASNLEP GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYDDLFTFGPGTKVDIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	370
iPS:361085	6A5.004.002	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNWYQQKPGKAPKLLIYDASNLEP GVPSRFSGSGSGTDFTLTISSLQPEDIATYYCQQYDDLFTFGPGTKVDIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	371
iPS:361091	6A5.004.003	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNWYQQKPGKAPKLLIYDASNLEP GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYDDLFTFGPGTKVDIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	372
iPS:361095	6A5.004.004	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNWYQQKPGKAPKLLIYDASNLEP GVPSRFSGSGSGTDFTFTISSLQPEDFATYYCQQYDDLFTFGPGTKVDIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	373
iPS:361101	6A5.004.005	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNWYQQKPGKAPKLLIYDASNLEP GVPSRFSGSGSGTDFTLTISSLQPEDIATYYCQQYDDLFTFGPGTKVDIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	374
iPS:361105	6A5.004.006	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNWYQQKPGKAPKLLIYDASNLEP GVPSRFSGSGSGTDFTFTISSLQPEDFATYYCQQYDDLFTFGPGTKVDIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	375
iPS:361109	6A5.004.007	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNWYQQKPGKAPKLLIYDASNLEP GVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQYDDLFTFGPGTKVDIKRTVAAPS	376

Identifier	Construct	LC	SEQ ID NO:
		VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	
iPS:361113	6A5.004.008	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNWYQQKPGKAPKLLIYDASNLEP GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYDDLFTFGPGTKVDIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	377
iPS:361120	6A5.004.009	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNWYQQKPGKAPKLLIYDASNLEP GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYDDLFTFGPGTKVDIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	378
iPS:359896	6A5.004.010	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNWYQQKPGKAPKLLIYDASNLEP GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYDDLFTFGQGTKVDIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	379
iPS:359890	6A5.004.011	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNWYQQKPGKAPKLLIYDASNLEP GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYDDLFTFGQGTKVDIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	380
iPS:359567	2A11.002	EIVLTQSPGTLSLSPGERATLSCRASQIFTSTYLAWYQQKPGQAPRLLIYGASSRAT GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPRFGQGTRLEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	381
iPS:333965	2A11.003	EIVLTQSPGTLSLSPGERATLSCRASQIFTSTYLAWYQQKPGQAPRLLIYGASSRAT GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPRFGQGTRLEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	382
iPS:361158	2A11.004	EIVLTQSPGTLSLSPGERATLSCRASQIFTSTYLAWYQQKPGQAPRLLIYGASSRAT GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPRFGQGTRLEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	383
iPS:361165	2A11.005	EIVLTQSPGTLSLSPGERATLSCRASQIFTSTYLAWYQQKPGQAPRLLIYGASSRAT GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPRFGQGTRLEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	384

Identifier	Construct	LC	SEQ ID NO:
iPS:361172	2G10_LC1.003	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGAATRAT GIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPLTFGGGTKVEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	385
iPS:361178	2G10_LC1.004	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGAATRAT GIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPLTFGGGTKVEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	386
iPS:361185	2G10_LC1.005	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGAATRAT GIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPLTFGGGTKVEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	387
iPS:361192	2G10_LC1.006	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGAATRAT GIPARVSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPLTFGGGTKVEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	388
iPS:359609	2G10_LC1.007	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGAATRAT GIPARFSGSGSGTEFTLTISSLEPEDFAVYYCQQYNNFPLTFGGGTKVEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	389
iPS:359615	2G10_LC1.008	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGAATRAT GIPARFSGSGSGTEFTLTISSLEPEDFAVYYCQQYNNYPLTFGGGTKVEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	390
iPS:361196	2G10_LC1.009	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGAATRAT GIPARFSGSGSGTEFTLTISSLEPEDFAVYYCQQYNNWPLTFGGGTKVEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	391
iPS:361202	2G10_LC1.010	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGAATRAT GIPARFSGSGSGTEFTLTISSLEPEDFAVYYCQQYNNWPLTFGGGTKVEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	392
iPS:359644	18E3.002	EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAWYQQKPGQAPRLLIYGASSRAT GIPDRFSGSGSGTDFTLTISRLEPDDFAVYYCQQYGSSPLTFGGGTKVEIKRTVAAP	393

Identifier	Construct	LC	SEQ ID NO:
		SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	
iPS:361206	18E3.003	EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAWYQQKPGQAPRLLIYGASSRAT GIPDRFSGSGSGTDFTLTISRQEPDDFAVYYCQQYGSSPLTFGGGTKVEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	394
iPS:359628	18E3.004	EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAWYQQKPGQAPRLLIYGASSRAT GIPDRFSGSGSGTDFTLTISRLEPDDFAVYYCQQYGSSPLTFGGGTKVEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	395
iPS:359637	18E3.005	EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAWYQQKPGQAPRLLIYGASSRAT GIPDRFSGSGSGTDFTLTISRLEPDDFAVYYCQQYGSSPLTFGGGTKVEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	396
iPS:361210	18E3.006	EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAWYQQKPGQAPRLLIYGASSRAT GIPDRFSGSGSGTDFTLTISRLEPDDFAVYYCQQYGSSPLTFGGGTKVEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	397
iPS:361214	18E3.007	EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAWYQQKPGQAPRLLIYGASSRAT GIPDRFSGSGSGTDFTLTISRQEPDDFAVYYCQQYGSSPLTFGGGTKVEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	398
iPS:361218	18E3.008	EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAWYQQKPGQAPRLLIYGASSRAT GIPDRFSGSGSGTDFTLTISRQEPDDFAVYYCQQYGSSPLTFGGGTKVEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	399
iPS:361222	5C2.006	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYIAWYQQQPGHPPKLLIYW ASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	400
iPS:361229	5C2.007	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYIAWYQQQPGHPPKLLIYW ASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	401

Identifier	Construct	LC	SEQ ID NO:
iPS:361236	5C2.008	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYIAWYQQQPGHPPKLLIYW ASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	402
iPS:359685	5C2.009	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYIAWYQQQPGHPPKLLIYW ASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	403
iPS:361240	5C2.010	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYIAWYQQQPGHPPKLLIYW ASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	404
iPS:361247	5C2.011	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYIAWYQQQPGHPPKLLIYW ASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	405
iPS:361254	5C2.012	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYIAWYQQQPGHPPKLLIYW ASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	406
iPS:361261	5C2.013	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYIAWYQQQPGHPPKLLIYW ASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	407
iPS:361268	5C2.014	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYIAWYQQQPGHPPKLLIYW ASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	408
iPS:359669	5C2.015	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYIAWYQQKPGQPPKLLIYW ASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	409
iPS:359678	5C2.016	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYIAWYQQKPGQPPKLLIYW ASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQGTKVEI	410

Identifier	Construct	LC	SEQ ID NO:
		KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	
iPS:361275	11C1.002	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIYW TSTRESGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	411
iPS:361282	11C1.003	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIYW TSTRESGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	412
iPS:361289	11C1.004	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIYW TSTRDSGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	413
iPS:359712	11C1.005	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIYW TSTRESGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	414
iPS:361293	11C1.006	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIYW TSTRESGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	415
iPS:361297	11C1.007	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIYW TSTRDSGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	416
iPS:361301	11C1.008	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIYW TSTRDSGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	417
iPS:359703	11C1.009	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPKLLIYW TSTRESGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	418

Identifier	Construct	LC	SEQ ID NO:
iPS:361305	11C1.010	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIYW TSTRESGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	419
iPS:361312	13H12.002	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYIAWYQQKPGHPPKLLIYW ASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	420
iPS:359744	13H12.003	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYIAWYQQKPGHPPKLLIYW ASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	421
iPS:361319	13H12.004	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYIAWYQQKPGQPPKLLIYW ASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	422
iPS:359737	13H12.005	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYIAWYQQKPGQPPKLLIYW ASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	423
iPS:361326	13H12.006	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYIAWYQQKPGQPPKLLIYW ASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	424
iPS:361330	12H11.002	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIYW TSTRDSGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	425
iPS:361337	12H11.003	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIYW TSTRDSGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	426
iPS:361344	12H11.004	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIYW TSTRDSGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTKVEI	427

Identifier	Construct	LC	SEQ ID NO:
		KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	
iPS:361351	12H11.005	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIYW TSTRDSGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	428
iPS:361358	12H11.006	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIYW TSTRDSGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	429
iPS:361365	12H11.007	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIYW TSTRDSGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	430
iPS:361372	12H11.008	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIYW TSTRDSGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	431
iPS:361379	12H11.009	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIYW TSTRESGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	432
iPS:361383	12H11.010	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIYW TSTRESGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	433
iPS:361387	12H11.011	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIYW TSTRESGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	434
iPS:361391	12H11.012	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPNLLIYW TSTRESGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	435

Identifier	Construct	LC	SEQ ID NO:
iPS:361395	12H11.013	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPKLLIYW TSTRDSGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	436
iPS:361402	12H11.014	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNKNYLAWYQQKPGQPPKLLIYW TSTRESGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	437
iPS:361406	2C2.005.001	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSQTVNWYQHLPGTAPKLLIYTNNQRPS GVPDRFSGSKSGTSASLAISGLQSEDEADYFCATFDESLSGPVFGGGTKLTVLGQPK AAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSK QSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	438
iPS:361412	2C2.005.002	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSQTVNWYQHLPGTAPKLLIYTNNQRPS GVPDRFSGSKSGTSASLAISGLQSEDEADYFCATFDESLQGPVFGGGTKLTVLGQP KAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPS KQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	439
iPS:361418	2C2.005.003	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVNWYQHLPGTAPKLLIYTNNQRPS GVPDRFSGSKSGTSASLAISGLQSEDEADYFCATFDESLSGPVFGGGTKLTVLGQPK AAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSK QSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	440
iPS:361424	2C2.005.004	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVNWYQHLPGTAPKLLIYTNNQRPS GVPDRFSGSKSGTSASLAISGLQSEDEADYFCATFDESLQGPVFGGGTKLTVLGQP KAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPS KQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	441
iPS:361430	2C2.005.005	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSQTVNWYQHLPGTAPKLLIYTNNQRPS GVPDRFSGSKSGTSASLAISGLQSEDEADYFCATFDDSLNGPVFGGGTKLTVLGQP KAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPS KQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	442
iPS:361436	2C2.005.006	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVNWYQHLPGTAPKLLIYTNNQRPS GVPDRFSGSKSGTSASLAISGLQSEDEADYFCATFDDSLNGPVFGGGTKLTVLGQP KAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPS KQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	443
iPS:361442	2C2.005.007	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQHLPGTAPKLLIYTNNQRPS GVPDRFSGSKSGTSASLAISGLQSEDEADYFCATFDESLNGPVFGGGTKLTVLGQP	444

Identifier	Construct	LC	SEQ ID NO:
		KAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPS KQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	
iPS:361448	2C2.005.008	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQHLPGTAPKLLIYTNNQRPS GVPDRFSGSKSGTSASLAISGLQSEDEADYFCATFDDSLQGPVFGGGTKLTVLGQP KAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPS KQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	445
iPS:361454	2C2.005.009	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQHLPGTAPKLLIYTNNQRPS GVPDRFSGSKSGTSASLAISGLQSEDEADYFCATFDDSLSGPVFGGGTKLTVLGQP KAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPS KQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	446
iPS:361460	2C2.005.010	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQHLPGTAPKLLIYTNNQRPS GVPDRFSGSKSGTSASLAISGLQSEDEADYFCATFDDSLNAPVFGGGTKLTVLGQP KAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPS KQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	447
iPS:361466	2C2.005.011	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQHLPGTAPKLLIYTNNQRPS GVPDRFSGSKSGTSASLAISGLQSEDEADYFCATFDSSLNGPVFGGGTKLTVLGQP KAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPS KQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	448
iPS:361472	2C2.005.012	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVNWYQHLPGTAPKLLIYTNNQRPS GVPDRFSGSKSGTSASLAISGLQSEDEADYFCATFDSSLNAPVFGGGTKLTVLGQP KAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPS KQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	449
iPS:361478	2C2.005.013	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVNWYQHLPGTAPKLLIYTNNQRPS GVPDRFSGSKSGTSASLAISGLQSEDEADYFCATFDSSLNAPVFGGGTKLTVLGQP KAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPS KQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	450
iPS:361485	2C2.005.014	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSQTVNWYQHLPGTAPKLLIYTNNQRPS GVPDRFSGSKSGTSASLAISGLQSEDEADYFCATFDESLSGPVFGGGTKLTVLGQPK AAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSK QSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	451
iPS:361845	18F2.013	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGWYQQKPGKAPKRLIYGASSLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	452

Identifier	Construct	LC	SEQ ID NO:
iPS:361851	6H1.009	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKRLIYGASSLQSG VPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	453
iPS:361855	2C2.005.015	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQQLPGTAPKLLIYTNNQRPS GVPDRFSGSKSGTSASLAISGLQSEDEADYFCATFDSSLSGPVFGGGTKLTVLGQPK AAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSK QSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	454
iPS:336067	5G12.006	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWYQQKPGKAPELLIYVASSLQSG VPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTLISFGQGTKLEITRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	455
iPS:336169	17B11.002	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYEQFPGTAPKLLIYDNNKRPS GIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAVVFGGGTKLTVLGQP KAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPS KQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	456
iPS:361127	5G12.006.001	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWYQQKPGKAPELLIYVASSLQSG VPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTLISFGQGTKLEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	457
iPS:361136	5G12.006.002	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWYQQKPGKAPELLIYVASSLQSG VPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTLISFGQGTKLEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	458
iPS:361140	5G12.006.003	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWYQQKPGKAPELLIYVASSLQSG VPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTLISFGQGTKLEITRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	459
iPS:359919	5G12.006.004	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWYQQKPGKAPKLLIYVASSLQSG VPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTLISFGQGTKLEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	460
iPS:361144	5G12.006.005	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWYQQKPGKAPELLIYVASSLQSG VPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTLISFGQGTKLEIKRTVAAPSV	461

Identifier	Construct	LC	SEQ ID NO:
		FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	
iPS:361151	5G12.006.006	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWYQQKPGKAPELLIYVASSLQSG VPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTLISFGQGTKLEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	462
iPS:361491	17B11.002.001	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPS GIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAVVFGGGTKLTVLGQP KAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPS KQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	463
iPS:361499	17B11.002.002	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPS GIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAVVFGGGTKLTVLGQP KAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPS KQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	464
iPS:361503	17B11.002.003	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYEQFPGTAPKLLIYDNNKRPS GIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAVVFGGGTKLTVLGQP KAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPS KQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	465
iPS:361507	17B11.002.004	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPS GIPDRFSGSKSGTSATLAITGLQTGDEADYYCGTFESSLSAVVFGGGTKLTVLGQP KAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPS KQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	466
iPS:361514	17B11.002.005	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPS GIPDRFSGSKSGTSATLAITGLQTGDEADYYCGTWDSSLSAVVFGGGTKLTVLGQP KAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPS KQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	467
iPS:360582	17B11.002.006	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPS GIPDRFSGSKSGTSATLAITGLQTGDEADYYCGTWDSSLSAVVFGGGTKLTVLGQP KAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPS KQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	468
iPS:361518	17B11.002.007	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPS GIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAVVFGGGTKLTVLGQP KAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPS KQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	469

Identifier	Construct	LC	SEQ ID NO:
iPS:360570	17B11.002.008	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPS GIPDRFSGSKSGTSATLAITGLQTGDEADYYCGTFESSLSAVVFGGGTKLTVLGQP KAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPS KQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	470
iPS:362051	5G12.005.001	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWYQQKPGKAPKLLIYVASSLQSG VPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTLLSFGQGTKLEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	471

Table 9. Heavy Chain (HC) Amino Acid Sequences of Exemplary Anti-GIPR Antibodies

Identifier	Construct	HC	SEQ ID NO:
iPS:336175	2C2.005	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWIN PNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGGDYVWGT YRPHYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	472
iPS:335914	4B1	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DGSNENYADSVKGRFTISRDNSKNTLYLHMNSLRVADTAVYYCARDGTIFGVVLG DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	473
iPS:335938	6H1	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAVIWY DGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGTIFGVLLG DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV	474

Identifier	Construct	HC	SEQ ID NO:
		EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	
iPS:335941	2F11	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWY DGSNKYYADSVKGRFTISSDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLD YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK	475
iPS:335970	5C2	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWINP DSGGTDYSQRFQGRFTMTRDTSISTAYMELNRLRSDDTAVYYCAREATIFGMVIVP FDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	476
iPS:335978	13H12	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWINP DSGGTDYSQRFQGRFTMTRDTSISTAYMELSRLRSDDTAVYYCAREATIFGMVIVP FDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	477
iPS:335986	11C1	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLVWMGWISP NSGDTSYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYFCTREATIFGMLIVP FDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW	478

Identifier	Construct	HC	SEQ ID NO:
		NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	
iPS:335994	12H11	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWISPN NGDTNYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYYCTREATIFGMLIVPF DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	479
iPS:336024	18E3	QVQLQESGPGLVKPSQTLSLTCTVSGDSISSGGYYWSWIRQHPGKGLEWIGYIYYS GSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFGVVMGGG MDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	480
iPS:336041	2G10_LC1	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGEGLEWVAAIWFD GSDKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQAIFGVVPD YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK	481
iPS:336077	4H9.004	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAVIWY DGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGTIFGVLLG	482

Identifier	Construct	HC	SEQ ID NO:
		DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	
iPS:336088	6A5.004	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQPPGKGLEWVAAIWYD GNNKYYADSVKGRFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLEY LGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK	483
iPS:336099	17H11.004	QVQLQESGPGLVKPSETLSLTCTVSQGSISSYYWSWIRQPAGKGLEWIGRIYTSGST NYNPSLKSRVTMSIDTSKNQFSLKLNSVTAADTAVYYCARDVAVAGFDYWGQGT LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS PGK	484
iPS:359621	17H11.004.001	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPAGKGLEWIGRIYTSGST NYNPSLKSRVTMSIDTSKNQFSLKLNSVTAADTAVYYCARDVAVAGFDYWGQGT LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS PGK	485

Identifier	Construct	HC	SEQ ID NO:
iPS:359781	4H9.004.001	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAVIWY DASNKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGTIFGVLL GDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	486
iPS:360929	4H9.004.002	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAVIWY DASNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGTIFGVLLG DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	487
iPS:360936	4H9.004.003	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAVIWY DGSNKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGTIFGVLL GDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	488
iPS:360943	4H9.004.004	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAVIWY DASNKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGTIFGVLL GDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE	489

Identifier	Construct	HC	SEQ ID NO:
		WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	
iPS:360949	4H9.004.005	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAVIWY DASNKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGTIFGVLL GDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	490
iPS:359761	4H9.004.006	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAVIWY DASNKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVLLG DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	491
iPS:360955	4B1.010	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DASNENYADAVKGRFTISRDNSKNTLYLQMNSLRVADTAVYYCARDGTIFGVVL GDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	492
iPS:360962	4B1.011	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DASNENYADAVKGRFTISRDNSKNTLYLQMNSLRVADTAVYYCARDGTIFGVVL GDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS	493

Identifier	Construct	HC	SEQ ID NO:
		NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	
iPS:360968	4B1.012	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DASNENYADAVKGRFTISRDNSKNTLYLQMNSLRVADTAVYYCARDGTIFGVVL GDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	494
iPS:360974	4B1.013	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DASNENYADSVKGRFTISRDNSKNTLYLHMNSLRVADTAVYYCARDGTIFGVVLG DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	495
iPS:360978	4B1.014	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DGSNENYADAVKGRFTISRDNSKNTLYLHMNSLRVADTAVYYCARDGTIFGVVL GDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	496
iPS:359785	4B1.015	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DASNENYADAVKGRFTISRDNSKNTLYLQMNSLRVEDTAVYYCARDRTIFGVVLG DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE	497

Identifier	Construct	HC	SEQ ID NO:
		VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	
iPS:360982	4B1.016	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DASNENYADAVKGRFTISRDNSKNTLYLQMNSLRVEDTAVYYCARDGTIFGVVL GDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	498
iPS:333922	18F2	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DGSNENYADSVKGRFTISRDNSKNTLYLHMNSLRAADTAVYYCARDGTIFGVVLG DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	499
iPS:360986	18F2.002	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DASNENYADAVKGRFTISRDNSKNTLYLQMNSLRAADTAVYYCARDGTIFGVVL GDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	500
iPS:360995	18F2.003	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DASNENYADAVKGRFTISRDNSKNTLYLHMNSLRAADTAVYYCARDGTIFGVVL GDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK	501

Identifier	Construct	HC	SEQ ID NO:
		VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	
iPS:360999	18F2.004	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DASNENYADAVKGRFTISRDNSKNTLYLQMNSLRAADTAVYYCARDGTIFGVVL GDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	502
iPS:361005	18F2.005	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DASNENYADAVKGRFTISRDNSKNTLYLQMNSLRAADTAVYYCARDGTIFGVVL GDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	503
iPS:361009	18F2.006	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DASNENYADAVKGRFTISRDNSKNTLYLHMNSLRAADTAVYYCARDGTIFGVVL GDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	504
iPS:361013	18F2.007	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DASNENYADAVKGRFTISRDNSKNTLYLHMNSLRAADTAVYYCARDGTIFGVVL GDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW	505

Identifier	Construct	HC	SEQ ID NO:
		NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	
iPS:361017	18F2.008	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DASNENYADAVKGRFTISRDNSKNTLYLQMNSLRAADTAVYYCARDGTIFGVVL GDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	506
iPS:361021	18F2.009	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DGSNENYADAVKGRFTISRDNSKNTLYLQMNSLRAADTAVYYCARDGTIFGVVL GDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	507
iPS:361028	18F2.010	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DASNENYADSVKGRFTISRDNSKNTLYLQMNSLRAADTAVYYCARDGTIFGVVLG DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	508
iPS:360535	18F2.011	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DASNENYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLG	509

Identifier	Construct	HC	SEQ ID NO:
		DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	
iPS:361035	18F2.012	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DASNENYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGTIFGVVL GDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	510
iPS:359940	2F11.002	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWY DASNKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVL DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	511
iPS:361039	2F11.003	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWY DASNKYYADAVKGRFTISSDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLD YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK	512

Identifier	Construct	HC	SEQ ID NO:
iPS:361043	2F11.004	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWY DASNKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVL DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	513
iPS:361049	2F11.005	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWY DASNKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVL DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	514
iPS:361055	2F11.006	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWY DASNKYYADAVKGRFTISSDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLD YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK	515
iPS:361059	2F11.007	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWY DASNKYYADAVKGRFTISSDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLD YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES	516

Identifier	Construct	HC	SEQ ID NO:
		NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK	
iPS:361063	2F11.008	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWY DASNKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVL DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	517
iPS:359949	2F11.009	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWY DASNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLD YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK	518
iPS:359956	2F11.010	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWY DGSNKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVL DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	519
iPS:359865	6H1.002	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAVIWY DASNKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGTIFGVLL GDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS	520

Identifier	Construct	HC	SEQ ID NO:
		NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	
iPS:359869	6H1.003	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAVIWY DASNKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVLLG DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	521
iPS:359873	6H1.004	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAVIWY DASNKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGTIFGVLL GDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	522
iPS:359877	6H1.005	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAVIWY DASNKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVLLG DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	523
iPS:361067	6H1.006	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAVIWY DGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGTIFGVLLG DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE	524

Identifier	Construct	HC	SEQ ID NO:
		VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	
iPS:361071	6H1.007	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAVIWY DASNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGTIFGVLLG DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	525
iPS:361075	6H1.008	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAVIWY DGSNKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGTIFGVLL GDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	526
iPS:361079	6A5.004.001	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQPPGKGLEWVAAIWYD ANNKYYADAVKGRFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLEY WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEP KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK	527
iPS:361085	6A5.004.002	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQPPGKGLEWVAAIWYD ANNKYYADAVKGRFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLEY WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEP	528

Identifier	Construct	HC	SEQ ID NO:
		KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK	
iPS:361091	6A5.004.003	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQPPGKGLEWVAAIWYD ANNKYYADAVKGRFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLEY LGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK	529
iPS:361095	6A5.004.004	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQPPGKGLEWVAAIWYD ANNKYYADAVKGRFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLEY WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEP KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK	530
iPS:361101	6A5.004.005	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQPPGKGLEWVAAIWYD ANNKYYADAVKGRFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLEY LGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK	531
iPS:361105	6A5.004.006	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQPPGKGLEWVAAIWYD ANNKYYADAVKGRFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLEY LGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA	532

Identifier	Construct	HC	SEQ ID NO:
		LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK	
iPS:361109	6A5.004.007	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQPPGKGLEWVAAIWYD ANNKYYADAVKGRFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLEY WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEP KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK	533
iPS:361113	6A5.004.008	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQPPGKGLEWVAAIWYD GNNKYYADAVKGRFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLEY WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEP KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK	534
iPS:361120	6A5.004.009	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQPPGKGLEWVAAIWYD ANNKYYADSVKGRFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLEY WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEP KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK	535
iPS:359896	6A5.004.010	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQPPGKGLEWVAAIWYD ANNKYYADAVKGRFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLEY	536

Identifier	Construct	HC	SEQ ID NO:
		WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEP KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK	
iPS:359890	6A5.004.011	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQPPGKGLEWVAAIWYD ANNKYYADAVKGRFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLEY LGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK	537
iPS:359567	2A11.002	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQAPGKGLEWVAVIWY DASNKYYEDAVKGRFTISRDNSKNTLFLQVNSLRAEDTAVYYCARGITIFGHGFEY WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEP KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK	538
iPS:335965	2A11.003	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQAPGKGLEWVAVIWY DGSNKYYEDSVKGRFTISRDNSKNTLFLQVNSLRAEDTAVYYCARGITIFGHGFEY WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEP KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK	539

Identifier	Construct	HC	SEQ ID NO:
iPS:361158	2A11.004	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQAPGKGLEWVAVIWY DGSNKYYEDAVKGRFTISRDNSKNTLFLQVNSLRAEDTAVYYCARGITIFGHGFEY WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEP KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK	540
iPS:361165	2A11.005	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQAPGKGLEWVAVIWY DASNKYYEDSVKGRFTISRDNSKNTLFLQVNSLRAEDTAVYYCARGITIFGHGFEY WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEP KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK	541
iPS:361172	2G10_LC1.003	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGEGLEWVAAIWFD ASDKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQAIFGVVPD YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK	542
iPS:361178	2G10_LC1.004	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGEGLEWVAAIWFD ASDKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQAIFGVVPD YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES	543

Identifier	Construct	HC	SEQ ID NO:
		NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK	
iPS:361185	2G10_LC1.005	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGEGLEWVAAIWFD GSDKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQAIFGVVPD YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK	544
iPS:361192	2G10_LC1.006	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGEGLEWVAAIWFD ASDKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQAIFGVVPD YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK	545
iPS:359609	2G10_LC1.007	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVAAIWF DASDKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQAIFGVVP DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	546
iPS:359615	2G10_LC1.008	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVAAIWF DASDKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQAIFGVVP DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN	547

Identifier	Construct	HC	SEQ ID NO:
		KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	
iPS:361196	2G10_LC1.009	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGEGLEWVAAIWFD ASDKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQAIFGVVPD YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK	548
iPS:361202	2G10_LC1.010	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVAAIWF DASDKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQAIFGVVP DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	549
iPS:359644	18E3.002	QVQLQESGPGLVKPSETLSLTCTVSGDSISSGGYYWSWIRQPPGKGLEWIGYIYYS GSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFGVVMGGG MDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	550
iPS:361206	18E3.003	QVQLQESGPGLVKPSETLSLTCTVSGDSISSGGYYWSWIRQPPGKGLEWIGYIYYS GSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFGVVMGGG MDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP	551

Identifier	Construct	HC	SEQ ID NO:
		EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	
iPS:359628	18E3.004	QVQLQESGPGLVKPSQTLSLTCTVSGDSISSGGYYWSWIRQPPGKGLEWIGYIYYS GSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFGVVMGGG MDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	552
iPS:359637	18E3.005	QVQLQESGPGLVKPSETLSLTCTVSGDSISSGGYYWSWIRQHPGKGLEWIGYIYYS GSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFGVVMGGG MDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	553
iPS:361210	18E3.006	QVQLQESGPGLVKPSQTLSLTCTVSGDSISSGGYYWSWIRQHPGKGLEWIGYIYYS GSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFGVVMGGG MDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	554
iPS:361214	18E3.007	QVQLQESGPGLVKPSETLSLTCTVSGDSISSGGYYWSWIRQHPGKGLEWIGYIYYS GSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFGVVMGGG MDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK	555

Identifier	Construct	HC	SEQ ID NO:
		VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	
iPS:361218	18E3.008	QVQLQESGPGLVKPSQTLSLTCTVSGDSISSGGYYWSWIRQPPGKGLEWIGYIYYS GSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFGVVMGGG MDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	556
iPS:361222	5C2.006	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWINP ESGGTDYSQRFQGRVTMTRDTSISTAYMELNRLRSDDTAVYYCAREATIFGMVIV PFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	557
iPS:361229	5C2.007	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWINPE SGGTDYSQRFQGRFTMTRDTSISTAYMELNRLRSDDTAVYYCAREATIFGMVIVPF DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	558
iPS:361236	5C2.008	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWINP DAGGTDYSQRFQGRVTMTRDTSISTAYMELNRLRSDDTAVYYCAREATIFGMVIV PFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW	559

Identifier	Construct	HC	SEQ ID NO:
		NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	
iPS:359685	5C2.009	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWINP DAGGTDYSQRFQGRFTMTRDTSISTAYMELNRLRSDDTAVYYCAREATIFGMVIV PFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	560
iPS:361240	5C2.010	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWINP DSGGTDYSQRFQGRVTMTRDTSISTAYMELNRLRSDDTAVYYCAREATIFGMVIV PFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	561
iPS:361247	5C2.011	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWINP DSGGTDYSQRFQGRFTMTRDTSISTAYMELNRLRSDDTAVYYCAREATIFGMVIVP FDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	562
iPS:361254	5C2.012	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWINP DSGGTDYSQRFQGRVTMTRDTSISTAYMELNRLRSDDTAVYYCAREATIFGMVIV	563

Identifier	Construct	HC	SEQ ID NO:
		PFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	
iPS:361261	5C2.013	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWINP DAGGTDYSQRFQGRFTMTRDTSISTAYMELNRLRSDDTAVYYCAREATIFGMVIV PFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	564
iPS:361268	5C2.014	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWINP DAGGTDYSQRFQGRVTMTRDTSISTAYMELNRLRSDDTAVYYCAREATIFGMVIV PFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	565
iPS:359669	5C2.015	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWINP DAGGTDYSQRFQGRVTMTRDTSISTAYMELNSLRSDDTAVYYCAREATIFGMVIV PFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	566

Identifier	Construct	HC	SEQ ID NO:
iPS:359678	5C2.016	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWINP ESGGTDYSQRFQGRVTMTRDTSISTAYMELNSLRSDDTAVYYCAREATIFGMVIVP FDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	567
iPS:361275	11C1.002	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLVWMGWISP NSGETSYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYYFCAREATIFGMLIVP FDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	568
iPS:361282	11C1.003	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLVWMGWISP NSGDTSYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYYFCAREATIFGMLIVP FDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	569
iPS:361289	11C1.004	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLVWMGWISP NSGETSYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYYFCAREATIFGMLIVP FDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE	570

Identifier	Construct	HC	SEQ ID NO:
		WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	
iPS:359712	11C1.005	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLVWMGWISP NSGETSYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYFCTREATIFGMLIVP FDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	571
iPS:361293	11C1.006	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLVWMGWISP NSGDTSYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYFCTREATIFGMLIVP FDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	572
iPS:361297	11C1.007	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLVWMGWISP NSGETSYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYFCTREATIFGMLIVP FDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	573
iPS:361301	11C1.008	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLVWMGWISP NSGDTSYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYFCAREATIFGMLIVP FDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS	574

Identifier	Construct	HC	SEQ ID NO:
		NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	
iPS:359703	11C1.009	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWISP NSGETSYAQKFQDRVTMTRDTSISTAYMELSSLRSDDTAVYFCAREATIFGMLIVP FDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	575
iPS:361305	11C1.010	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWISP NSGETSYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYFCAREATIFGMLIVP FDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	576
iPS:361312	13H12.002	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWINPE SGGTDYSQRFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCAREATIFGMVIVPF DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	577
iPS:359744	13H12.003	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWINPE SGGTDYSQRFQGRFTMTRDTSISTAYMELSRLRSDDTAVYYCAREATIFGMVIVPF DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE	578

Identifier	Construct	HC	SEQ ID NO:
		VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	
iPS:361319	13H12.004	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWINP DSGGTDYSQRFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCAREATIFGMVIVP FDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	579
iPS:359737	13H12.005	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWINP ESGGTDYSQRFQGRVTMTRDTSISTAYMELSSLRSDDTAVYYCAREATIFGMVIVP FDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	580
iPS:361326	13H12.006	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWINPE SGGTDYSQRFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCAREATIFGMVIVPF DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	581
iPS:361330	12H11.002	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWISPN QGETNYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYYCAREATIFGMLIVPF DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV	582

Identifier	Construct	HC	SEQ ID NO:
		EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	
iPS:361337	12H11.003	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWISPN QGDTNYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYYCAREATIFGMLIVP FDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	583
iPS:361344	12H11.004	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWISPN QGETNYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYYCTREATIFGMLIVPF DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	584
iPS:361351	12H11.005	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWISPN NGETNYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYYCAREATIFGMLIVPF DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	585
iPS:361358	12H11.006	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWISPN NGDTNYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYYCAREATIFGMLIVP FDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW	586

Identifier	Construct	HC	SEQ ID NO:
		NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	
iPS:361365	12H11.007	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWISPN QGDTNYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYYCTREATIFGMLIVPF DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	587
iPS:361372	12H11.008	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWISPN NGETNYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYYCTREATIFGMLIVPF DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	588
iPS:361379	12H11.009	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWISPN QGETNYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYYCAREATIFGMLIVPF DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	589
iPS:361383	12H11.010	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWISPN NGDTNYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYYCAREATIFGMLIVP	590

Identifier	Construct	HC	SEQ ID NO:
		FDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	
iPS:361387	12H11.011	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWISPN QGDTNYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYYCAREATIFGMLIVP FDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	591
iPS:361391	12H11.012	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWISPN NGETNYAQKFQDRVTMTRDTSISTAYMELSRLRSDDTAVYYCAREATIFGMLIVPF DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	592
iPS:361395	12H11.013	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWISP NQGETNYAQKFQDRVTMTRDTSISTAYMELSSLRSDDTAVYYCAREATIFGMLIV PFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	593

Identifier	Construct	HC	SEQ ID NO:
iPS:361402	12H11.014	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGWISP NQGETNYAQKFQDRVTMTRDTSISTAYMELSSLRSDDTAVYYCAREATIFGMLIV PFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	594
iPS:361406	2C2.005.001	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWIN PNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGGDYVWGT YRPHYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	595
iPS:361412	2C2.005.002	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWIN PNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGGDYVWGT YRPHYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	596
iPS:361418	2C2.005.003	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWIN PNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGGDYVWGT YRPHYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF	597

Identifier	Construct	HC	SEQ ID NO:
		YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	
iPS:361424	2C2.005.004	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWIN PNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGGDYVWGT YRPHYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	598
iPS:361430	2C2.005.005	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWIN PNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGGDYVWGT YRPHYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	599
iPS:361436	2C2.005.006	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWIN PNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGGDYVWGT YRPHYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	600
iPS:361442	2C2.005.007	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWIN PNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGGDYVWGT YRPHYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNG	601

Identifier	Construct	HC	SEQ ID NO:
		KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	
iPS:361448	2C2.005.008	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWIN PNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGGDYVWGT YRPHYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	602
iPS:361454	2C2.005.009	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWIN PNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGGDYVWGT YRPHYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	603
iPS:361460	2C2.005.010	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWIN PNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGGDYVWGT YRPHYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	604
iPS:361466	2C2.005.011	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWIN PNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGGDYVWGT YRPHYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV	605

Identifier	Construct	HC	SEQ ID NO:
		VDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	
iPS:361472	2C2.005.012	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWIN PNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGGDYVWGT YRPHYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	606
iPS:361478	2C2.005.013	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWIN PNSGGTNYAQKFQGRVTMTRDTSISTAYMELSSLRSDDTAVYYCARGGDYVFGT YRPHYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	607
iPS:361485	2C2.005.014	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWIN PNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGGDYVFGT YRPHYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	608
iPS:361845	18F2.013	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAVIWY DASNENYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLG DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV	609

Identifier	Construct	HC	SEQ ID NO:
		EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	
iPS:361851	6H1.009	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAVIWY DASNKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVLLG DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	610
iPS:361855	2C2.005.015	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWIN PNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGGDYVWGT YRPHYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	611
iPS:336067	5G12.006	QVQLVESGGGVVQPGRSLRLSCTASGFTFSSYGIHWVRQAPGKGLEWVAVIWYD GSNKFHADSVKGRFTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKVAGMPEAF EIWGQGTKVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK	612
iPS:336169	17B11.002	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN PNSGNTGYAQKFQGRVTMTRDTSISTAYMELSSLRSQDTAVYYCARGGDYVWGS YRPYYYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD	613

Identifier	Construct	HC	SEQ ID NO:
		YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWL NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK	
iPS:361127	5G12.006.001	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGIHWVRQAPGKGLEWVAVIWYD ASNKFHADAVKGRFTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKVAGMPEAF EIWGQGTKVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK	614
iPS:361136	5G12.006.002	QVQLVESGGGVVQPGRSLRLSCTASGFTFSSYGIHWVRQAPGKGLEWVAVIWYD ASNKFHADAVKGRFTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKVAGMPEAF EIWGQGTKVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK	615
iPS:361140	5G12.006.003	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGIHWVRQAPGKGLEWVAVIWYD ASNKFHADAVKGRFTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKVAGMPEAF EIWGQGTKVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK	616
iPS:359919	5G12.006.004	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGIHWVRQAPGKGLEWVAVIWYD ASNKFHADAVKGRFTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKVAGMPEAF	617

Identifier	Construct	HC	SEQ ID NO:
		EIWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK	
iPS:361144	5G12.006.005	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGIHWVRQAPGKGLEWVAVIWYD ASNKFHADSVKGRFTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKVAGMPEAF EIWGQGTKVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK	618
iPS:361151	5G12.006.006	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGIHWVRQAPGKGLEWVAVIWYD GSNKFHADAVKGRFTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKVAGMPEAF EIWGQGTKVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK	619
iPS:361491	17B11.002.001	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN PNSGGTGYAQKFQGRVTMTRDTSISTAYMELSSLRSQDTAVYYCARGGDYVWGS YRPYYYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWL NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK	620

Identifier	Construct	HC	SEQ ID NO:
iPS:361499	17B11.002.002	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN PNSGNTGYAQKFQGRVTMTRDTSISTAYMELSSLRSQDTAVYYCARGGDYVWGS YRPYYYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWL NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK	621
iPS:361503	17B11.002.003	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN PNSGGTGYAQKFQGRVTMTRDTSISTAYMELSSLRSQDTAVYYCARGGDYVWGS YRPYYYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWL NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK	622
iPS:361507	17B11.002.004	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQAPGQGLEWMGWMN PNSGGTGYAQKFQGRVTMTRDTSISTAYMELSSLRSDDTAVYYCARGGDYVWGS YRPYYYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWL NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK	623
iPS:361514	17B11.002.005	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN PNSGGTGYAQKFQGRVTMTRDTSISTAYMELSSLRSQDTAVYYCARGGDYVWGS YRPYYYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWL NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK	624

Identifier	Construct	HC	SEQ ID NO:
		GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK	
iPS:360582	17B11.002.006	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQAPGQGLEWMGWMN PNSGNTGYAQKFQGRVTMTRDTSISTAYMELSSLRSDDTAVYYCARGGDYVWGS YRPYYYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWL NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK	625
iPS:361518	17B11.002.007	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN PNSGGTGYAQKFQGRVTMTRDTSISTAYMELSSLRSQDTAVYYCARGGDYVFGS YRPYYYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWL NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK	626
iPS:360570	17B11.002.008	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQAPGQGLEWMGWMN PNSGGTGYAQKFQGRVTMTRDTSISTAYMELSSLRSDDTAVYYCARGGDYVFGS YRPYYYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWL NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK	627
iPS:362051	5G12.005.001	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGIHWVRQAPGKGLEWVAVIWYD ASNKFHADAVKGRFTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKVAGMPEAF EIWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK	628

Identifier	Construct	HC	SEQ ID NO:
		ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK	

Table 10. Light Chain (LC) Amino Acid Sequences of Example Anti-GIPR Antibodies with Cysteine Modifications

Description	LC	SEQ ID NO:
aGIPR 2G10 SEFL2 E384C	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGAATRATGI PARVSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPLTFGGGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	388
aGIPR 5G12 SEFL2 E384C	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWYQQKPGKAPELLIYVASSLQSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTLISFGQGTKLEITRTVAAPSVFIFPPS DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	455
aGIPR 2G10.007 SEFL2 E384C	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGAATRATGI PARFSGSGSGTEFTLTISSLEPEDFAVYYCQQYNNFPLTFGGGTKVEIKRTVAAPSVFIF PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	389
aGIPR 5G12 SEFL2 T487C	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWYQQKPGKAPELLIYVASSLQSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTLISFGQGTKLEITRTVAAPSVFIFPPS DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	455
aGIPR 5G12 SEFL2 D88C	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWYQQKPGKAPELLIYVASSLQSGVPS RFSGSGSGT**C**FTLTISSLQPEDFATYYCQQSYSTLISFGQGTKLEITRTVAAPSVFIFPPS DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	1594

Table 11. Heavy Chain (HC) Amino Acid Sequences of Example Anti-GIPR Antibodies with Cysteine Modifications

Description	HC	SEQ ID NO:
aGIPR 2G10 SEFL2 E384C	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGEGLEWVAAIWFDAS DKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQAIFGVVPDYWGQ GTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP**C**VKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1571
aGIPR 5G12 SEFL2 E384C	QVQLVESGGGVVQPGRSLRLSCTASGFTFSSYGIHWVRQAPGKGLEWVAVIWYDGS NKFHADSVKGRFTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKVAGMPEAFEIWG QGTKVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP**C**VKFNWYVDGV EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1595
aGIPR 2G10.007 SEFL2 E384C	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVAAIWFDAS DKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQAIFGVVPDYWGQ GTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP**C**VKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	1596
aGIPR 5G12 SEFL2 T487C	QVQLVESGGGVVQPGRSLRLSCTASGFTFSSYGIHWVRQAPGKGLEWVAVIWYDGS NKFHADSVKGRFTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKVAGMPEAFEIWG QGTKVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA	1597

Description	HC	SEQ ID NO:
	KGQPREPQVYTLPPSREEMCKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	
aGIPR 5G12 SEFL2 D88C	QVQLVESGGGVVQPGRSLRLSCTASGFTFSSYGIHWVRQAPGKGLEWVAVIWYDGS NKFHADSVKGRFTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKVAGMPEAFEIWG QGTKVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	612

[0192] In one embodiment, the antagonist anti-GIPR antibody of the conjugate molecule comprises a light chain variable region, where the light chain variable region comprises light chain complementarity determining region 1 (CDRL1), a CDRL2, a CDRL3. In one embodiment, the CDRL1 of the antibody comprises an amino acid sequence of any one of SEQ ID NOs: 629-785 of Table 6; the CDRL2 comprises an amino acid sequence of any one of SEQ ID NOs: 786-942 of Table 6; and the CDRL3 comprises an amino acid sequence of any one of SEQ ID NOs: 943-1099 of Table 6. In one embodiment, the antagonist anti-GIPR antibody of the conjugate molecule comprises a heavy chain variable region, where the heavy chain variable region comprises a heavy chain complementarity determining region 1 (CDRH1), a CDRH2, a CDRH3. In one embodiment, the CDRH1 of the antibody comprises an amino acid sequence of any one of SEQ ID NOs: 1100-1256 as disclosed in Table 7; the CDRH2 comprises an amino acid sequence of any one of SEQ ID NOs: 1257-1413 of Table 7; and the CDRH3 comprises an amino acid sequence of any one of SEQ ID NOs: 1414-1570 of Table 7.

[0193] In one embodiment, the anti-GIPR antibody of the conjugate molecule comprises a light chain variable region comprising CDRL1, CDRL2, CDRL3 amino acid sequences as listed in one of the rows for one of the antibodies listed in Table 3. In one embodiment, the anti-GIPR antibody of the conjugate molecule comprises a heavy chain variable region comprising CDRH1, CDRH2, CDRH3 amino acid sequences as listed in one of the rows for one of the antibodies listed in Table 3.

[0194] In one embodiment, the anti-GIPR antibody of the conjugate molecule described herein comprises a combination of CDRL1, CDRL2, CDRL3, CDRH1, CDRH2, and CDRH3 sequences as listed in one of the rows for one of the antibodies listed in Table 3. In one embodiment, the CDRL1, the CDRL2, the CDRL3, the CDRH1, the CDRH2, and the CDRH3 of the antagonist anti-GIPR antibody comprise the amino acid sequences selected from:

i. SEQ ID NO: 629, SEQ ID NO: 786, SEQ ID NO: 943, SEQ ID NO: 1100, SEQ ID NO: 1257, and SEQ ID NO: 1414, respectively;

ii. SEQ ID NO: 630, SEQ ID NO: 787, SEQ ID NO: 944, SEQ ID NO: 1101, SEQ ID NO: 1258, and SEQ ID NO: 1415, respectively;

iii. SEQ ID NO: 631, SEQ ID NO: 788, SEQ ID NO: 945, SEQ ID NO: 1102, SEQ ID NO: 1259, and SEQ ID NO: 1416, respectively;

iv. SEQ ID NO: 632, SEQ ID NO: 789, SEQ ID NO: 946, SEQ ID NO: 1103, SEQ ID NO: 1260, and SEQ ID NO: 1417, respectively;

v. SEQ ID NO: 633, SEQ ID NO: 790, SEQ ID NO: 947, SEQ ID NO: 1104, SEQ ID NO: 1261, and SEQ ID NO: 1418, respectively;

vi. SEQ ID NO: 634, SEQ ID NO: 791, SEQ ID NO: 948, SEQ ID NO: 1105, SEQ ID NO: 1262, and SEQ ID NO: 1419, respectively;

vii. SEQ ID NO: 635, SEQ ID NO: 792, SEQ ID NO: 949, SEQ ID NO: 1106, SEQ ID NO: 1263, and SEQ ID NO: 1420, respectively;

viii. SEQ ID NO: 636, SEQ ID NO: 793, SEQ ID NO: 950, SEQ ID NO: 1107, SEQ ID NO: 1264, and SEQ ID NO: 1421, respectively;

ix. SEQ ID NO: 637, SEQ ID NO: 794, SEQ ID NO: 951, SEQ ID NO: 1108, SEQ ID NO: 1265, and SEQ ID NO: 1422, respectively;

x. SEQ ID NO: 638, SEQ ID NO: 795, SEQ ID NO: 952, SEQ ID NO: 1109, SEQ ID NO: 1266, and SEQ ID NO: 1423, respectively;

xi. SEQ ID NO: 639, SEQ ID NO: 796, SEQ ID NO: 953, SEQ ID NO: 1110, SEQ ID NO: 1267, and SEQ ID NO: 1424, respectively;

xii. SEQ ID NO: 640, SEQ ID NO: 797, SEQ ID NO: 954, SEQ ID NO: 1111, SEQ ID NO: 1268, and SEQ ID NO: 1425, respectively;

xiii. SEQ ID NO: 641, SEQ ID NO: 798, SEQ ID NO: 955, SEQ ID NO: 1112, SEQ ID NO: 1269, and SEQ ID NO: 1426, respectively;

xiv. SEQ ID NO: 642, SEQ ID NO: 799, SEQ ID NO: 956, SEQ ID NO: 1113, SEQ ID NO: 1270, and SEQ ID NO: 1427, respectively;

xv. SEQ ID NO: 643, SEQ ID NO: 800, SEQ ID NO: 957, SEQ ID NO: 1114, SEQ ID NO: 1271, and SEQ ID NO: 1428, respectively;

xvi. SEQ ID NO: 644, SEQ ID NO: 801, SEQ ID NO: 958, SEQ ID NO: 1115, SEQ ID NO: 1272, and SEQ ID NO: 1429, respectively;

xvii. SEQ ID NO: 645, SEQ ID NO: 802, SEQ ID NO: 959, SEQ ID NO: 1116, SEQ ID NO: 1273, and SEQ ID NO: 1430, respectively;

xviii. SEQ ID NO: 646, SEQ ID NO: 803, SEQ ID NO: 960, SEQ ID NO: 1117, SEQ ID NO: 1274, and SEQ ID NO: 1431, respectively;

xix. SEQ ID NO: 647, SEQ ID NO: 804, SEQ ID NO: 961, SEQ ID NO: 1118, SEQ ID NO: 1275, and SEQ ID NO: 1432, respectively;

xx. SEQ ID NO: 648, SEQ ID NO: 805, SEQ ID NO: 962, SEQ ID NO: 1119, SEQ ID NO: 1276, and SEQ ID NO: 1433, respectively;

xxi. SEQ ID NO: 649, SEQ ID NO: 806, SEQ ID NO: 963, SEQ ID NO: 1120, SEQ ID NO: 1277, and SEQ ID NO: 1434, respectively;

xxii. SEQ ID NO: 650, SEQ ID NO: 807, SEQ ID NO: 964, SEQ ID NO: 1121, SEQ ID NO: 1278, and SEQ ID NO: 1435, respectively;

xxiii. SEQ ID NO: 651, SEQ ID NO: 808, SEQ ID NO: 965, SEQ ID NO: 1122, SEQ ID NO: 1279, and SEQ ID NO: 1436, respectively;

xxiv. SEQ ID NO: 652, SEQ ID NO: 809, SEQ ID NO: 966, SEQ ID NO: 1123, SEQ ID NO: 1280, and SEQ ID NO: 1437, respectively;

xxv. SEQ ID NO: 653, SEQ ID NO: 810, SEQ ID NO: 967, SEQ ID NO: 1124, SEQ ID NO: 1281, and SEQ ID NO: 1438, respectively;

xxvi. SEQ ID NO: 654, SEQ ID NO: 811, SEQ ID NO: 968, SEQ ID NO: 1125, SEQ ID NO: 1282, and SEQ ID NO: 1439, respectively;

xxvii. SEQ ID NO: 655, SEQ ID NO: 812, SEQ ID NO: 969, SEQ ID NO: 1126, SEQ ID NO: 1283, and SEQ ID NO: 1440, respectively;

xxviii. SEQ ID NO: 656, SEQ ID NO: 813, SEQ ID NO: 970, SEQ ID NO: 1127, SEQ ID NO: 1284, and SEQ ID NO: 1441, respectively;

xxix. SEQ ID NO: 657, SEQ ID NO: 814, SEQ ID NO: 971, SEQ ID NO: 1128, SEQ ID NO: 1285, and SEQ ID NO: 1442, respectively;

xxx. SEQ ID NO: 658, SEQ ID NO: 815, SEQ ID NO: 972, SEQ ID NO: 1129, SEQ ID NO: 1286, and SEQ ID NO: 1443, respectively;

xxxi. SEQ ID NO: 659, SEQ ID NO: 816, SEQ ID NO: 973, SEQ ID NO: 1130, SEQ ID NO: 1287, and SEQ ID NO: 1444, respectively;

xxxii. SEQ ID NO: 660, SEQ ID NO: 817, SEQ ID NO: 974, SEQ ID NO: 1131, SEQ ID NO: 1288, and SEQ ID NO: 1445, respectively;

xxxiii. SEQ ID NO: 661, SEQ ID NO: 818, SEQ ID NO: 975, SEQ ID NO: 1132, SEQ ID NO: 1289, and SEQ ID NO: 1446, respectively;

xxxiv. SEQ ID NO: 662, SEQ ID NO: 819, SEQ ID NO: 976, SEQ ID NO: 1133, SEQ ID NO: 1290, and SEQ ID NO: 1447, respectively;

xxxv. SEQ ID NO: 663, SEQ ID NO: 820, SEQ ID NO: 977, SEQ ID NO: 1134, SEQ ID NO: 1291, and SEQ ID NO: 1448, respectively;

xxxvi. SEQ ID NO: 664, SEQ ID NO: 821, SEQ ID NO: 978, SEQ ID NO: 1135, SEQ ID NO: 1292, and SEQ ID NO: 1449, respectively;

xxxvii. SEQ ID NO: 665, SEQ ID NO: 822, SEQ ID NO: 979, SEQ ID NO: 1136, SEQ ID NO: 1293, and SEQ ID NO: 1450, respectively;

xxxviii. SEQ ID NO: 666, SEQ ID NO: 823, SEQ ID NO: 980, SEQ ID NO: 1137, SEQ ID NO: 1294, and SEQ ID NO: 1451, respectively;

xxxix. SEQ ID NO: 667, SEQ ID NO: 824, SEQ ID NO: 981, SEQ ID NO: 1138, SEQ ID NO: 1295, and SEQ ID NO: 1452, respectively;

xl. SEQ ID NO: 668, SEQ ID NO: 825, SEQ ID NO: 982, SEQ ID NO: 1139, SEQ ID NO: 1296, and SEQ ID NO: 1453, respectively;

xli. SEQ ID NO: 669, SEQ ID NO: 826, SEQ ID NO: 983, SEQ ID NO: 1140, SEQ ID NO: 1297, and SEQ ID NO: 1454, respectively;

xlii. SEQ ID NO: 670, SEQ ID NO: 827, SEQ ID NO: 984, SEQ ID NO: 1141, SEQ ID NO: 1298, and SEQ ID NO: 1455, respectively;

xliii. SEQ ID NO: 671, SEQ ID NO: 828, SEQ ID NO: 985, SEQ ID NO: 1142, SEQ ID NO: 1299, and SEQ ID NO: 1456, respectively;

xliv. SEQ ID NO: 672, SEQ ID NO: 829, SEQ ID NO: 986, SEQ ID NO: 1143, SEQ ID NO: 1300, and SEQ ID NO: 1457, respectively;

xlv. SEQ ID NO: 673, SEQ ID NO: 830, SEQ ID NO: 987, SEQ ID NO: 1144, SEQ ID NO: 1301, and SEQ ID NO: 1458, respectively;

xlvi. SEQ ID NO: 674, SEQ ID NO: 831, SEQ ID NO: 988, SEQ ID NO: 1145, SEQ ID NO: 1302, and SEQ ID NO: 1459, respectively;

xlvii. SEQ ID NO: 675, SEQ ID NO: 832, SEQ ID NO: 989, SEQ ID NO: 1146, SEQ ID NO: 1303, and SEQ ID NO: 1460, respectively;

xlviii. SEQ ID NO: 676, SEQ ID NO: 833, SEQ ID NO: 990, SEQ ID NO: 1147, SEQ ID NO: 1304, and SEQ ID NO: 1461, respectively;

xlix. SEQ ID NO: 677, SEQ ID NO: 834, SEQ ID NO: 991, SEQ ID NO: 1148, SEQ ID NO: 1305, and SEQ ID NO: 1462, respectively;

l. SEQ ID NO: 678, SEQ ID NO: 835, SEQ ID NO: 992, SEQ ID NO: 1149, SEQ ID NO: 1306, and SEQ ID NO: 1463, respectively;

li. SEQ ID NO: 679, SEQ ID NO: 836, SEQ ID NO: 993, SEQ ID NO: 1150, SEQ ID NO: 1307, and SEQ ID NO: 1464, respectively;

lii. SEQ ID NO: 680, SEQ ID NO: 837, SEQ ID NO: 994, SEQ ID NO: 1151, SEQ ID NO: 1308, and SEQ ID NO: 1465, respectively;

liii. SEQ ID NO: 681, SEQ ID NO: 838, SEQ ID NO: 995, SEQ ID NO: 1152, SEQ ID NO: 1309, and SEQ ID NO: 1466, respectively;

liv. SEQ ID NO: 682, SEQ ID NO: 839, SEQ ID NO: 996, SEQ ID NO: 1153, SEQ ID NO: 1310, and SEQ ID NO: 1467, respectively;

lv. SEQ ID NO: 683, SEQ ID NO: 840, SEQ ID NO: 997, SEQ ID NO: 1154, SEQ ID NO: 1311, and SEQ ID NO: 1468, respectively;

lvi. SEQ ID NO: 684, SEQ ID NO: 841, SEQ ID NO: 998, SEQ ID NO: 1155, SEQ ID NO: 1312, and SEQ ID NO: 1469, respectively;

lvii. SEQ ID NO: 685, SEQ ID NO: 842, SEQ ID NO: 999, SEQ ID NO: 1156, SEQ ID NO: 1313, and SEQ ID NO: 1470, respectively;

lviii. SEQ ID NO: 686, SEQ ID NO: 843, SEQ ID NO: 1000, SEQ ID NO: 1157, SEQ ID NO: 1314, and SEQ ID NO: 1471, respectively;

lix. SEQ ID NO: 687, SEQ ID NO: 844, SEQ ID NO: 1001, SEQ ID NO: 1158, SEQ ID NO: 1315, and SEQ ID NO: 1472, respectively;

lx. SEQ ID NO: 688, SEQ ID NO: 845, SEQ ID NO: 1002, SEQ ID NO: 1159, SEQ ID NO: 1316, and SEQ ID NO: 1473, respectively;

lxi. SEQ ID NO: 689, SEQ ID NO: 846, SEQ ID NO: 1003, SEQ ID NO: 1160, SEQ ID NO: 1317, and SEQ ID NO: 1474, respectively;

lxii. SEQ ID NO: 690, SEQ ID NO: 847, SEQ ID NO: 1004, SEQ ID NO: 1161, SEQ ID NO: 1318, and SEQ ID NO: 1475, respectively;

lxiii. SEQ ID NO: 691, SEQ ID NO: 848, SEQ ID NO: 1005, SEQ ID NO: 1162, SEQ ID NO: 1319, and SEQ ID NO: 1476, respectively;

lxiv. SEQ ID NO: 692, SEQ ID NO: 849, SEQ ID NO: 1006, SEQ ID NO: 1163, SEQ ID NO: 1320, and SEQ ID NO: 1477, respectively;

lxv. SEQ ID NO: 693, SEQ ID NO: 850, SEQ ID NO: 1007, SEQ ID NO: 1164, SEQ ID NO: 1321, and SEQ ID NO: 1478, respectively;

lxvi. SEQ ID NO: 694, SEQ ID NO: 851, SEQ ID NO: 1008, SEQ ID NO: 1165, SEQ ID NO: 1322, and SEQ ID NO: 1479, respectively;

lxvii. SEQ ID NO: 695, SEQ ID NO: 852, SEQ ID NO: 1009, SEQ ID NO: 1166, SEQ ID NO: 1323, and SEQ ID NO: 1480, respectively;

lxviii. SEQ ID NO: 696, SEQ ID NO: 853, SEQ ID NO: 1010, SEQ ID NO: 1167, SEQ ID NO: 1324, and SEQ ID NO: 1481, respectively;

lxix. SEQ ID NO: 697, SEQ ID NO: 854, SEQ ID NO: 1011, SEQ ID NO: 1168, SEQ ID NO: 1325, and SEQ ID NO: 1482, respectively;

lxx. SEQ ID NO: 698, SEQ ID NO: 855, SEQ ID NO: 1012, SEQ ID NO: 1169, SEQ ID NO: 1326, and SEQ ID NO: 1483, respectively;

lxxi. SEQ ID NO: 699, SEQ ID NO: 856, SEQ ID NO: 1013, SEQ ID NO: 1170, SEQ ID NO: 1327, and SEQ ID NO: 1484, respectively;

lxxii. SEQ ID NO: 700, SEQ ID NO: 857, SEQ ID NO: 1014, SEQ ID NO: 1171, SEQ ID NO: 1328, and SEQ ID NO: 1485, respectively;

lxxiii. SEQ ID NO: 701, SEQ ID NO: 858, SEQ ID NO: 1015, SEQ ID NO: 1172, SEQ ID NO: 1329, and SEQ ID NO: 1486, respectively;

lxxiv. SEQ ID NO: 702, SEQ ID NO: 859, SEQ ID NO: 1016, SEQ ID NO: 1173, SEQ ID NO: 1330, and SEQ ID NO: 1487, respectively;

lxxv. SEQ ID NO: 703, SEQ ID NO: 860, SEQ ID NO: 1017, SEQ ID NO: 1174, SEQ ID NO: 1331, and SEQ ID NO: 1488, respectively;

lxxvi. SEQ ID NO: 704, SEQ ID NO: 861, SEQ ID NO: 1018, SEQ ID NO: 1175, SEQ ID NO: 1332, and SEQ ID NO: 1489, respectively;

lxxvii. SEQ ID NO: 705, SEQ ID NO: 862, SEQ ID NO: 1019, SEQ ID NO: 1176, SEQ ID NO: 1333, and SEQ ID NO: 1490, respectively;

lxxviii. SEQ ID NO: 706, SEQ ID NO: 863, SEQ ID NO: 1020, SEQ ID NO: 1177, SEQ ID NO: 1334, and SEQ ID NO: 1491, respectively;

lxxix. SEQ ID NO: 707, SEQ ID NO: 864, SEQ ID NO: 1021, SEQ ID NO: 1178, SEQ ID NO: 1335, and SEQ ID NO: 1492, respectively;

lxxx. SEQ ID NO: 708, SEQ ID NO: 865, SEQ ID NO: 1022, SEQ ID NO: 1179, SEQ ID NO: 1336, and SEQ ID NO: 1493, respectively;

lxxxi. SEQ ID NO: 709, SEQ ID NO: 866, SEQ ID NO: 1023, SEQ ID NO: 1180, SEQ ID NO: 1337, and SEQ ID NO: 1494, respectively;

lxxxii. SEQ ID NO: 710, SEQ ID NO: 867, SEQ ID NO: 1024, SEQ ID NO: 1181, SEQ ID NO: 1338, and SEQ ID NO: 1495, respectively;

lxxxiii. SEQ ID NO: 711, SEQ ID NO: 868, SEQ ID NO: 1025, SEQ ID NO: 1182, SEQ ID NO: 1339, and SEQ ID NO: 1496, respectively;

lxxxiv. SEQ ID NO: 712, SEQ ID NO: 869, SEQ ID NO: 1026, SEQ ID NO: 1183, SEQ ID NO: 1340, and SEQ ID NO: 1497, respectively;

lxxxv. SEQ ID NO: 713, SEQ ID NO: 870, SEQ ID NO: 1027, SEQ ID NO: 1184, SEQ ID NO: 1341, and SEQ ID NO: 1498, respectively;

lxxxvi. SEQ ID NO: 714, SEQ ID NO: 871, SEQ ID NO: 1028, SEQ ID NO: 1185, SEQ ID NO: 1342, and SEQ ID NO: 1499, respectively;

lxxxvii. SEQ ID NO: 715, SEQ ID NO: 872, SEQ ID NO: 1029, SEQ ID NO: 1186, SEQ ID NO: 1343, and SEQ ID NO: 1500, respectively;

lxxxviii. SEQ ID NO: 716, SEQ ID NO: 873, SEQ ID NO: 1030, SEQ ID NO: 1187, SEQ ID NO: 1344, and SEQ ID NO: 1501, respectively;

lxxxix. SEQ ID NO: 717, SEQ ID NO: 874, SEQ ID NO: 1031, SEQ ID NO: 1188, SEQ ID NO: 1345, and SEQ ID NO: 1502, respectively;

xc. SEQ ID NO: 718, SEQ ID NO: 875, SEQ ID NO: 1032, SEQ ID NO: 1189, SEQ ID NO: 1346, and SEQ ID NO: 1503, respectively;

xci. SEQ ID NO: 719, SEQ ID NO: 876, SEQ ID NO: 1033, SEQ ID NO: 1190, SEQ ID NO: 1347, and SEQ ID NO: 1504, respectively;

xcii. SEQ ID NO: 720, SEQ ID NO: 877, SEQ ID NO: 1034, SEQ ID NO: 1191, SEQ ID NO: 1348, and SEQ ID NO: 1505, respectively;

xciii. SEQ ID NO: 721, SEQ ID NO: 878, SEQ ID NO: 1035, SEQ ID NO: 1192, SEQ ID NO: 1349, and SEQ ID NO: 1506, respectively;

xciv. SEQ ID NO: 722, SEQ ID NO: 879, SEQ ID NO: 1036, SEQ ID NO: 1193, SEQ ID NO: 1350, and SEQ ID NO: 1507, respectively;

xcv. SEQ ID NO: 723, SEQ ID NO: 880, SEQ ID NO: 1037, SEQ ID NO: 1194, SEQ ID NO: 1351, and SEQ ID NO: 1508, respectively;

xcvi. SEQ ID NO: 724, SEQ ID NO: 881, SEQ ID NO: 1038, SEQ ID NO: 1195, SEQ ID NO: 1352, and SEQ ID NO: 1509, respectively;

xcvii. SEQ ID NO: 725, SEQ ID NO: 882, SEQ ID NO: 1039, SEQ ID NO: 1196, SEQ ID NO: 1353, and SEQ ID NO: 1510, respectively;

xcviii. SEQ ID NO: 726, SEQ ID NO: 883, SEQ ID NO: 1040, SEQ ID NO: 1197, SEQ ID NO: 1354, and SEQ ID NO: 1511, respectively;

xcix. SEQ ID NO: 727, SEQ ID NO: 884, SEQ ID NO: 1041, SEQ ID NO: 1198, SEQ ID NO: 1355, and SEQ ID NO: 1512, respectively;

c. SEQ ID NO: 728, SEQ ID NO: 885, SEQ ID NO: 1042, SEQ ID NO: 1199, SEQ ID NO: 1356, and SEQ ID NO: 1513, respectively;

ci. SEQ ID NO: 729, SEQ ID NO: 886, SEQ ID NO: 1043, SEQ ID NO: 1200, SEQ ID NO: 1357, and SEQ ID NO: 1514, respectively;

cii. SEQ ID NO: 730, SEQ ID NO: 887, SEQ ID NO: 1044, SEQ ID NO: 1201, SEQ ID NO: 1358, and SEQ ID NO: 1515, respectively;

ciii. SEQ ID NO: 731, SEQ ID NO: 888, SEQ ID NO: 1045, SEQ ID NO: 1202, SEQ ID NO: 1359, and SEQ ID NO: 1516, respectively;

civ. SEQ ID NO: 732, SEQ ID NO: 889, SEQ ID NO: 1046, SEQ ID NO: 1203, SEQ ID NO: 1360, and SEQ ID NO: 1517, respectively;

cv. SEQ ID NO: 733, SEQ ID NO: 890, SEQ ID NO: 1047, SEQ ID NO: 1204, SEQ ID NO: 1361, and SEQ ID NO: 1518, respectively;

cvi. SEQ ID NO: 734, SEQ ID NO: 891, SEQ ID NO: 1048, SEQ ID NO: 1205, SEQ ID NO: 1362, and SEQ ID NO: 1519, respectively;

cvii. SEQ ID NO: 735, SEQ ID NO: 892, SEQ ID NO: 1049, SEQ ID NO: 1206, SEQ ID NO: 1363, and SEQ ID NO: 1520, respectively;

cviii. SEQ ID NO: 736, SEQ ID NO: 893, SEQ ID NO: 1050, SEQ ID NO: 1207, SEQ ID NO: 1364, and SEQ ID NO: 1521, respectively;

cix. SEQ ID NO: 737, SEQ ID NO: 894, SEQ ID NO: 1051, SEQ ID NO: 1208, SEQ ID NO: 1365, and SEQ ID NO: 1522, respectively;

cx. SEQ ID NO: 738, SEQ ID NO: 895, SEQ ID NO: 1052, SEQ ID NO: 1209, SEQ ID NO: 1366, and SEQ ID NO: 1523, respectively;

cxi. SEQ ID NO: 739, SEQ ID NO: 896, SEQ ID NO: 1053, SEQ ID NO: 1210, SEQ ID NO: 1367, and SEQ ID NO: 1524, respectively;

cxii. SEQ ID NO: 740, SEQ ID NO: 897, SEQ ID NO: 1054, SEQ ID NO: 1211, SEQ ID NO: 1368, and SEQ ID NO: 1525, respectively;

cxiii. SEQ ID NO: 741, SEQ ID NO: 898, SEQ ID NO: 1055, SEQ ID NO: 1212, SEQ ID NO: 1369, and SEQ ID NO: 1526, respectively;

cxiv. SEQ ID NO: 742, SEQ ID NO: 899, SEQ ID NO: 1056, SEQ ID NO: 1213, SEQ ID NO: 1370, and SEQ ID NO: 1527, respectively;

cxv. SEQ ID NO: 743, SEQ ID NO: 900, SEQ ID NO: 1057, SEQ ID NO: 1214, SEQ ID NO: 1371, and SEQ ID NO: 1528, respectively;

cxvi. SEQ ID NO: 744, SEQ ID NO: 901, SEQ ID NO: 1058, SEQ ID NO: 1215, SEQ ID NO: 1372, and SEQ ID NO: 1529, respectively;

cxvii. SEQ ID NO: 745, SEQ ID NO: 902, SEQ ID NO: 1059, SEQ ID NO: 1216, SEQ ID NO: 1373, and SEQ ID NO: 1530, respectively;

cxviii. SEQ ID NO: 746, SEQ ID NO: 903, SEQ ID NO: 1060, SEQ ID NO: 1217, SEQ ID NO: 1374, and SEQ ID NO: 1531, respectively;

cxix. SEQ ID NO: 747, SEQ ID NO: 904, SEQ ID NO: 1061, SEQ ID NO: 1218, SEQ ID NO: 1375, and SEQ ID NO: 1532, respectively;

cxx. SEQ ID NO: 748, SEQ ID NO: 905, SEQ ID NO: 1062, SEQ ID NO: 1219, SEQ ID NO: 1376, and SEQ ID NO: 1533, respectively;

cxxi. SEQ ID NO: 749, SEQ ID NO: 906, SEQ ID NO: 1063, SEQ ID NO: 1220, SEQ ID NO: 1377, and SEQ ID NO: 1534, respectively;

cxxii. SEQ ID NO: 750, SEQ ID NO: 907, SEQ ID NO: 1064, SEQ ID NO: 1221, SEQ ID NO: 1378, and SEQ ID NO: 1535, respectively;

cxxiii. SEQ ID NO: 751, SEQ ID NO: 908, SEQ ID NO: 1065, SEQ ID NO: 1222, SEQ ID NO: 1379, and SEQ ID NO: 1536, respectively;

cxxiv. SEQ ID NO: 752, SEQ ID NO: 909, SEQ ID NO: 1066, SEQ ID NO: 1223, SEQ ID NO: 1380, and SEQ ID NO: 1537, respectively;

cxxv. SEQ ID NO: 753, SEQ ID NO: 910, SEQ ID NO: 1067, SEQ ID NO: 1224, SEQ ID NO: 1381, and SEQ ID NO: 1538, respectively;

cxxvi. SEQ ID NO: 754, SEQ ID NO: 911, SEQ ID NO: 1068, SEQ ID NO: 1225, SEQ ID NO: 1382, and SEQ ID NO: 1539, respectively;

cxxvii. SEQ ID NO: 755, SEQ ID NO: 912, SEQ ID NO: 1069, SEQ ID NO: 1226, SEQ ID NO: 1383, and SEQ ID NO: 1540, respectively;

cxxviii. SEQ ID NO: 756, SEQ ID NO: 913, SEQ ID NO: 1070, SEQ ID NO: 1227, SEQ ID NO: 1384, and SEQ ID NO: 1541, respectively;

cxxix. SEQ ID NO: 757, SEQ ID NO: 914, SEQ ID NO: 1071, SEQ ID NO: 1228, SEQ ID NO: 1385, and SEQ ID NO: 1542, respectively;

cxxx. SEQ ID NO: 758, SEQ ID NO: 915, SEQ ID NO: 1072, SEQ ID NO: 1229, SEQ ID NO: 1386, and SEQ ID NO: 1543, respectively;

cxxxi. SEQ ID NO: 759, SEQ ID NO: 916, SEQ ID NO: 1073, SEQ ID NO: 1230, SEQ ID NO: 1387, and SEQ ID NO: 1544, respectively;

cxxxii. SEQ ID NO: 760, SEQ ID NO: 917, SEQ ID NO: 1074, SEQ ID NO: 1231, SEQ ID NO: 1388, and SEQ ID NO: 1545, respectively;

cxxxiii. SEQ ID NO: 761, SEQ ID NO: 918, SEQ ID NO: 1075, SEQ ID NO: 1232, SEQ ID NO: 1389, and SEQ ID NO: 1546, respectively;

cxxxiv. SEQ ID NO: 762, SEQ ID NO: 919, SEQ ID NO: 1076, SEQ ID NO: 1233, SEQ ID NO: 1390, and SEQ ID NO: 1547, respectively;

cxxxv. SEQ ID NO: 763, SEQ ID NO: 920, SEQ ID NO: 1077, SEQ ID NO: 1234, SEQ ID NO: 1391, and SEQ ID NO: 1548, respectively;

cxxxvi. SEQ ID NO: 764, SEQ ID NO: 921, SEQ ID NO: 1078, SEQ ID NO: 1235, SEQ ID NO: 1392, and SEQ ID NO: 1549, respectively;

cxxxvii. SEQ ID NO: 765, SEQ ID NO: 922, SEQ ID NO: 1079, SEQ ID NO: 1236, SEQ ID NO: 1393, and SEQ ID NO: 1550, respectively;

cxxxviii. SEQ ID NO: 766, SEQ ID NO: 923, SEQ ID NO: 1080, SEQ ID NO: 1237, SEQ ID NO: 1394, and SEQ ID NO: 1551, respectively;

cxxxix. SEQ ID NO: 767, SEQ ID NO: 924, SEQ ID NO: 1081, SEQ ID NO: 1238, SEQ ID NO: 1395, and SEQ ID NO: 1552, respectively;

cxl. SEQ ID NO: 768, SEQ ID NO: 925, SEQ ID NO: 1082, SEQ ID NO: 1239, SEQ ID NO: 1396, and SEQ ID NO: 1553, respectively;

cxli. SEQ ID NO: 769, SEQ ID NO: 926, SEQ ID NO: 1083, SEQ ID NO: 1240, SEQ ID NO: 1397, and SEQ ID NO: 1554, respectively;

cxlii. SEQ ID NO: 770, SEQ ID NO: 927, SEQ ID NO: 1084, SEQ ID NO: 1241, SEQ ID NO: 1398, and SEQ ID NO: 1555, respectively;

cxliii. SEQ ID NO: 771, SEQ ID NO: 928, SEQ ID NO: 1085, SEQ ID NO: 1242, SEQ ID NO: 1399, and SEQ ID NO: 1556, respectively;

cxliv. SEQ ID NO: 772, SEQ ID NO: 929, SEQ ID NO: 1086, SEQ ID NO: 1243, SEQ ID NO: 1400, and SEQ ID NO: 1557, respectively;

cxlv. SEQ ID NO: 773, SEQ ID NO: 930, SEQ ID NO: 1087, SEQ ID NO: 1244, SEQ ID NO: 1401, and SEQ ID NO: 1558, respectively;

cxlvi. SEQ ID NO: 774, SEQ ID NO: 931, SEQ ID NO: 1088, SEQ ID NO: 1245, SEQ ID NO: 1402, and SEQ ID NO: 1559, respectively;

cxlvii. SEQ ID NO: 775, SEQ ID NO: 932, SEQ ID NO: 1089, SEQ ID NO: 1246, SEQ ID NO: 1403, and SEQ ID NO: 1560, respectively;

cxlviii. SEQ ID NO: 776, SEQ ID NO: 933, SEQ ID NO: 1090, SEQ ID NO: 1247, SEQ ID NO: 1404, and SEQ ID NO: 1561, respectively;

cxlix. SEQ ID NO: 777, SEQ ID NO: 934, SEQ ID NO: 1091, SEQ ID NO: 1248, SEQ ID NO: 1405, and SEQ ID NO: 1562, respectively;

cl. SEQ ID NO: 778, SEQ ID NO: 935, SEQ ID NO: 1092, SEQ ID NO: 1249, SEQ ID NO: 1406, and SEQ ID NO: 1563, respectively;

cli. SEQ ID NO: 779, SEQ ID NO: 936, SEQ ID NO: 1093, SEQ ID NO: 1250, SEQ ID NO: 1407, and SEQ ID NO: 1564, respectively;

clii. SEQ ID NO: 780, SEQ ID NO: 937, SEQ ID NO: 1094, SEQ ID NO: 1251, SEQ ID NO: 1408, and SEQ ID NO: 1565, respectively;

cliii. SEQ ID NO: 781, SEQ ID NO: 938, SEQ ID NO: 1095, SEQ ID NO: 1252, SEQ ID NO: 1409, and SEQ ID NO: 1566, respectively;

cliv. SEQ ID NO: 782, SEQ ID NO: 939, SEQ ID NO: 1096, SEQ ID NO: 1253, SEQ ID NO: 1410, and SEQ ID NO: 1567, respectively;

clv. SEQ ID NO: 783, SEQ ID NO: 940, SEQ ID NO: 1097, SEQ ID NO: 1254, SEQ ID NO: 1411, and SEQ ID NO: 1568, respectively;

clvi. SEQ ID NO: 784, SEQ ID NO: 941, SEQ ID NO: 1098, SEQ ID NO: 1255, SEQ ID NO: 1412, and SEQ ID NO: 1569, respectively; and

clvii. SEQ ID NO: 785, SEQ ID NO: 942, SEQ ID NO: 1099, SEQ ID NO: 1256, SEQ ID NO: 1413, and SEQ ID NO: 1570, respectively.

[0195] In one embodiment, the antagonist anti-GIPR antibody of the conjugate molecule as described herein comprises light chain CDRL1, CDRL2, and CDRL3 comprising the amino acid sequences of SEQ ID NOs: 702, 859, 1016, respectively and heavy chain HCDR1, HCDR2, and HCDR3 comprising the amino acid sequences of SEQ ID NOs: 1173, 1330, and 1487, respectively. An exemplary antibody disclosed herein comprising these light and heavy chain CDRs is referred to as the 2G10_LC1.006 anti-GIPR antibody.

[0196] In one embodiment, the anti-GIPR antibody of the conjugate molecule comprises a light chain variable region comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-157 and a heavy chain variable region comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 158-314.

[0197] In one embodiment, the antagonist anti-GIPR antibody of the conjugate molecule comprises a light chain variable region comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-157 and a heavy chain variable region comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 158-314, wherein the antibody comprises at least one cysteine conjugation site at a position selected from the group consisting of 88 (e.g., D88) of the light chain, 384 (e.g., E384) of the heavy chain, and 487 (e.g., T487) of the heavy chain, all according to AHo numbering.

[0198] In one embodiment, the anti-GIPR antibody of the conjugate molecule comprises a light chain variable region and a heavy chain variable region as listed in one of the rows for one of the antibodies listed in Table 3. In one embodiment, the anti-GIPR antibody comprises a light chain variable region and a heavy chain variable region as listed in one of the rows for one of the antibodies listed in Table 3, except that one or both of the light chain variable region and

the heavy chain variable region differs from the sequence specified in Table 4 (VL) or Table 5 (VH) at 1, 2, 3, 4, or 5 amino acid residues (combined), wherein each such sequence difference is independently either a single amino acid deletion, insertion, or substitution, with the deletions, insertions and/or substitutions resulting in no more than 1, 2, 3, 4, or 5 amino acid changes (combined) relative to the light chain variable region and heavy chain variable region sequences specified in Table 4 (VL) or Table 5 (VH).

[0199] In one embodiment, the anti-GIPR antibody of the conjugate molecule comprises light chain variable regions and heavy chain variable regions as listed in one of the rows for one of the antibodies listed in Tables 3, except that one or both of the variable regions differs from the amino acid sequence specified in Table 5 (VH) or Table 4 (VL) in that the heavy chain variable region and/or light chain variable region comprises or consists of a sequence of amino acids that has at least 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequences of the heavy chain variable region or light chain variable domain region as specified in Table 5 or Table 4, respectively.

[0200] In one embodiment the antagonist anti-GIPR of the molecule described herein comprises a combination of light chain variable region and a heavy chain variable region selected from the group consisting of: a light chain variable region comprising SEQ ID NO: 1 and a heavy chain variable region comprising SEQ ID NO: 158; a light chain variable region comprising SEQ ID NO: 2 and a heavy chain variable region comprising SEQ ID NO: 159; a light chain variable region comprising SEQ ID NO: 3 and a heavy chain variable region comprising SEQ ID NO: 160; a light chain variable region comprising SEQ ID NO: 4 and a heavy chain variable region comprising SEQ ID NO: 161; a light chain variable region comprising SEQ ID NO: 5 and a heavy chain variable region comprising SEQ ID NO: 162; a light chain variable region comprising SEQ ID NO: 6 and a heavy chain variable region comprising SEQ ID NO: 163; a light chain variable region comprising SEQ ID NO: 7 and a heavy chain variable region comprising SEQ ID NO: 164; a light chain variable region comprising SEQ ID NO: 8 and a heavy chain variable region comprising SEQ ID NO: 165; a light chain variable region comprising SEQ ID NO: 9 and a heavy chain variable region comprising SEQ ID NO: 166; a light chain variable region comprising SEQ ID NO: 10 and a heavy chain variable region comprising SEQ ID NO: 167; a light chain variable region comprising SEQ ID NO: 11 and a heavy chain variable region comprising SEQ ID NO: 168; a

light chain variable region comprising SEQ ID NO: 12 and a heavy chain variable region comprising SEQ ID NO: 169; a light chain variable region comprising SEQ ID NO: 13 and a heavy chain variable region comprising SEQ ID NO: 170; a light chain variable region comprising SEQ ID NO: 14 and a heavy chain variable region comprising SEQ ID NO: 171; a light chain variable region comprising SEQ ID NO: 15 and a heavy chain variable region comprising SEQ ID NO: 172; a light chain variable region comprising SEQ ID NO: 16 and a heavy chain variable region comprising SEQ ID NO: 173; a light chain variable region comprising SEQ ID NO: 17 and a heavy chain variable region comprising SEQ ID NO: 174; a light chain variable region comprising SEQ ID NO: 18 and a heavy chain variable region comprising SEQ ID NO: 175; a light chain variable region comprising SEQ ID NO: 19 and a heavy chain variable region comprising SEQ ID NO: 176; a light chain variable region comprising SEQ ID NO: 20 and a heavy chain variable region comprising SEQ ID NO: 177; a light chain variable region comprising SEQ ID NO: 21 and a heavy chain variable region comprising SEQ ID NO: 178; a light chain variable region comprising SEQ ID NO: 22 and a heavy chain variable region comprising SEQ ID NO: 179; a light chain variable region comprising SEQ ID NO: 23 and a heavy chain variable region comprising SEQ ID NO: 180; a light chain variable region comprising SEQ ID NO: 24 and a heavy chain variable region comprising SEQ ID NO: 181; a light chain variable region comprising SEQ ID NO: 25 and a heavy chain variable region comprising SEQ ID NO: 182; a light chain variable region comprising SEQ ID NO: 26 and a heavy chain variable region comprising SEQ ID NO: 183; a light chain variable region comprising SEQ ID NO: 27 and a heavy chain variable region comprising SEQ ID NO: 184; a light chain variable region comprising SEQ ID NO: 28 and a heavy chain variable region comprising SEQ ID NO: 185; a light chain variable region comprising SEQ ID NO: 29 and a heavy chain variable region comprising SEQ ID NO: 186; a light chain variable region comprising SEQ ID NO: 30 and a heavy chain variable region comprising SEQ ID NO: 187; a light chain variable region comprising SEQ ID NO: 31 and a heavy chain variable region comprising SEQ ID NO: 188; a light chain variable region comprising SEQ ID NO: 32 and a heavy chain variable region comprising SEQ ID NO: 189; a light chain variable region comprising SEQ ID NO: 33 and a heavy chain variable region comprising SEQ ID NO: 190; a light chain variable region comprising SEQ ID NO: 34 and a heavy chain variable region comprising SEQ ID NO: 191; a light chain variable region

comprising SEQ ID NO: 35 and a heavy chain variable region comprising SEQ ID NO: 192; a light chain variable region comprising SEQ ID NO: 36 and a heavy chain variable region comprising SEQ ID NO: 193; a light chain variable region comprising SEQ ID NO: 37 and a heavy chain variable region comprising SEQ ID NO: 194; a light chain variable region comprising SEQ ID NO: 38 and a heavy chain variable region comprising SEQ ID NO: 195; a light chain variable region comprising SEQ ID NO: 39 and a heavy chain variable region comprising SEQ ID NO: 196; a light chain variable region comprising SEQ ID NO: 40 and a heavy chain variable region comprising SEQ ID NO: 197; a light chain variable region comprising SEQ ID NO: 41 and a heavy chain variable region comprising SEQ ID NO: 198; a light chain variable region comprising SEQ ID NO: 42 and a heavy chain variable region comprising SEQ ID NO: 199; a light chain variable region comprising SEQ ID NO: 43 and a heavy chain variable region comprising SEQ ID NO: 200; a light chain variable region comprising SEQ ID NO: 44 and a heavy chain variable region comprising SEQ ID NO: 201; a light chain variable region comprising SEQ ID NO: 45 and a heavy chain variable region comprising SEQ ID NO: 202; a light chain variable region comprising SEQ ID NO: 46 and a heavy chain variable region comprising SEQ ID NO: 203; a light chain variable region comprising SEQ ID NO: 47 and a heavy chain variable region comprising SEQ ID NO: 204; a light chain variable region comprising SEQ ID NO: 48 and a heavy chain variable region comprising SEQ ID NO: 205; a light chain variable region comprising SEQ ID NO: 49 and a heavy chain variable region comprising SEQ ID NO: 206; a light chain variable region comprising SEQ ID NO: 50 and a heavy chain variable region comprising SEQ ID NO: 207; a light chain variable region comprising SEQ ID NO: 51 and a heavy chain variable region comprising SEQ ID NO: 208; a light chain variable region comprising SEQ ID NO: 52 and a heavy chain variable region comprising SEQ ID NO: 209; a light chain variable region comprising SEQ ID NO: 53 and a heavy chain variable region comprising SEQ ID NO: 210; a light chain variable region comprising SEQ ID NO: 54 and a heavy chain variable region comprising SEQ ID NO: 211; a light chain variable region comprising SEQ ID NO: 55 and a heavy chain variable region comprising SEQ ID NO: 212; a light chain variable region comprising SEQ ID NO: 56 and a heavy chain variable region comprising SEQ ID NO: 213; a light chain variable region comprising SEQ ID NO: 57 and a heavy chain variable region comprising SEQ ID NO: 214; a light chain variable region comprising SEQ ID NO: 58 and a

heavy chain variable region comprising SEQ ID NO: 215; a light chain variable region comprising SEQ ID NO: 59 and a heavy chain variable region comprising SEQ ID NO: 216; a light chain variable region comprising SEQ ID NO: 60 and a heavy chain variable region comprising SEQ ID NO: 217; a light chain variable region comprising SEQ ID NO: 61 and a heavy chain variable region comprising SEQ ID NO: 218; a light chain variable region comprising SEQ ID NO: 62 and a heavy chain variable region comprising SEQ ID NO: 219; a light chain variable region comprising SEQ ID NO: 63 and a heavy chain variable region comprising SEQ ID NO: 220; a light chain variable region comprising SEQ ID NO: 64 and a heavy chain variable region comprising SEQ ID NO: 221; a light chain variable region comprising SEQ ID NO: 65 and a heavy chain variable region comprising SEQ ID NO: 222; a light chain variable region comprising SEQ ID NO: 66 and a heavy chain variable region comprising SEQ ID NO: 223; a light chain variable region comprising SEQ ID NO: 67 and a heavy chain variable region comprising SEQ ID NO: 224; a light chain variable region comprising SEQ ID NO: 68 and a heavy chain variable region comprising SEQ ID NO: 225; a light chain variable region comprising SEQ ID NO: 69 and a heavy chain variable region comprising SEQ ID NO: 226; a light chain variable region comprising SEQ ID NO: 70 and a heavy chain variable region comprising SEQ ID NO: 227; a light chain variable region comprising SEQ ID NO: 71 and a heavy chain variable region comprising SEQ ID NO: 228; a light chain variable region comprising SEQ ID NO: 72 and a heavy chain variable region comprising SEQ ID NO: 229; a light chain variable region comprising SEQ ID NO: 73 and a heavy chain variable region comprising SEQ ID NO: 230; a light chain variable region comprising SEQ ID NO: 74 and a heavy chain variable region comprising SEQ ID NO: 231; a light chain variable region comprising SEQ ID NO: 75 and a heavy chain variable region comprising SEQ ID NO: 232; a light chain variable region comprising SEQ ID NO: 76 and a heavy chain variable region comprising SEQ ID NO: 233; a light chain variable region comprising SEQ ID NO: 77 and a heavy chain variable region comprising SEQ ID NO: 234; a light chain variable region comprising SEQ ID NO: 78 and a heavy chain variable region comprising SEQ ID NO: 235; a light chain variable region comprising SEQ ID NO: 79 and a heavy chain variable region comprising SEQ ID NO: 236; a light chain variable region comprising SEQ ID NO: 80 and a heavy chain variable region comprising SEQ ID NO: 237; a light chain variable region comprising SEQ ID NO: 81 and a heavy chain variable region

comprising SEQ ID NO: 238; a light chain variable region comprising SEQ ID NO: 82 and a heavy chain variable region comprising SEQ ID NO: 239; a light chain variable region comprising SEQ ID NO: 83 and a heavy chain variable region comprising SEQ ID NO: 240; a light chain variable region comprising SEQ ID NO: 84 and a heavy chain variable region comprising SEQ ID NO: 241; a light chain variable region comprising SEQ ID NO: 85 and a heavy chain variable region comprising SEQ ID NO: 242; a light chain variable region comprising SEQ ID NO: 86 and a heavy chain variable region comprising SEQ ID NO: 243; a light chain variable region comprising SEQ ID NO: 87 and a heavy chain variable region comprising SEQ ID NO: 244; a light chain variable region comprising SEQ ID NO: 88 and a heavy chain variable region comprising SEQ ID NO: 245; a light chain variable region comprising SEQ ID NO: 89 and a heavy chain variable region comprising SEQ ID NO: 246; a light chain variable region comprising SEQ ID NO: 90 and a heavy chain variable region comprising SEQ ID NO: 247; a light chain variable region comprising SEQ ID NO: 91 and a heavy chain variable region comprising SEQ ID NO: 248; a light chain variable region comprising SEQ ID NO: 92 and a heavy chain variable region comprising SEQ ID NO: 249; a light chain variable region comprising SEQ ID NO: 93 and a heavy chain variable region comprising SEQ ID NO: 250; a light chain variable region comprising SEQ ID NO: 94 and a heavy chain variable region comprising SEQ ID NO: 251; a light chain variable region comprising SEQ ID NO: 95 and a heavy chain variable region comprising SEQ ID NO: 252; a light chain variable region comprising SEQ ID NO: 96 and a heavy chain variable region comprising SEQ ID NO: 253; a light chain variable region comprising SEQ ID NO: 97 and a heavy chain variable region comprising SEQ ID NO: 254; a light chain variable region comprising SEQ ID NO: 98 and a heavy chain variable region comprising SEQ ID NO: 255; a light chain variable region comprising SEQ ID NO: 99 and a heavy chain variable region comprising SEQ ID NO: 256; a light chain variable region comprising SEQ ID NO: 100 and a heavy chain variable region comprising SEQ ID NO: 257; a light chain variable region comprising SEQ ID NO: 101 and a heavy chain variable region comprising SEQ ID NO: 258; a light chain variable region comprising SEQ ID NO: 102 and a heavy chain variable region comprising SEQ ID NO: 259; a light chain variable region comprising SEQ ID NO: 103 and a heavy chain variable region comprising SEQ ID NO: 260; a light chain variable region comprising SEQ ID NO: 104 and a heavy chain variable region comprising SEQ ID NO: 261; a

light chain variable region comprising SEQ ID NO: 105 and a heavy chain variable region comprising SEQ ID NO: 262; a light chain variable region comprising SEQ ID NO: 106 and a heavy chain variable region comprising SEQ ID NO: 263; a light chain variable region comprising SEQ ID NO: 107 and a heavy chain variable region comprising SEQ ID NO: 264; a light chain variable region comprising SEQ ID NO: 108 and a heavy chain variable region comprising SEQ ID NO: 265; a light chain variable region comprising SEQ ID NO: 109 and a heavy chain variable region comprising SEQ ID NO: 266; a light chain variable region comprising SEQ ID NO: 110 and a heavy chain variable region comprising SEQ ID NO: 267; a light chain variable region comprising SEQ ID NO: 111 and a heavy chain variable region comprising SEQ ID NO: 268; a light chain variable region comprising SEQ ID NO: 112 and a heavy chain variable region comprising SEQ ID NO: 269; a light chain variable region comprising SEQ ID NO: 113 and a heavy chain variable region comprising SEQ ID NO: 270; a light chain variable region comprising SEQ ID NO: 114 and a heavy chain variable region comprising SEQ ID NO: 271; a light chain variable region comprising SEQ ID NO: 115 and a heavy chain variable region comprising SEQ ID NO: 272; a light chain variable region comprising SEQ ID NO: 116 and a heavy chain variable region comprising SEQ ID NO: 273; a light chain variable region comprising SEQ ID NO: 117 and a heavy chain variable region comprising SEQ ID NO: 274; a light chain variable region comprising SEQ ID NO: 118 and a heavy chain variable region comprising SEQ ID NO: 275; a light chain variable region comprising SEQ ID NO: 119 and a heavy chain variable region comprising SEQ ID NO: 276; a light chain variable region comprising SEQ ID NO: 120 and a heavy chain variable region comprising SEQ ID NO: 277; a light chain variable region comprising SEQ ID NO: 121 and a heavy chain variable region comprising SEQ ID NO: 278; a light chain variable region comprising SEQ ID NO: 122 and a heavy chain variable region comprising SEQ ID NO: 279; a light chain variable region comprising SEQ ID NO: 123 and a heavy chain variable region comprising SEQ ID NO: 280; a light chain variable region comprising SEQ ID NO: 124 and a heavy chain variable region comprising SEQ ID NO: 281; a light chain variable region comprising SEQ ID NO: 125 and a heavy chain variable region comprising SEQ ID NO: 282; a light chain variable region comprising SEQ ID NO: 126 and a heavy chain variable region comprising SEQ ID NO: 283; a light chain variable region comprising SEQ ID NO: 127 and a heavy chain variable region comprising SEQ ID NO: 284; a light chain variable region

comprising SEQ ID NO: 128 and a heavy chain variable region comprising SEQ ID NO: 285; a light chain variable region comprising SEQ ID NO: 129 and a heavy chain variable region comprising SEQ ID NO: 286; a light chain variable region comprising SEQ ID NO: 130 and a heavy chain variable region comprising SEQ ID NO: 287; a light chain variable region comprising SEQ ID NO: 131 and a heavy chain variable region comprising SEQ ID NO: 288; a light chain variable region comprising SEQ ID NO: 132 and a heavy chain variable region comprising SEQ ID NO: 289; a light chain variable region comprising SEQ ID NO: 133 and a heavy chain variable region comprising SEQ ID NO: 290; a light chain variable region comprising SEQ ID NO: 134 and a heavy chain variable region comprising SEQ ID NO: 291; a light chain variable region comprising SEQ ID NO: 135 and a heavy chain variable region comprising SEQ ID NO: 292; a light chain variable region comprising SEQ ID NO: 136 and a heavy chain variable region comprising SEQ ID NO: 293; a light chain variable region comprising SEQ ID NO: 137 and a heavy chain variable region comprising SEQ ID NO: 294; a light chain variable region comprising SEQ ID NO: 138 and a heavy chain variable region comprising SEQ ID NO: 295; a light chain variable region comprising SEQ ID NO: 139 and a heavy chain variable region comprising SEQ ID NO: 296; a light chain variable region comprising SEQ ID NO: 140 and a heavy chain variable region comprising SEQ ID NO: 297; a light chain variable region comprising SEQ ID NO: 141 and a heavy chain variable region comprising SEQ ID NO: 298; a light chain variable region comprising SEQ ID NO: 142 and a heavy chain variable region comprising SEQ ID NO: 299; a light chain variable region comprising SEQ ID NO: 143 and a heavy chain variable region comprising SEQ ID NO: 300; a light chain variable region comprising SEQ ID NO: 144 and a heavy chain variable region comprising SEQ ID NO: 301; a light chain variable region comprising SEQ ID NO: 145 and a heavy chain variable region comprising SEQ ID NO: 302; a light chain variable region comprising SEQ ID NO: 146 and a heavy chain variable region comprising SEQ ID NO: 303; a light chain variable region comprising SEQ ID NO: 147 and a heavy chain variable region comprising SEQ ID NO: 304; a light chain variable region comprising SEQ ID NO: 148 and a heavy chain variable region comprising SEQ ID NO: 305; a light chain variable region comprising SEQ ID NO: 149 and a heavy chain variable region comprising SEQ ID NO: 306; a light chain variable region comprising SEQ ID NO: 150 and a heavy chain variable region comprising SEQ ID NO: 307; a light chain variable region comprising SEQ ID NO: 151 and a

heavy chain variable region comprising SEQ ID NO: 308; a light chain variable region comprising SEQ ID NO: 152 and a heavy chain variable region comprising SEQ ID NO: 309; a light chain variable region comprising SEQ ID NO: 153 and a heavy chain variable region comprising SEQ ID NO: 310; a light chain variable region comprising SEQ ID NO: 154 and a heavy chain variable region comprising SEQ ID NO: 311; a light chain variable region comprising SEQ ID NO: 155 and a heavy chain variable region comprising SEQ ID NO: 312; a light chain variable region comprising SEQ ID NO: 156 and a heavy chain variable region comprising SEQ ID NO: 313; and a light chain variable region comprising SEQ ID NO: 157 and a heavy chain variable region comprising SEQ ID NO: 314. The anti-GIPR antibody comprising anyone of the above combinations of light chain variable and heavy chain variable regions may further comprise a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s). In one embodiment, the conjugation site is at position 88 of the light chain according to AHo numbering.

[0201] In one embodiment, the antagonist anti-GIPR antibody of the conjugate molecule as described herein comprises the light chain variable region amino acid sequence of SEQ ID NO: 74 and the heavy chain variable region amino acid sequence of SEQ ID NO: 231. An exemplary antibody disclosed herein comprising these light and heavy chain variable regions is referred to as the 2G10_LC1.006 anti-GIPR antibody.

[0202] In one embodiment the antagonist anti-GIPR of the conjugate molecule described herein comprises a light chain comprising a sequence selected from the group consisting of SEQ ID NOs: 315-471 and a heavy chain comprising a sequence selected from the group consisting of SEQ ID NOs: 472-628, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of 88 in the antibody light chain according to AHo numbering, position 384 of the antibody heavy chain according to AHo numbering, and position 487 of the antibody heavy chain according to AHo numbering.

[0203] Antagonist anti-GIPR antibodies suitable for incorporation in the conjugate molecules described herein, i.e., molecules comprising a GLP-1 receptor agonist polypeptide conjugated to an anti-GIPR antibody, may comprise a full length light chain and a full length heavy chain as listed in one of the rows for one of the antibodies listed in Table 3. Some antibodies that are provided comprise a full length light chain and a full length heavy chain as

listed in one of the rows for one of the antibodies listed in Table 3, except that one or both of the chains differs from the sequence specified in the table at only 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acid residues, wherein each such sequence difference is independently either a single amino acid deletion, insertion or substitution, with the deletions, insertions and/or substitutions resulting in no more than 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acid changes relative to the full length sequences specified in Tables 8 and 9. In one embodiment the anti-GIPR antibody comprises a full length light chain from Table 8 and/or a full length heavy chain from Table 9 with the N-terminal methionine, if present, deleted. In one embodiment the anti-GIPR antibody comprises a full length light chain from Table 8 and/or a full length heavy chain from Table 9 with the C-terminal lysine, if present, deleted. Other anti-GIPR antibodies also comprise a full length light chain and a full length heavy chain as listed in one of the rows for one of the antibodies listed in Table 3, except that one or both of the chains differs from the sequence specified in the table in that the light chain and/or heavy chain comprises or consists of a sequence of amino acids that has at least 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequences of the light chain or heavy chain sequences as specified in Table 3.

[0204] In one embodiment the antagonist anti-GIPR antibody of the conjugate molecule described herein comprises a combination of a light chain and a heavy chain selected from the group consisting of: a light chain comprising SEQ ID NO: 315 and a heavy chain comprising SEQ ID NO: 472; a light chain comprising SEQ ID NO: 316 and a heavy chain comprising SEQ ID NO: 473; a light chain comprising SEQ ID NO: 317 and a heavy chain comprising SEQ ID NO: 474; a light chain comprising SEQ ID NO: 318 and a heavy chain comprising SEQ ID NO: 475; a light chain comprising SEQ ID NO: 319 and a heavy chain comprising SEQ ID NO: 476; a light chain comprising SEQ ID NO: 320 and a heavy chain comprising SEQ ID NO: 477; a light chain comprising SEQ ID NO: 321 and a heavy chain comprising SEQ ID NO: 478; a light chain comprising SEQ ID NO: 322 and a heavy chain comprising SEQ ID NO: 479; a light chain comprising SEQ ID NO: 323 and a heavy chain comprising SEQ ID NO: 480; a light chain comprising SEQ ID NO: 324 and a heavy chain comprising SEQ ID NO: 481; a light chain comprising SEQ ID NO: 325 and a heavy chain comprising SEQ ID NO: 482; a light chain comprising SEQ ID NO: 326 and a heavy chain comprising SEQ ID NO: 483; a light chain comprising SEQ ID NO: 327 and a heavy chain comprising SEQ ID NO: 484; a light chain comprising SEQ ID NO: 328 and a heavy chain comprising SEQ ID NO: 485; a light chain

comprising SEQ ID NO: 329 and a heavy chain comprising SEQ ID NO: 486; a light chain comprising SEQ ID NO: 330 and a heavy chain comprising SEQ ID NO: 487; a light chain comprising SEQ ID NO: 331 and a heavy chain comprising SEQ ID NO: 488; a light chain comprising SEQ ID NO: 332 and a heavy chain comprising SEQ ID NO: 489; a light chain comprising SEQ ID NO: 333 and a heavy chain comprising SEQ ID NO: 490; a light chain comprising SEQ ID NO: 334 and a heavy chain comprising SEQ ID NO: 491; a light chain comprising SEQ ID NO: 335 and a heavy chain comprising SEQ ID NO: 492; a light chain comprising SEQ ID NO: 336 and a heavy chain comprising SEQ ID NO: 493; a light chain comprising SEQ ID NO: 337 and a heavy chain comprising SEQ ID NO: 494; a light chain comprising SEQ ID NO: 338 and a heavy chain comprising SEQ ID NO: 495; a light chain comprising SEQ ID NO: 339 and a heavy chain comprising SEQ ID NO: 496; a light chain comprising SEQ ID NO: 340 and a heavy chain comprising SEQ ID NO: 497; a light chain comprising SEQ ID NO: 341 and a heavy chain comprising SEQ ID NO: 498; a light chain comprising SEQ ID NO: 342 and a heavy chain comprising SEQ ID NO: 499; a light chain comprising SEQ ID NO: 343 and a heavy chain comprising SEQ ID NO: 500; a light chain comprising SEQ ID NO: 344 and a heavy chain comprising SEQ ID NO: 501; a light chain comprising SEQ ID NO: 345 and a heavy chain comprising SEQ ID NO: 502; a light chain comprising SEQ ID NO: 346 and a heavy chain comprising SEQ ID NO: 503; a light chain comprising SEQ ID NO: 347 and a heavy chain comprising SEQ ID NO: 504; a light chain comprising SEQ ID NO: 348 and a heavy chain comprising SEQ ID NO: 505; a light chain comprising SEQ ID NO: 349 and a heavy chain comprising SEQ ID NO: 506; a light chain comprising SEQ ID NO: 350 and a heavy chain comprising SEQ ID NO: 507; a light chain comprising SEQ ID NO: 351 and a heavy chain comprising SEQ ID NO: 508; a light chain comprising SEQ ID NO: 352 and a heavy chain comprising SEQ ID NO: 509; a light chain comprising SEQ ID NO: 353 and a heavy chain comprising SEQ ID NO: 510; a light chain comprising SEQ ID NO: 354 and a heavy chain comprising SEQ ID NO: 511; a light chain comprising SEQ ID NO: 355 and a heavy chain comprising SEQ ID NO: 512; a light chain comprising SEQ ID NO: 356 and a heavy chain comprising SEQ ID NO: 513; a light chain comprising SEQ ID NO: 357 and a heavy chain comprising SEQ ID NO: 514; a light chain comprising SEQ ID NO: 358 and a heavy chain comprising SEQ ID NO: 515; a light chain comprising SEQ ID NO: 359 and a heavy chain comprising SEQ ID NO: 516; a light chain

comprising SEQ ID NO: 360 and a heavy chain comprising SEQ ID NO: 517; a light chain comprising SEQ ID NO: 361 and a heavy chain comprising SEQ ID NO: 518; a light chain comprising SEQ ID NO: 362 and a heavy chain comprising SEQ ID NO: 519; a light chain comprising SEQ ID NO: 363 and a heavy chain comprising SEQ ID NO: 520; a light chain comprising SEQ ID NO: 364 and a heavy chain comprising SEQ ID NO: 521; a light chain comprising SEQ ID NO: 365 and a heavy chain comprising SEQ ID NO: 522; a light chain comprising SEQ ID NO: 366 and a heavy chain comprising SEQ ID NO: 523; a light chain comprising SEQ ID NO: 367 and a heavy chain comprising SEQ ID NO: 524; a light chain comprising SEQ ID NO: 368 and a heavy chain comprising SEQ ID NO: 525; a light chain comprising SEQ ID NO: 369 and a heavy chain comprising SEQ ID NO: 526; a light chain comprising SEQ ID NO: 370 and a heavy chain comprising SEQ ID NO: 527; a light chain comprising SEQ ID NO: 371 and a heavy chain comprising SEQ ID NO: 528; a light chain comprising SEQ ID NO: 372 and a heavy chain comprising SEQ ID NO: 529; a light chain comprising SEQ ID NO: 373 and a heavy chain comprising SEQ ID NO: 530; a light chain comprising SEQ ID NO: 374 and a heavy chain comprising SEQ ID NO: 531; a light chain comprising SEQ ID NO: 375 and a heavy chain comprising SEQ ID NO: 532; a light chain comprising SEQ ID NO: 376 and a heavy chain comprising SEQ ID NO: 533; a light chain comprising SEQ ID NO: 377 and a heavy chain comprising SEQ ID NO: 534; a light chain comprising SEQ ID NO: 378 and a heavy chain comprising SEQ ID NO: 535; a light chain comprising SEQ ID NO: 379 and a heavy chain comprising SEQ ID NO: 536; a light chain comprising SEQ ID NO: 380 and a heavy chain comprising SEQ ID NO: 537; a light chain comprising SEQ ID NO: 381 and a heavy chain comprising SEQ ID NO: 538; a light chain comprising SEQ ID NO: 382 and a heavy chain comprising SEQ ID NO: 539; a light chain comprising SEQ ID NO: 383 and a heavy chain comprising SEQ ID NO: 540; a light chain comprising SEQ ID NO: 384 and a heavy chain comprising SEQ ID NO: 541; a light chain comprising SEQ ID NO: 385 and a heavy chain comprising SEQ ID NO: 542; a light chain comprising SEQ ID NO: 386 and a heavy chain comprising SEQ ID NO: 543; a light chain comprising SEQ ID NO: 387 and a heavy chain comprising SEQ ID NO: 544; a light chain comprising SEQ ID NO: 388 and a heavy chain comprising SEQ ID NO: 545; a light chain comprising SEQ ID NO: 389 and a heavy chain comprising SEQ ID NO: 546; a light chain comprising SEQ ID NO: 390 and a heavy chain comprising SEQ ID NO: 547; a light chain

comprising SEQ ID NO: 391 and a heavy chain comprising SEQ ID NO: 548; a light chain comprising SEQ ID NO: 392 and a heavy chain comprising SEQ ID NO: 549; a light chain comprising SEQ ID NO: 393 and a heavy chain comprising SEQ ID NO: 550; a light chain comprising SEQ ID NO: 394 and a heavy chain comprising SEQ ID NO: 551; a light chain comprising SEQ ID NO: 395 and a heavy chain comprising SEQ ID NO: 552; a light chain comprising SEQ ID NO: 396 and a heavy chain comprising SEQ ID NO: 553; a light chain comprising SEQ ID NO: 397 and a heavy chain comprising SEQ ID NO: 554; a light chain comprising SEQ ID NO: 398 and a heavy chain comprising SEQ ID NO: 555; a light chain comprising SEQ ID NO: 399 and a heavy chain comprising SEQ ID NO: 556; a light chain comprising SEQ ID NO: 400 and a heavy chain comprising SEQ ID NO: 557; a light chain comprising SEQ ID NO: 401 and a heavy chain comprising SEQ ID NO: 558; a light chain comprising SEQ ID NO: 402 and a heavy chain comprising SEQ ID NO: 559; a light chain comprising SEQ ID NO: 403 and a heavy chain comprising SEQ ID NO: 560; a light chain comprising SEQ ID NO: 404 and a heavy chain comprising SEQ ID NO: 561; a light chain comprising SEQ ID NO: 405 and a heavy chain comprising SEQ ID NO: 562; a light chain comprising SEQ ID NO: 406 and a heavy chain comprising SEQ ID NO: 563; a light chain comprising SEQ ID NO: 407 and a heavy chain comprising SEQ ID NO: 564; a light chain comprising SEQ ID NO: 408 and a heavy chain comprising SEQ ID NO: 565; a light chain comprising SEQ ID NO: 409 and a heavy chain comprising SEQ ID NO: 566; a light chain comprising SEQ ID NO: 410 and a heavy chain comprising SEQ ID NO: 567; a light chain comprising SEQ ID NO: 411 and a heavy chain comprising SEQ ID NO: 568; a light chain comprising SEQ ID NO: 412 and a heavy chain comprising SEQ ID NO: 569; a light chain comprising SEQ ID NO: 413 and a heavy chain comprising SEQ ID NO: 570; a light chain comprising SEQ ID NO: 414 and a heavy chain comprising SEQ ID NO: 571; a light chain comprising SEQ ID NO: 415 and a heavy chain comprising SEQ ID NO: 572; a light chain comprising SEQ ID NO: 416 and a heavy chain comprising SEQ ID NO: 573; a light chain comprising SEQ ID NO: 417 and a heavy chain comprising SEQ ID NO: 574; a light chain comprising SEQ ID NO: 418 and a heavy chain comprising SEQ ID NO: 575; a light chain comprising SEQ ID NO: 419 and a heavy chain comprising SEQ ID NO: 576; a light chain comprising SEQ ID NO: 420 and a heavy chain comprising SEQ ID NO: 577; a light chain comprising SEQ ID NO: 421 and a heavy chain comprising SEQ ID NO: 578; a light chain

comprising SEQ ID NO: 422 and a heavy chain comprising SEQ ID NO: 579; a light chain comprising SEQ ID NO: 423 and a heavy chain comprising SEQ ID NO: 580; a light chain comprising SEQ ID NO: 424 and a heavy chain comprising SEQ ID NO: 581; a light chain comprising SEQ ID NO: 425 and a heavy chain comprising SEQ ID NO: 582; a light chain comprising SEQ ID NO: 426 and a heavy chain comprising SEQ ID NO: 583; a light chain comprising SEQ ID NO: 427 and a heavy chain comprising SEQ ID NO: 584; a light chain comprising SEQ ID NO: 428 and a heavy chain comprising SEQ ID NO: 585; a light chain comprising SEQ ID NO: 429 and a heavy chain comprising SEQ ID NO: 586; a light chain comprising SEQ ID NO: 430 and a heavy chain comprising SEQ ID NO: 587; a light chain comprising SEQ ID NO: 431 and a heavy chain comprising SEQ ID NO: 588; a light chain comprising SEQ ID NO: 432 and a heavy chain comprising SEQ ID NO: 589; a light chain comprising SEQ ID NO: 433 and a heavy chain comprising SEQ ID NO: 590; a light chain comprising SEQ ID NO: 434 and a heavy chain comprising SEQ ID NO: 591; a light chain comprising SEQ ID NO: 435 and a heavy chain comprising SEQ ID NO: 592; a light chain comprising SEQ ID NO: 436 and a heavy chain comprising SEQ ID NO: 593; a light chain comprising SEQ ID NO: 437 and a heavy chain comprising SEQ ID NO: 594; a light chain comprising SEQ ID NO: 438 and a heavy chain comprising SEQ ID NO: 595; a light chain comprising SEQ ID NO: 439 and a heavy chain comprising SEQ ID NO: 596; a light chain comprising SEQ ID NO: 440 and a heavy chain comprising SEQ ID NO: 597; a light chain comprising SEQ ID NO: 441 and a heavy chain comprising SEQ ID NO: 598; a light chain comprising SEQ ID NO: 442 and a heavy chain comprising SEQ ID NO: 599; a light chain comprising SEQ ID NO: 443 and a heavy chain comprising SEQ ID NO: 600; a light chain comprising SEQ ID NO: 444 and a heavy chain comprising SEQ ID NO: 601; a light chain comprising SEQ ID NO: 445 and a heavy chain comprising SEQ ID NO: 602; a light chain comprising SEQ ID NO: 446 and a heavy chain comprising SEQ ID NO: 603; a light chain comprising SEQ ID NO: 447 and a heavy chain comprising SEQ ID NO: 604; a light chain comprising SEQ ID NO: 448 and a heavy chain comprising SEQ ID NO: 605; a light chain comprising SEQ ID NO: 449 and a heavy chain comprising SEQ ID NO: 606; a light chain comprising SEQ ID NO: 450 and a heavy chain comprising SEQ ID NO: 607; a light chain comprising SEQ ID NO: 451 and a heavy chain comprising SEQ ID NO: 608; a light chain comprising SEQ ID NO: 452 and a heavy chain comprising SEQ ID NO: 609; a light chain

comprising SEQ ID NO: 453 and a heavy chain comprising SEQ ID NO: 610; a light chain comprising SEQ ID NO: 454 and a heavy chain comprising SEQ ID NO: 611; a light chain comprising SEQ ID NO: 455 and a heavy chain comprising SEQ ID NO: 612; a light chain comprising SEQ ID NO: 456 and a heavy chain comprising SEQ ID NO: 613; a light chain comprising SEQ ID NO: 457 and a heavy chain comprising SEQ ID NO: 614; a light chain comprising SEQ ID NO: 458 and a heavy chain comprising SEQ ID NO: 615; a light chain comprising SEQ ID NO: 459 and a heavy chain comprising SEQ ID NO: 616; a light chain comprising SEQ ID NO: 460 and a heavy chain comprising SEQ ID NO: 617; a light chain comprising SEQ ID NO: 461 and a heavy chain comprising SEQ ID NO: 618; a light chain comprising SEQ ID NO: 462 and a heavy chain comprising SEQ ID NO: 619; a light chain comprising SEQ ID NO: 463 and a heavy chain comprising SEQ ID NO: 620; a light chain comprising SEQ ID NO: 464 and a heavy chain comprising SEQ ID NO: 621; a light chain comprising SEQ ID NO: 465 and a heavy chain comprising SEQ ID NO: 622; a light chain comprising SEQ ID NO: 466 and a heavy chain comprising SEQ ID NO: 623; a light chain comprising SEQ ID NO: 467 and a heavy chain comprising SEQ ID NO: 624; a light chain comprising SEQ ID NO: 468 and a heavy chain comprising SEQ ID NO: 625; a light chain comprising SEQ ID NO: 469 and a heavy chain comprising SEQ ID NO: 626; a light chain comprising SEQ ID NO: 470 and a heavy chain comprising SEQ ID NO: 627; and a light chain comprising SEQ ID NO: 471 and a heavy chain comprising SEQ ID NO: 628, wherein the antibody comprises one or more cysteine amino acid substitution(s) at one or more position(s) selected from 88 of the light chain, 384 of the heavy chain, or 487 of the heavy chain, according to AHo numbering.

[0205] In one embodiment, the antagonist anti-GIPR antibody of the conjugate molecule as described herein comprises the light chain amino acid sequence of SEQ ID NO: 388 and the heavy chain amino acid sequence of SEQ ID NO: 545, wherein the antibody comprises one or more cysteine amino acid substitution(s) at one or more position(s) selected from 88 of the light chain, 384 of the heavy chain, or 487 of the heavy chain, according to AHo numbering. An exemplary antibody disclosed herein comprising these light and heavy chains is referred to as the 2G10_LC1.006 anti-GIPR antibody.

[0206] In one embodiment, an antagonist anti-GIPR antibody of the conjugate molecule comprising a cysteine amino acid substitution (i.e., a conjugation site) at position 88 of the light

chain (according to AHo numbering) comprises a light chain amino acid sequence of SEQ ID NO: 1594 and heavy chain amino acid sequence of SEQ ID NO: 612.

[0207] In one embodiment, an antagonist anti-GIPR antibody of the conjugate molecule comprising a cysteine amino acid substitution (i.e., a conjugation site) at position 384 of the heavy chain (according to AHo numbering) comprises a light chain amino acid sequence of SEQ ID NO: 388 and heavy chain amino acid sequence of SEQ ID NO: 1571.

[0208] In one embodiment, an antagonist anti-GIPR antibody of the conjugate molecule comprising a cysteine amino acid substitution (i.e., a conjugation site) at position 384 of the heavy chain (according to AHo numbering) comprises a light chain amino acid sequence of SEQ ID NO: 389 and heavy chain amino acid sequence of SEQ ID NO: 1596.

[0209] In one embodiment, an exemplary anti-GIPR/GLP-1 conjugate molecule of the present disclosure comprises an antagonist anti-GIPR antibody, wherein said antibody comprises: a first and second light chain, each light chain comprising a CDRL1, a CDRL2, and a CDRL3 of SEQ ID NO: 702, SEQ ID NO: 859, and SEQ ID NO: 1016, respectively, and a first and second heavy chain, each heavy chain comprising a CDRH1, a CDRH2, and a CDRH3 of SEQ ID NO: 1173, SEQ ID NO: 1330, and SEQ ID NO: 1487, respectively. The molecule further comprises a first and second GLP-1 receptor agonist polypeptide, wherein each GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1579; and a first and second peptide linker, wherein each peptide linker comprises the amino acid sequence of SEQ ID NO: 1592. The first GLP-1 receptor agonist polypeptide of the molecule is conjugated, at its C-terminus via the first linker, to the first heavy chain of the GIPR antibody at a cysteine residue at position 384 of the first heavy chain according to AHo numbering (which corresponds to position 275 of SEQ ID NO: 1571), and the second GLP-1 receptor agonist polypeptide is conjugated, at its C-terminus via the second linker, to the second heavy chain of the GIPR antibody at a cysteine residue at position 384 of the second heavy chain according to AHo numbering (which corresponds to position 275 of SEQ ID NO: 1571). In one embodiment, each light chain comprises a VL of SEQ ID NO: 74, and each heavy chain comprises a VH of SEQ ID NO: 231. In one embodiment, each light chain comprises the amino acid sequence of SEQ ID NO: 388, and each heavy chain comprises the amino acid sequence of SEQ ID NO: 1571.

[0210] In one embodiment, an exemplary anti-GIPR/GLP-1 conjugate molecule of the present disclosure comprises an antagonist anti-GIPR antibody, wherein said antibody

comprises: a first and second light chain, each light chain comprising a CDRL1, a CDRL2, and a CDRL3 of SEQ ID NO: 702, SEQ ID NO: 859, and SEQ ID NO: 1016, respectively, and a first and second heavy chain, each heavy chain comprising a CDRH1, a CDRH2, and a CDRH3 of SEQ ID NO: 1173, SEQ ID NO: 1330, and SEQ ID NO: 1487, respectively. The molecule further comprises a first and second GLP-1 receptor agonist polypeptide, wherein each GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1580; and a first and second peptide linker, wherein each peptide linker comprises the amino acid sequence of SEQ ID NO: 1591. The first GLP-1 receptor agonist polypeptide of the molecule is conjugated, at its C-terminus via the first linker, to the first heavy chain of the GIPR antibody at a cysteine residue at position 384 of the first heavy chain according to AHo numbering (which corresponds to position 275 of SEQ ID NO: 1571), and the second GLP-1 receptor agonist polypeptide is conjugated, at its C-terminus via the second linker, to the second heavy chain of the GIPR antibody at a cysteine residue at position 384 of the second heavy chain according to AHo numbering (which corresponds to position 275 of SEQ ID NO: 1571). In one embodiment, each light chain comprises a VL of SEQ ID NO: 74, and each heavy chain comprises a VH of SEQ ID NO: 231. In one embodiment, each light chain comprises the amino acid sequence of SEQ ID NO: 388, and each heavy chain comprises the amino acid sequence of SEQ ID NO: 1571.

[0211] In one embodiment, an exemplary anti-GIPR/GLP-1 conjugate molecule of the present disclosure comprises an antagonist anti-GIPR antibody, wherein said antibody comprises: a first and second light chain, each light chain comprising a CDRL1, a CDRL2, and a CDRL3 of SEQ ID NO: 702, SEQ ID NO: 859, and SEQ ID NO: 1016, respectively, and a first and second heavy chain, each heavy chain comprising a CDRH1, a CDRH2, and a CDRH3 of SEQ ID NO: 1173, SEQ ID NO: 1330, and SEQ ID NO: 1487, respectively. The molecule further comprises a first and second GLP-1 receptor agonist polypeptide, wherein each GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1581; and a first and second peptide linker, wherein each peptide linker comprises the amino acid sequence of SEQ ID NO: 1586. The first GLP-1 receptor agonist polypeptide of the molecule is conjugated, at its C-terminus via the first linker, to the first heavy chain of the GIPR antibody at a cysteine residue at position 384 of the first heavy chain according to AHo numbering (which corresponds to position 275 of SEQ ID NO: 1571), and the second GLP-1 receptor agonist polypeptide is conjugated, at its C-terminus via the second linker, to the second heavy chain of

the GIPR antibody at a cysteine residue at position 384 of the second heavy chain according to AHo numbering (which corresponds to position 275 of SEQ ID NO: 1571). In one embodiment, each light chain comprises a VL of SEQ ID NO: 74, and each heavy chain comprises a VH of SEQ ID NO: 231. In one embodiment, each light chain comprises the amino acid sequence of SEQ ID NO: 388, and each heavy chain comprises the amino acid sequence of SEQ ID NO: 1571.

[0212] In one embodiment, an exemplary anti-GIPR/GLP-1 conjugate molecule of the present disclosure comprises an antagonist anti-GIPR antibody, wherein said antibody comprises: a first and second light chain, each light chain comprising a CDRL1, a CDRL2, and a CDRL3 of SEQ ID NO: 702, SEQ ID NO: 859, and SEQ ID NO: 1016, respectively, and a first and second heavy chain, each heavy chain comprising a CDRH1, a CDRH2, and a CDRH3 of SEQ ID NO: 1173, SEQ ID NO: 1330, and SEQ ID NO: 1487, respectively. The molecule further comprises a first and second GLP-1 receptor agonist polypeptide, wherein each GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1581; and a first and second peptide linker, wherein each peptide linker comprises the amino acid sequence of SEQ ID NO: 1585. The first GLP-1 receptor agonist polypeptide of the molecule is conjugated, at its C-terminus via the first linker, to the first heavy chain of the GIPR antibody at a cysteine residue at position 384 of the first heavy chain according to AHo numbering (which corresponds to position 275 of SEQ ID NO: 1571), and the second GLP-1 receptor agonist polypeptide is conjugated, at its C-terminus via the second linker, to the second heavy chain of the GIPR antibody at a cysteine residue at position 384 of the second heavy chain according to AHo numbering (which corresponds to position 275 of SEQ ID NO: 1571). In one embodiment, each light chain comprises a VL of SEQ ID NO: 74, and each heavy chain comprises a VH of SEQ ID NO: 231. In one embodiment, each light chain comprises the amino acid sequence of SEQ ID NO: 388, and each heavy chain comprises the amino acid sequence of SEQ ID NO: 1571.

[0213] In one embodiment, the antagonist anti-GIPR antibodies of the conjugate molecules herein are monoclonal antibodies that bind to GIPR. Monoclonal antibodies may be produced using any technique known in the art, e.g., by immortalizing spleen cells harvested from a transgenic animal capable of producing human antibodies (e.g., XenoMouse®) 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.

[0214] In some instances, a hybridoma cell line is produced by immunizing an animal (e.g., a transgenic animal capable of producing human immunoglobulin sequences) with a GIPR 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 a GIPR polypeptide. Anti-GIPR monoclonal antibodies produced by these hybridoma cells are suitable for inclusion in the molecules described herein.

[0215] Anti-GIPR monoclonal antibodies secreted by a hybridoma cell line can be purified using any technique known in the art. Hybridomas or mAbs may be further screened to identify mAbs with particular properties, such as the ability to antagonize GIPR activity.

[0216] Anti-GIPR chimeric and humanized antibodies are also suitable for use in the conjugate molecules described herein. The anti-GIPR antibody sequences disclosed herein may be modified in various ways prior to use. One example is a chimeric antibody, which is an antibody composed of protein segments from different antibodies that are covalently joined to produce functional immunoglobulin light or heavy chains or immunologically functional portions thereof. Generally, a portion of the heavy chain and/or light chain is identical with or homologous to a corresponding sequence in antibodies derived from a particular species or belonging to a particular antibody class or subclass, while the remainder of the chain(s) is/are identical with or homologous to a corresponding sequence in antibodies derived from another species or belonging to another antibody class or subclass. For methods relating to chimeric antibodies, *see*, for example, United States Patent No. 4,816,567; and Morrison *et al.*, 1985, *Proc. Natl. Acad. Sci. USA* 81:6851-6855, which are hereby incorporated by reference. CDR grafting is described, for example, in United States Patent No. 6,180,370, No. 5,693,762, No. 5,693,761, No. 5,585,089, and No. 5,530,101.

[0217] Generally, the goal of making a chimeric antibody is to create a chimera in which the number of amino acids from the intended subject species is maximized. One example is the "CDR-grafted" antibody, in which the antibody comprises one or more complementarity determining regions (CDRs) from a particular species or belonging to a particular antibody class or subclass, while the remainder of the antibody chain(s) is/are identical with or homologous to a corresponding sequence in antibodies derived from another species or belonging to another antibody class or subclass. For use in humans, the variable region or selected CDRs from a rodent antibody often are grafted into a human antibody, replacing the naturally-occurring variable regions or CDRs of the human antibody.

[0218] In one aspect, the CDRs of the light and heavy chain variable regions of the antibodies provided herein are grafted to framework regions (FRs) from antibodies from the same, or a different, phylogenetic species. For example, the CDRs of the heavy and light chain variable regions V_H1, V_H2, V_H3, V_H4, V_H5, V_H6, V_H7, V_H8, V_H9, V_H10, V_H11, V_H12 and/or V_L1, and V_L2 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. In other embodiments, the FRs of a heavy chain or light chain disclosed herein are replaced with the FRs from a different heavy chain or light chain. In one aspect, rare amino acids in the FRs of the heavy and light chains of GIPR antibodies are not replaced, while the rest of the FR amino acids are replaced. A "rare amino acid" is a specific amino acid that is in a position in which this particular amino acid is not usually found in an FR. Alternatively, the grafted variable regions from the one heavy or light chain may be used with a constant region that is different from the constant region of that particular heavy or light chain as disclosed herein.

[0219] Human antagonist anti-GIPR antibodies are also provided. Methods are available for making human antibodies specific for a given antigen without exposing human beings to the antigen. One specific means provided for implementing the production of 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 human monoclonal antibodies (mAbs) in mouse, an animal that can be immunized with any desirable antigen. Using 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.

[0220] 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. 5,545,807; 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, and in EP 546073B1 and EP 546073A1.

[0221] Suitable human antibodies can alternatively be derived from phage-display libraries (as disclosed in Hoogenboom *et al.*, 1991, *J. Mol. Biol.* 227:381; and Marks *et al.*, 1991, *J. Mol. Biol.* 222:581). Phage display techniques mimic immune selection through the display of antibody repertoires on the surface of filamentous bacteriophage, and subsequent selection of phage by their binding to an antigen of choice. One such technique is described in PCT Publication No. WO 99/10494 (hereby incorporated by reference).

[0222] The anti-GIPR antibody used in the molecules described herein may be prepared by any of a number of conventional techniques. For example, antibodies can be produced by recombinant expression systems. *See, e.g.,* Monoclonal Antibodies, Hybridomas: A New Dimension in Biological Analyses, Kennet et al. (eds.) Plenum Press, New York (1980); and

Antibodies: A Laboratory Manual, Harlow and Lane (eds.), Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1988).

[0223] In one embodiment, the anti-GIPR antibodies provided herein are expressed in hybridoma cell lines or in cell lines other than hybridomas. Expression constructs encoding the anti-GIPR antibodies can be used to transform a mammalian, insect or microbial host cell. Transformation can be performed using any known method for introducing polynucleotides into a host cell, including, for example, packaging the polynucleotide in a virus or bacteriophage and transducing a host cell with the construct by transfection procedures known in the art, as exemplified by United States Patent No. 4,399,216; No. 4,912,040; No. 4,740,461; No. 4,959,455. The choice of transformation procedure used will depend upon which type of host cell is being transformed. Methods for introduction of heterologous polynucleotides into mammalian cells are known in the art and include, but are not limited to, dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, mixing nucleic acid with positively-charged lipids, and direct microinjection of the DNA into nuclei.

[0224] Recombinant expression constructs typically comprise a nucleic acid molecule encoding a polypeptide comprising one or more of the following: one or more light chain CDRs; one or more heavy chain CDRs; a light chain constant region; a light chain variable region; a heavy chain constant region (e.g., C_H1, C_H2 and/or C_H3); and a heavy chain variable region of an anti-GIPR antibody. These nucleic acid sequences are inserted into an appropriate expression vector using standard ligation techniques. In one embodiment, the heavy or light chain constant region is appended to the C-terminus of the anti-GIPR specific heavy or light chain variable region and is ligated into an expression vector. The vector is typically selected to be functional in the particular host cell employed (i.e., the vector is compatible with the host cell machinery, permitting amplification, and/or expression of the gene can occur).

[0225] Typically, expression vectors used in any of the host cells will contain sequences for plasmid maintenance and for cloning and expression of exogenous nucleotide sequences. Such sequences, collectively referred to as “flanking sequences,” can include one or more of the following nucleotide sequences: a promoter, one or more enhancer sequences, an origin of replication, a transcriptional termination sequence, a complete intron sequence containing a donor and acceptor splice site, a sequence encoding a leader sequence for polypeptide secretion,

a ribosome binding site, a polyadenylation sequence, a polylinker region for inserting the nucleic acid encoding the polypeptide to be expressed, and a selectable marker element.

[0226] Flanking sequences may be homologous (i.e., from the same species and/or strain as the host cell), heterologous (i.e., from a species other than the host cell species or strain), hybrid (i.e., a combination of flanking sequences from more than one source), synthetic, or native. As such, the source of a flanking sequence may be any prokaryotic or eukaryotic organism, any vertebrate or invertebrate organism, or any plant, provided that the flanking sequence is functional in, and can be activated by, the host cell machinery.

[0227] Flanking sequences useful in the vectors can be obtained by methods known in the art. Typically, flanking sequences will have been previously identified by mapping and/or by restriction endonuclease digestion and can thus be isolated from the proper tissue source using the appropriate restriction endonucleases. In some cases, the full nucleotide sequence of a flanking sequence may be known. The flanking sequence may be synthesized using conventional methods for nucleic acid synthesis or cloning.

[0228] An origin of replication is typically a part of commercially available prokaryotic expression vectors; the origin of replication aids in the amplification of the vector in a host cell. If the vector of choice does not contain an origin of replication site, one may be chemically synthesized based on a known sequence and ligated into the vector. For example, the origin of replication from the plasmid pBR322 (New England Biolabs, Beverly, MA) is suitable for most gram-negative bacteria and various viral origins (e.g., SV40, polyoma, adenovirus, vesicular stomatitus virus (VSV), or papillomaviruses, such as, e.g., HPV or BPV). Generally, the origin of replication component is not needed for mammalian expression vectors (for example, the SV40 origin is often used only because it also contains the virus early promoter).

[0229] A transcription termination sequence is typically located 3′ to the end of a polypeptide coding region and serves to terminate transcription. Usually, a transcription termination sequence in prokaryotic cells is a G-C rich fragment followed by a poly-T sequence. While the sequence is easily cloned from a library or even purchased commercially as part of a vector, it can also be readily synthesized using conventional methods for nucleic acid synthesis.

[0230] A selectable marker gene encodes a protein necessary for the survival and growth of a host cell grown in a selective culture medium. Typical selection marker genes encode proteins that (a) confer resistance to antibiotics or other toxins, e.g., ampicillin, tetracycline, or

kanamycin for prokaryotic host cells; (b) complement auxotrophic deficiencies of the cell; or (c) supply critical nutrients not available from complex or defined media. Specific selectable markers are the kanamycin resistance gene, the ampicillin resistance gene, and the tetracycline resistance gene. Advantageously, a neomycin resistance gene may also be used for selection in both prokaryotic and eukaryotic host cells.

[0231] Other selectable genes may be used to amplify the gene that will be expressed. Amplification is the process wherein genes that are required for production of a protein critical for growth or cell survival are reiterated in tandem within the chromosomes of successive generations of recombinant cells. Examples of suitable selectable markers for mammalian cells include dihydrofolate reductase (DHFR) and promoter-less thymidine kinase genes. Mammalian cell transformants are placed under selection pressure wherein only the transformants are uniquely adapted to survive by virtue of the selectable gene present in the vector. Selection pressure is imposed by culturing the transformed cells under conditions in which the concentration of selection agent in the medium is successively increased, thereby leading to the amplification of both the selectable gene and the DNA that encodes another gene, such as an antibody that binds GIPR polypeptide. As a result, increased quantities of a polypeptide such as an anti-GIPR antibody are synthesized from the amplified DNA.

[0232] A ribosome-binding site is usually necessary for translation initiation of mRNA and is characterized by a Shine-Dalgarno sequence (prokaryotes) or a Kozak sequence (eukaryotes). The element is typically located 3' to the promoter and 5' to the coding sequence of the polypeptide to be expressed.

[0233] In some cases, such as where glycosylation is desired in a eukaryotic host cell expression system, one may manipulate the various pre- or pro-sequences to improve glycosylation or yield. For example, one may alter the peptidase cleavage site of a particular signal peptide, or add prosequences, which also may affect glycosylation. The final protein product may have, in the -1 position (relative to the first amino acid of the mature protein), one or more additional amino acids incident to expression, which may not have been totally removed. For example, the final protein product may have one or two amino acid residues found in the peptidase cleavage site, attached to the amino-terminus. Alternatively, use of some enzyme cleavage sites may result in a slightly truncated form of the desired polypeptide, if the enzyme cuts at such area within the mature polypeptide.

[0234] Expression and cloning will typically contain a promoter that is recognized by the host organism and operably linked to the molecule encoding the anti-GIPR antibody. Promoters are untranscribed sequences located upstream (i.e., 5') to the start codon of a structural gene (generally within about 100 to 1000 bp) that control transcription of the structural gene. Promoters are conventionally grouped into one of two classes: inducible promoters and constitutive promoters. Inducible promoters initiate increased levels of transcription from DNA under their control in response to some change in culture conditions, such as the presence or absence of a nutrient or a change in temperature. Constitutive promoters, on the other hand, uniformly transcribe a gene to which they are operably linked, that is, with little or no control over gene expression. A large number of promoters, recognized by a variety of potential host cells, are known. A suitable promoter is operably linked to the DNA encoding heavy chain or light chain comprising a GIPR antibody by removing the promoter from the source DNA by restriction enzyme digestion and inserting the desired promoter sequence into the vector.

[0235] Suitable promoters for use with yeast hosts are also known in the art. Yeast enhancers are advantageously used with yeast promoters. Suitable promoters for use with mammalian host cells are known and include, but are not limited to, those obtained from the genomes of viruses such as polyoma virus, fowlpox virus, adenovirus (such as, e.g., Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, retroviruses, hepatitis-B virus, and Simian Virus 40 (SV40). Other suitable mammalian promoters include, but are not limited to, heterologous mammalian promoters, for example, heat-shock promoters and the actin promoter.

[0236] An enhancer sequence may be inserted into the vector to increase transcription of DNA encoding the light chain or heavy chain of an anti-GIPR antibody by higher eukaryotes. Enhancers are cis-acting elements of DNA, usually about 10-300 bp in length, which act on the promoter to increase transcription. Enhancers are relatively orientation and position independent, having been found at positions both 5' and 3' to the transcription unit. Several enhancer sequences available from mammalian genes are known (e.g., globin, elastase, albumin, alpha-feto-protein and insulin). Alternatively, an enhancer from a virus can be used. The SV40 enhancer, the cytomegalovirus early promoter enhancer, the polyoma enhancer, and adenovirus enhancers known in the art are non-limiting examples of enhancing elements for the activation of eukaryotic promoters. While an enhancer may be positioned in the vector either 5' or 3' to a

coding sequence, it is typically located at a site 5' from the promoter. A sequence encoding an appropriate native or heterologous signal sequence (leader sequence or signal peptide) can be incorporated into an expression vector, e.g., to promote extracellular secretion of the antibody. The choice of signal peptide or leader depends on the type of host cells in which the antibody is to be produced, and a heterologous signal sequence can replace the native signal sequence. Non-limiting examples of signal peptides that are functional in mammalian host cells include the following: the signal sequence for interleukin-7 (IL-7) described in US Patent No. 4,965,195; the signal sequence for interleukin-2 receptor described in Cosman *et al.*,1984, *Nature* 312:768; the interleukin-4 receptor signal peptide described in EP Patent No. 0367 566; the type I interleukin-1 receptor signal peptide described in U.S. Patent No. 4,968,607; the type II interleukin-1 receptor signal peptide described in EP Patent No. 0 460 846.

[0237] In one embodiment the leader sequence comprises SEQ ID NO: 1655 (MDMRVPAQLL GLLLLWLRGA RC). In another embodiment the leader sequence comprises SEQ ID NO: 1656 (MAWALLLLTL LTQGTGSWA).

[0238] Expression vectors may be constructed from a starting vector such as a commercially available vector. Such vectors may or may not contain all of the desired flanking sequences. Where one or more of the flanking sequences described herein are not already present in the vector, they may be individually obtained and ligated into the vector. Methods used for obtaining each of the flanking sequences are known to one skilled in the art.

[0239] Optionally, the vector may contain a "tag"-encoding sequence, i.e., an oligonucleotide molecule located at the 5′ or 3′ end of the GIPR antibody coding sequence; the oligonucleotide sequence encodes polyHis (such as hexaHis), or another "tag" such as FLAG®, HA (hemagglutinin influenza virus), or myc, for which commercially available antibodies exist. This tag is typically fused to the polypeptide upon expression of the polypeptide, and can serve as a means for affinity purification or detection of the antibody from the host cell. Affinity purification can be accomplished, for example, by column chromatography using antibodies against the tag as an affinity matrix. Optionally, the tag can subsequently be removed from the purified antibody by various means such as using certain peptidases for cleavage.

[0240] After the vector has been constructed and a nucleic acid molecule encoding a light chain, a heavy chain, or a light chain and a heavy chain has been inserted into the proper site of the vector, the completed vector may be inserted into a suitable host cell for amplification and/or

polypeptide expression. The transformation of an expression vector encoding an antibody into a selected host cell may be accomplished by conventional methods including, but not limited to, transfection, infection, calcium phosphate co-precipitation, electroporation, microinjection, lipofection, DEAE-dextran mediated transfection, or other known techniques. The method selected will in part be a function of the type of host cell to be used.

[0241] A host cell, when cultured under appropriate conditions, synthesizes an anti-GIPR antibody that can subsequently be collected from the culture medium (if the host cell secretes it into the medium) or directly from the host cell producing it (if it is not secreted). The selection of an appropriate host cell will depend upon various factors, such as, e.g., desired expression levels, polypeptide modifications that are desirable or necessary for activity (such as, e.g., glycosylation or phosphorylation), and ease of folding into a biologically active molecule.

[0242] Mammalian cell lines available as hosts for expression are known in the art and include, but are not limited to, immortalized cell lines available from the American Type Culture Collection (ATCC), including, but not limited to, Chinese hamster ovary (CHO) cells, HeLa cells, baby hamster kidney (BHK) cells, monkey kidney cells (COS), human hepatocellular carcinoma cells (*e.g.*, Hep G2), and a number of other cell lines. In one embodiment, a host cell line can be selected by determining which cell lines have high expression levels and constitutively produce the desired anti-GIPR antibody. In one embodiment, a cell line from the B cell lineage that does not make its own antibody but has a capacity to make and secrete a heterologous antibody can be selected.

[0243] Additionally, in one embodiment, a mammalian cell line modified to provide for reduced cleavage of peptides that will be conjugated to polypeptides expressed by the cells (e.g., a cathepsin D knock-out cell line) can be used. In one embodiment, a mammalian cell line (e.g., a CHO cell line) in which both alleles of cathepsin D are knocked out (e.g., using CRISPR or zinc-finger technology) can be used. An example of a cathepsin D knock-out cell that can be used to produce an antibody-peptide conjugate of the disclosure is described in WO 2023/086790, which is incorporated by reference herein.

PHARMACEUTICAL COMPOSITIONS

[0244] While it may be possible to administer a GLP-1 receptor agonist polypeptide or anti-GIPR/GLP-1 conjugate molecule disclosed herein alone in the uses described herein, the

GLP-1 receptor agonist polypeptide or conjugate molecule will normally be administered as an active ingredient in a pharmaceutical composition. Thus, further provided herein is a pharmaceutical composition comprising a GLP-1 receptor agonist polypeptide or anti-GIPR/GLP-1 conjugate molecule disclosed herein and a pharmaceutically acceptable excipient. Non-limiting examples of pharmaceutically acceptable excipients include calcium carbonate, calcium phosphate, sugars (e.g., lactose, glucose, or sucrose), starches, cellulose derivatives, gelatin, vegetable oils, polyethylene glycols, and physiologically compatible solvents. *See, e.g.*, Remington: The Science and Practice of Pharmacy, Volume I and Volume II, twenty-second edition, edited by Loyd V. Allen Jr., Philadelphia, PA, Pharmaceutical Press, 2012; Pharmaceutical Dosage Forms (Vol. 1-3), Liberman et al., Eds., Marcel Dekker, New York, NY, 1992; Handbook of Pharmaceutical Excipients (3rd Ed.), edited by Arthur H. Kibbe, American Pharmaceutical Association, Washington, 2000; Pharmaceutical Formulation: The Science and Technology of Dosage Forms (Drug Discovery), first edition, edited by GD Tovey, Royal Society of Chemistry, 2018.

[0245] In some cases, the pharmaceutical composition described herein comprises a therapeutically effective amount of a GLP-1 receptor agonist polypeptide or anti-GIPR/GLP-1 conjugate molecule disclosed herein. In one embodiment, the pharmaceutical composition is made in the form of a dosage unit containing a particular amount of the active ingredient.

[0246] The GLP-1 receptor agonist polypeptides or anti-GIPR/GLP-1 conjugate molecules disclosed herein may be administered by any suitable route in the form of a pharmaceutical composition adapted to such a route and in a dose effective for the treatment intended. The polypeptides, molecules, and compositions presented herein may, for example, be administered orally, mucosally, transdermally, parentally, intravenously, intraperitoneally, subcutaneously, intramuscularly, by infusion techniques, in dosage unit formulations containing conventional pharmaceutically acceptable excipients. For example, in one embodiment, a pharmaceutical composition disclosed herein may be provided for peripheral administration, such as parenteral (e.g., subcutaneous, intravenous, intramuscular), continuous infusion (e.g., intravenous drip, intravenous bolus, intravenous infusion), topical, nasal, or oral administration.

[0247] Pharmaceutical compositions disclosed herein may be sterilized by conventional sterilization techniques or may be sterile-filtered. In one embodiment, such compositions comprise sterile water. In one embodiment, such compositions can contain pharmaceutically

acceptable auxiliary substances as required to approximate physiological conditions, such as, e.g., pH buffering agents (e.g., an acetic acid buffer).

[0248] In one embodiment, the pharmaceutical composition comprises sterile water and sodium chloride. In one embodiment, the pharmaceutical composition comprises sterile water and dextrose. In one embodiment, the pharmaceutical composition comprises sterile water, sodium chloride, and dextrose.

[0249] In one embodiment, the pharmaceutical composition comprises an aqueous carrier. In one embodiment, the aqueous carrier is an isotonic buffer solution at a pH in the range of 3.0 to 8.0 (such as, e.g., in the range of 3.0 to 5.0).

[0250] In one embodiment, the pharmaceutical composition is a parenteral composition. In one embodiment, the pharmaceutical composition is a parenteral composition for injection. In one embodiment, the pharmaceutical composition is a parenteral composition for infusion.

[0251] In one embodiment, a form of repository or "depot" slow release preparation may be used so that therapeutically effective amounts of the preparation are delivered into the bloodstream over many hours or days following subcutaneous injection, transdermal injection, or other delivery method. The desired isotonicity may be accomplished using sodium chloride or other pharmaceutically acceptable excipients, such as, e.g., dextrose, boric acid, sodium tartrate, propylene glycol, polyols (such as, e.g., mannitol and sorbitol), or other inorganic or organic solutes.

METHODS OF TREATMENT

[0252] The GLP-1 receptor agonist polypeptides and conjugate molecules comprising these GLP-1 receptor agonist polypeptides, e.g., the anti-GIPR antibody/GLP-1 receptor agonist conjugate molecules, as disclosed herein are useful for reducing body weight of a subject in need thereof. The GLP-1 receptor agonist polypeptides and conjugate molecules comprising these GLP-1 receptor agonist polypeptides as disclosed herein are also useful for reducing food intake in a subject in need thereof. The GLP-1 receptor agonist polypeptides and conjugate molecules comprising these GLP-1 receptor agonist polypeptides as disclosed herein are also useful for reducing hypertension and/or blood sugar levels in a subject in need thereof. The GLP-1 receptor agonist polypeptides and conjugate molecules comprising these GLP-1 receptor agonist polypeptides are also useful for treating obesity in a subject in need thereof, and for treating and

preventing obesity-related conditions in a subject in need thereof. Obesity-related conditions include, without limitation, cardiovascular disease, in particular hypertension, heart failure, and atherosclerotic cardiovascular (ASCVD); sleep apnea; dyslipidemia; chronic kidney disease; and metabolic dysfunction-associated steatohepatitis (MASH). The GLP-1 receptor agonist polypeptides and conjugate molecules comprising these GLP-1 receptor agonist polypeptides are also useful for treating type 2 diabetes in a subject in need thereof, and for treating and preventing conditions associated with type 2 diabetes in a subject in need thereof. Conditions associated with type 2 diabetes include, without limitation, hypertension, high blood sugar, cardiovascular disease, diabetic kidney disease, and diabetic kidney failure.

[0253] Accordingly, in one aspect, the present disclosure provides a method for preventing or treating obesity, obesity-related conditions, type 2 diabetes, and/or type 2 diabetes related conditions in a subject in need thereof. In one embodiment, this method involves administering, to the subject, the anti-GIPR antibody/GLP-1 receptor agonist conjugate molecule disclosed herein, or a pharmaceutical composition comprising the same, at a dose of about 21 mg to about 840 mg. In one embodiment, the anti-GIPR antibody/GLP-1 receptor agonist conjugate molecule, or pharmaceutical composition comprising the same, is administered to the subject at a dose of about 21 mg to about 840 mg every four weeks, at a dose of about 21 mg to about 840 mg every six weeks, at a dose of about 21 mg to about 840 mg every eight weeks, or at a dose of about 21 mg to about 840 mg every twelve weeks. In one embodiment, the anti-GIPR antibody/GLP-1 receptor agonist conjugate molecule, or pharmaceutical composition comprising the same, is administered to the subject at a dose of about 21 mg to about 840 mg every month, at a dose of about 21 mg to about 840 mg every one and a half months, at a dose of about 21 mg to about 840 mg every two months, or at a dose of about 21 mg to about 840 mg every three months. In one embodiment, the subject has obesity. In one embodiment, the subject has or is at risk of having an obesity-related condition. In one embodiment, the subject has sleep apnea. In one embodiment, the subject has dyslipidemia. In one embodiment, the subject has or is at risk of having a cardiovascular disease. In one embodiment, the subject has or is at risk of having ASCVD. In one embodiment, the subject has heart failure. In one embodiment, the subject has hypertension. In one embodiment, the subject has chronic kidney failure. In one embodiment, the subject has MASH. In one embodiment, the subject has type 2 diabetes. In one embodiment, the subject a type 2 diabetes related condition. In one embodiment, the subject has hypertension

and/or high blood sugar. In one embodiment, the subject has diabetic kidney disease or diabetic kidney failure. In one embodiment, the subject has cardiovascular disease.

[0254] In another aspect, the present disclosure provides a method for reducing body weight or reducing food intake in a subject in need thereof. This method involves administering, to the subject, the anti-GIPR antibody/GLP-1 receptor agonist conjugate molecule disclosed herein, or pharmaceutical composition comprising the same, at a dose of about 21 mg to about 840 mg. In one embodiment, the anti-GIPR antibody/GLP-1 receptor agonist conjugate molecule, or pharmaceutical composition comprising the same, is administered to the subject at a dose of about 21 mg to about 840 mg every four weeks, at a dose of about 21 mg to about 840 mg every six weeks, at a dose of about 21 mg to about 840 mg every eight weeks, or at a dose of about 21 mg to about 840 mg every twelve weeks. In one embodiment, the anti-GIPR antibody/GLP-1 receptor agonist conjugate molecule, or pharmaceutical composition comprising the same, is administered to the subject at a dose of about 21 mg to about 840 mg every month, at a dose of about 21 mg to about 840 mg every one and a half months, at a dose of about 21 mg to about 840 mg every two months, or at a dose of about 21 mg to about 840 mg every three months. In one embodiment, the subject has or is at risk of having an obesity related condition. In one embodiment, the subject has sleep apnea. In one embodiment, the subject has dyslipidemia. In one embodiment, the subject has or is at risk of having a cardiovascular disease. In one embodiment, the subject has or is at risk of having ASCVD. In one embodiment, the subject has heart failure. In one embodiment, the subject has hypertension. In one embodiment, the subject has chronic kidney failure. In one embodiment, the subject has MASH. In one embodiment, the subject has type 2 diabetes. In one embodiment, the subject a type 2 diabetes related condition. In one embodiment, the subject has hypertension and/or high blood sugar. In one embodiment, the subject has diabetic kidney disease or diabetic kidney failure. In one embodiment, the subject has cardiovascular disease.

[0255] In another aspect, the present disclosure provides a method for reducing blood pressure and/or reducing blood sugar levels in a subject in need thereof. This method involves administering, to the subject, the anti-GIPR antibody/GLP-1 receptor agonist conjugate molecule disclosed herein, or pharmaceutical composition comprising the same, at a dose of about 21 mg to about 840 mg. In one embodiment, the anti-GIPR antibody/GLP-1 receptor agonist conjugate molecule, or pharmaceutical composition comprising the same, is administered to the subject at a

dose of about 21 mg to about 840 mg every four weeks, at a dose of about 21 mg to about 840 mg every six weeks, at a dose of about 21 mg to about 840 mg every eight weeks, or at a dose of about 21 mg to about 840 mg every twelve weeks. In one embodiment, the anti-GIPR antibody/GLP-1 receptor agonist conjugate molecule, or pharmaceutical composition comprising the same, is administered to the subject at a dose of about 21 mg to about 840 mg every month, at a dose of about 21 mg to about 840 mg every one and a half months, at a dose of about 21 mg to about 840 mg every two months, or at a dose of about 21 mg to about 840 mg every three months. In one embodiment, the subject has obesity. In one embodiment, the subject has or is at risk of having an obesity related condition. In one embodiment, the subject has sleep apnea. In one embodiment, the subject has dyslipidemia. In one embodiment, the subject has or is at risk of having a cardiovascular disease. In one embodiment, the subject has or is at risk of having ASCVD. In one embodiment, the subject has heart failure. In one embodiment, the subject has hypertension. In one embodiment, the subject has chronic kidney failure. In one embodiment, the subject has MASH. In one embodiment, the subject has type 2 diabetes. In one embodiment, the subject a type 2 diabetes related condition. In one embodiment, the subject has hypertension and/or high blood sugar. In one embodiment, the subject has diabetic kidney disease or diabetic kidney failure. In one embodiment, the subject has cardiovascular disease.

[0256] In another aspect, the present disclosure provides the use of the anti-GIPR antibody/GLP-1 receptor agonist conjugate molecule disclosed herein for preparation of a medicament for preventing or treating obesity, an obesity related condition, type 2 diabetes, or a type 2 diabetes related condition in a subject in need thereof. In one embodiment, the medicament is formulated for administration at a dose of about 21 mg to about 840 mg. In one embodiment, the medicament, formulated at a dose of about 21 mg to about 840 mg, is administered to the subject every four weeks, every six weeks, every eight weeks, or every twelve weeks. In one embodiment, the medicament, formulated at a dose of about 21 mg to about 840 mg, is administered to the subject every month, every one and a half months, every two months, or every three month. In one embodiment, the subject has obesity. In one embodiment, the subject has or is at risk of having an obesity related condition. In one embodiment, the subject has from sleep apnea. In one embodiment, the subject has dyslipidemia. In one embodiment, the subject has or is at risk of having a cardiovascular disease. In one embodiment, the subject has or is at risk of having ASCVD. In one embodiment, the

subject has heart failure. In one embodiment, the subject has hypertension. In one embodiment, the subject has chronic kidney failure. In one embodiment, the subject has MASH. In one embodiment, the subject has type 2 diabetes. In one embodiment, the subject a type 2 diabetes related condition. In one embodiment, the subject has hypertension and/or high blood sugar. In one embodiment, the subject has diabetic kidney disease or diabetic kidney failure. In one embodiment, the subject has cardiovascular disease.

[0257] In another aspect, the present disclosure is directed to the use of the anti-GIPR antibody/GLP-1 receptor agonist conjugate molecule disclosed herein for preparation of a medicament for reducing body weight or reducing food intake in a subject in need thereof. The medicament is formulated for administration at a dose of about 21 mg to about 840 mg. In one embodiment, the medicament, formulated at a dose of about 21 mg to about 840 mg, is administered to the subject every four weeks, every six weeks, every eight weeks, or every twelve weeks. In one embodiment, the medicament, formulated at a dose of about 21 mg to about 840 mg, is administered to the subject every month, every one and a half months, every two months, or every three month. In one embodiment, the subject has obesity. In one embodiment, the subject has or is at risk of having an obesity related condition. In one embodiment, the subject has sleep apnea. In one embodiment, the subject has dyslipidemia. In one embodiment, the subject has or is at risk of having a cardiovascular disease. In one embodiment, the subject has or is at risk of having ASCVD. In one embodiment, the subject has heart failure. In one embodiment, the subject has hypertension. In one embodiment, the subject has chronic kidney failure. In one embodiment, the subject has MASH. In one embodiment, the subject has type 2 diabetes. In one embodiment, the subject a type 2 diabetes related condition. In one embodiment, the subject has hypertension and/or high blood sugar. In one embodiment, the subject has diabetic kidney disease or diabetic kidney failure. In one embodiment, the subject has cardiovascular disease.

[0258] In another aspect, the present disclosure is directed to the use of the anti-GIPR antibody/GLP-1 receptor agonist conjugate molecule disclosed herein for preparation of a medicament for reducing blood pressure and/or reducing blood sugar levels in a subject in need thereof. The medicament is formulated for administration at a dose of about 21 mg to about 840 mg. In one embodiment, the medicament, formulated at a dose of about 21 mg to about 840 mg, is administered to the subject every four weeks, every six weeks, every eight weeks, or every

twelve weeks. In one embodiment, the medicament, formulated at a dose of about 21 mg to about 840 mg, is administered to the subject every month, every one and a half months, every two months, or every three month. In one embodiment, the subject has obesity. In one embodiment, the subject has or is at risk of having an obesity related condition. In one embodiment, the subject has sleep apnea. In one embodiment, the subject has dyslipidemia. In one embodiment, the subject has or is at risk of having a cardiovascular disease. In one embodiment, the subject has or is at risk of having ASCVD. In one embodiment, the subject has heart failure. In one embodiment, the subject has hypertension. In one embodiment, the subject has chronic kidney failure. In one embodiment, the subject has MASH. In one embodiment, the subject has type 2 diabetes. In one embodiment, the subject a type 2 diabetes related condition. In one embodiment, the subject has hypertension and/or high blood sugar. In one embodiment, the subject has diabetic kidney disease or diabetic kidney failure. In one embodiment, the subject has cardiovascular disease.

[0259] In one embodiment, the weekly and monthly dosing schedules of the anti-GIPR antibody/GLP-1 receptor agonist conjugate molecule is similar among subjects regardless of body weight. Alternatively, the monthly dose of the anti-GIPR antibody/GLP-1 receptor agonist conjugate molecule may be based upon a subject's body weight.

[0260] The dose of the anti-GIPR antibody/GLP-1 receptor agonist conjugate molecule described herein can be administered in a single administration or divided among multiple administrations over the course of the dosing frequency period. For example, in one embodiment, the therapeutically effective dose of anti-GIPR antibody/GLP-1 receptor agonist conjugate molecule is administered in a single administration each frequency period. Thus, in one embodiment, any of the doses of anti-GIPR antibody/GLP-1 receptor agonist conjugate molecule described herein can be administered to the subject once a month (QM dosing). Subjects on a QM dosing regimen are typically administered the anti-GIPR antibody/GLP-1 receptor agonist conjugate molecule every 24 to 36 days, preferably, every 28 to 35 days, more preferably, every 28 to 31 days, or even more preferably, every 28 days or every 30 days. In these and other embodiments, the monthly dose is administered to the subject as a bolus injection, for example, using a self-injection device as described herein.

[0261] In alternative embodiments, the doses of the anti-GIPR antibody/GLP-1 receptor agonist conjugate molecule are divided among two or more administrations over the course of

the dosing frequency period. For example, for a dosing frequency period of one month, the monthly dose may be divided into four doses and administered on a weekly basis or divided into two doses and administered every two weeks. Any of the doses of anti-GIPR antibody/GLP-1 receptor agonist conjugate molecule described herein can be divided among two or more administrations. The number of administrations and intervening interval can be adjusted for a particular subject depending on the severity of the condition (e.g., obesity, type 2 diabetes, or an obesity or type 2 diabetes related condition), the age of the subject, the physical health of the subject, concomitant treatment with other medications, and/or the presence of other conditions

[0262] In one embodiment, a subject suitable for treatment in accordance with the methods and compositions described herein is a subject who has or is diagnosed with type 2 diabetes. In one embodiment, the subject having type 2 diabetes is a subject having a hemoglobin A1C (HbA1c) level of $\geq$ 6.5% and $\leq$ 10% (48 to 86 mmol/mol), where administration of the anti-GIPR antibody/GLP-1 receptor agonist conjugate molecule at the dose and frequency disclosed herein lowers the subject's HbA1c level. In one embodiment, administration of the anti-GIPR antibody/GLP-1 receptor agonist conjugate molecule at the dose and frequency disclosed herein lowers the subject's HbA1c level by about 0.5%, about 1%, about 1.5%, about 2%, or >2%. In one embodiment, a subject suitable for treatment in accordance with the methods and compositions described herein is a subject having type 2 diabetes who has been treated with metformin, a sulfonylurea, or a sodium-glucose cotransporter 2 (SGLT2) inhibitor as monotherapy or combination therapy.

[0263] In one embodiment, the subject has obesity, but does not have type 2 diabetes. In one embodiment, the subject has not previously received therapy for obesity.

[0264] In one embodiment, a subject suitable for treatment in accordance with the method and compositions described herein is a subject having a body mass index ("BMI") of $\geq$ 25 kg/m^2. In one embodiment, the subject has a BMI of $\geq$ 27 kg/m^2. In one embodiment, the subject has a BMI of $\geq$ 30 kg/m^2. Body Mass Index (BMI) is a person's weight in kilograms (or pounds) divided by the square of height in meters (or feet). A high BMI can indicate high body fatness. In one embodiment, the subject has a BMI of $\geq$ 35 kg/m^2. In one embodiment, the subject has a BMI of $\geq$ 40 kg/m^2. In one embodiment, the subject has a BMI greater than 25 kg/m2 and less than 40 kg/m2. In one embodiment, the subject has a BMI greater than 27 kg/m2 and less than 40 kg/m2. In one embodiment, the subject has a BMI greater than 30 kg/m2 and

less than 35 kg/m2. The measurements can also be converted to lbs/in^2. In one embodiment, the subject having a BMI of $\geq$ 25 kg/m^2, $\geq$ 27 kg/m^2, or $\geq$ 30 kg/m^2 further comprises one or more obesity associated conditions, e.g., hypertension, dyslipidemia, sleep apnea, or cardiovascular disease.

[0265] In one embodiment, treating obesity comprises promoting weight loss in a subject. Accordingly, the present disclosure is directed to a method of treating obesity wherein the subject loses about 5% of body weight over 52 weeks, about 10% of body weight over 52 weeks, about 15% of body weight over 52 weeks, about 20% of body weight over 52 weeks, about 25% of body weight over 52 weeks, or about 30% of body weight over 52 weeks. "Body weight" as used in the forgoing context is referring to a subject's weight before the first administration of the anti-GIPR antibody/GLP-1 receptor agonist conjugate molecule disclosed herein, or a pharmaceutical composition comprising the same.

[0266] In one embodiment, treating obesity comprises maintaining a subject's body weight by administering a maintenance dose of the anti-GIPR antibody/GLP-1 receptor agonist to subject. Accordingly, the present disclosure is directed to a method of maintaining a subject's body weight wherein the subject's body weight does not fluctuate more than ±0.5% of goal body weight, ±1.0% of goal body weight, ±1.5% of goal body weight, ±2.0% of goal body weight, ±2.5% of goal body weight, ±3.0% of goal body weight, ±3.5% of goal body weight, ±4.0% of goal body weight, ±4.5% of goal body weight, or ±5.0% of goal body weight. "Goal body weight" as used in the foregoing context refers to the body weight a subject means to maintain. A maintenance dose can be the same amount and frequency as a dose that promotes weight loss. Alternatively, a maintenance dose can be 1) a lower amount of the anti-GIPR antibody/GLP-1 receptor agonist conjugate than a dose that promotes weight loss, 2) a dose administered less frequently than a dose that promotes weight loss, or 3) a dose that is both a lower amount than a dose that promotes weight loss and administered less frequently than a dose that promotes weight loss.

[0267] In one embodiment of the methods described herein, the anti-GIPR antibody/GLP-1 receptor agonist conjugate molecule is administered to the subject parenterally. Parenteral administration includes intraperitoneal, intramuscular, intravenous, intradermal, and subcutaneous administration. In a preferred embodiment, the pharmaceutical composition comprising a therapeutically effective amount of an anti-GIPR antibody/GLP-1 receptor agonist

conjugate molecule is administered to the subject subcutaneously. In these and other embodiments in which the pharmaceutical composition is administered by parenteral injection, the pharmaceutical composition can be administered to the subject with a syringe. In one embodiment, the syringe is pre-filled with the pharmaceutical composition. In other embodiments in which the pharmaceutical composition is administered to the subject by parenteral injection, such as subcutaneous injection, the pharmaceutical composition is administered with an injection device, including devices for self-administration. Such devices are commercially available and include, but are not limited to, autoinjectors, dosing pens, microinfusion pumps, and pre-filled syringes. Exemplary devices for administering a pharmaceutical composition comprising a therapeutically effective amount of an anti-GIPR antibody/GLP-1 receptor agonist conjugate molecule according to the methods of the invention include autoinjectors (*e.g.*, SureClick®, EverGentle®, Avanti®, DosePro®, Molly®, and Leva®), pen injection devices (e.g., Madie® pen injector, DCP™ pen injector, BD Vystra™ disposable pen, BD™ reusable pen), and pre-filled syringes (BD Sterifill™, BD Hypak™, prefilled syringes from Baxter). In one embodiment, the pharmaceutical composition comprising a therapeutically effective amount of an anti-GIPR antibody/GLP-1 receptor agonist conjugate molecule is administered to the subject with a pre-filled syringe. In one embodiment, the pharmaceutical composition comprising a therapeutically effective amount of an anti-GIPR antibody/GLP-1 receptor agonist conjugate molecule is administered to the subject with an autoinjector. In one embodiment, the injection volume is about 3mL or less, about 2mL or less, or about 1 mL or less.

[0268] In one embodiment, the anti-GIPR antibody/GLP-1 receptor agonist conjugate molecule as disclosed herein is administered to the subject over the course of a set treatment period. A "treatment period" begins upon administration of a first dose of the anti-GIPR antibody/GLP-1 receptor agonist conjugate molecule and ends upon administration of a final dose of the conjugate molecule. The treatment period may comprise from about 1 month to about 36 months, such as about 2 months, about 3 months, about 4 months, about 5 months, about 6 months, about 7 months, about 8 months, about 9 months, about 10 months, about 11 months, about 12 months, about 13 months, about 14 months, about 15 months, about 18 months, about 21 months, about 24 months, about 27 months, about 30 months, or about 33 months. In one embodiment, the treatment period is about 6 months. In one embodiment, the

treatment period is about 7 months. In one embodiment, the treatment period is about 12 months. In one embodiment, the treatment period can be longer than 36 months, such as 48 or 60 or 64 months or more.

[0269] Administration of an anti-GIPR antibody/GLP-1 receptor agonist conjugate molecule according to the methods disclosed herein preferably causes few or no adverse side effects in the subject being treated. As used herein, the term "adverse side effect" refers to any abnormality, defect, mutation, lesion, degeneration, harmful or undesirable reaction, symptom, or injury, which may be caused by taking the drug. In one embodiment, administration of the anti-GIPR antibody/GLP-1 receptor agonist conjugate molecule does not substantially cause one or more adverse side effects associated with other obesity treatments. Side effects associated with other weight loss treatments include, but are not limited to, fatigue, nausea, dizziness, insomnia, depression, reduced exercise tolerance, tremor, paresthesia, teratogenicity, and cognitive difficulty. In one embodiment, administration of the anti-GIPR antibody/GLP-1 receptor agonist conjugate molecule is associated with a lower rate or number of adverse side effects as compared to the rate or number of adverse side effects associated with other obesity treatments. In one embodiment, administration of the anti-GIPR antibody/GLP-1 receptor agonist conjugate molecule is associated with a lower rate of discontinuation due to adverse side effects as compared to the rate of discontinuation due to adverse side effects associated with other weight loss treatments. In one embodiment, the number and type of adverse side effects associated with administration of the anti-GIPR antibody/GLP-1 receptor agonist conjugate molecule is not statistically different than the number and type of adverse side effects associated with administration of placebo.

EMBODIMENTS

[0270] Embodiment 1 is a human glucagon-like peptide 1 (GLP-1) receptor agonist polypeptide comprising the amino acid sequence of H[Aib]EGTFTSDYSSYLEEX_{17}AAX_{20}EFIX_{24}WL$X_{27}X_{28}$GGG (SEQ ID NO: 1575), wherein X_{17} is Q, K, E, or R; X_{20} is K, R, Q, or homoarginine (hArg); X_{24} is A, E, Q, D, d-Ala, G, N, K, (1S,2S)-2-Aminocyclopentanecarboxylic acid (ACPC), (3S,4R)-4-Amino-3-pyrrolidinecarboxylic acid (APCA), T, S, or Y; X_{27} is V, K, Aib, N, S, T, Y, Q, or R; and X_{28} is K, E, R, Q, D, N, G, S, or T; and wherein the GLP-1 receptor agonist polypeptide does not comprise the amino acid sequence of SEQ ID NO: 1574 (H[Aib]EGTFTSDYSSYLEEQAAKEFIAWLVKGGG).

[0271] Embodiment 2 is the GLP-1 receptor agonist polypeptide of embodiment 1, wherein the GLP-1 receptor agonist polypeptide comprises the amino acid sequence of H[Aib]EGTFTSDYSSYLEEX_{17}AAX_{20}EFIX_{24}WL$X_{27}X_{28}$GGG (SEQ ID NO: 1576), wherein X_{17} is Q or K; X_{20} is K or R; X_{24} is A, E, or Q; X_{27} is V or K; and X_{28} is K, E, or R.

[0272] Embodiment 3 is the GLP-1 receptor agonist polypeptide of embodiment 1, wherein the GLP-1 receptor agonist polypeptide comprises the amino acid sequence of H[Aib]EGTFTSDYSSYLEEX_{17}AAREFIX_{24}WL$X_{27}X_{28}$GGG (SEQ ID NO: 1577) wherein X_{17} is Q or K; X_{24} is A, E, or Q; X_{27} is V or K; and X_{28} is K, E, or R.

[0273] Embodiment 4 is the GLP-1 receptor agonist polypeptide of embodiment 1, wherein the GLP-1 receptor agonist polypeptide comprises the amino acid sequence of H[Aib]EGTFTSDYSSYLEEX_{17}AAX_{20}EFIX_{24}WLKX_{28}GGG (SEQ ID NO: 1578), wherein X_{17} is Q or K; X_{20} is K or R; X_{24} is A, E, or Q; and X_{28} is K, E, or R.

[0274] Embodiment 5 is the GLP-1 receptor agonist polypeptide of any one of embodiments 1-4, where the GLP-1 receptor agonist polypeptide comprises the amino acid sequence of any one of SEQ ID NO: 1579, SEQ ID NO: 1580, SEQ ID NO: 1581, SEQ ID NO: 1582, or SEQ ID NO: 1583.

[0275] Embodiment 6 is a human glucagon-like peptide 1 (GLP-1) receptor agonist polypeptide, wherein: the polypeptide comprises 31 amino acids and comprises an amino acid sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 1580; and wherein the polypeptide comprises an α-amino-isobutyric acid (Aib) at position 2; a tyrosine at position 10; a glutamic acid at positions 16, 24, and 28; an arginine at position 20; a lysine at positions 17 and 27; and a glycine at position 31.

[0276] Embodiment 7 is a human glucagon-like peptide 1 (GLP-1) receptor agonist polypeptide, wherein: the GLP-1 receptor agonist polypeptide comprises 31 amino acids and comprises an amino acid sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 1579; and wherein the GLP-1 receptor agonist polypeptide comprises an Aib at position 2; a tyrosine at position 10; a glutamic acid at positions 16 and 24; an arginine at position 20; a lysine at positions 27; and a glycine at position 30.

[0277] Embodiment 8 is a human glucagon-like peptide 1 (GLP-1) receptor agonist polypeptide, wherein: the GLP-1 receptor agonist polypeptide comprises 31 amino acids and comprises an amino acid sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 1581; and wherein the GLP-1 receptor agonist polypeptide comprises an Aib at position 2; a tyrosine at position 10;

a glutamic acid at positions 16 and 24; an arginine at position 20; a lysine at positions 17, 27; and a glycine at position 30.

[0278] Embodiment 9 is a human glucagon-like peptide 1 (GLP-1) receptor agonist polypeptide, wherein: the GLP-1 receptor agonist polypeptide comprises 31 amino acids and comprises an amino acid sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 1583; and wherein the GLP-1 receptor agonist polypeptide comprises an Aib at position 2; a tyrosine at position 10; a glutamic acid at positions 16 and 28; an arginine at position 20; a lysine at positions 17, 27; a glutamine at position 24; and a glycine at position 30.

[0279] Embodiment 10 is a human glucagon-like peptide 1 (GLP-1) receptor agonist polypeptide, wherein: the GLP-1 receptor agonist polypeptide comprises 31 amino acids and comprises an amino acid sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 1582; and wherein the GLP-1 receptor agonist polypeptide comprises an Aib at position 2; a tyrosine at position 10; a glutamic acid at positions 16 and 24; an arginine at positions 20 and 28; a lysine at positions 27; and a glycine at position 30.

[0280] Embodiment 11 is a molecule comprising: a first human glucagon-like peptide 1 (GLP-1) receptor agonist polypeptide comprising the amino acid sequence of H[Aib]EGTFTSDYSSYLEEX_{17}AAX_{20}EFIX_{24}WL$X_{27}X_{28}$GGG (SEQ ID NO: 1575), wherein X_{17} is Q, K, E, or R; X_{20} is K, R, Q, or homoarginine (hArg); X_{24} is A, E, Q, D, d-Ala, G, N, K, (1S,2S)-2-Aminocyclopentanecarboxylic acid (ACPC), (3S,4R)-4-Amino-3-pyrrolidinecarboxylic acid (APCA), T, S, or Y; X_{27} is V, K, Aib, N, S, T, Y, Q, or R; and X_{28} is K, E, R, Q, D, N, G, S, or T, and wherein the GLP-1 receptor agonist polypeptide does not comprise the amino acid sequence of SEQ ID NO: 1574; and a half-life extending moiety.

[0281] Embodiment 12 is the molecule of embodiment 11, wherein the first GLP-1 receptor agonist polypeptide comprises the amino acid sequence of H[Aib]EGTFTSDYSSYLEEX_{17}AAX_{20}EFIX_{24}WL$X_{27}X_{28}$GGG (SEQ ID NO: 1576), wherein X_{17} is Q or K; X_{20} is K or R; X_{24} is A, E, or Q; X_{27} is V or K; and X_{28} is K, E, or R.

[0282] Embodiment 13 is the molecule of embodiment 11, wherein the first GLP-1 receptor agonist polypeptide comprises the amino acid sequence of H[Aib]EGTFTSDYSSYLEEX_{17}AAR_{20}EFIX_{24}WL$X_{27}X_{28}$GGG (SEQ ID NO: 1577) wherein X_{17} is Q or K; X_{24} is A, E, or Q; X_{27} is V or K; and X_{28} is K, E, or R.

[0283] Embodiment 14 is the molecule of embodiment 11, wherein the first GLP-1 receptor agonist polypeptide comprises the amino acid sequence of

H[Aib]EGTFTSDYSSYLEEX_{17}AAX_{20}EFIX_{24}WLK$_{27}X_{28}$GGG (SEQ ID NO: 1578), wherein X_{17} is Q or K; X_{20} is K or R; X_{24} is A, E, or Q; and X_{28} is K, E, or R.

[0284] Embodiment 15 is the molecule of embodiment 11, wherein the first GLP-1 receptor agonist polypeptide comprises the amino acid sequence of any one of SEQ ID NO: 1579, SEQ ID NO: 1580, SEQ ID NO: 1581, SEQ ID NO: 1582, or SEQ ID NO: 1583.

[0285] Embodiment 16 is the molecule of any one of embodiments 11–15, wherein the half-life extending moiety is an antibody.

[0286] Embodiment 17 is a conjugate molecule comprising: (i) a first human glucagon-like peptide 1 (GLP-1) receptor agonist polypeptide comprising the amino acid sequence of H[Aib]EGTFTSDYSSYLEEX_{17}AAX_{20}EFIX_{24}WL$X_{27}X_{28}$GGG (SEQ ID NO: 1575), wherein X_{17} is Q, K, E, or R; X_{20} is K, R, Q, or homoarginine (hArg); X_{24} is A, E, Q, D, d-Ala, G, N, K, (1S,2S)-2-Aminocyclopentanecarboxylic acid (ACPC), (3S,4R)-4-Amino-3-pyrrolidinecarboxylic acid (APCA), T, S, or Y; X_{27} is V, K, Aib, N, S, T, Y, Q, or R; and X_{28} is K, E, R, Q, D, N, G, S, or T, and wherein the GLP-1 receptor agonist polypeptide does not comprise the amino acid sequence of SEQ ID NO: 1574; and (ii) an antagonist anti-glucose-dependent insulinotropic polypeptide receptor (GIPR) human antibody.

[0287] Embodiment 18 is the conjugate molecule of embodiment 17, wherein the anti-GIPR antibody antagonizes human GIPR.

[0288] Embodiment 19 is the conjugate molecule of embodiment 17 or 18, wherein the first GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1575.

[0289] Embodiment 20 is the conjugate molecule of embodiment 17 or 18, wherein the first GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1576.

[0290] Embodiment 21 is the conjugate molecule of embodiment 17 or 18, wherein the first GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1577.

[0291] Embodiment 22 is the conjugate molecule of embodiment 17 or 18, wherein the first GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1578.

[0292] Embodiment 23 is the conjugate molecule of embodiment 17 or 18, wherein the first GLP-1 receptor agonist polypeptide comprises the amino acid sequence of any one of SEQ ID NO: 1579, SEQ ID NO: 1580, SEQ ID NO: 1581, SEQ ID NO: 1582, or SEQ ID NO: 1583.

[0293] Embodiment 24 is the conjugate molecule of embodiment 17 or 18, wherein the anti-GIPR antibody comprises a first cysteine conjugation site within a light chain or heavy chain of the

antibody, and wherein the first GLP-1 receptor agonist polypeptide is conjugated, at its C-terminus, to the first cysteine conjugation site of the anti-GIPR antibody.

[0294] Embodiment 25 is the conjugate molecule of embodiment 24, wherein the first GLP-1 receptor agonist polypeptide is conjugated, at its C-terminus, to the first cysteine conjugation site of the anti-GIPR antibody via a first linker moiety.

[0295] Embodiment 26 is the conjugate molecule of embodiment 25, wherein the first linker moiety is a peptide linker and the peptide linker comprises the amino acid sequence of any one of SEQ ID NOs: 1585–1593.

[0296] Embodiment 27 is the conjugate molecule of embodiment 25, wherein the first linker moiety is a PEG linker.

[0297] Embodiment 28 is the conjugate molecule of any one of embodiments 24 to 27, wherein the first cysteine conjugation site of the anti-GIPR antibody is at position 88 of the light chain, position 384 of the heavy chain, or position 487 of the heavy chain according to AHo numbering.

[0298] Embodiment 29 is the conjugate molecule of anyone of embodiments 17 to 28, wherein the molecule further comprises: a second GLP-1 receptor agonist polypeptide, wherein the second GLP-1 receptor agonist polypeptide is conjugated, at its C-terminus, to a second cysteine conjugation site of the anti-GIPR antibody.

[0299] Embodiment 30 is the conjugate molecule of embodiment 29, wherein the second GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1575.

[0300] Embodiment 31 is the conjugate molecule of embodiment 29, wherein the second GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1576.

[0301] Embodiment 32 is the conjugate molecule of embodiment 29 wherein the second GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1577.

[0302] Embodiment 33 is the conjugate molecule of embodiment 29, wherein the second GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1578.

[0303] Embodiment 34 is the conjugate molecule of embodiment 29, wherein the second GLP-1 receptor agonist polypeptide comprises the amino acid sequence of any one of SEQ ID NO: 1579, SEQ ID NO: 1580, SEQ ID NO: 1581, SEQ ID NO: 1582, or SEQ ID NO: 1583.

[0304] Embodiment 35 is the conjugate molecule of embodiment 29, wherein the second GLP-1 receptor agonist polypeptide comprises the same amino acid sequence as the first GLP-1 receptor agonist polypeptide.

[0305] Embodiment 36 is the conjugate molecule of any one of embodiments 29 to 35, wherein the second GLP-1 receptor agonist polypeptide is conjugated, at its C-terminus, to the second cysteine conjugation site of the anti-GIPR antibody via a second linker moiety.

[0306] Embodiment 37 is the conjugate molecule of embodiment 36, wherein the second linker moiety is a peptide linker and the peptide linker comprises the amino acid sequence of any one of SEQ ID NOs: 1585–1593.

[0307] Embodiment 38 is the conjugate molecule of embodiment 36, wherein the second linker moiety is a PEG linker.

[0308] Embodiment 39 is the conjugate molecule of embodiment 29, wherein the first and second conjugation sites of the anti-GIPR antibody are at position 88 of each light chain, position 384 of each heavy chain, or position 487 of each heavy chain according to AHo numbering.

[0309] Embodiment 40 is the conjugate molecule of any one of embodiments 17 to 39, wherein the anti-GIPR antibody comprises a light chain complementarity determining region 1 (CDRL1), a CDRL2, a CDRL3, a heavy chain complementarity determining region 1 (CDRH1), a CDRH2, and a CDRH3, wherein the CDRL1, the CDRL2, the CDRL3, the CDRH1, the CDRH2, and the CDRH3 comprise the amino acid sequences selected from:

i. SEQ ID NO: 629, SEQ ID NO: 786, SEQ ID NO: 943, SEQ ID NO: 1100, SEQ ID NO: 1257, and SEQ ID NO: 1414, respectively;

ii. SEQ ID NO: 630, SEQ ID NO: 787, SEQ ID NO: 944, SEQ ID NO: 1101, SEQ ID NO: 1258, and SEQ ID NO: 1415, respectively;

iii. SEQ ID NO: 631, SEQ ID NO: 788, SEQ ID NO: 945, SEQ ID NO: 1102, SEQ ID NO: 1259, and SEQ ID NO: 1416, respectively;

iv. SEQ ID NO: 632, SEQ ID NO: 789, SEQ ID NO: 946, SEQ ID NO: 1103, SEQ ID NO: 1260, and SEQ ID NO: 1417, respectively;

v. SEQ ID NO: 633, SEQ ID NO: 790, SEQ ID NO: 947, SEQ ID NO: 1104, SEQ ID NO: 1261, and SEQ ID NO: 1418, respectively;

vi. SEQ ID NO: 634, SEQ ID NO: 791, SEQ ID NO: 948, SEQ ID NO: 1105, SEQ ID NO: 1262, and SEQ ID NO: 1419, respectively;

vii. SEQ ID NO: 635, SEQ ID NO: 792, SEQ ID NO: 949, SEQ ID NO: 1106, SEQ ID NO: 1263, and SEQ ID NO: 1420, respectively;

viii. SEQ ID NO: 636, SEQ ID NO: 793, SEQ ID NO: 950, SEQ ID NO: 1107, SEQ ID NO: 1264, and SEQ ID NO: 1421, respectively;

ix. SEQ ID NO: 637, SEQ ID NO: 794, SEQ ID NO: 951, SEQ ID NO: 1108, SEQ ID NO: 1265, and SEQ ID NO: 1422, respectively;

x. SEQ ID NO: 638, SEQ ID NO: 795, SEQ ID NO: 952, SEQ ID NO: 1109, SEQ ID NO: 1266, and SEQ ID NO: 1423, respectively;

xi. SEQ ID NO: 639, SEQ ID NO: 796, SEQ ID NO: 953, SEQ ID NO: 1110, SEQ ID NO: 1267, and SEQ ID NO: 1424, respectively;

xii. SEQ ID NO: 640, SEQ ID NO: 797, SEQ ID NO: 954, SEQ ID NO: 1111, SEQ ID NO: 1268, and SEQ ID NO: 1425, respectively;

xiii. SEQ ID NO: 641, SEQ ID NO: 798, SEQ ID NO: 955, SEQ ID NO: 1112, SEQ ID NO: 1269, and SEQ ID NO: 1426, respectively;

xiv. SEQ ID NO: 642, SEQ ID NO: 799, SEQ ID NO: 956, SEQ ID NO: 1113, SEQ ID NO: 1270, and SEQ ID NO: 1427, respectively;

xv. SEQ ID NO: 643, SEQ ID NO: 800, SEQ ID NO: 957, SEQ ID NO: 1114, SEQ ID NO: 1271, and SEQ ID NO: 1428, respectively;

xvi. SEQ ID NO: 644, SEQ ID NO: 801, SEQ ID NO: 958, SEQ ID NO: 1115, SEQ ID NO: 1272, and SEQ ID NO: 1429, respectively;

xvii. SEQ ID NO: 645, SEQ ID NO: 802, SEQ ID NO: 959, SEQ ID NO: 1116, SEQ ID NO: 1273, and SEQ ID NO: 1430, respectively;

xviii. SEQ ID NO: 646, SEQ ID NO: 803, SEQ ID NO: 960, SEQ ID NO: 1117, SEQ ID NO: 1274, and SEQ ID NO: 1431, respectively;

xix. SEQ ID NO: 647, SEQ ID NO: 804, SEQ ID NO: 961, SEQ ID NO: 1118, SEQ ID NO: 1275, and SEQ ID NO: 1432, respectively;

xx. SEQ ID NO: 648, SEQ ID NO: 805, SEQ ID NO: 962, SEQ ID NO: 1119, SEQ ID NO: 1276, and SEQ ID NO: 1433, respectively;

xxi. SEQ ID NO: 649, SEQ ID NO: 806, SEQ ID NO: 963, SEQ ID NO: 1120, SEQ ID NO: 1277, and SEQ ID NO: 1434, respectively;

xxii. SEQ ID NO: 650, SEQ ID NO: 807, SEQ ID NO: 964, SEQ ID NO: 1121, SEQ ID NO: 1278, and SEQ ID NO: 1435, respectively;

xxiii. SEQ ID NO: 651, SEQ ID NO: 808, SEQ ID NO: 965, SEQ ID NO: 1122, SEQ ID NO: 1279, and SEQ ID NO: 1436, respectively;

xxiv. SEQ ID NO: 652, SEQ ID NO: 809, SEQ ID NO: 966, SEQ ID NO: 1123, SEQ ID NO: 1280, and SEQ ID NO: 1437, respectively;

xxv. SEQ ID NO: 653, SEQ ID NO: 810, SEQ ID NO: 967, SEQ ID NO: 1124, SEQ ID NO: 1281, and SEQ ID NO: 1438, respectively;

xxvi. SEQ ID NO: 654, SEQ ID NO: 811, SEQ ID NO: 968, SEQ ID NO: 1125, SEQ ID NO: 1282, and SEQ ID NO: 1439, respectively;

xxvii. SEQ ID NO: 655, SEQ ID NO: 812, SEQ ID NO: 969, SEQ ID NO: 1126, SEQ ID NO: 1283, and SEQ ID NO: 1440, respectively;

xxviii. SEQ ID NO: 656, SEQ ID NO: 813, SEQ ID NO: 970, SEQ ID NO: 1127, SEQ ID NO: 1284, and SEQ ID NO: 1441, respectively;

xxix. SEQ ID NO: 657, SEQ ID NO: 814, SEQ ID NO: 971, SEQ ID NO: 1128, SEQ ID NO: 1285, and SEQ ID NO: 1442, respectively;

xxx. SEQ ID NO: 658, SEQ ID NO: 815, SEQ ID NO: 972, SEQ ID NO: 1129, SEQ ID NO: 1286, and SEQ ID NO: 1443, respectively;

xxxi. SEQ ID NO: 659, SEQ ID NO: 816, SEQ ID NO: 973, SEQ ID NO: 1130, SEQ ID NO: 1287, and SEQ ID NO: 1444, respectively;

xxxii. SEQ ID NO: 660, SEQ ID NO: 817, SEQ ID NO: 974, SEQ ID NO: 1131, SEQ ID NO: 1288, and SEQ ID NO: 1445, respectively;

xxxiii. SEQ ID NO: 661, SEQ ID NO: 818, SEQ ID NO: 975, SEQ ID NO: 1132, SEQ ID NO: 1289, and SEQ ID NO: 1446, respectively;

xxxiv. SEQ ID NO: 662, SEQ ID NO: 819, SEQ ID NO: 976, SEQ ID NO: 1133, SEQ ID NO: 1290, and SEQ ID NO: 1447, respectively;

xxxv. SEQ ID NO: 663, SEQ ID NO: 820, SEQ ID NO: 977, SEQ ID NO: 1134, SEQ ID NO: 1291, and SEQ ID NO: 1448, respectively;

xxxvi. SEQ ID NO: 664, SEQ ID NO: 821, SEQ ID NO: 978, SEQ ID NO: 1135, SEQ ID NO: 1292, and SEQ ID NO: 1449, respectively;

xxxvii. SEQ ID NO: 665, SEQ ID NO: 822, SEQ ID NO: 979, SEQ ID NO: 1136, SEQ ID NO: 1293, and SEQ ID NO: 1450, respectively;

xxxviii. SEQ ID NO: 666, SEQ ID NO: 823, SEQ ID NO: 980, SEQ ID NO: 1137, SEQ ID NO: 1294, and SEQ ID NO: 1451, respectively;

xxxix. SEQ ID NO: 667, SEQ ID NO: 824, SEQ ID NO: 981, SEQ ID NO: 1138, SEQ ID NO: 1295, and SEQ ID NO: 1452, respectively;

xl. SEQ ID NO: 668, SEQ ID NO: 825, SEQ ID NO: 982, SEQ ID NO: 1139, SEQ ID NO: 1296, and SEQ ID NO: 1453, respectively;

xli. SEQ ID NO: 669, SEQ ID NO: 826, SEQ ID NO: 983, SEQ ID NO: 1140, SEQ ID NO: 1297, and SEQ ID NO: 1454, respectively;

xlii. SEQ ID NO: 670, SEQ ID NO: 827, SEQ ID NO: 984, SEQ ID NO: 1141, SEQ ID NO: 1298, and SEQ ID NO: 1455, respectively;

xliii. SEQ ID NO: 671, SEQ ID NO: 828, SEQ ID NO: 985, SEQ ID NO: 1142, SEQ ID NO: 1299, and SEQ ID NO: 1456, respectively;

xliv. SEQ ID NO: 672, SEQ ID NO: 829, SEQ ID NO: 986, SEQ ID NO: 1143, SEQ ID NO: 1300, and SEQ ID NO: 1457, respectively;

xlv. SEQ ID NO: 673, SEQ ID NO: 830, SEQ ID NO: 987, SEQ ID NO: 1144, SEQ ID NO: 1301, and SEQ ID NO: 1458, respectively;

xlvi. SEQ ID NO: 674, SEQ ID NO: 831, SEQ ID NO: 988, SEQ ID NO: 1145, SEQ ID NO: 1302, and SEQ ID NO: 1459, respectively;

xlvii. SEQ ID NO: 675, SEQ ID NO: 832, SEQ ID NO: 989, SEQ ID NO: 1146, SEQ ID NO: 1303, and SEQ ID NO: 1460, respectively;

xlviii. SEQ ID NO: 676, SEQ ID NO: 833, SEQ ID NO: 990, SEQ ID NO: 1147, SEQ ID NO: 1304, and SEQ ID NO: 1461, respectively;

xlix. SEQ ID NO: 677, SEQ ID NO: 834, SEQ ID NO: 991, SEQ ID NO: 1148, SEQ ID NO: 1305, and SEQ ID NO: 1462, respectively;

l. SEQ ID NO: 678, SEQ ID NO: 835, SEQ ID NO: 992, SEQ ID NO: 1149, SEQ ID NO: 1306, and SEQ ID NO: 1463, respectively;

li. SEQ ID NO: 679, SEQ ID NO: 836, SEQ ID NO: 993, SEQ ID NO: 1150, SEQ ID NO: 1307, and SEQ ID NO: 1464, respectively;

lii. SEQ ID NO: 680, SEQ ID NO: 837, SEQ ID NO: 994, SEQ ID NO: 1151, SEQ ID NO: 1308, and SEQ ID NO: 1465, respectively;

liii. SEQ ID NO: 681, SEQ ID NO: 838, SEQ ID NO: 995, SEQ ID NO: 1152, SEQ ID NO: 1309, and SEQ ID NO: 1466, respectively;

liv. SEQ ID NO: 682, SEQ ID NO: 839, SEQ ID NO: 996, SEQ ID NO: 1153, SEQ ID NO: 1310, and SEQ ID NO: 1467, respectively;

lv. SEQ ID NO: 683, SEQ ID NO: 840, SEQ ID NO: 997, SEQ ID NO: 1154, SEQ ID NO: 1311, and SEQ ID NO: 1468, respectively;

lvi. SEQ ID NO: 684, SEQ ID NO: 841, SEQ ID NO: 998, SEQ ID NO: 1155, SEQ ID NO: 1312, and SEQ ID NO: 1469, respectively;

lvii. SEQ ID NO: 685, SEQ ID NO: 842, SEQ ID NO: 999, SEQ ID NO: 1156, SEQ ID NO: 1313, and SEQ ID NO: 1470, respectively;

lviii. SEQ ID NO: 686, SEQ ID NO: 843, SEQ ID NO: 1000, SEQ ID NO: 1157, SEQ ID NO: 1314, and SEQ ID NO: 1471, respectively;

lix. SEQ ID NO: 687, SEQ ID NO: 844, SEQ ID NO: 1001, SEQ ID NO: 1158, SEQ ID NO: 1315, and SEQ ID NO: 1472, respectively;

lx. SEQ ID NO: 688, SEQ ID NO: 845, SEQ ID NO: 1002, SEQ ID NO: 1159, SEQ ID NO: 1316, and SEQ ID NO: 1473, respectively;

lxi. SEQ ID NO: 689, SEQ ID NO: 846, SEQ ID NO: 1003, SEQ ID NO: 1160, SEQ ID NO: 1317, and SEQ ID NO: 1474, respectively;

lxii. SEQ ID NO: 690, SEQ ID NO: 847, SEQ ID NO: 1004, SEQ ID NO: 1161, SEQ ID NO: 1318, and SEQ ID NO: 1475, respectively;

lxiii. SEQ ID NO: 691, SEQ ID NO: 848, SEQ ID NO: 1005, SEQ ID NO: 1162, SEQ ID NO: 1319, and SEQ ID NO: 1476, respectively;

lxiv. SEQ ID NO: 692, SEQ ID NO: 849, SEQ ID NO: 1006, SEQ ID NO: 1163, SEQ ID NO: 1320, and SEQ ID NO: 1477, respectively;

lxv. SEQ ID NO: 693, SEQ ID NO: 850, SEQ ID NO: 1007, SEQ ID NO: 1164, SEQ ID NO: 1321, and SEQ ID NO: 1478, respectively;

lxvi. SEQ ID NO: 694, SEQ ID NO: 851, SEQ ID NO: 1008, SEQ ID NO: 1165, SEQ ID NO: 1322, and SEQ ID NO: 1479, respectively;

lxvii. SEQ ID NO: 695, SEQ ID NO: 852, SEQ ID NO: 1009, SEQ ID NO: 1166, SEQ ID NO: 1323, and SEQ ID NO: 1480, respectively;

lxviii. SEQ ID NO: 696, SEQ ID NO: 853, SEQ ID NO: 1010, SEQ ID NO: 1167, SEQ ID NO: 1324, and SEQ ID NO: 1481, respectively;

lxix. SEQ ID NO: 697, SEQ ID NO: 854, SEQ ID NO: 1011, SEQ ID NO: 1168, SEQ ID NO: 1325, and SEQ ID NO: 1482, respectively;

lxx. SEQ ID NO: 698, SEQ ID NO: 855, SEQ ID NO: 1012, SEQ ID NO: 1169, SEQ ID NO: 1326, and SEQ ID NO: 1483, respectively;

lxxi. SEQ ID NO: 699, SEQ ID NO: 856, SEQ ID NO: 1013, SEQ ID NO: 1170, SEQ ID NO: 1327, and SEQ ID NO: 1484, respectively;

lxxii. SEQ ID NO: 700, SEQ ID NO: 857, SEQ ID NO: 1014, SEQ ID NO: 1171, SEQ ID NO: 1328, and SEQ ID NO: 1485, respectively;

lxxiii. SEQ ID NO: 701, SEQ ID NO: 858, SEQ ID NO: 1015, SEQ ID NO: 1172, SEQ ID NO: 1329, and SEQ ID NO: 1486, respectively;

lxxiv. SEQ ID NO: 702, SEQ ID NO: 859, SEQ ID NO: 1016, SEQ ID NO: 1173, SEQ ID NO: 1330, and SEQ ID NO: 1487, respectively;

lxxv. SEQ ID NO: 703, SEQ ID NO: 860, SEQ ID NO: 1017, SEQ ID NO: 1174, SEQ ID NO: 1331, and SEQ ID NO: 1488, respectively;

lxxvi. SEQ ID NO: 704, SEQ ID NO: 861, SEQ ID NO: 1018, SEQ ID NO: 1175, SEQ ID NO: 1332, and SEQ ID NO: 1489, respectively;

lxxvii. SEQ ID NO: 705, SEQ ID NO: 862, SEQ ID NO: 1019, SEQ ID NO: 1176, SEQ ID NO: 1333, and SEQ ID NO: 1490, respectively;

lxxviii. SEQ ID NO: 706, SEQ ID NO: 863, SEQ ID NO: 1020, SEQ ID NO: 1177, SEQ ID NO: 1334, and SEQ ID NO: 1491, respectively;

lxxix. SEQ ID NO: 707, SEQ ID NO: 864, SEQ ID NO: 1021, SEQ ID NO: 1178, SEQ ID NO: 1335, and SEQ ID NO: 1492, respectively;

lxxx. SEQ ID NO: 708, SEQ ID NO: 865, SEQ ID NO: 1022, SEQ ID NO: 1179, SEQ ID NO: 1336, and SEQ ID NO: 1493, respectively;

lxxxi. SEQ ID NO: 709, SEQ ID NO: 866, SEQ ID NO: 1023, SEQ ID NO: 1180, SEQ ID NO: 1337, and SEQ ID NO: 1494, respectively;

lxxxii. SEQ ID NO: 710, SEQ ID NO: 867, SEQ ID NO: 1024, SEQ ID NO: 1181, SEQ ID NO: 1338, and SEQ ID NO: 1495, respectively;

lxxxiii. SEQ ID NO: 711, SEQ ID NO: 868, SEQ ID NO: 1025, SEQ ID NO: 1182, SEQ ID NO: 1339, and SEQ ID NO: 1496, respectively;

lxxxiv. SEQ ID NO: 712, SEQ ID NO: 869, SEQ ID NO: 1026, SEQ ID NO: 1183, SEQ ID NO: 1340, and SEQ ID NO: 1497, respectively;

lxxxv. SEQ ID NO: 713, SEQ ID NO: 870, SEQ ID NO: 1027, SEQ ID NO: 1184, SEQ ID NO: 1341, and SEQ ID NO: 1498, respectively;

lxxxvi. SEQ ID NO: 714, SEQ ID NO: 871, SEQ ID NO: 1028, SEQ ID NO: 1185, SEQ ID NO: 1342, and SEQ ID NO: 1499, respectively;

lxxxvii. SEQ ID NO: 715, SEQ ID NO: 872, SEQ ID NO: 1029, SEQ ID NO: 1186, SEQ ID NO: 1343, and SEQ ID NO: 1500, respectively;

lxxxviii. SEQ ID NO: 716, SEQ ID NO: 873, SEQ ID NO: 1030, SEQ ID NO: 1187, SEQ ID NO: 1344, and SEQ ID NO: 1501, respectively;

lxxxix. SEQ ID NO: 717, SEQ ID NO: 874, SEQ ID NO: 1031, SEQ ID NO: 1188, SEQ ID NO: 1345, and SEQ ID NO: 1502, respectively;

xc. SEQ ID NO: 718, SEQ ID NO: 875, SEQ ID NO: 1032, SEQ ID NO: 1189, SEQ ID NO: 1346, and SEQ ID NO: 1503, respectively;

xci. SEQ ID NO: 719, SEQ ID NO: 876, SEQ ID NO: 1033, SEQ ID NO: 1190, SEQ ID NO: 1347, and SEQ ID NO: 1504, respectively;

xcii. SEQ ID NO: 720, SEQ ID NO: 877, SEQ ID NO: 1034, SEQ ID NO: 1191, SEQ ID NO: 1348, and SEQ ID NO: 1505, respectively;

xciii. SEQ ID NO: 721, SEQ ID NO: 878, SEQ ID NO: 1035, SEQ ID NO: 1192, SEQ ID NO: 1349, and SEQ ID NO: 1506, respectively;

xciv. SEQ ID NO: 722, SEQ ID NO: 879, SEQ ID NO: 1036, SEQ ID NO: 1193, SEQ ID NO: 1350, and SEQ ID NO: 1507, respectively;

xcv. SEQ ID NO: 723, SEQ ID NO: 880, SEQ ID NO: 1037, SEQ ID NO: 1194, SEQ ID NO: 1351, and SEQ ID NO: 1508, respectively;

xcvi. SEQ ID NO: 724, SEQ ID NO: 881, SEQ ID NO: 1038, SEQ ID NO: 1195, SEQ ID NO: 1352, and SEQ ID NO: 1509, respectively;

xcvii. SEQ ID NO: 725, SEQ ID NO: 882, SEQ ID NO: 1039, SEQ ID NO: 1196, SEQ ID NO: 1353, and SEQ ID NO: 1510, respectively;

xcviii. SEQ ID NO: 726, SEQ ID NO: 883, SEQ ID NO: 1040, SEQ ID NO: 1197, SEQ ID NO: 1354, and SEQ ID NO: 1511, respectively;

xcix. SEQ ID NO: 727, SEQ ID NO: 884, SEQ ID NO: 1041, SEQ ID NO: 1198, SEQ ID NO: 1355, and SEQ ID NO: 1512, respectively;

c. SEQ ID NO: 728, SEQ ID NO: 885, SEQ ID NO: 1042, SEQ ID NO: 1199, SEQ ID NO: 1356, and SEQ ID NO: 1513, respectively;

ci. SEQ ID NO: 729, SEQ ID NO: 886, SEQ ID NO: 1043, SEQ ID NO: 1200, SEQ ID NO: 1357, and SEQ ID NO: 1514, respectively;

cii. SEQ ID NO: 730, SEQ ID NO: 887, SEQ ID NO: 1044, SEQ ID NO: 1201, SEQ ID NO: 1358, and SEQ ID NO: 1515, respectively;

ciii. SEQ ID NO: 731, SEQ ID NO: 888, SEQ ID NO: 1045, SEQ ID NO: 1202, SEQ ID NO: 1359, and SEQ ID NO: 1516, respectively;

civ. SEQ ID NO: 732, SEQ ID NO: 889, SEQ ID NO: 1046, SEQ ID NO: 1203, SEQ ID NO: 1360, and SEQ ID NO: 1517, respectively;

cv. SEQ ID NO: 733, SEQ ID NO: 890, SEQ ID NO: 1047, SEQ ID NO: 1204, SEQ ID NO: 1361, and SEQ ID NO: 1518, respectively;

cvi. SEQ ID NO: 734, SEQ ID NO: 891, SEQ ID NO: 1048, SEQ ID NO: 1205, SEQ ID NO: 1362, and SEQ ID NO: 1519, respectively;

cvii. SEQ ID NO: 735, SEQ ID NO: 892, SEQ ID NO: 1049, SEQ ID NO: 1206, SEQ ID NO: 1363, and SEQ ID NO: 1520, respectively;

cviii. SEQ ID NO: 736, SEQ ID NO: 893, SEQ ID NO: 1050, SEQ ID NO: 1207, SEQ ID NO: 1364, and SEQ ID NO: 1521, respectively;

cix. SEQ ID NO: 737, SEQ ID NO: 894, SEQ ID NO: 1051, SEQ ID NO: 1208, SEQ ID NO: 1365, and SEQ ID NO: 1522, respectively;

cx. SEQ ID NO: 738, SEQ ID NO: 895, SEQ ID NO: 1052, SEQ ID NO: 1209, SEQ ID NO: 1366, and SEQ ID NO: 1523, respectively;

cxi. SEQ ID NO: 739, SEQ ID NO: 896, SEQ ID NO: 1053, SEQ ID NO: 1210, SEQ ID NO: 1367, and SEQ ID NO: 1524, respectively;

cxii. SEQ ID NO: 740, SEQ ID NO: 897, SEQ ID NO: 1054, SEQ ID NO: 1211, SEQ ID NO: 1368, and SEQ ID NO: 1525, respectively;

cxiii. SEQ ID NO: 741, SEQ ID NO: 898, SEQ ID NO: 1055, SEQ ID NO: 1212, SEQ ID NO: 1369, and SEQ ID NO: 1526, respectively;

cxiv. SEQ ID NO: 742, SEQ ID NO: 899, SEQ ID NO: 1056, SEQ ID NO: 1213, SEQ ID NO: 1370, and SEQ ID NO: 1527, respectively;

cxv. SEQ ID NO: 743, SEQ ID NO: 900, SEQ ID NO: 1057, SEQ ID NO: 1214, SEQ ID NO: 1371, and SEQ ID NO: 1528, respectively;

cxvi. SEQ ID NO: 744, SEQ ID NO: 901, SEQ ID NO: 1058, SEQ ID NO: 1215, SEQ ID NO: 1372, and SEQ ID NO: 1529, respectively;

cxvii. SEQ ID NO: 745, SEQ ID NO: 902, SEQ ID NO: 1059, SEQ ID NO: 1216, SEQ ID NO: 1373, and SEQ ID NO: 1530, respectively;

cxviii. SEQ ID NO: 746, SEQ ID NO: 903, SEQ ID NO: 1060, SEQ ID NO: 1217, SEQ ID NO: 1374, and SEQ ID NO: 1531, respectively;

cxix. SEQ ID NO: 747, SEQ ID NO: 904, SEQ ID NO: 1061, SEQ ID NO: 1218, SEQ ID NO: 1375, and SEQ ID NO: 1532, respectively;

cxx. SEQ ID NO: 748, SEQ ID NO: 905, SEQ ID NO: 1062, SEQ ID NO: 1219, SEQ ID NO: 1376, and SEQ ID NO: 1533, respectively;

cxxi. SEQ ID NO: 749, SEQ ID NO: 906, SEQ ID NO: 1063, SEQ ID NO: 1220, SEQ ID NO: 1377, and SEQ ID NO: 1534, respectively;

cxxii. SEQ ID NO: 750, SEQ ID NO: 907, SEQ ID NO: 1064, SEQ ID NO: 1221, SEQ ID NO: 1378, and SEQ ID NO: 1535, respectively;

cxxiii. SEQ ID NO: 751, SEQ ID NO: 908, SEQ ID NO: 1065, SEQ ID NO: 1222, SEQ ID NO: 1379, and SEQ ID NO: 1536, respectively;

cxxiv. SEQ ID NO: 752, SEQ ID NO: 909, SEQ ID NO: 1066, SEQ ID NO: 1223, SEQ ID NO: 1380, and SEQ ID NO: 1537, respectively;

cxxv. SEQ ID NO: 753, SEQ ID NO: 910, SEQ ID NO: 1067, SEQ ID NO: 1224, SEQ ID NO: 1381, and SEQ ID NO: 1538, respectively;

cxxvi. SEQ ID NO: 754, SEQ ID NO: 911, SEQ ID NO: 1068, SEQ ID NO: 1225, SEQ ID NO: 1382, and SEQ ID NO: 1539, respectively;

cxxvii. SEQ ID NO: 755, SEQ ID NO: 912, SEQ ID NO: 1069, SEQ ID NO: 1226, SEQ ID NO: 1383, and SEQ ID NO: 1540, respectively;

cxxviii. SEQ ID NO: 756, SEQ ID NO: 913, SEQ ID NO: 1070, SEQ ID NO: 1227, SEQ ID NO: 1384, and SEQ ID NO: 1541, respectively;

cxxix. SEQ ID NO: 757, SEQ ID NO: 914, SEQ ID NO: 1071, SEQ ID NO: 1228, SEQ ID NO: 1385, and SEQ ID NO: 1542, respectively;

cxxx. SEQ ID NO: 758, SEQ ID NO: 915, SEQ ID NO: 1072, SEQ ID NO: 1229, SEQ ID NO: 1386, and SEQ ID NO: 1543, respectively;

cxxxi. SEQ ID NO: 759, SEQ ID NO: 916, SEQ ID NO: 1073, SEQ ID NO: 1230, SEQ ID NO: 1387, and SEQ ID NO: 1544, respectively;

cxxxii. SEQ ID NO: 760, SEQ ID NO: 917, SEQ ID NO: 1074, SEQ ID NO: 1231, SEQ ID NO: 1388, and SEQ ID NO: 1545, respectively;

cxxxiii. SEQ ID NO: 761, SEQ ID NO: 918, SEQ ID NO: 1075, SEQ ID NO: 1232, SEQ ID NO: 1389, and SEQ ID NO: 1546, respectively;

cxxxiv. SEQ ID NO: 762, SEQ ID NO: 919, SEQ ID NO: 1076, SEQ ID NO: 1233, SEQ ID NO: 1390, and SEQ ID NO: 1547, respectively;

cxxxv. SEQ ID NO: 763, SEQ ID NO: 920, SEQ ID NO: 1077, SEQ ID NO: 1234, SEQ ID NO: 1391, and SEQ ID NO: 1548, respectively;

cxxxvi. SEQ ID NO: 764, SEQ ID NO: 921, SEQ ID NO: 1078, SEQ ID NO: 1235, SEQ ID NO: 1392, and SEQ ID NO: 1549, respectively;

cxxxvii. SEQ ID NO: 765, SEQ ID NO: 922, SEQ ID NO: 1079, SEQ ID NO: 1236, SEQ ID NO: 1393, and SEQ ID NO: 1550, respectively;

cxxxviii. SEQ ID NO: 766, SEQ ID NO: 923, SEQ ID NO: 1080, SEQ ID NO: 1237, SEQ ID NO: 1394, and SEQ ID NO: 1551, respectively;

cxxxix. SEQ ID NO: 767, SEQ ID NO: 924, SEQ ID NO: 1081, SEQ ID NO: 1238, SEQ ID NO: 1395, and SEQ ID NO: 1552, respectively;

cxl. SEQ ID NO: 768, SEQ ID NO: 925, SEQ ID NO: 1082, SEQ ID NO: 1239, SEQ ID NO: 1396, and SEQ ID NO: 1553, respectively;

cxli. SEQ ID NO: 769, SEQ ID NO: 926, SEQ ID NO: 1083, SEQ ID NO: 1240, SEQ ID NO: 1397, and SEQ ID NO: 1554, respectively;

cxlii. SEQ ID NO: 770, SEQ ID NO: 927, SEQ ID NO: 1084, SEQ ID NO: 1241, SEQ ID NO: 1398, and SEQ ID NO: 1555, respectively;

cxliii. SEQ ID NO: 771, SEQ ID NO: 928, SEQ ID NO: 1085, SEQ ID NO: 1242, SEQ ID NO: 1399, and SEQ ID NO: 1556, respectively;

cxliv. SEQ ID NO: 772, SEQ ID NO: 929, SEQ ID NO: 1086, SEQ ID NO: 1243, SEQ ID NO: 1400, and SEQ ID NO: 1557, respectively;

cxlv. SEQ ID NO: 773, SEQ ID NO: 930, SEQ ID NO: 1087, SEQ ID NO: 1244, SEQ ID NO: 1401, and SEQ ID NO: 1558, respectively;

cxlvi. SEQ ID NO: 774, SEQ ID NO: 931, SEQ ID NO: 1088, SEQ ID NO: 1245, SEQ ID NO: 1402, and SEQ ID NO: 1559, respectively;

cxlvii. SEQ ID NO: 775, SEQ ID NO: 932, SEQ ID NO: 1089, SEQ ID NO: 1246, SEQ ID NO: 1403, and SEQ ID NO: 1560, respectively;

cxlviii. SEQ ID NO: 776, SEQ ID NO: 933, SEQ ID NO: 1090, SEQ ID NO: 1247, SEQ ID NO: 1404, and SEQ ID NO: 1561, respectively;

cxlix. SEQ ID NO: 777, SEQ ID NO: 934, SEQ ID NO: 1091, SEQ ID NO: 1248, SEQ ID NO: 1405, and SEQ ID NO: 1562, respectively;

cl. SEQ ID NO: 778, SEQ ID NO: 935, SEQ ID NO: 1092, SEQ ID NO: 1249, SEQ ID NO: 1406, and SEQ ID NO: 1563, respectively;

cli. SEQ ID NO: 779, SEQ ID NO: 936, SEQ ID NO: 1093, SEQ ID NO: 1250, SEQ ID NO: 1407, and SEQ ID NO: 1564, respectively;

clii. SEQ ID NO: 780, SEQ ID NO: 937, SEQ ID NO: 1094, SEQ ID NO: 1251, SEQ ID NO: 1408, and SEQ ID NO: 1565, respectively;

cliii. SEQ ID NO: 781, SEQ ID NO: 938, SEQ ID NO: 1095, SEQ ID NO: 1252, SEQ ID NO: 1409, and SEQ ID NO: 1566, respectively;

cliv. SEQ ID NO: 782, SEQ ID NO: 939, SEQ ID NO: 1096, SEQ ID NO: 1253, SEQ ID NO: 1410, and SEQ ID NO: 1567, respectively;

clv. SEQ ID NO: 783, SEQ ID NO: 940, SEQ ID NO: 1097, SEQ ID NO: 1254, SEQ ID NO: 1411, and SEQ ID NO: 1568, respectively;

clvi. SEQ ID NO: 784, SEQ ID NO: 941, SEQ ID NO: 1098, SEQ ID NO: 1255, SEQ ID NO: 1412, and SEQ ID NO: 1569, respectively; and

clvii. SEQ ID NO: 785, SEQ ID NO: 942, SEQ ID NO: 1099, SEQ ID NO: 1256, SEQ ID NO: 1413, and SEQ ID NO: 1570, respectively.

[0310] Embodiment 41 is the conjugate molecule of embodiment 40, wherein the anti-GIPR antibody comprises the CDRL1, the CDRL2, the CDRL3, the CDRH1, the CDRH2, and the CDRH3 of SEQ ID NO: 702, SEQ ID NO: 859, SEQ ID NO: 1016, SEQ ID NO: 1173, SEQ ID NO: 1330, and SEQ ID NO: 1487, respectively.

[0311] Embodiment 42 is the conjugate molecule of any one of embodiments 17 to 39, wherein the anti-GIPR antibody comprises a light chain variable region (V_L) and a heavy chain variable region (V_H), wherein the V_L and the V_H comprise amino acid sequences selected from:

i. SEQ ID NO: 1 and SEQ ID NO: 158, respectively;
ii. SEQ ID NO: 2 and SEQ ID NO: 159, respectively;
iii. SEQ ID NO: 3 and SEQ ID NO: 160, respectively;
iv. SEQ ID NO: 4 and SEQ ID NO: 161, respectively;
v. SEQ ID NO: 5 and SEQ ID NO: 162, respectively;
vi. SEQ ID NO: 6 and SEQ ID NO: 163, respectively;
vii. SEQ ID NO: 7 and SEQ ID NO: 164, respectively;
viii. SEQ ID NO: 8 and SEQ ID NO: 165, respectively;
ix. SEQ ID NO: 9 and SEQ ID NO: 166, respectively;
x. SEQ ID NO: 10 and SEQ ID NO: 167, respectively;
xi. SEQ ID NO: 11 and SEQ ID NO: 168, respectively;
xii. SEQ ID NO: 12 and SEQ ID NO: 169, respectively;
xiii. SEQ ID NO: 13 and SEQ ID NO: 170, respectively;
xiv. SEQ ID NO: 14 and SEQ ID NO: 171, respectively;
xv. SEQ ID NO: 15 and SEQ ID NO: 172, respectively;
xvi. SEQ ID NO: 16 and SEQ ID NO: 173, respectively;
xvii. SEQ ID NO: 17 and SEQ ID NO: 174, respectively;
xviii. SEQ ID NO: 18 and SEQ ID NO: 175, respectively;
xix. SEQ ID NO: 19 and SEQ ID NO: 176, respectively;
xx. SEQ ID NO: 20 and SEQ ID NO: 177, respectively;
xxi. SEQ ID NO: 21 and SEQ ID NO: 178, respectively;
xxii. SEQ ID NO: 22 and SEQ ID NO: 179, respectively;
xxiii. SEQ ID NO: 23 and SEQ ID NO: 180, respectively;
xxiv. SEQ ID NO: 24 and SEQ ID NO: 181, respectively;
xxv. SEQ ID NO: 25 and SEQ ID NO: 182, respectively;
xxvi. SEQ ID NO: 26 and SEQ ID NO: 183, respectively;
xxvii. SEQ ID NO: 27 and SEQ ID NO: 184, respectively;
xxviii. SEQ ID NO: 28 and SEQ ID NO: 185, respectively;
xxix. SEQ ID NO: 29 and SEQ ID NO: 186, respectively;
xxx. SEQ ID NO: 30 and SEQ ID NO: 187, respectively;
xxxi. SEQ ID NO: 31 and SEQ ID NO: 188, respectively;

xxxii. SEQ ID NO: 32 and SEQ ID NO: 189, respectively;
xxxiii. SEQ ID NO: 33 and SEQ ID NO: 190, respectively;
xxxiv. SEQ ID NO: 34 and SEQ ID NO: 191, respectively;
xxxv. SEQ ID NO: 35 and SEQ ID NO: 192, respectively;
xxxvi. SEQ ID NO: 36 and SEQ ID NO: 193, respectively;
xxxvii. SEQ ID NO: 37 and SEQ ID NO: 194, respectively;
xxxviii. SEQ ID NO: 38 and SEQ ID NO: 195, respectively;
xxxix. SEQ ID NO: 39 and SEQ ID NO: 196, respectively;
xl. SEQ ID NO: 40 and SEQ ID NO: 197, respectively;
xli. SEQ ID NO: 41 and SEQ ID NO: 198, respectively;
xlii. SEQ ID NO: 42 and SEQ ID NO: 199, respectively;
xliii. SEQ ID NO: 43 and SEQ ID NO: 200, respectively;
xliv. SEQ ID NO: 44 and SEQ ID NO: 201, respectively;
xlv. SEQ ID NO: 45 and SEQ ID NO: 202, respectively;
xlvi. SEQ ID NO: 46 and SEQ ID NO: 203, respectively;
xlvii. SEQ ID NO: 47 and SEQ ID NO: 204, respectively;
xlviii. SEQ ID NO: 48 and SEQ ID NO: 205, respectively;
xlix. SEQ ID NO: 49 and SEQ ID NO: 206, respectively;
l. SEQ ID NO: 50 and SEQ ID NO: 207, respectively;
li. SEQ ID NO: 51 and SEQ ID NO: 208, respectively;
lii. SEQ ID NO: 52 and SEQ ID NO: 209, respectively;
liii. SEQ ID NO: 53 and SEQ ID NO: 210, respectively;
liv. SEQ ID NO: 54 and SEQ ID NO: 211, respectively;
lv. SEQ ID NO: 55 and SEQ ID NO: 212, respectively;
lvi. SEQ ID NO: 56 and SEQ ID NO: 213, respectively;
lvii. SEQ ID NO: 57 and SEQ ID NO: 214, respectively;
lviii. SEQ ID NO: 58 and SEQ ID NO: 215, respectively;
lix. SEQ ID NO: 59 and SEQ ID NO: 216, respectively;
lx. SEQ ID NO: 60 and SEQ ID NO: 217, respectively;
lxi. SEQ ID NO: 61 and SEQ ID NO: 218, respectively;
lxii. SEQ ID NO: 62 and SEQ ID NO: 219, respectively;
lxiii. SEQ ID NO: 63 and SEQ ID NO: 220, respectively;
lxiv. SEQ ID NO: 64 and SEQ ID NO: 221, respectively;
lxv. SEQ ID NO: 65 and SEQ ID NO: 222, respectively;

lxvi. SEQ ID NO: 66 and SEQ ID NO: 223, respectively;
lxvii. SEQ ID NO: 67 and SEQ ID NO: 224, respectively;
lxviii. SEQ ID NO: 68 and SEQ ID NO: 225, respectively;
lxix. SEQ ID NO: 69 and SEQ ID NO: 226, respectively;
lxx. SEQ ID NO: 70 and SEQ ID NO: 227, respectively;
lxxi. SEQ ID NO: 71 and SEQ ID NO: 228, respectively;
lxxii. SEQ ID NO: 72 and SEQ ID NO: 229, respectively;
lxxiii. SEQ ID NO: 73 and SEQ ID NO: 230, respectively;
lxxiv. SEQ ID NO: 74 and SEQ ID NO: 231, respectively;
lxxv. SEQ ID NO: 75 and SEQ ID NO: 232, respectively;
lxxvi. SEQ ID NO: 76 and SEQ ID NO: 233, respectively;
lxxvii. SEQ ID NO: 77 and SEQ ID NO: 234, respectively;
lxxviii. SEQ ID NO: 78 and SEQ ID NO: 235, respectively;
lxxix. SEQ ID NO: 79 and SEQ ID NO: 236, respectively;
lxxx. SEQ ID NO: 80 and SEQ ID NO: 237, respectively;
lxxxi. SEQ ID NO: 81 and SEQ ID NO: 238, respectively;
lxxxii. SEQ ID NO: 82 and SEQ ID NO: 239, respectively;
lxxxiii. SEQ ID NO: 83 and SEQ ID NO: 240, respectively;
lxxxiv. SEQ ID NO: 84 and SEQ ID NO: 241, respectively;
lxxxv. SEQ ID NO: 85 and SEQ ID NO: 242, respectively;
lxxxvi. SEQ ID NO: 86 and SEQ ID NO: 243, respectively;
lxxxvii. SEQ ID NO: 87 and SEQ ID NO: 244, respectively;
lxxxviii. SEQ ID NO: 88 and SEQ ID NO: 245, respectively;
lxxxix. SEQ ID NO: 89 and SEQ ID NO: 246, respectively;
xc. SEQ ID NO: 90 and SEQ ID NO: 247, respectively;
xci. SEQ ID NO: 91 and SEQ ID NO: 248, respectively;
xcii. SEQ ID NO: 92 and SEQ ID NO: 249, respectively;
xciii. SEQ ID NO: 93 and SEQ ID NO: 250, respectively;
xciv. SEQ ID NO: 94 and SEQ ID NO: 251, respectively;
xcv. SEQ ID NO: 95 and SEQ ID NO: 252, respectively;
xcvi. SEQ ID NO: 96 and SEQ ID NO: 253, respectively;
xcvii. SEQ ID NO: 97 and SEQ ID NO: 254, respectively;
xcviii. SEQ ID NO: 98 and SEQ ID NO: 255, respectively;
xcix. SEQ ID NO: 99 and SEQ ID NO: 256, respectively;

c. SEQ ID NO: 100 and SEQ ID NO: 257, respectively;
ci. SEQ ID NO: 101 and SEQ ID NO: 258, respectively;
cii. SEQ ID NO: 102 and SEQ ID NO: 259, respectively;
ciii. SEQ ID NO: 103 and SEQ ID NO: 260, respectively;
civ. SEQ ID NO: 104 and SEQ ID NO: 261, respectively;
cv. SEQ ID NO: 105 and SEQ ID NO: 262, respectively;
cvi. SEQ ID NO: 106 and SEQ ID NO: 263, respectively;
cvii. SEQ ID NO: 107 and SEQ ID NO: 264, respectively;
cviii. SEQ ID NO: 108 and SEQ ID NO: 265, respectively;
cix. SEQ ID NO: 109 and SEQ ID NO: 266, respectively;
cx. SEQ ID NO: 110 and SEQ ID NO: 267, respectively;
cxi. SEQ ID NO: 111 and SEQ ID NO: 268, respectively;
cxii. SEQ ID NO: 112 and SEQ ID NO: 269, respectively;
cxiii. SEQ ID NO: 113 and SEQ ID NO: 270, respectively;
cxiv. SEQ ID NO: 114 and SEQ ID NO: 271, respectively;
cxv. SEQ ID NO: 115 and SEQ ID NO: 272, respectively;
cxvi. SEQ ID NO: 116 and SEQ ID NO: 273, respectively;
cxvii. SEQ ID NO: 117 and SEQ ID NO: 274, respectively;
cxviii. SEQ ID NO: 118 and SEQ ID NO: 275, respectively;
cxix. SEQ ID NO: 119 and SEQ ID NO: 276, respectively;
cxx. SEQ ID NO: 120 and SEQ ID NO: 277, respectively;
cxxi. SEQ ID NO: 121 and SEQ ID NO: 278, respectively;
cxxii. SEQ ID NO: 122 and SEQ ID NO: 279, respectively;
cxxiii. SEQ ID NO: 123 and SEQ ID NO: 280, respectively;
cxxiv. SEQ ID NO: 124 and SEQ ID NO: 281, respectively;
cxxv. SEQ ID NO: 125 and SEQ ID NO: 282, respectively;
cxxvi. SEQ ID NO: 126 and SEQ ID NO: 283, respectively;
cxxvii. SEQ ID NO: 127 and SEQ ID NO: 284, respectively;
cxxviii. SEQ ID NO: 128 and SEQ ID NO: 285, respectively;
cxxix. SEQ ID NO: 129 and SEQ ID NO: 286, respectively;
cxxx. SEQ ID NO: 130 and SEQ ID NO: 287, respectively;
cxxxi. SEQ ID NO: 131 and SEQ ID NO: 288, respectively;
cxxxii. SEQ ID NO: 132 and SEQ ID NO: 289, respectively;
cxxxiii. SEQ ID NO: 133 and SEQ ID NO: 290, respectively;

cxxxiv. SEQ ID NO: 134 and SEQ ID NO: 291, respectively;
cxxxv. SEQ ID NO: 135 and SEQ ID NO: 292, respectively;
cxxxvi. SEQ ID NO: 136 and SEQ ID NO: 293, respectively;
cxxxvii. SEQ ID NO: 137 and SEQ ID NO: 294, respectively;
cxxxviii. SEQ ID NO: 138 and SEQ ID NO: 295, respectively;
cxxxix. SEQ ID NO: 139 and SEQ ID NO: 296, respectively;
cxl. SEQ ID NO: 140 and SEQ ID NO: 297, respectively;
cxli. SEQ ID NO: 141 and SEQ ID NO: 298, respectively;
cxlii. SEQ ID NO: 142 and SEQ ID NO: 299, respectively;
cxliii. SEQ ID NO: 143 and SEQ ID NO: 300, respectively;
cxliv. SEQ ID NO: 144 and SEQ ID NO: 301, respectively;
cxlv. SEQ ID NO: 145 and SEQ ID NO: 302, respectively;
cxlvi. SEQ ID NO: 146 and SEQ ID NO: 303, respectively;
cxlvii. SEQ ID NO: 147 and SEQ ID NO: 304, respectively;
cxlviii. SEQ ID NO: 148 and SEQ ID NO: 305, respectively;
cxlix. SEQ ID NO: 149 and SEQ ID NO: 306, respectively;
cl. SEQ ID NO: 150 and SEQ ID NO: 307, respectively;
cli. SEQ ID NO: 151 and SEQ ID NO: 308, respectively;
clii. SEQ ID NO: 152 and SEQ ID NO: 309, respectively;
cliii. SEQ ID NO: 153 and SEQ ID NO: 310, respectively;
cliv. SEQ ID NO: 154 and SEQ ID NO: 311, respectively;
clv. SEQ ID NO: 155 and SEQ ID NO: 312, respectively;
clvi. SEQ ID NO: 156 and SEQ ID NO: 313, respectively; and
clvii. SEQ ID NO: 157 and SEQ ID NO: 314, respectively.

[0312] Embodiment 43 is the conjugate molecule of embodiment 42, wherein the anti-GIPR antibody comprises the V_L and V_H of SEQ ID NO: 74 and SEQ ID NO: 231, respectively.

[0313] Embodiment 44 is the conjugate molecule of any one of embodiments 17 to 39, wherein the anti-GIPR antibody comprises a light chain and a heavy chain, wherein the light chain and heavy chain comprise amino acid sequences selected from:

i. SEQ ID NO: 315 and SEQ ID NO: 472, respectively;
ii. SEQ ID NO: 316 and SEQ ID NO: 473, respectively;
iii. SEQ ID NO: 317 and SEQ ID NO: 474, respectively;
iv. SEQ ID NO: 318 and SEQ ID NO: 475, respectively;

v. SEQ ID NO: 319 and SEQ ID NO: 476, respectively;
vi. SEQ ID NO: 320 and SEQ ID NO: 477, respectively;
vii. SEQ ID NO: 321 and SEQ ID NO: 478, respectively;
viii. SEQ ID NO: 322 and SEQ ID NO: 479, respectively;
ix. SEQ ID NO: 323 and SEQ ID NO: 480, respectively;
x. SEQ ID NO: 324 and SEQ ID NO: 481, respectively;
xi. SEQ ID NO: 325 and SEQ ID NO: 482, respectively;
xii. SEQ ID NO: 326 and SEQ ID NO: 483, respectively;
xiii. SEQ ID NO: 327 and SEQ ID NO: 484, respectively;
xiv. SEQ ID NO: 328 and SEQ ID NO: 485, respectively;
xv. SEQ ID NO: 329 and SEQ ID NO: 486, respectively;
xvi. SEQ ID NO: 330 and SEQ ID NO: 487, respectively;
xvii. SEQ ID NO: 331 and SEQ ID NO: 488, respectively;
xviii. SEQ ID NO: 332 and SEQ ID NO: 489, respectively;
xix. SEQ ID NO: 333 and SEQ ID NO: 490, respectively;
xx. SEQ ID NO: 334 and SEQ ID NO: 491, respectively;
xxi. SEQ ID NO: 335 and SEQ ID NO: 492, respectively;
xxii. SEQ ID NO: 336 and SEQ ID NO: 493, respectively;
xxiii. SEQ ID NO: 337 and SEQ ID NO: 494, respectively;
xxiv. SEQ ID NO: 338 and SEQ ID NO: 495, respectively;
xxv. SEQ ID NO: 339 and SEQ ID NO: 496, respectively;
xxvi. SEQ ID NO: 340 and SEQ ID NO: 497, respectively;
xxvii. SEQ ID NO: 341 and SEQ ID NO: 498, respectively;
xxviii. SEQ ID NO: 342 and SEQ ID NO: 499, respectively;
xxix. SEQ ID NO: 343 and SEQ ID NO: 500, respectively;
xxx. SEQ ID NO: 344 and SEQ ID NO: 501, respectively;
xxxi. SEQ ID NO: 345 and SEQ ID NO: 502, respectively;
xxxii. SEQ ID NO: 346 and SEQ ID NO: 503, respectively;
xxxiii. SEQ ID NO: 347 and SEQ ID NO: 504, respectively;
xxxiv. SEQ ID NO: 348 and SEQ ID NO: 505, respectively;
xxxv. SEQ ID NO: 349 and SEQ ID NO: 506, respectively;
xxxvi. SEQ ID NO: 350 and SEQ ID NO: 507, respectively;
xxxvii. SEQ ID NO: 351 and SEQ ID NO: 508, respectively;
xxxviii. SEQ ID NO: 352 and SEQ ID NO: 509, respectively;

xxxix. SEQ ID NO: 353 and SEQ ID NO: 510, respectively;
xl. SEQ ID NO: 354 and SEQ ID NO: 511, respectively;
xli. SEQ ID NO: 355 and SEQ ID NO: 512, respectively;
xlii. SEQ ID NO: 356 and SEQ ID NO: 513, respectively;
xliii. SEQ ID NO: 357 and SEQ ID NO: 514, respectively;
xliv. SEQ ID NO: 358 and SEQ ID NO: 515, respectively;
xlv. SEQ ID NO: 359 and SEQ ID NO: 516, respectively;
xlvi. SEQ ID NO: 360 and SEQ ID NO: 517, respectively;
xlvii. SEQ ID NO: 361 and SEQ ID NO: 518, respectively;
xlviii. SEQ ID NO: 362 and SEQ ID NO: 519, respectively;
xlix. SEQ ID NO: 363 and SEQ ID NO: 520, respectively;
l. SEQ ID NO: 364 and SEQ ID NO: 521, respectively;
li. SEQ ID NO: 365 and SEQ ID NO: 522, respectively;
lii. SEQ ID NO: 366 and SEQ ID NO: 523, respectively;
liii. SEQ ID NO: 367 and SEQ ID NO: 524, respectively;
liv. SEQ ID NO: 368 and SEQ ID NO: 525, respectively;
lv. SEQ ID NO: 369 and SEQ ID NO: 526, respectively;
lvi. SEQ ID NO: 370 and SEQ ID NO: 527, respectively;
lvii. SEQ ID NO: 371 and SEQ ID NO: 528, respectively;
lviii. SEQ ID NO: 372 and SEQ ID NO: 529, respectively;
lix. SEQ ID NO: 373 and SEQ ID NO: 530, respectively;
lx. SEQ ID NO: 374 and SEQ ID NO: 531, respectively;
lxi. SEQ ID NO: 375 and SEQ ID NO: 532, respectively;
lxii. SEQ ID NO: 376 and SEQ ID NO: 533, respectively;
lxiii. SEQ ID NO: 377 and SEQ ID NO: 534, respectively;
lxiv. SEQ ID NO: 378 and SEQ ID NO: 535, respectively;
lxv. SEQ ID NO: 379 and SEQ ID NO: 536, respectively;
lxvi. SEQ ID NO: 380 and SEQ ID NO: 537, respectively;
lxvii. SEQ ID NO: 381 and SEQ ID NO: 538, respectively;
lxviii. SEQ ID NO: 382 and SEQ ID NO: 539, respectively;
lxix. SEQ ID NO: 383 and SEQ ID NO: 540, respectively;
lxx. SEQ ID NO: 384 and SEQ ID NO: 541, respectively;
lxxi. SEQ ID NO: 385 and SEQ ID NO: 542, respectively;
lxxii. SEQ ID NO: 386 and SEQ ID NO: 543, respectively;

lxxiii. SEQ ID NO: 387 and SEQ ID NO: 544, respectively;
lxxiv. SEQ ID NO: 388 and SEQ ID NO: 545, respectively;
lxxv. SEQ ID NO: 389 and SEQ ID NO: 546, respectively;
lxxvi. SEQ ID NO: 390 and SEQ ID NO: 547, respectively;
lxxvii. SEQ ID NO: 391 and SEQ ID NO: 548, respectively;
lxxviii. SEQ ID NO: 392 and SEQ ID NO: 549, respectively;
lxxix. SEQ ID NO: 393 and SEQ ID NO: 550, respectively;
lxxx. SEQ ID NO: 394 and SEQ ID NO: 551, respectively;
lxxxi. SEQ ID NO: 395 and SEQ ID NO: 552, respectively;
lxxxii. SEQ ID NO: 396 and SEQ ID NO: 553, respectively;
lxxxiii. SEQ ID NO: 397 and SEQ ID NO: 554, respectively;
lxxxiv. SEQ ID NO: 398 and SEQ ID NO: 555, respectively;
lxxxv. SEQ ID NO: 399 and SEQ ID NO: 556, respectively;
lxxxvi. SEQ ID NO: 400 and SEQ ID NO: 557, respectively;
lxxxvii. SEQ ID NO: 401 and SEQ ID NO: 558, respectively;
lxxxviii. SEQ ID NO: 402 and SEQ ID NO: 559, respectively;
lxxxix. SEQ ID NO: 403 and SEQ ID NO: 560, respectively;
xc. SEQ ID NO: 404 and SEQ ID NO: 561, respectively;
xci. SEQ ID NO: 405 and SEQ ID NO: 562, respectively;
xcii. SEQ ID NO: 406 and SEQ ID NO: 563, respectively;
xciii. SEQ ID NO: 407 and SEQ ID NO: 564, respectively;
xciv. SEQ ID NO: 408 and SEQ ID NO: 565, respectively;
xcv. SEQ ID NO: 409 and SEQ ID NO: 566, respectively;
xcvi. SEQ ID NO: 410 and SEQ ID NO: 567, respectively;
xcvii. SEQ ID NO: 411 and SEQ ID NO: 568, respectively;
xcviii. SEQ ID NO: 412 and SEQ ID NO: 569, respectively;
xcix. SEQ ID NO: 413 and SEQ ID NO: 570, respectively;
c. SEQ ID NO: 414 and SEQ ID NO: 571, respectively;
ci. SEQ ID NO: 415 and SEQ ID NO: 572, respectively;
cii. SEQ ID NO: 416 and SEQ ID NO: 573, respectively;
ciii. SEQ ID NO: 417 and SEQ ID NO: 574, respectively;
civ. SEQ ID NO: 418 and SEQ ID NO: 575, respectively;
cv. SEQ ID NO: 419 and SEQ ID NO: 576, respectively;
cvi. SEQ ID NO: 420 and SEQ ID NO: 577, respectively;

cvii. SEQ ID NO: 421 and SEQ ID NO: 578, respectively;
cviii. SEQ ID NO: 422 and SEQ ID NO: 579, respectively;
cix. SEQ ID NO: 423 and SEQ ID NO: 580, respectively;
cx. SEQ ID NO: 424 and SEQ ID NO: 581, respectively;
cxi. SEQ ID NO: 425 and SEQ ID NO: 582, respectively;
cxii. SEQ ID NO: 426 and SEQ ID NO: 583, respectively;
cxiii. SEQ ID NO: 427 and SEQ ID NO: 584, respectively;
cxiv. SEQ ID NO: 428 and SEQ ID NO: 585, respectively;
cxv. SEQ ID NO: 429 and SEQ ID NO: 586, respectively;
cxvi. SEQ ID NO: 430 and SEQ ID NO: 587, respectively;
cxvii. SEQ ID NO: 431 and SEQ ID NO: 588, respectively;
cxviii. SEQ ID NO: 432 and SEQ ID NO: 589, respectively;
cxix. SEQ ID NO: 433 and SEQ ID NO: 590, respectively;
cxx. SEQ ID NO: 434 and SEQ ID NO: 591, respectively;
cxxi. SEQ ID NO: 435 and SEQ ID NO: 592, respectively;
cxxii. SEQ ID NO: 436 and SEQ ID NO: 593, respectively;
cxxiii. SEQ ID NO: 437 and SEQ ID NO: 594, respectively;
cxxiv. SEQ ID NO: 438 and SEQ ID NO: 595, respectively;
cxxv. SEQ ID NO: 439 and SEQ ID NO: 596, respectively;
cxxvi. SEQ ID NO: 440 and SEQ ID NO: 597, respectively;
cxxvii. SEQ ID NO: 441 and SEQ ID NO: 598, respectively;
cxxviii. SEQ ID NO: 442 and SEQ ID NO: 599, respectively;
cxxix. SEQ ID NO: 443 and SEQ ID NO: 600, respectively;
cxxx. SEQ ID NO: 444 and SEQ ID NO: 601, respectively;
cxxxi. SEQ ID NO: 445 and SEQ ID NO: 602, respectively;
cxxxii. SEQ ID NO: 446 and SEQ ID NO: 603, respectively;
cxxxiii. SEQ ID NO: 447 and SEQ ID NO: 604, respectively;
cxxxiv. SEQ ID NO: 448 and SEQ ID NO: 605, respectively;
cxxxv. SEQ ID NO: 449 and SEQ ID NO: 606, respectively;
cxxxvi. SEQ ID NO: 450 and SEQ ID NO: 607, respectively;
cxxxvii. SEQ ID NO: 451 and SEQ ID NO: 608, respectively;
cxxxviii. SEQ ID NO: 452 and SEQ ID NO: 609, respectively;
cxxxix. SEQ ID NO: 453 and SEQ ID NO: 610, respectively;
cxl. SEQ ID NO: 454 and SEQ ID NO: 611, respectively;

cxli. SEQ ID NO: 455 and SEQ ID NO: 612, respectively;
cxlii. SEQ ID NO: 456 and SEQ ID NO: 613, respectively;
cxliii. SEQ ID NO: 457 and SEQ ID NO: 614, respectively;
cxliv. SEQ ID NO: 458 and SEQ ID NO: 615, respectively;
cxlv. SEQ ID NO: 459 and SEQ ID NO: 616, respectively;
cxlvi. SEQ ID NO: 460 and SEQ ID NO: 617, respectively;
cxlvii. SEQ ID NO: 461 and SEQ ID NO: 618, respectively;
cxlviii. SEQ ID NO: 462 and SEQ ID NO: 619, respectively;
cxlix. SEQ ID NO: 463 and SEQ ID NO: 620, respectively;
cl. SEQ ID NO: 464 and SEQ ID NO: 621, respectively;
cli. SEQ ID NO: 465 and SEQ ID NO: 622, respectively;
clii. SEQ ID NO: 466 and SEQ ID NO: 623, respectively;
cliii. SEQ ID NO: 467 and SEQ ID NO: 624, respectively;
cliv. SEQ ID NO: 468 and SEQ ID NO: 625, respectively;
clv. SEQ ID NO: 469 and SEQ ID NO: 626, respectively;
clvi. SEQ ID NO: 470 and SEQ ID NO: 627, respectively; and
clvii. SEQ ID NO: 471 and SEQ ID NO: 628, respectively,

wherein the antibody comprises one or more cysteine amino acid substitution(s) at one or more position(s) selected from 88 of the light chain, 384 of the heavy chain, or 487 of the heavy chain, according to AHo numbering.

[0314] Embodiment 45 is the conjugate molecule of embodiment 44, wherein the anti-GIPR antibody comprises the light chain and heavy chain of SEQ ID NO: 388 and SEQ ID NO: 545, respectively.

[0315] Embodiment 46 is a conjugate molecule comprising: (i) an antagonist anti-glucose-dependent insulinotropic polypeptide receptor (GIPR) antibody, wherein the anti-GIPR antibody comprises: a first and second light chain, each light chain comprising a CDRL1, a CDRL2, and a CDRL3 of SEQ ID NO: 702, SEQ ID NO: 859, and SEQ ID NO: 1016, respectively, and a first and second heavy chain, each heavy chain comprising a CDRH1, a CDRH2, and a CDRH3 of SEQ ID NO: 1173, SEQ ID NO: 1330, and SEQ ID NO: 1487, respectively; (ii) a first and second GLP-1 receptor agonist polypeptide, wherein each GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1579; and (iii) a first and second peptide linker, wherein each peptide linker comprises the amino acid sequence of SEQ ID NO: 1592; wherein the first GLP-1 receptor agonist polypeptide is conjugated, at its C-terminus via the first linker, to the first heavy chain of the anti-GIPR antibody at a

cysteine residue at position 384 of the first heavy chain according to AHo numbering, and wherein the second GLP-1 receptor agonist polypeptide is conjugated, at its C-terminus via the second linker, to the second heavy chain of the anti-GIPR antibody at a cysteine residue at position 384 of the second heavy chain according to AHo numbering.

[0316] Embodiment 47 is the conjugate molecule of embodiment 46, wherein each light chain comprises a VL of SEQ ID NO: 74, and each heavy chain comprises a VH of SEQ ID NO: 231.

[0317] Embodiment 48 is the conjugate molecule of embodiment 46, wherein each light chain comprises the amino acid sequence of SEQ ID NO: 388, and each heavy chain comprises the amino acid sequence of SEQ ID NO: 1571.

[0318] Embodiment 49 is the conjugate molecule comprising: (i) an antagonist anti-glucose-dependent insulinotropic polypeptide receptor (GIPR) antibody, wherein the anti-GIPR antibody comprises: a first and second light chain, each light chain comprising a CDRL1, a CDRL2, and a CDRL3 of SEQ ID NO: 702, SEQ ID NO: 859, and SEQ ID NO: 1016, respectively, and a first and second heavy chain, each heavy chain comprising a CDRH1, a CDRH2, and a CDRH3 of SEQ ID NO: 1173, SEQ ID NO: 1330, and SEQ ID NO: 1487, respectively; a first and second GLP-1 receptor agonist polypeptide, wherein each GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1580; and (ii) a first and second peptide linker, wherein each peptide linker comprises the amino acid sequence of SEQ ID NO: 1591; wherein the first GLP-1 receptor agonist polypeptide is conjugated, at its C-terminus via the first linker, to the first heavy chain of the anti-GIPR antibody at a cysteine residue at position 384 of the first heavy chain according to AHo numbering, and wherein the second GLP-1 receptor agonist polypeptide is conjugated, at its C-terminus via the second linker, to the second heavy chain of the anti-GIPR antibody at a cysteine residue at position 384 of the second heavy chain according to AHo numbering.

[0319] Embodiment 50 is the conjugate molecule of embodiment 49, wherein each light chain comprises a VL of SEQ ID NO: 74, and each heavy chain comprises a VH of SEQ ID NO: 231.

[0320] Embodiment 51 is the conjugate molecule of embodiment 49, wherein each light chain comprises the amino acid sequence of SEQ ID NO: 388, and each heavy chain comprises the amino acid sequence of SEQ ID NO: 1571.

[0321] Embodiment 52 is a conjugate molecule comprising: (i) an antagonist anti-glucose-dependent insulinotropic polypeptide receptor (GIPR) antibody, wherein the anti-GIPR antibody comprises: a first and second light chain, each light chain comprising a CDRL1, a CDRL2, and a CDRL3 of SEQ ID NO: 702, SEQ ID NO: 859, and SEQ ID NO: 1016, respectively, and a first and second heavy

chain, each heavy chain comprising a CDRH1, a CDRH2, and a CDRH3 of SEQ ID NO: 1173, SEQ ID NO: 1330, and SEQ ID NO: 1487, respectively; (ii) a first and second GLP-1 receptor agonist polypeptide, wherein each GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1581; and (iii) a first and second peptide linker, wherein each peptide linker comprises the amino acid sequence of SEQ ID NO: 1586; wherein the first GLP-1 receptor agonist polypeptide is conjugated, at its C-terminus via the first linker, to the first heavy chain of the anti-GIPR antibody at a cysteine residue at position 384 of the first heavy chain according to AHo numbering, and wherein the second GLP-1 receptor agonist polypeptide is conjugated, at its C-terminus via the second linker, to the second heavy chain of the anti-GIPR antibody at a cysteine residue at position 384 of the second heavy chain according to AHo numbering.

[0322] Embodiment 53 is the conjugate molecule of embodiment 52, wherein each light chain comprises a VL of SEQ ID NO: 74, and each heavy chain comprises a VH of SEQ ID NO: 231.

[0323] Embodiment 54 is the conjugate molecule of embodiment 52, wherein each light chain comprises the amino acid sequence of SEQ ID NO: 388, and each heavy chain comprises the amino acid sequence of SEQ ID NO: 1571.

[0324] Embodiment 55 is a conjugate molecule comprising: (i) an antagonist anti-glucose-dependent insulinotropic polypeptide receptor (GIPR) antibody, wherein the anti-GIPR antibody comprises: a first and second light chain, each light chain comprising a CDRL1, a CDRL2, and a CDRL3 of SEQ ID NO: 702, SEQ ID NO: 859, and SEQ ID NO: 1016, respectively, and a first and second heavy chain, each heavy chain comprising a CDRH1, a CDRH2, and a CDRH3 of SEQ ID NO: 1173, SEQ ID NO: 1330, and SEQ ID NO: 1487, respectively; (ii) a first and second GLP-1 receptor agonist polypeptide, wherein each GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1581; and (iii) a first and second peptide linker, wherein each peptide linker comprises the amino acid sequence of SEQ ID NO: 1585; wherein the first GLP-1 receptor agonist polypeptide is conjugated, at its C-terminus via the first linker, to the first heavy chain of the anti-GIPR antibody at a cysteine residue at position 275 of the first heavy chain, and wherein the second GLP-1 receptor agonist polypeptide is conjugated, at its C-terminus via the second linker, to the second heavy chain of the anti-GIPR antibody at a cysteine residue at position 275 of the second heavy chain.

[0325] Embodiment 56 is the conjugate molecule of embodiment 55, wherein each light chain comprises a VL of SEQ ID NO: 74, and each heavy chain comprises a VH of SEQ ID NO: 231.

[0326] Embodiment 57 is the conjugate molecule of embodiment 55, wherein each light chain comprises the amino acid sequence of SEQ ID NO: 388, and each heavy chain comprises the amino acid sequence of SEQ ID NO: 1571.

[0327] Embodiment 58 is a pharmaceutical composition comprising: a GLP-1 receptor agonist polypeptide of any one of embodiments 1 to 10, the molecule of any one of embodiments 11 to 16, or the conjugate molecule of any one of embodiments 17 to 57; and a pharmaceutically acceptable excipient.

[0328] Embodiment 59 is a method of reducing body weight and/or food intake in a subject in need thereof, the method comprising: administering the GLP-1 receptor agonist polypeptide of any one of embodiments 1 to 10, the molecule of any one of embodiments 11 to 16, the conjugate molecule of any one of embodiments 17 to 57, or the pharmaceutical composition of embodiment 58 to the subject.

[0329] Embodiment 60 is a method of treating obesity or an obesity related condition in a subject in need thereof, the method comprising: administering, to the subject, the GLP-1 receptor agonist polypeptide of any one of embodiments 1 to 10, the molecule of any one of embodiments 11 to 16, the conjugate molecule of any one of embodiments 17 to 57, or the pharmaceutical composition of embodiment 58.

[0330] Embodiment 61 is the method of embodiment 60, wherein the obesity related condition is selected from the group consisting of sleep apnea, dyslipidemia, atherosclerotic cardiovascular disease, heart failure, hypertension, chronic kidney failure, and metabolic dysfunction-associated steatohepatitis.

[0331] Embodiment 62 is a method of treating type 2 diabetes or a type 2 diabetes related condition in a subject in need thereof, the method comprising: administering, to the subject, the GLP-1 receptor agonist polypeptide of any one of embodiments 1 to 10, the molecule of any one of embodiments 11 to 17, the conjugate molecule of any one of embodiments 17 to 57, or the pharmaceutical composition of embodiment 58.

[0332] Embodiment 63 is the method of embodiment 62, wherein the type 2 diabetes related conditions is selected from the group consisting of hypertension, high blood sugar, diabetic kidney disease, and diabetic kidney failure.

[0333] Embodiment 64 is the GLP-1 receptor agonist polypeptide of any one of embodiments 1 to 10, the molecule of any one of embodiments 11 to 16, or the conjugate molecule of any one of embodiments 17 to 57 for use as a medicament.

EXAMPLES

Example 1: Generation of Bis-Cysteamine-Capped Anti-GIPR cys mAb (2 g Scale)

[0334] Anti-GIPR monoclonal antibodies with a specific cysteine mutation (anti-GIPR cys mAb, 2 g) were incubated with 800 mL solution of 2.5 mM cystamine and 1 mM cysteamine in 40 mM HEPES buffer, pH 7.5-8.5 for 15-20 h. The reaction mixture was filtered using 0.22 μm filter, and diluted in 1200 mL of 100 mM sodium acetate buffer pH 5. Cation exchange chromatography was used to purify the bis-cysteamine-capped anti-GIPR cys mAb from the reaction mixture. First, 2 L of reaction mixture diluted in 100 mM sodium acetate buffer pH 5 was loaded onto 240 mL SP HP column at 20 mL/min. The column was washed with 2 column volumes of 100 mM sodium acetate pH 5, followed by a 0-20% gradient of 100 mM sodium acetate with 1 M NaCl pH 5. The main peak containing bis-cysteamine-capped anti-GIPR cys mAb was collected and buffer exchanged to 10 mM sodium acetate with 9% sucrose pH 5.2 using tangential flow filtration.

Example 2: Generation of Anti-GIPR/GLP-1 Peptide Conjugates

[0335] The reaction scheme for the generation of anti-GIPR/GLP-1 peptide conjugates is shown in FIG. 1. Bis-cysteamine-capped anti-GIPR cys mAb (6 mg/mL in 10 mM sodium acetate with 9% sucrose) was partially reduced using 3-4 equivalents of triphenylphosphine-3,3′,3″-trisulfonic acid trisodium salt (TPPTS) at RT for 60-90 min. TPPTS was removed, and partially reduced cys mAb was buffer exchanged to 50 mM sodium phosphate buffer containing 2 mM ethylenediaminetetraacetic acid (EDTA) pH 7.5. To the partially reduced cys mAb was added 6-10 equivalents of dehydroascorbic acid (DHAA), and oxidation was carried out until only trace amount of partially reduced mAb species were observed (30-120 min). Without removing DHAA, 3-8 equivalents of bromoacetyl-GLP-1 peptide was added to the reaction mixture and incubated for 12-16 hrs. Either cation exchange chromatography or hydrophobic interaction chromatography were used to purify the conjugates. For cation exchange, first the reaction was diluted in 100 mM sodium acetate buffer pH 5 and loaded on a 5 mL SPHP column at 5 mL/min. The column was then washed with 2 column volumes of 20 mM sodium acetate pH 5, followed by a 0-20% gradient of 20 mM sodium acetate with 1 M NaCl pH5. For hydrophobic interaction chromatography, first the reaction was diluted in a buffer containing 1 M ammonium sulfate and 20 mM sodium acetate pH 5. The sample was then loaded on a 5 mL Butyl HP

column at 5 mL/min. The column was washed with 2 column volumes of a buffer containing 1 M ammonium sulfate and 20 mM sodium acetate pH 5, followed by a 0-100% gradient of a buffer containing 20 mM sodium acetate and 10% acetonitrile pH5. The main peak containing the anti-GIPR/GLP-1 conjugates comprising a drug-to-antibody ratio of 2:1 (DAR2) was collected and buffer exchanged into 10 mM sodium acetate with 9% sucrose pH5.2 using spin concentration.

Example 3: GLP-1 Receptor Agonist Activity

[0336] CHOK1 cells stably expressing the human GLP-1 receptor were used to measure GLP-1 receptor agonist-induced cAMP production by the anti-GIPR antibody/GLP-1 agonist conjugate molecules of the disclosure in a homogeneous time-resolved fluorescence (HTRF) assay (CISBIO, cat #62AM4PEJ). Serial diluted anti-GIPR/GLP-1 conjugate molecules were incubated with 40,000 cells in assay buffer (0.1% BSA, 500 uM IBMX in F12 media) for 15 min at 37°C. Cells were then lysed with lysis buffer containing cAMP-d2 and cAMP cryptate (CISBIO) and incubated for 1 hour at room temperature before measured in Envision plate reader (PerkinElmer). The cAMP levels are expressed as a fluorescence ratio of 665/620 nm. Representative anti-GIPR/GLP-1 conjugate-induced cAMP levels for 5G12 and 2G10 GIPR antibody conjugate molecules comprising the GLP-1 receptor agonist polypeptides disclosed herein is provided in Table 12 below. 5G12 antibody conjugates comprise the indicated GLP-1 receptor agonist polypeptide conjugated to the anti-GIPR antibody of 5G12.006 (see Table 3) ("5G12 conjugate") which is cross-reactive to mouse GIPR. 2G10 antibody conjugates comprise the indicated GLP-1 receptor agonist polypeptide conjugated to the anti-GIPR antibody 2G10_LC1.006 (see Table 3) ("2G10 conjugate"), which is cross-reactive to human, but not mouse GIPR.

Example 4: *In Vivo* Pharmacodynamic Studies

[0337] Naïve male C57BL6 mice from either Envigo (study 2023-10 and 2023-13) or Jackson Laboratories (study 2023-03) were fed high fat diet (D12492 HFD from Research Diets Inc) for 14-15 weeks starting at 5-6 weeks of age. These mice are defined as Diet-Induced Obesity (DIO) mice. Mice were acclimated to all study related procedures prior to study initiation (single housing, handling, weighing, dosing). On day -1, mice were sorted into

treatment groups with equal distribution of body weight across all groups with n=7 mice per group.

[0338] For single injection studies, mice received a single intraperitoneal injection of either vehicle (2.5mL/kg; 10mM sodium acetate, 9% sucrose, pH5.2) or anti-GIPR antibody/GLP-1 receptor agonist surrogate conjugates at 0.5 mg/kg (2.5mL/kg). The surrogate molecules (identified as 5G12 conjugates) comprise the GLP-1 receptor agonist polypeptides described herein conjugated to the antagonist anti-GIPR antibody of 5G12.006 (see Table 3 for structural details) that cross-reacts with mouse GIPR. Body weight and food intake were measured every other day at the same time in the morning. The graphs of FIGs. 10-14 show the percent change in body weight from baseline (day 0) over the number of days indicated in DIO mice receiving the single dose of the anti-GIPR antibody/GLP-1 receptor agonist conjugate molecules at day 0. The maximum percent body weight loss observed over the course of the study following the single injection is provided in Table 12 below ("Single Dose BW Loss").

[0339] For chronic studies, mice received an intraperitoneal injection of day 0 and day 10 of either vehicle, the reference anti-GIPR/GLP-1 receptor agonist conjugate (5G12 Conjugate ID 1238), or anti-GIPR antibody/GLP-1 receptor agonist conjugate molecules comprising the GLP-1 receptor agonist polypeptides disclosed herein (*i.e.*, 5G12 Conjugate ID Nos. 59112, 62207, 65296, 65300, 59117, 69730, 69850, and 73313). Body weight and food intake were measured every other day throughout the study (until day 24) at the same time in the morning. Percent change in body weight from baseline (day 0) over the number of days indicated in mice receiving the conjugate molecule versus the mice receiving vehicle was the main endpoint for these studies.

[0340] The graphs of FIGs. 15-17 show the percent change in body weight from baseline (day 0) over the number of days indicated in DIO mice receiving two doses of the anti-GIPR antibody/GLP-1 receptor agonist conjugate molecules (chronic study). The percent BW loss at days 10 and 16 for each treatment group is also provided in Table 12 below. Also provided is the additional percent BW loss achieved at day 16 by the indicated conjugate over the BW loss achieved in mice administered the reference anti-GIPR/GLP-1 receptor agonist conjugate in the same study.

Table. 12 Summary of *In vitro* and *In vivo* anti-GIPR/GLP-1R agonist Activity

GLP-1R Agonist AA Subst.	GLP-1R Agonist SEQ ID NO: 5G12 Conjugate ID	Linker (SEQ ID NO)	GLP-1R EC50 (pM) 5G12/ 2G10	Single dose BW loss	Chronic DIO BW loss			Percent extra BW loss over 1238 at D16
					Study#	D10	D16	
Aib2;Y10;E16;E24;R20;K27;G30	1579 65300	$(G_2S)_5$-K (1592)	14.5/17.8	-13.3%	2023-10	-16.9%	-21.7%	-1.5%
Aib2;Y10;E16;E24;E28;R20;K17;K27;G30	1580 59117	$K(G_4S)_3$ (1591)	13.7/14.3	-12.1%	2023-13	-18.1%	-22.9%	-1.0%
Aib2;Y10;E16;E24;R20;K17,K27;G30	1581 73313	$(G_4Q)_3$-K (1586)	22.4/14.2	Not Tested	2023-13	-20.6%	-25.5%	-3.6%
Aib2;Y10;E16;E24;R20;K17,K27;G30	1581 59112	$(G_4S)_3$-K (1593)	21.8/46.1	-12.6%	2023-03	-12.2%	-17%	-4.3%
Aib2;Y10;E16;E24;R20;K17,K27;G30	1581 65296	(G_2Q)5-K (1585)	20.6/15.7	-22.2%	2023-10	-16.7%	-21.2%	-1.0%
Aib2;Y10;E16;E24;R20;R28;K27;G30	1582 69850	K-(G-PEG20)	10.4/14.9	-13.5%	2023-13	-16.9%	-22.1%	0%
Aib2;Y10;E16;E24;R20;K17,K27;G30	1581 62207	K-(G-PEG20)	11.7/19.0	-23.4%,	2023-10	-15.7%	-20.4%	0%
Aib2;Y10;E16;E28;K17;K27;R20;Q24;G30	1583 69730	K-(G-PEG20)	7.9/31.3	-12.8%	2023-13	-16.5%	-24.6%	-2.6%

Example 5: Pharmacokinetic Studies

[0341] Preliminary pharmacokinetic (PK) studies were conducted with CD-1 mice. Plasma concentrations of Intact and Total GIPR-GLP-1 molecules were measured at every time point. Plasma concentration of Intact GIPR-GLP-1 molecule is defined as the concentration of molecules having at least one intact GLP-1 peptide conjugated to the anti-GIPR mAb. Plasma concentration of Total GIPR-GLP-1 molecule is defined as the concentration of all the molecules containing the anti-GIPR mAb. The general design of the PK studies is in the table below. Anti-GIPR-GLP-1 receptor agonist conjugate molecules were dosed to Male CD-1 mice by intravenous bolus administration at a dose of 5 mg/kg via intravenous administration. Blood samples were taken at each time point (0.083, 24, 72, 168, 336 hours) post-dose (table below). All plasma specimens were stored at approximately −70° C (±10° C) until transferred for subsequent analysis.

Experimental Design

Test System #	Test Article	Route	Dose (mg/kg)	Dose Solution Conc. (mg/mL)	Dose Volume (mL/kg)	[1]Approx. Dose Vol. (mL)
1-6	anti-GIPR-GLP-1 receptor agonist conjugate	IV	5	1	5	0.15

[1] Approximate dose volume is based on an average test system body weight of 0.03 kg per mouse and is adjusted to each test system's individual body weight the morning of dose administration.

Test Systems

Species	Strain Name	Sex	Source	Age	No. per Cage
Mouse	CD-1	Male	Charles River Laboratory, Hollister, CA	7-8 weeks	3

[0342] **Test Article Storage, Handling, and Dilutions**. The stock test articles were removed from −70°C (±10°C) storage and placed at 2-8°C to thaw overnight on the day before

dose administration. On the morning of dosing, the stock test articles were removed from 2-8°C storage, mixed by gentle inversion, and placed on wet ice for the dilution procedures. The vehicle was removed from 2-8°C storage mixed by gentle inversion and placed on wet ice for the dilution procedures. For all groups, the stock test articles were diluted in the appropriate formulation buffer to obtain the final dose solution concentrations listed in the Experimental Design table. Following dose solution preparation, all remaining vehicle (if applicable) was returned to 2-8°C storage. The dose solutions remained on wet ice throughout the dose administration phase. Following dose administration, all remaining stock test articles (if applicable) and remaining dosing solutions (if applicable) were placed at −70° (±10°C) and transferred to storage.

[0343] **Dose Administration.** Test systems receive a 5 mg/kg intravenous bolus dose of the appropriate dosing solution via the lateral tail vein.

[0344] **Blood Collection.** SARSTEDT Microvette® K_2EDTA plasma separation tubes were used to collect approximately 0.1 mL of whole blood per test system at each serial time point for each analysis via submandibular venipuncture. At each terminal time point, test systems were euthanized by CO2(g) asphyxiation and as much whole blood as possible, ≥ 0.6 mL, is collected by cardiocentesis. After putting the whole blood into the SARSTEDT Microvette® plasma tubes, the tubes were mixed by 8-10 gentle inversions and placed on wet ice. The specimens were centrifuged using a calibrated Eppendorf 5417R Centrifuge System (Brinkmann Instruments, Inc., Westbury, NY 11590). Blood specimens were centrifuged at 2-8°C at approximately 14,000 rcf for 5 minutes. The collected plasma specimens were transferred into each test system's pre-labeled, freezer-safe storage tube. All plasma specimens were stored at approximately -70°C (±10°C) until transferred for subsequent analysis.

Sub Group	Test System #	Time Points (hr)					
		0.083	24	72	168	240	336
A	1-3	X		X		X	
B	4-6		X		X		X

X = Blood specimens are collected for PK plasma drug analysis

[0345] **Pharmacokinetic Bioanalytical Assay.** For LC-MS/MS, GIPR-GLP-1 conjugate molecule stock solutions (1 mg/mL) were made from reference standards in A5Su

buffer and stored at −70° C. 1 mg/mL GIPR-GLP-1 conjugate molecule stock solutions were used to prepare 100 µg/mL working solution in A5Su buffer and were stored in a refrigerator at 2 to 8° C. Standard samples were prepared in CD-1 mouse plasma. Standards concentrations of 100, 250, 500, 1,000, 2,500, 5,000, 7,500, and 10,000 ng/mL were prepared by serial dilution of a freshly prepared 10,000 ng/mL solution in mouse plasma using the 100 µg/mL mAb conjugate molecule working solution. 10 µl mouse plasma samples were aliquoted into the appropriate well of a 96-well plate, followed by the addition of 10 µL of magnetic beads immobilized with anti-human Fc capture antibody Ab35. Samples were then incubated for 30 min at room temperature. After washing with 250 mM NH4HCO3 buffer, the beads were denatured using 8 M urea and reduced by tris(2-carboxyethyl) phosphine (TCEP), followed by trypsin digestion. After quenched with formic acid, samples were centrifuged, and the supernatant was transferred to a 96-well plate then injected (20 µL) onto the LC-MS/MS system for analysis.

[0346] The LC-MS/MS consisted of Shimadzu Nexera X2 system (Shimadzu Corporation, Kyoto, Japan) coupled with a Sciex 6500 plus mass spectrometer (AB Sciex, Toronto, Canada) with a Turbo IonSpray® ionization source. The analytical column was a MAC MOD HALO Protein ES-C18 column (3.4 µm, 50 x 2.1 mm). The mobile phases were 0.1% formic acid in water (mobile phase A) and 0.1% formic acid in acetonitrile (mobile phase B). Data was collected and processed using AB Sciex Analyst® software (version 1.6.1). The LC-MS/MS methods are GIPR-GLP-1 molecule-specific depending on the GLP-1 peptide amino acid sequences.

[0347] The calibration curve was derived from the peak area ratios (GIPR-GLP-1 conjugate construct tryptic surrogate peptide/internal standard) versus the concentrations of the corresponding GIPR-GLP-1 conjugate construct standards using 1/x2 weighted linear least-squares regression. The regression equations from the calibration standards were used to back-calculate the measured concentrations for each standard and plasma sample.

[0348] **Noncompartmental Analysis.** Noncompartmental analysis was performed on individual mouse plasma concentration-nominal time data using Phoenix® WinNonlin® (version 6.4; Certara, Princeton, N.J.). Individual concentration values less than the lower limit of qualification (LLOQ 100 ng/mL) were reported as below the quantitation limit (BQL) and set to zero for the calculation of summary statistics. Mean concentration values less than the LLOQ were not reported or plotted. All concentration values less than the LLOQ were excluded from

the non-compartmental analysis. Nominal doses and nominal sampling times were used for PK analysis.

[0349] The following PK parameters were estimated:

(i) The initial concentration (C0) value after intravenous administration was estimated by back extrapolation to time zero using the first 2 observed declining concentration values.

(ii) The area under the concentration-time curve from time zero to infinity (AUCinf) was calculated by the linear trapezoidal method.

(iii) The terminal-phase half-life (t1/2,z) was calculated as ln 2/2λz. λz is the first-order rate constant of drug associated with the terminal portion of the curve

(iv) Systemic clearance (CL) was calculated as:

CL=Dose/AUCinf after intravenous administration

(v) The intact to total GIPR-GLP-1 molecule $AUC_{0\text{-}t}$ ratio was calculated as:

$$intact\ to\ total\ GIPR-GLP1\ AUC\ ratio = \frac{intact\ GIPR-GLP1\ AUC_{0-t}}{total\ GIPR-GLP1\ AUC_{0-t}}$$

Where t=336 hours

[0350] The elimination of intact GIPR-GLP-1 conjugate molecule was more rapid than that of the total GIPR-GLP-1 conjugate molecule and likely resulted from the gradual clipping of the GLP-1 moiety from the conjugate molecule circulating in mice. Hence, the intact to total AUC ratio indicates the stability of the GLP-1 peptide. The GLP-1 peptide is the same between 5G12 mouse surrogate and 2G10 human format. Hence, the intact to total $AUC_{0\text{-}t}$ ratio is likely to be consistent between human 2G10 and its corresponding 5G12 mouse surrogate format.

Table 13. GIPR-GLP-1 Conjugate Molecule Stability

GLP-1 Receptor Agonist AA Substitutions	GLP-1R Agonist SEQ ID NO:	Linker (SEQ ID NO)	Antibody Conjugate	Stability of Conjugate Intact/Total AUC Ratio
Aib2;Y10;E16;E24; R20;K27;G30	1579	1592	2G10	0.76
Aib2;Y10;E16;E24; E28;R20;K17;K27; G30	1580	1593	2G10	0.813
Aib2;Y10;E16;E24; R20;K17,K27;G30	1581	1586	2G10	0.845
Aib2;Y10;E16;E24; R20;K17,K27;G30	1581	1593	2G10	0.816
Aib2;Y10;E16;E24; R20;K17,K27;G30	1581	1585	2G10	0.86
Aib2;Y10;E16;E24; R20;R28;K27;G30	1582	K-(G-PEG20)	2G10	0.844
Aib2;Y10;E16;E24; R20;K17,K27;G30	1581	K-(G-PEG20)	2G10	0.94
Aib2;Y10;E16;E28; K17;K27;R20;Q24; G30	1583	K-(G-PEG20)	2G10	0.848
Aib2;Y10;E16; G30	1574	1593	5G12	0.59

[0351] The disclosed subject matter is not intended to be limited in scope by the specific embodiments described herein, which are instead intended as non-limiting illustrations of individual aspects of the disclosure. Functionally equivalent methods and components are within

the scope of the disclosure. Indeed, various modifications of the disclosed subject matter, in addition to those shown and described herein, will be apparent to those skilled in the art from the foregoing description and accompanying drawing(s). Such modifications are intended to fall within the scope of the disclosed subject matter.

What is Claimed:

1. A human glucagon-like peptide 1 (GLP-1) receptor agonist polypeptide comprising the amino acid sequence of H[Aib]EGTFTSDYSSYLEEX_{17}AAX_{20}EFIX_{24}WL$X_{27}X_{28}$GGG (SEQ ID NO: 1575),

wherein X_{17} is Q, K, E, or R; X_{20} is K, R, Q, or homoarginine (hArg); X_{24} is A, E, Q, D, d-Ala, G, N, K, (1S,2S)-2-Aminocyclopentanecarboxylic acid (ACPC), (3S,4R)-4-Amino-3-pyrrolidinecarboxylic acid (APCA), T, S, or Y; X_{27} is V, K, Aib, N, S, T, Y, Q, or R; and X_{28} is K, E, R, Q, D, N, G, S, or T; and

wherein the GLP-1 receptor agonist polypeptide does not comprise the amino acid sequence of SEQ ID NO: 1574 (H[Aib]EGTFTSDYSSYLEEQAAKEFIAWLVKGGG).

2. The GLP-1 receptor agonist polypeptide of claim 1, wherein the GLP-1 receptor agonist polypeptide comprises the amino acid sequence of H[Aib]EGTFTSDYSSYLEEX_{17}AAX_{20}EFIX_{24}WL$X_{27}X_{28}$GGG (SEQ ID NO: 1576), wherein X_{17} is Q or K; X_{20} is K or R; X_{24} is A, E, or Q; X_{27} is V or K; and X_{28} is K, E, or R.

3. The GLP-1 receptor agonist polypeptide of claim 1, wherein the GLP-1 receptor agonist polypeptide comprises the amino acid sequence of H[Aib]EGTFTSDYSSYLEEX_{17}AAREFIX_{24}WL$X_{27}X_{28}$GGG (SEQ ID NO: 1577) wherein X_{17} is Q or K; X_{24} is A, E, or Q; X_{27} is V or K; and X_{28} is K, E, or R.

4. The GLP-1 receptor agonist polypeptide of claim 1, wherein the GLP-1 receptor agonist polypeptide comprises the amino acid sequence of H[Aib]EGTFTSDYSSYLEEX_{17}AAX_{20}EFIX_{24}WLKX_{28}GGG (SEQ ID NO: 1578), wherein X_{17} is Q or K; X_{20} is K or R; X_{24} is A, E, or Q; and X_{28} is K, E, or R.

5. The GLP-1 receptor agonist polypeptide of claim 1, where the GLP-1 receptor agonist polypeptide comprises the amino acid sequence of any one of SEQ ID NO: 1579, SEQ ID NO: 1580, SEQ ID NO: 1581, SEQ ID NO: 1582, or SEQ ID NO: 1583.

6. A human glucagon-like peptide 1 (GLP-1) receptor agonist polypeptide, wherein:

the polypeptide comprises 31 amino acids and comprises an amino acid sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 1580; and

wherein the polypeptide comprises an α-amino-isobutyric acid (Aib) at position 2; a tyrosine at position 10; a glutamic acid at positions 16, 24, and 28; an arginine at position 20; a lysine at positions 17 and 27; and a glycine at position 31.

7. A human glucagon-like peptide 1 (GLP-1) receptor agonist polypeptide, wherein:

the GLP-1 receptor agonist polypeptide comprises 31 amino acids and comprises an amino acid sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 1579; and

wherein the GLP-1 receptor agonist polypeptide comprises an Aib at position 2; a tyrosine at position 10; a glutamic acid at positions 16 and 24; an arginine at position 20; a lysine at positions 27; and a glycine at position 30.

8. A human glucagon-like peptide 1 (GLP-1) receptor agonist polypeptide, wherein:

the GLP-1 receptor agonist polypeptide comprises 31 amino acids and comprises an amino acid sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 1581; and

wherein the GLP-1 receptor agonist polypeptide comprises an Aib at position 2; a tyrosine at position 10; a glutamic acid at positions 16 and 24; an arginine at position 20; a lysine at positions 17, 27; and a glycine at position 30.

9. A human glucagon-like peptide 1 (GLP-1) receptor agonist polypeptide, wherein:

the GLP-1 receptor agonist polypeptide comprises 31 amino acids and comprises an amino acid sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 1583; and

wherein the GLP-1 receptor agonist polypeptide comprises an Aib at position 2; a tyrosine at position 10; a glutamic acid at positions 16 and 28; an arginine at position 20; a lysine at positions 17, 27; a glutamine at position 24; and a glycine at position 30.

10. A human glucagon-like peptide 1 (GLP-1) receptor agonist polypeptide, wherein:

the GLP-1 receptor agonist polypeptide comprises 31 amino acids and comprises an amino acid sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 1582; and

wherein the GLP-1 receptor agonist polypeptide comprises an Aib at position 2; a tyrosine at position 10; a glutamic acid at positions 16 and 24; an arginine at positions 20 and 28; a lysine at positions 27; and a glycine at position 30.

11. A molecule comprising:

a first human glucagon-like peptide 1 (GLP-1) receptor agonist polypeptide comprising the amino acid sequence of H[Aib]EGTFTSDYSSYLEEX_{17}AAX_{20}EFIX_{24}WL$X_{27}X_{28}$GGG (SEQ ID NO: 1575),

wherein X_{17} is Q, K, E, or R; X_{20} is K, R, Q, or homoarginine (hArg); X_{24} is A, E, Q, D, d-Ala, G, N, K, (1S,2S)-2-Aminocyclopentanecarboxylic acid (ACPC), (3S,4R)-4-Amino-3-pyrrolidinecarboxylic acid (APCA), T, S, or Y; X_{27} is V, K, Aib, N, S, T, Y, Q, or R; and X_{28} is K, E, R, Q, D, N, G, S, or T, and

wherein the GLP-1 receptor agonist polypeptide does not comprise the amino acid sequence of SEQ ID NO: 1574; and

a half-life extending moiety.

12. The molecule of claim 11, wherein the first GLP-1 receptor agonist polypeptide comprises the amino acid sequence of H[Aib]EGTFTSDYSSYLEEX_{17}AAX_{20}EFIX_{24}WL$X_{27}X_{28}$GGG (SEQ ID NO: 1576), wherein X_{17} is Q or K; X_{20} is K or R; X_{24} is A, E, or Q; X_{27} is V or K; and X_{28} is K, E, or R.

13. The molecule of claim 11, wherein the first GLP-1 receptor agonist polypeptide comprises the amino acid sequence of H[Aib]EGTFTSDYSSYLEEX_{17}AAR_{20}EFIX_{24}WL$X_{27}X_{28}$GGG (SEQ ID NO: 1577) wherein X_{17} is Q or K; X_{24} is A, E, or Q; X_{27} is V or K; and X_{28} is K, E, or R.

14. The molecule of claim 11, wherein the first GLP-1 receptor agonist polypeptide comprises the amino acid sequence of H[Aib]EGTFTSDYSSYLEEX_{17}AAX_{20}EFIX_{24}WL$K_{27}X_{28}$GGG (SEQ ID NO: 1578), wherein X_{17} is Q or K; X_{20} is K or R; X_{24} is A, E, or Q; and X_{28} is K, E, or R.

15. The molecule of claim 11, wherein the first GLP-1 receptor agonist polypeptide comprises the amino acid sequence of any one of SEQ ID NO: 1579, SEQ ID NO: 1580, SEQ ID NO: 1581, SEQ ID NO: 1582, or SEQ ID NO: 1583.

16. The molecule of any one of claims 11–15, wherein the half-life extending moiety is an antibody.

17. A conjugate molecule comprising:

a first human glucagon-like peptide 1 (GLP-1) receptor agonist polypeptide comprising the amino acid sequence of H[Aib]EGTFTSDYSSYLEEX_{17}AAX_{20}EFIX_{24}WL$X_{27}X_{28}$GGG (SEQ ID NO: 1575),

wherein X_{17} is Q, K, E, or R; X_{20} is K, R, Q, or homoarginine (hArg); X_{24} is A, E, Q, D, d-Ala, G, N, K, (1S,2S)-2-Aminocyclopentanecarboxylic acid (ACPC), (3S,4R)-4-Amino-3-pyrrolidinecarboxylic acid (APCA), T, S, or Y; X_{27} is V, K, Aib, N, S, T, Y, Q, or R; and X_{28} is K, E, R, Q, D, N, G, S, or T, and

wherein the GLP-1 receptor agonist polypeptide does not comprise the amino acid sequence of SEQ ID NO: 1574; and

an antagonist anti-glucose-dependent insulinotropic polypeptide receptor (GIPR) human antibody.

18. The conjugate molecule of claim 17, wherein the anti-GIPR antibody antagonizes human GIPR.

19. The conjugate molecule of claim 17, wherein the first GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1575.

20. The conjugate molecule of claim 17, wherein the first GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1576.

21. The conjugate molecule of claim 17, wherein the first GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1577.

22. The conjugate molecule of claim 17, wherein the first GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1578.

23. The conjugate molecule of claim 17, wherein the first GLP-1 receptor agonist polypeptide comprises the amino acid sequence of any one of SEQ ID NO: 1579, SEQ ID NO: 1580, SEQ ID NO: 1581, SEQ ID NO: 1582, or SEQ ID NO: 1583.

24. The conjugate molecule of claim 17 or claim 18, wherein the anti-GIPR antibody comprises a first cysteine conjugation site within a light chain or heavy chain of the antibody, and

wherein the first GLP-1 receptor agonist polypeptide is conjugated, at its C-terminus, to the first cysteine conjugation site of the anti-GIPR antibody.

25. The conjugate molecule of claim 24, wherein the first GLP-1 receptor agonist polypeptide is conjugated, at its C-terminus, to the first cysteine conjugation site of the anti-GIPR antibody via a first linker moiety.

26. The conjugate molecule of claim 25, wherein the first linker moiety is a peptide linker and the peptide linker comprises the amino acid sequence of any one of SEQ ID NOs: 1585–1593.

27. The conjugate molecule of claim 25, wherein the first linker moiety is a PEG linker.

28. The conjugate molecule of any one of claims 24 to 27, wherein the first cysteine conjugation site of the anti-GIPR antibody is at position 88 of the light chain, position 384 of the heavy chain, or position 487 of the heavy chain according to AHo numbering.

29. The conjugate molecule of anyone of claims 17 to 28, wherein the molecule further comprises:

a second GLP-1 receptor agonist polypeptide, wherein the second GLP-1 receptor agonist polypeptide is conjugated, at its C-terminus, to a second cysteine conjugation site of the anti-GIPR antibody.

30. The conjugate molecule of claim 29, wherein the second GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1575.

31. The conjugate molecule of claim 29, wherein the second GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1576.

32. The conjugate molecule of claim 29 wherein the second GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1577.

33. The conjugate molecule of claim 29, wherein the second GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1578.

34. The conjugate molecule of claim 29, wherein the second GLP-1 receptor agonist polypeptide comprises the amino acid sequence of any one of SEQ ID NO: 1579, SEQ ID NO: 1580, SEQ ID NO: 1581, SEQ ID NO: 1582, or SEQ ID NO: 1583.

35. The conjugate molecule of claim 29, wherein the second GLP-1 receptor agonist polypeptide comprises the same amino acid sequence as the first GLP-1 receptor agonist polypeptide.

36. The conjugate molecule of any one of claims 29 to 35, wherein the second GLP-1 receptor agonist polypeptide is conjugated, at its C-terminus, to the second cysteine conjugation site of the anti-GIPR antibody via a second linker moiety.

37. The conjugate molecule of claim 36, wherein the second linker moiety is a peptide linker and the peptide linker comprises the amino acid sequence of any one of SEQ ID NOs: 1585–1593.

38. The conjugate molecule of claim 36, wherein the second linker moiety is a PEG linker.

39. The conjugate molecule of claim 29, wherein the first and second conjugation sites of the anti-GIPR antibody are at position 88 of each light chain, position 384 of each heavy chain, or position 487 of each heavy chain according to AHo numbering.

40. The conjugate molecule of any one of embodiments 17 to 39, wherein the anti-GIPR antibody comprises a light chain complementarity determining region 1 (CDRL1), a CDRL2, a CDRL3, a heavy chain complementarity determining region 1 (CDRH1), a CDRH2, and a CDRH3, wherein the CDRL1, the CDRL2, the CDRL3, the CDRH1, the CDRH2, and the CDRH3 comprise the amino acid sequences selected from:

i. SEQ ID NO: 629, SEQ ID NO: 786, SEQ ID NO: 943, SEQ ID NO: 1100, SEQ ID NO: 1257, and SEQ ID NO: 1414, respectively;
ii. SEQ ID NO: 630, SEQ ID NO: 787, SEQ ID NO: 944, SEQ ID NO: 1101, SEQ ID NO: 1258, and SEQ ID NO: 1415, respectively;
iii. SEQ ID NO: 631, SEQ ID NO: 788, SEQ ID NO: 945, SEQ ID NO: 1102, SEQ ID NO: 1259, and SEQ ID NO: 1416, respectively;
iv. SEQ ID NO: 632, SEQ ID NO: 789, SEQ ID NO: 946, SEQ ID NO: 1103, SEQ ID NO: 1260, and SEQ ID NO: 1417, respectively;
v. SEQ ID NO: 633, SEQ ID NO: 790, SEQ ID NO: 947, SEQ ID NO: 1104, SEQ ID NO: 1261, and SEQ ID NO: 1418, respectively;
vi. SEQ ID NO: 634, SEQ ID NO: 791, SEQ ID NO: 948, SEQ ID NO: 1105, SEQ ID NO: 1262, and SEQ ID NO: 1419, respectively;
vii. SEQ ID NO: 635, SEQ ID NO: 792, SEQ ID NO: 949, SEQ ID NO: 1106, SEQ ID NO: 1263, and SEQ ID NO: 1420, respectively;
viii. SEQ ID NO: 636, SEQ ID NO: 793, SEQ ID NO: 950, SEQ ID NO: 1107, SEQ ID NO: 1264, and SEQ ID NO: 1421, respectively;
ix. SEQ ID NO: 637, SEQ ID NO: 794, SEQ ID NO: 951, SEQ ID NO: 1108, SEQ ID NO: 1265, and SEQ ID NO: 1422, respectively;

x. SEQ ID NO: 638, SEQ ID NO: 795, SEQ ID NO: 952, SEQ ID NO: 1109, SEQ ID NO: 1266, and SEQ ID NO: 1423, respectively;

xi. SEQ ID NO: 639, SEQ ID NO: 796, SEQ ID NO: 953, SEQ ID NO: 1110, SEQ ID NO: 1267, and SEQ ID NO: 1424, respectively;

xii. SEQ ID NO: 640, SEQ ID NO: 797, SEQ ID NO: 954, SEQ ID NO: 1111, SEQ ID NO: 1268, and SEQ ID NO: 1425, respectively;

xiii. SEQ ID NO: 641, SEQ ID NO: 798, SEQ ID NO: 955, SEQ ID NO: 1112, SEQ ID NO: 1269, and SEQ ID NO: 1426, respectively;

xiv. SEQ ID NO: 642, SEQ ID NO: 799, SEQ ID NO: 956, SEQ ID NO: 1113, SEQ ID NO: 1270, and SEQ ID NO: 1427, respectively;

xv. SEQ ID NO: 643, SEQ ID NO: 800, SEQ ID NO: 957, SEQ ID NO: 1114, SEQ ID NO: 1271, and SEQ ID NO: 1428, respectively;

xvi. SEQ ID NO: 644, SEQ ID NO: 801, SEQ ID NO: 958, SEQ ID NO: 1115, SEQ ID NO: 1272, and SEQ ID NO: 1429, respectively;

xvii. SEQ ID NO: 645, SEQ ID NO: 802, SEQ ID NO: 959, SEQ ID NO: 1116, SEQ ID NO: 1273, and SEQ ID NO: 1430, respectively;

xviii. SEQ ID NO: 646, SEQ ID NO: 803, SEQ ID NO: 960, SEQ ID NO: 1117, SEQ ID NO: 1274, and SEQ ID NO: 1431, respectively;

xix. SEQ ID NO: 647, SEQ ID NO: 804, SEQ ID NO: 961, SEQ ID NO: 1118, SEQ ID NO: 1275, and SEQ ID NO: 1432, respectively;

xx. SEQ ID NO: 648, SEQ ID NO: 805, SEQ ID NO: 962, SEQ ID NO: 1119, SEQ ID NO: 1276, and SEQ ID NO: 1433, respectively;

xxi. SEQ ID NO: 649, SEQ ID NO: 806, SEQ ID NO: 963, SEQ ID NO: 1120, SEQ ID NO: 1277, and SEQ ID NO: 1434, respectively;

xxii. SEQ ID NO: 650, SEQ ID NO: 807, SEQ ID NO: 964, SEQ ID NO: 1121, SEQ ID NO: 1278, and SEQ ID NO: 1435, respectively;

xxiii. SEQ ID NO: 651, SEQ ID NO: 808, SEQ ID NO: 965, SEQ ID NO: 1122, SEQ ID NO: 1279, and SEQ ID NO: 1436, respectively;

xxiv. SEQ ID NO: 652, SEQ ID NO: 809, SEQ ID NO: 966, SEQ ID NO: 1123, SEQ ID NO: 1280, and SEQ ID NO: 1437, respectively;

xxv. SEQ ID NO: 653, SEQ ID NO: 810, SEQ ID NO: 967, SEQ ID NO: 1124, SEQ ID NO: 1281, and SEQ ID NO: 1438, respectively;

xxvi. SEQ ID NO: 654, SEQ ID NO: 811, SEQ ID NO: 968, SEQ ID NO: 1125, SEQ ID NO: 1282, and SEQ ID NO: 1439, respectively;

xxvii. SEQ ID NO: 655, SEQ ID NO: 812, SEQ ID NO: 969, SEQ ID NO: 1126, SEQ ID NO: 1283, and SEQ ID NO: 1440, respectively;

xxviii. SEQ ID NO: 656, SEQ ID NO: 813, SEQ ID NO: 970, SEQ ID NO: 1127, SEQ ID NO: 1284, and SEQ ID NO: 1441, respectively;

xxix. SEQ ID NO: 657, SEQ ID NO: 814, SEQ ID NO: 971, SEQ ID NO: 1128, SEQ ID NO: 1285, and SEQ ID NO: 1442, respectively;

xxx. SEQ ID NO: 658, SEQ ID NO: 815, SEQ ID NO: 972, SEQ ID NO: 1129, SEQ ID NO: 1286, and SEQ ID NO: 1443, respectively;

xxxi. SEQ ID NO: 659, SEQ ID NO: 816, SEQ ID NO: 973, SEQ ID NO: 1130, SEQ ID NO: 1287, and SEQ ID NO: 1444, respectively;

xxxii. SEQ ID NO: 660, SEQ ID NO: 817, SEQ ID NO: 974, SEQ ID NO: 1131, SEQ ID NO: 1288, and SEQ ID NO: 1445, respectively;

xxxiii. SEQ ID NO: 661, SEQ ID NO: 818, SEQ ID NO: 975, SEQ ID NO: 1132, SEQ ID NO: 1289, and SEQ ID NO: 1446, respectively;

xxxiv. SEQ ID NO: 662, SEQ ID NO: 819, SEQ ID NO: 976, SEQ ID NO: 1133, SEQ ID NO: 1290, and SEQ ID NO: 1447, respectively;

xxxv. SEQ ID NO: 663, SEQ ID NO: 820, SEQ ID NO: 977, SEQ ID NO: 1134, SEQ ID NO: 1291, and SEQ ID NO: 1448, respectively;

xxxvi. SEQ ID NO: 664, SEQ ID NO: 821, SEQ ID NO: 978, SEQ ID NO: 1135, SEQ ID NO: 1292, and SEQ ID NO: 1449, respectively;

xxxvii. SEQ ID NO: 665, SEQ ID NO: 822, SEQ ID NO: 979, SEQ ID NO: 1136, SEQ ID NO: 1293, and SEQ ID NO: 1450, respectively;

xxxviii. SEQ ID NO: 666, SEQ ID NO: 823, SEQ ID NO: 980, SEQ ID NO: 1137, SEQ ID NO: 1294, and SEQ ID NO: 1451, respectively;

xxxix. SEQ ID NO: 667, SEQ ID NO: 824, SEQ ID NO: 981, SEQ ID NO: 1138, SEQ ID NO: 1295, and SEQ ID NO: 1452, respectively;

xl. SEQ ID NO: 668, SEQ ID NO: 825, SEQ ID NO: 982, SEQ ID NO: 1139, SEQ ID NO: 1296, and SEQ ID NO: 1453, respectively;

xli. SEQ ID NO: 669, SEQ ID NO: 826, SEQ ID NO: 983, SEQ ID NO: 1140, SEQ ID NO: 1297, and SEQ ID NO: 1454, respectively;

xlii. SEQ ID NO: 670, SEQ ID NO: 827, SEQ ID NO: 984, SEQ ID NO: 1141, SEQ ID NO: 1298, and SEQ ID NO: 1455, respectively;

xliii. SEQ ID NO: 671, SEQ ID NO: 828, SEQ ID NO: 985, SEQ ID NO: 1142, SEQ ID NO: 1299, and SEQ ID NO: 1456, respectively;

xliv. SEQ ID NO: 672, SEQ ID NO: 829, SEQ ID NO: 986, SEQ ID NO: 1143, SEQ ID NO: 1300, and SEQ ID NO: 1457, respectively;

xlv. SEQ ID NO: 673, SEQ ID NO: 830, SEQ ID NO: 987, SEQ ID NO: 1144, SEQ ID NO: 1301, and SEQ ID NO: 1458, respectively;

xlvi. SEQ ID NO: 674, SEQ ID NO: 831, SEQ ID NO: 988, SEQ ID NO: 1145, SEQ ID NO: 1302, and SEQ ID NO: 1459, respectively;

xlvii. SEQ ID NO: 675, SEQ ID NO: 832, SEQ ID NO: 989, SEQ ID NO: 1146, SEQ ID NO: 1303, and SEQ ID NO: 1460, respectively;

xlviii. SEQ ID NO: 676, SEQ ID NO: 833, SEQ ID NO: 990, SEQ ID NO: 1147, SEQ ID NO: 1304, and SEQ ID NO: 1461, respectively;

xlix. SEQ ID NO: 677, SEQ ID NO: 834, SEQ ID NO: 991, SEQ ID NO: 1148, SEQ ID NO: 1305, and SEQ ID NO: 1462, respectively;

l. SEQ ID NO: 678, SEQ ID NO: 835, SEQ ID NO: 992, SEQ ID NO: 1149, SEQ ID NO: 1306, and SEQ ID NO: 1463, respectively;

li. SEQ ID NO: 679, SEQ ID NO: 836, SEQ ID NO: 993, SEQ ID NO: 1150, SEQ ID NO: 1307, and SEQ ID NO: 1464, respectively;

lii. SEQ ID NO: 680, SEQ ID NO: 837, SEQ ID NO: 994, SEQ ID NO: 1151, SEQ ID NO: 1308, and SEQ ID NO: 1465, respectively;

liii. SEQ ID NO: 681, SEQ ID NO: 838, SEQ ID NO: 995, SEQ ID NO: 1152, SEQ ID NO: 1309, and SEQ ID NO: 1466, respectively;

liv. SEQ ID NO: 682, SEQ ID NO: 839, SEQ ID NO: 996, SEQ ID NO: 1153, SEQ ID NO: 1310, and SEQ ID NO: 1467, respectively;

lv. SEQ ID NO: 683, SEQ ID NO: 840, SEQ ID NO: 997, SEQ ID NO: 1154, SEQ ID NO: 1311, and SEQ ID NO: 1468, respectively;

lvi. SEQ ID NO: 684, SEQ ID NO: 841, SEQ ID NO: 998, SEQ ID NO: 1155, SEQ ID NO: 1312, and SEQ ID NO: 1469, respectively;

lvii. SEQ ID NO: 685, SEQ ID NO: 842, SEQ ID NO: 999, SEQ ID NO: 1156, SEQ ID NO: 1313, and SEQ ID NO: 1470, respectively;

lviii. SEQ ID NO: 686, SEQ ID NO: 843, SEQ ID NO: 1000, SEQ ID NO: 1157, SEQ ID NO: 1314, and SEQ ID NO: 1471, respectively;

lix. SEQ ID NO: 687, SEQ ID NO: 844, SEQ ID NO: 1001, SEQ ID NO: 1158, SEQ ID NO: 1315, and SEQ ID NO: 1472, respectively;

lx. SEQ ID NO: 688, SEQ ID NO: 845, SEQ ID NO: 1002, SEQ ID NO: 1159, SEQ ID NO: 1316, and SEQ ID NO: 1473, respectively;

lxi. SEQ ID NO: 689, SEQ ID NO: 846, SEQ ID NO: 1003, SEQ ID NO: 1160, SEQ ID NO: 1317, and SEQ ID NO: 1474, respectively;

lxii. SEQ ID NO: 690, SEQ ID NO: 847, SEQ ID NO: 1004, SEQ ID NO: 1161, SEQ ID NO: 1318, and SEQ ID NO: 1475, respectively;

lxiii. SEQ ID NO: 691, SEQ ID NO: 848, SEQ ID NO: 1005, SEQ ID NO: 1162, SEQ ID NO: 1319, and SEQ ID NO: 1476, respectively;

lxiv. SEQ ID NO: 692, SEQ ID NO: 849, SEQ ID NO: 1006, SEQ ID NO: 1163, SEQ ID NO: 1320, and SEQ ID NO: 1477, respectively;

lxv. SEQ ID NO: 693, SEQ ID NO: 850, SEQ ID NO: 1007, SEQ ID NO: 1164, SEQ ID NO: 1321, and SEQ ID NO: 1478, respectively;

lxvi. SEQ ID NO: 694, SEQ ID NO: 851, SEQ ID NO: 1008, SEQ ID NO: 1165, SEQ ID NO: 1322, and SEQ ID NO: 1479, respectively;

lxvii. SEQ ID NO: 695, SEQ ID NO: 852, SEQ ID NO: 1009, SEQ ID NO: 1166, SEQ ID NO: 1323, and SEQ ID NO: 1480, respectively;

lxviii. SEQ ID NO: 696, SEQ ID NO: 853, SEQ ID NO: 1010, SEQ ID NO: 1167, SEQ ID NO: 1324, and SEQ ID NO: 1481, respectively;

lxix. SEQ ID NO: 697, SEQ ID NO: 854, SEQ ID NO: 1011, SEQ ID NO: 1168, SEQ ID NO: 1325, and SEQ ID NO: 1482, respectively;

lxx. SEQ ID NO: 698, SEQ ID NO: 855, SEQ ID NO: 1012, SEQ ID NO: 1169, SEQ ID NO: 1326, and SEQ ID NO: 1483, respectively;

lxxi. SEQ ID NO: 699, SEQ ID NO: 856, SEQ ID NO: 1013, SEQ ID NO: 1170, SEQ ID NO: 1327, and SEQ ID NO: 1484, respectively;

lxxii. SEQ ID NO: 700, SEQ ID NO: 857, SEQ ID NO: 1014, SEQ ID NO: 1171, SEQ ID NO: 1328, and SEQ ID NO: 1485, respectively;

lxxiii. SEQ ID NO: 701, SEQ ID NO: 858, SEQ ID NO: 1015, SEQ ID NO: 1172, SEQ ID NO: 1329, and SEQ ID NO: 1486, respectively;

lxxiv. SEQ ID NO: 702, SEQ ID NO: 859, SEQ ID NO: 1016, SEQ ID NO: 1173, SEQ ID NO: 1330, and SEQ ID NO: 1487, respectively;

lxxv. SEQ ID NO: 703, SEQ ID NO: 860, SEQ ID NO: 1017, SEQ ID NO: 1174, SEQ ID NO: 1331, and SEQ ID NO: 1488, respectively;

lxxvi. SEQ ID NO: 704, SEQ ID NO: 861, SEQ ID NO: 1018, SEQ ID NO: 1175, SEQ ID NO: 1332, and SEQ ID NO: 1489, respectively;

lxxvii. SEQ ID NO: 705, SEQ ID NO: 862, SEQ ID NO: 1019, SEQ ID NO: 1176, SEQ ID NO: 1333, and SEQ ID NO: 1490, respectively;

lxxviii. SEQ ID NO: 706, SEQ ID NO: 863, SEQ ID NO: 1020, SEQ ID NO: 1177, SEQ ID NO: 1334, and SEQ ID NO: 1491, respectively;

lxxix. SEQ ID NO: 707, SEQ ID NO: 864, SEQ ID NO: 1021, SEQ ID NO: 1178, SEQ ID NO: 1335, and SEQ ID NO: 1492, respectively;

lxxx. SEQ ID NO: 708, SEQ ID NO: 865, SEQ ID NO: 1022, SEQ ID NO: 1179, SEQ ID NO: 1336, and SEQ ID NO: 1493, respectively;

lxxxi. SEQ ID NO: 709, SEQ ID NO: 866, SEQ ID NO: 1023, SEQ ID NO: 1180, SEQ ID NO: 1337, and SEQ ID NO: 1494, respectively;

lxxxii. SEQ ID NO: 710, SEQ ID NO: 867, SEQ ID NO: 1024, SEQ ID NO: 1181, SEQ ID NO: 1338, and SEQ ID NO: 1495, respectively;

lxxxiii. SEQ ID NO: 711, SEQ ID NO: 868, SEQ ID NO: 1025, SEQ ID NO: 1182, SEQ ID NO: 1339, and SEQ ID NO: 1496, respectively;

lxxxiv. SEQ ID NO: 712, SEQ ID NO: 869, SEQ ID NO: 1026, SEQ ID NO: 1183, SEQ ID NO: 1340, and SEQ ID NO: 1497, respectively;

lxxxv. SEQ ID NO: 713, SEQ ID NO: 870, SEQ ID NO: 1027, SEQ ID NO: 1184, SEQ ID NO: 1341, and SEQ ID NO: 1498, respectively;

lxxxvi. SEQ ID NO: 714, SEQ ID NO: 871, SEQ ID NO: 1028, SEQ ID NO: 1185, SEQ ID NO: 1342, and SEQ ID NO: 1499, respectively;

lxxxvii. SEQ ID NO: 715, SEQ ID NO: 872, SEQ ID NO: 1029, SEQ ID NO: 1186, SEQ ID NO: 1343, and SEQ ID NO: 1500, respectively;

lxxxviii. SEQ ID NO: 716, SEQ ID NO: 873, SEQ ID NO: 1030, SEQ ID NO: 1187, SEQ ID NO: 1344, and SEQ ID NO: 1501, respectively;

lxxxix. SEQ ID NO: 717, SEQ ID NO: 874, SEQ ID NO: 1031, SEQ ID NO: 1188, SEQ ID NO: 1345, and SEQ ID NO: 1502, respectively;

xc. SEQ ID NO: 718, SEQ ID NO: 875, SEQ ID NO: 1032, SEQ ID NO: 1189, SEQ ID NO: 1346, and SEQ ID NO: 1503, respectively;

xci. SEQ ID NO: 719, SEQ ID NO: 876, SEQ ID NO: 1033, SEQ ID NO: 1190, SEQ ID NO: 1347, and SEQ ID NO: 1504, respectively;

xcii. SEQ ID NO: 720, SEQ ID NO: 877, SEQ ID NO: 1034, SEQ ID NO: 1191, SEQ ID NO: 1348, and SEQ ID NO: 1505, respectively;

xciii. SEQ ID NO: 721, SEQ ID NO: 878, SEQ ID NO: 1035, SEQ ID NO: 1192, SEQ ID NO: 1349, and SEQ ID NO: 1506, respectively;

xciv. SEQ ID NO: 722, SEQ ID NO: 879, SEQ ID NO: 1036, SEQ ID NO: 1193, SEQ ID NO: 1350, and SEQ ID NO: 1507, respectively;

xcv. SEQ ID NO: 723, SEQ ID NO: 880, SEQ ID NO: 1037, SEQ ID NO: 1194, SEQ ID NO: 1351, and SEQ ID NO: 1508, respectively;

xcvi. SEQ ID NO: 724, SEQ ID NO: 881, SEQ ID NO: 1038, SEQ ID NO: 1195, SEQ ID NO: 1352, and SEQ ID NO: 1509, respectively;

xcvii. SEQ ID NO: 725, SEQ ID NO: 882, SEQ ID NO: 1039, SEQ ID NO: 1196, SEQ ID NO: 1353, and SEQ ID NO: 1510, respectively;

xcviii. SEQ ID NO: 726, SEQ ID NO: 883, SEQ ID NO: 1040, SEQ ID NO: 1197, SEQ ID NO: 1354, and SEQ ID NO: 1511, respectively;

xcix. SEQ ID NO: 727, SEQ ID NO: 884, SEQ ID NO: 1041, SEQ ID NO: 1198, SEQ ID NO: 1355, and SEQ ID NO: 1512, respectively;

c. SEQ ID NO: 728, SEQ ID NO: 885, SEQ ID NO: 1042, SEQ ID NO: 1199, SEQ ID NO: 1356, and SEQ ID NO: 1513, respectively;

ci. SEQ ID NO: 729, SEQ ID NO: 886, SEQ ID NO: 1043, SEQ ID NO: 1200, SEQ ID NO: 1357, and SEQ ID NO: 1514, respectively;

cii. SEQ ID NO: 730, SEQ ID NO: 887, SEQ ID NO: 1044, SEQ ID NO: 1201, SEQ ID NO: 1358, and SEQ ID NO: 1515, respectively;

ciii. SEQ ID NO: 731, SEQ ID NO: 888, SEQ ID NO: 1045, SEQ ID NO: 1202, SEQ ID NO: 1359, and SEQ ID NO: 1516, respectively;

civ. SEQ ID NO: 732, SEQ ID NO: 889, SEQ ID NO: 1046, SEQ ID NO: 1203, SEQ ID NO: 1360, and SEQ ID NO: 1517, respectively;

cv. SEQ ID NO: 733, SEQ ID NO: 890, SEQ ID NO: 1047, SEQ ID NO: 1204, SEQ ID NO: 1361, and SEQ ID NO: 1518, respectively;

cvi. SEQ ID NO: 734, SEQ ID NO: 891, SEQ ID NO: 1048, SEQ ID NO: 1205, SEQ ID NO: 1362, and SEQ ID NO: 1519, respectively;

cvii. SEQ ID NO: 735, SEQ ID NO: 892, SEQ ID NO: 1049, SEQ ID NO: 1206, SEQ ID NO: 1363, and SEQ ID NO: 1520, respectively;

cviii. SEQ ID NO: 736, SEQ ID NO: 893, SEQ ID NO: 1050, SEQ ID NO: 1207, SEQ ID NO: 1364, and SEQ ID NO: 1521, respectively;

cix. SEQ ID NO: 737, SEQ ID NO: 894, SEQ ID NO: 1051, SEQ ID NO: 1208, SEQ ID NO: 1365, and SEQ ID NO: 1522, respectively;

cx. SEQ ID NO: 738, SEQ ID NO: 895, SEQ ID NO: 1052, SEQ ID NO: 1209, SEQ ID NO: 1366, and SEQ ID NO: 1523, respectively;

cxi. SEQ ID NO: 739, SEQ ID NO: 896, SEQ ID NO: 1053, SEQ ID NO: 1210, SEQ ID NO: 1367, and SEQ ID NO: 1524, respectively;

cxii. SEQ ID NO: 740, SEQ ID NO: 897, SEQ ID NO: 1054, SEQ ID NO: 1211, SEQ ID NO: 1368, and SEQ ID NO: 1525, respectively;

cxiii. SEQ ID NO: 741, SEQ ID NO: 898, SEQ ID NO: 1055, SEQ ID NO: 1212, SEQ ID NO: 1369, and SEQ ID NO: 1526, respectively;

cxiv. SEQ ID NO: 742, SEQ ID NO: 899, SEQ ID NO: 1056, SEQ ID NO: 1213, SEQ ID NO: 1370, and SEQ ID NO: 1527, respectively;

cxv. SEQ ID NO: 743, SEQ ID NO: 900, SEQ ID NO: 1057, SEQ ID NO: 1214, SEQ ID NO: 1371, and SEQ ID NO: 1528, respectively;

cxvi. SEQ ID NO: 744, SEQ ID NO: 901, SEQ ID NO: 1058, SEQ ID NO: 1215, SEQ ID NO: 1372, and SEQ ID NO: 1529, respectively;

cxvii. SEQ ID NO: 745, SEQ ID NO: 902, SEQ ID NO: 1059, SEQ ID NO: 1216, SEQ ID NO: 1373, and SEQ ID NO: 1530, respectively;

cxviii. SEQ ID NO: 746, SEQ ID NO: 903, SEQ ID NO: 1060, SEQ ID NO: 1217, SEQ ID NO: 1374, and SEQ ID NO: 1531, respectively;

cxix. SEQ ID NO: 747, SEQ ID NO: 904, SEQ ID NO: 1061, SEQ ID NO: 1218, SEQ ID NO: 1375, and SEQ ID NO: 1532, respectively;

cxx. SEQ ID NO: 748, SEQ ID NO: 905, SEQ ID NO: 1062, SEQ ID NO: 1219, SEQ ID NO: 1376, and SEQ ID NO: 1533, respectively;

cxxi. SEQ ID NO: 749, SEQ ID NO: 906, SEQ ID NO: 1063, SEQ ID NO: 1220, SEQ ID NO: 1377, and SEQ ID NO: 1534, respectively;

cxxii. SEQ ID NO: 750, SEQ ID NO: 907, SEQ ID NO: 1064, SEQ ID NO: 1221, SEQ ID NO: 1378, and SEQ ID NO: 1535, respectively;

cxxiii. SEQ ID NO: 751, SEQ ID NO: 908, SEQ ID NO: 1065, SEQ ID NO: 1222, SEQ ID NO: 1379, and SEQ ID NO: 1536, respectively;

cxxiv. SEQ ID NO: 752, SEQ ID NO: 909, SEQ ID NO: 1066, SEQ ID NO: 1223, SEQ ID NO: 1380, and SEQ ID NO: 1537, respectively;

cxxv. SEQ ID NO: 753, SEQ ID NO: 910, SEQ ID NO: 1067, SEQ ID NO: 1224, SEQ ID NO: 1381, and SEQ ID NO: 1538, respectively;

cxxvi. SEQ ID NO: 754, SEQ ID NO: 911, SEQ ID NO: 1068, SEQ ID NO: 1225, SEQ ID NO: 1382, and SEQ ID NO: 1539, respectively;

cxxvii. SEQ ID NO: 755, SEQ ID NO: 912, SEQ ID NO: 1069, SEQ ID NO: 1226, SEQ ID NO: 1383, and SEQ ID NO: 1540, respectively;

cxxviii. SEQ ID NO: 756, SEQ ID NO: 913, SEQ ID NO: 1070, SEQ ID NO: 1227, SEQ ID NO: 1384, and SEQ ID NO: 1541, respectively;

cxxix. SEQ ID NO: 757, SEQ ID NO: 914, SEQ ID NO: 1071, SEQ ID NO: 1228, SEQ ID NO: 1385, and SEQ ID NO: 1542, respectively;

cxxx. SEQ ID NO: 758, SEQ ID NO: 915, SEQ ID NO: 1072, SEQ ID NO: 1229, SEQ ID NO: 1386, and SEQ ID NO: 1543, respectively;

cxxxi. SEQ ID NO: 759, SEQ ID NO: 916, SEQ ID NO: 1073, SEQ ID NO: 1230, SEQ ID NO: 1387, and SEQ ID NO: 1544, respectively;

cxxxii. SEQ ID NO: 760, SEQ ID NO: 917, SEQ ID NO: 1074, SEQ ID NO: 1231, SEQ ID NO: 1388, and SEQ ID NO: 1545, respectively;

cxxxiii. SEQ ID NO: 761, SEQ ID NO: 918, SEQ ID NO: 1075, SEQ ID NO: 1232, SEQ ID NO: 1389, and SEQ ID NO: 1546, respectively;

cxxxiv. SEQ ID NO: 762, SEQ ID NO: 919, SEQ ID NO: 1076, SEQ ID NO: 1233, SEQ ID NO: 1390, and SEQ ID NO: 1547, respectively;

cxxxv. SEQ ID NO: 763, SEQ ID NO: 920, SEQ ID NO: 1077, SEQ ID NO: 1234, SEQ ID NO: 1391, and SEQ ID NO: 1548, respectively;

cxxxvi. SEQ ID NO: 764, SEQ ID NO: 921, SEQ ID NO: 1078, SEQ ID NO: 1235, SEQ ID NO: 1392, and SEQ ID NO: 1549, respectively;

cxxxvii. SEQ ID NO: 765, SEQ ID NO: 922, SEQ ID NO: 1079, SEQ ID NO: 1236, SEQ ID NO: 1393, and SEQ ID NO: 1550, respectively;

cxxxviii. SEQ ID NO: 766, SEQ ID NO: 923, SEQ ID NO: 1080, SEQ ID NO: 1237, SEQ ID NO: 1394, and SEQ ID NO: 1551, respectively;

cxxxix. SEQ ID NO: 767, SEQ ID NO: 924, SEQ ID NO: 1081, SEQ ID NO: 1238, SEQ ID NO: 1395, and SEQ ID NO: 1552, respectively;

cxl. SEQ ID NO: 768, SEQ ID NO: 925, SEQ ID NO: 1082, SEQ ID NO: 1239, SEQ ID NO: 1396, and SEQ ID NO: 1553, respectively;

cxli. SEQ ID NO: 769, SEQ ID NO: 926, SEQ ID NO: 1083, SEQ ID NO: 1240, SEQ ID NO: 1397, and SEQ ID NO: 1554, respectively;

cxlii. SEQ ID NO: 770, SEQ ID NO: 927, SEQ ID NO: 1084, SEQ ID NO: 1241, SEQ ID NO: 1398, and SEQ ID NO: 1555, respectively;

cxliii. SEQ ID NO: 771, SEQ ID NO: 928, SEQ ID NO: 1085, SEQ ID NO: 1242, SEQ ID NO: 1399, and SEQ ID NO: 1556, respectively;

cxliv. SEQ ID NO: 772, SEQ ID NO: 929, SEQ ID NO: 1086, SEQ ID NO: 1243, SEQ ID NO: 1400, and SEQ ID NO: 1557, respectively;

cxlv. SEQ ID NO: 773, SEQ ID NO: 930, SEQ ID NO: 1087, SEQ ID NO: 1244, SEQ ID NO: 1401, and SEQ ID NO: 1558, respectively;

cxlvi. SEQ ID NO: 774, SEQ ID NO: 931, SEQ ID NO: 1088, SEQ ID NO: 1245, SEQ ID NO: 1402, and SEQ ID NO: 1559, respectively;

cxlvii. SEQ ID NO: 775, SEQ ID NO: 932, SEQ ID NO: 1089, SEQ ID NO: 1246, SEQ ID NO: 1403, and SEQ ID NO: 1560, respectively;

cxlviii. SEQ ID NO: 776, SEQ ID NO: 933, SEQ ID NO: 1090, SEQ ID NO: 1247, SEQ ID NO: 1404, and SEQ ID NO: 1561, respectively;

cxlix. SEQ ID NO: 777, SEQ ID NO: 934, SEQ ID NO: 1091, SEQ ID NO: 1248, SEQ ID NO: 1405, and SEQ ID NO: 1562, respectively;

cl. SEQ ID NO: 778, SEQ ID NO: 935, SEQ ID NO: 1092, SEQ ID NO: 1249, SEQ ID NO: 1406, and SEQ ID NO: 1563, respectively;

cli. SEQ ID NO: 779, SEQ ID NO: 936, SEQ ID NO: 1093, SEQ ID NO: 1250, SEQ ID NO: 1407, and SEQ ID NO: 1564, respectively;

clii. SEQ ID NO: 780, SEQ ID NO: 937, SEQ ID NO: 1094, SEQ ID NO: 1251, SEQ ID NO: 1408, and SEQ ID NO: 1565, respectively;

cliii. SEQ ID NO: 781, SEQ ID NO: 938, SEQ ID NO: 1095, SEQ ID NO: 1252, SEQ ID NO: 1409, and SEQ ID NO: 1566, respectively;

cliv. SEQ ID NO: 782, SEQ ID NO: 939, SEQ ID NO: 1096, SEQ ID NO: 1253, SEQ ID NO: 1410, and SEQ ID NO: 1567, respectively;

clv. SEQ ID NO: 783, SEQ ID NO: 940, SEQ ID NO: 1097, SEQ ID NO: 1254, SEQ ID NO: 1411, and SEQ ID NO: 1568, respectively;

clvi. SEQ ID NO: 784, SEQ ID NO: 941, SEQ ID NO: 1098, SEQ ID NO: 1255, SEQ ID NO: 1412, and SEQ ID NO: 1569, respectively; and

clvii. SEQ ID NO: 785, SEQ ID NO: 942, SEQ ID NO: 1099, SEQ ID NO: 1256, SEQ ID NO: 1413, and SEQ ID NO: 1570, respectively.

41. The conjugate molecule of claim 40, wherein the anti-GIPR antibody comprises the CDRL1, the CDRL2, the CDRL3, the CDRH1, the CDRH2, and the CDRH3 of SEQ ID NO: 702, SEQ ID NO: 859, SEQ ID NO: 1016, SEQ ID NO: 1173, SEQ ID NO: 1330, and SEQ ID NO: 1487, respectively.

42. The conjugate molecule of any one of claims 17 to 39, wherein the anti-GIPR antibody comprises a light chain variable region (V_L) and a heavy chain variable region (V_H), wherein the V_L and the V_H comprise amino acid sequences selected from:

i. SEQ ID NO: 1 and SEQ ID NO: 158, respectively;

ii. SEQ ID NO: 2 and SEQ ID NO: 159, respectively;
iii. SEQ ID NO: 3 and SEQ ID NO: 160, respectively;
iv. SEQ ID NO: 4 and SEQ ID NO: 161, respectively;
v. SEQ ID NO: 5 and SEQ ID NO: 162, respectively;
vi. SEQ ID NO: 6 and SEQ ID NO: 163, respectively;
vii. SEQ ID NO: 7 and SEQ ID NO: 164, respectively;
viii. SEQ ID NO: 8 and SEQ ID NO: 165, respectively;
ix. SEQ ID NO: 9 and SEQ ID NO: 166, respectively;
x. SEQ ID NO: 10 and SEQ ID NO: 167, respectively;
xi. SEQ ID NO: 11 and SEQ ID NO: 168, respectively;
xii. SEQ ID NO: 12 and SEQ ID NO: 169, respectively;
xiii. SEQ ID NO: 13 and SEQ ID NO: 170, respectively;
xiv. SEQ ID NO: 14 and SEQ ID NO: 171, respectively;
xv. SEQ ID NO: 15 and SEQ ID NO: 172, respectively;
xvi. SEQ ID NO: 16 and SEQ ID NO: 173, respectively;
xvii. SEQ ID NO: 17 and SEQ ID NO: 174, respectively;
xviii. SEQ ID NO: 18 and SEQ ID NO: 175, respectively;
xix. SEQ ID NO: 19 and SEQ ID NO: 176, respectively;
xx. SEQ ID NO: 20 and SEQ ID NO: 177, respectively;
xxi. SEQ ID NO: 21 and SEQ ID NO: 178, respectively;
xxii. SEQ ID NO: 22 and SEQ ID NO: 179, respectively;
xxiii. SEQ ID NO: 23 and SEQ ID NO: 180, respectively;
xxiv. SEQ ID NO: 24 and SEQ ID NO: 181, respectively;
xxv. SEQ ID NO: 25 and SEQ ID NO: 182, respectively;
xxvi. SEQ ID NO: 26 and SEQ ID NO: 183, respectively;
xxvii. SEQ ID NO: 27 and SEQ ID NO: 184, respectively;
xxviii. SEQ ID NO: 28 and SEQ ID NO: 185, respectively;
xxix. SEQ ID NO: 29 and SEQ ID NO: 186, respectively;
xxx. SEQ ID NO: 30 and SEQ ID NO: 187, respectively;
xxxi. SEQ ID NO: 31 and SEQ ID NO: 188, respectively;
xxxii. SEQ ID NO: 32 and SEQ ID NO: 189, respectively;
xxxiii. SEQ ID NO: 33 and SEQ ID NO: 190, respectively;
xxxiv. SEQ ID NO: 34 and SEQ ID NO: 191, respectively;
xxxv. SEQ ID NO: 35 and SEQ ID NO: 192, respectively;

xxxvi. SEQ ID NO: 36 and SEQ ID NO: 193, respectively;
xxxvii. SEQ ID NO: 37 and SEQ ID NO: 194, respectively;
xxxviii. SEQ ID NO: 38 and SEQ ID NO: 195, respectively;
xxxix. SEQ ID NO: 39 and SEQ ID NO: 196, respectively;
xl. SEQ ID NO: 40 and SEQ ID NO: 197, respectively;
xli. SEQ ID NO: 41 and SEQ ID NO: 198, respectively;
xlii. SEQ ID NO: 42 and SEQ ID NO: 199, respectively;
xliii. SEQ ID NO: 43 and SEQ ID NO: 200, respectively;
xliv. SEQ ID NO: 44 and SEQ ID NO: 201, respectively;
xlv. SEQ ID NO: 45 and SEQ ID NO: 202, respectively;
xlvi. SEQ ID NO: 46 and SEQ ID NO: 203, respectively;
xlvii. SEQ ID NO: 47 and SEQ ID NO: 204, respectively;
xlviii. SEQ ID NO: 48 and SEQ ID NO: 205, respectively;
xlix. SEQ ID NO: 49 and SEQ ID NO: 206, respectively;
l. SEQ ID NO: 50 and SEQ ID NO: 207, respectively;
li. SEQ ID NO: 51 and SEQ ID NO: 208, respectively;
lii. SEQ ID NO: 52 and SEQ ID NO: 209, respectively;
liii. SEQ ID NO: 53 and SEQ ID NO: 210, respectively;
liv. SEQ ID NO: 54 and SEQ ID NO: 211, respectively;
lv. SEQ ID NO: 55 and SEQ ID NO: 212, respectively;
lvi. SEQ ID NO: 56 and SEQ ID NO: 213, respectively;
lvii. SEQ ID NO: 57 and SEQ ID NO: 214, respectively;
lviii. SEQ ID NO: 58 and SEQ ID NO: 215, respectively;
lix. SEQ ID NO: 59 and SEQ ID NO: 216, respectively;
lx. SEQ ID NO: 60 and SEQ ID NO: 217, respectively;
lxi. SEQ ID NO: 61 and SEQ ID NO: 218, respectively;
lxii. SEQ ID NO: 62 and SEQ ID NO: 219, respectively;
lxiii. SEQ ID NO: 63 and SEQ ID NO: 220, respectively;
lxiv. SEQ ID NO: 64 and SEQ ID NO: 221, respectively;
lxv. SEQ ID NO: 65 and SEQ ID NO: 222, respectively;
lxvi. SEQ ID NO: 66 and SEQ ID NO: 223, respectively;
lxvii. SEQ ID NO: 67 and SEQ ID NO: 224, respectively;
lxviii. SEQ ID NO: 68 and SEQ ID NO: 225, respectively;
lxix. SEQ ID NO: 69 and SEQ ID NO: 226, respectively;

lxx. SEQ ID NO: 70 and SEQ ID NO: 227, respectively;
lxxi. SEQ ID NO: 71 and SEQ ID NO: 228, respectively;
lxxii. SEQ ID NO: 72 and SEQ ID NO: 229, respectively;
lxxiii. SEQ ID NO: 73 and SEQ ID NO: 230, respectively;
lxxiv. SEQ ID NO: 74 and SEQ ID NO: 231, respectively;
lxxv. SEQ ID NO: 75 and SEQ ID NO: 232, respectively;
lxxvi. SEQ ID NO: 76 and SEQ ID NO: 233, respectively;
lxxvii. SEQ ID NO: 77 and SEQ ID NO: 234, respectively;
lxxviii. SEQ ID NO: 78 and SEQ ID NO: 235, respectively;
lxxix. SEQ ID NO: 79 and SEQ ID NO: 236, respectively;
lxxx. SEQ ID NO: 80 and SEQ ID NO: 237, respectively;
lxxxi. SEQ ID NO: 81 and SEQ ID NO: 238, respectively;
lxxxii. SEQ ID NO: 82 and SEQ ID NO: 239, respectively;
lxxxiii. SEQ ID NO: 83 and SEQ ID NO: 240, respectively;
lxxxiv. SEQ ID NO: 84 and SEQ ID NO: 241, respectively;
lxxxv. SEQ ID NO: 85 and SEQ ID NO: 242, respectively;
lxxxvi. SEQ ID NO: 86 and SEQ ID NO: 243, respectively;
lxxxvii. SEQ ID NO: 87 and SEQ ID NO: 244, respectively;
lxxxviii. SEQ ID NO: 88 and SEQ ID NO: 245, respectively;
lxxxix. SEQ ID NO: 89 and SEQ ID NO: 246, respectively;
xc. SEQ ID NO: 90 and SEQ ID NO: 247, respectively;
xci. SEQ ID NO: 91 and SEQ ID NO: 248, respectively;
xcii. SEQ ID NO: 92 and SEQ ID NO: 249, respectively;
xciii. SEQ ID NO: 93 and SEQ ID NO: 250, respectively;
xciv. SEQ ID NO: 94 and SEQ ID NO: 251, respectively;
xcv. SEQ ID NO: 95 and SEQ ID NO: 252, respectively;
xcvi. SEQ ID NO: 96 and SEQ ID NO: 253, respectively;
xcvii. SEQ ID NO: 97 and SEQ ID NO: 254, respectively;
xcviii. SEQ ID NO: 98 and SEQ ID NO: 255, respectively;
xcix. SEQ ID NO: 99 and SEQ ID NO: 256, respectively;
c. SEQ ID NO: 100 and SEQ ID NO: 257, respectively;
ci. SEQ ID NO: 101 and SEQ ID NO: 258, respectively;
cii. SEQ ID NO: 102 and SEQ ID NO: 259, respectively;
ciii. SEQ ID NO: 103 and SEQ ID NO: 260, respectively;

civ. SEQ ID NO: 104 and SEQ ID NO: 261, respectively;
cv. SEQ ID NO: 105 and SEQ ID NO: 262, respectively;
cvi. SEQ ID NO: 106 and SEQ ID NO: 263, respectively;
cvii. SEQ ID NO: 107 and SEQ ID NO: 264, respectively;
cviii. SEQ ID NO: 108 and SEQ ID NO: 265, respectively;
cix. SEQ ID NO: 109 and SEQ ID NO: 266, respectively;
cx. SEQ ID NO: 110 and SEQ ID NO: 267, respectively;
cxi. SEQ ID NO: 111 and SEQ ID NO: 268, respectively;
cxii. SEQ ID NO: 112 and SEQ ID NO: 269, respectively;
cxiii. SEQ ID NO: 113 and SEQ ID NO: 270, respectively;
cxiv. SEQ ID NO: 114 and SEQ ID NO: 271, respectively;
cxv. SEQ ID NO: 115 and SEQ ID NO: 272, respectively;
cxvi. SEQ ID NO: 116 and SEQ ID NO: 273, respectively;
cxvii. SEQ ID NO: 117 and SEQ ID NO: 274, respectively;
cxviii. SEQ ID NO: 118 and SEQ ID NO: 275, respectively;
cxix. SEQ ID NO: 119 and SEQ ID NO: 276, respectively;
cxx. SEQ ID NO: 120 and SEQ ID NO: 277, respectively;
cxxi. SEQ ID NO: 121 and SEQ ID NO: 278, respectively;
cxxii. SEQ ID NO: 122 and SEQ ID NO: 279, respectively;
cxxiii. SEQ ID NO: 123 and SEQ ID NO: 280, respectively;
cxxiv. SEQ ID NO: 124 and SEQ ID NO: 281, respectively;
cxxv. SEQ ID NO: 125 and SEQ ID NO: 282, respectively;
cxxvi. SEQ ID NO: 126 and SEQ ID NO: 283, respectively;
cxxvii. SEQ ID NO: 127 and SEQ ID NO: 284, respectively;
cxxviii. SEQ ID NO: 128 and SEQ ID NO: 285, respectively;
cxxix. SEQ ID NO: 129 and SEQ ID NO: 286, respectively;
cxxx. SEQ ID NO: 130 and SEQ ID NO: 287, respectively;
cxxxi. SEQ ID NO: 131 and SEQ ID NO: 288, respectively;
cxxxii. SEQ ID NO: 132 and SEQ ID NO: 289, respectively;
cxxxiii. SEQ ID NO: 133 and SEQ ID NO: 290, respectively;
cxxxiv. SEQ ID NO: 134 and SEQ ID NO: 291, respectively;
cxxxv. SEQ ID NO: 135 and SEQ ID NO: 292, respectively;
cxxxvi. SEQ ID NO: 136 and SEQ ID NO: 293, respectively;
cxxxvii. SEQ ID NO: 137 and SEQ ID NO: 294, respectively;

cxxxviii. SEQ ID NO: 138 and SEQ ID NO: 295, respectively;
cxxxix. SEQ ID NO: 139 and SEQ ID NO: 296, respectively;
cxl. SEQ ID NO: 140 and SEQ ID NO: 297, respectively;
cxli. SEQ ID NO: 141 and SEQ ID NO: 298, respectively;
cxlii. SEQ ID NO: 142 and SEQ ID NO: 299, respectively;
cxliii. SEQ ID NO: 143 and SEQ ID NO: 300, respectively;
cxliv. SEQ ID NO: 144 and SEQ ID NO: 301, respectively;
cxlv. SEQ ID NO: 145 and SEQ ID NO: 302, respectively;
cxlvi. SEQ ID NO: 146 and SEQ ID NO: 303, respectively;
cxlvii. SEQ ID NO: 147 and SEQ ID NO: 304, respectively;
cxlviii. SEQ ID NO: 148 and SEQ ID NO: 305, respectively;
cxlix. SEQ ID NO: 149 and SEQ ID NO: 306, respectively;
cl. SEQ ID NO: 150 and SEQ ID NO: 307, respectively;
cli. SEQ ID NO: 151 and SEQ ID NO: 308, respectively;
clii. SEQ ID NO: 152 and SEQ ID NO: 309, respectively;
cliii. SEQ ID NO: 153 and SEQ ID NO: 310, respectively;
cliv. SEQ ID NO: 154 and SEQ ID NO: 311, respectively;
clv. SEQ ID NO: 155 and SEQ ID NO: 312, respectively;
clvi. SEQ ID NO: 156 and SEQ ID NO: 313, respectively; and
clvii. SEQ ID NO: 157 and SEQ ID NO: 314, respectively.

43. The conjugate molecule of claim 42, wherein the anti-GIPR antibody comprises the V_L and V_H of SEQ ID NO: 74 and SEQ ID NO: 231, respectively.

44. The conjugate molecule of any one of claims 17 to 39, wherein the anti-GIPR antibody comprises a light chain and a heavy chain, wherein the light chain and heavy chain comprise amino acid sequences selected from:

i. SEQ ID NO: 315 and SEQ ID NO: 472, respectively;
ii. SEQ ID NO: 316 and SEQ ID NO: 473, respectively;
iii. SEQ ID NO: 317 and SEQ ID NO: 474, respectively;
iv. SEQ ID NO: 318 and SEQ ID NO: 475, respectively;
v. SEQ ID NO: 319 and SEQ ID NO: 476, respectively;
vi. SEQ ID NO: 320 and SEQ ID NO: 477, respectively;
vii. SEQ ID NO: 321 and SEQ ID NO: 478, respectively;

viii. SEQ ID NO: 322 and SEQ ID NO: 479, respectively;
ix. SEQ ID NO: 323 and SEQ ID NO: 480, respectively;
x. SEQ ID NO: 324 and SEQ ID NO: 481, respectively;
xi. SEQ ID NO: 325 and SEQ ID NO: 482, respectively;
xii. SEQ ID NO: 326 and SEQ ID NO: 483, respectively;
xiii. SEQ ID NO: 327 and SEQ ID NO: 484, respectively;
xiv. SEQ ID NO: 328 and SEQ ID NO: 485, respectively;
xv. SEQ ID NO: 329 and SEQ ID NO: 486, respectively;
xvi. SEQ ID NO: 330 and SEQ ID NO: 487, respectively;
xvii. SEQ ID NO: 331 and SEQ ID NO: 488, respectively;
xviii. SEQ ID NO: 332 and SEQ ID NO: 489, respectively;
xix. SEQ ID NO: 333 and SEQ ID NO: 490, respectively;
xx. SEQ ID NO: 334 and SEQ ID NO: 491, respectively;
xxi. SEQ ID NO: 335 and SEQ ID NO: 492, respectively;
xxii. SEQ ID NO: 336 and SEQ ID NO: 493, respectively;
xxiii. SEQ ID NO: 337 and SEQ ID NO: 494, respectively;
xxiv. SEQ ID NO: 338 and SEQ ID NO: 495, respectively;
xxv. SEQ ID NO: 339 and SEQ ID NO: 496, respectively;
xxvi. SEQ ID NO: 340 and SEQ ID NO: 497, respectively;
xxvii. SEQ ID NO: 341 and SEQ ID NO: 498, respectively;
xxviii. SEQ ID NO: 342 and SEQ ID NO: 499, respectively;
xxix. SEQ ID NO: 343 and SEQ ID NO: 500, respectively;
xxx. SEQ ID NO: 344 and SEQ ID NO: 501, respectively;
xxxi. SEQ ID NO: 345 and SEQ ID NO: 502, respectively;
xxxii. SEQ ID NO: 346 and SEQ ID NO: 503, respectively;
xxxiii. SEQ ID NO: 347 and SEQ ID NO: 504, respectively;
xxxiv. SEQ ID NO: 348 and SEQ ID NO: 505, respectively;
xxxv. SEQ ID NO: 349 and SEQ ID NO: 506, respectively;
xxxvi. SEQ ID NO: 350 and SEQ ID NO: 507, respectively;
xxxvii. SEQ ID NO: 351 and SEQ ID NO: 508, respectively;
xxxviii. SEQ ID NO: 352 and SEQ ID NO: 509, respectively;
xxxix. SEQ ID NO: 353 and SEQ ID NO: 510, respectively;
xl. SEQ ID NO: 354 and SEQ ID NO: 511, respectively;
xli. SEQ ID NO: 355 and SEQ ID NO: 512, respectively;

xlii. SEQ ID NO: 356 and SEQ ID NO: 513, respectively;
xliii. SEQ ID NO: 357 and SEQ ID NO: 514, respectively;
xliv. SEQ ID NO: 358 and SEQ ID NO: 515, respectively;
xlv. SEQ ID NO: 359 and SEQ ID NO: 516, respectively;
xlvi. SEQ ID NO: 360 and SEQ ID NO: 517, respectively;
xlvii. SEQ ID NO: 361 and SEQ ID NO: 518, respectively;
xlviii. SEQ ID NO: 362 and SEQ ID NO: 519, respectively;
xlix. SEQ ID NO: 363 and SEQ ID NO: 520, respectively;
l. SEQ ID NO: 364 and SEQ ID NO: 521, respectively;
li. SEQ ID NO: 365 and SEQ ID NO: 522, respectively;
lii. SEQ ID NO: 366 and SEQ ID NO: 523, respectively;
liii. SEQ ID NO: 367 and SEQ ID NO: 524, respectively;
liv. SEQ ID NO: 368 and SEQ ID NO: 525, respectively;
lv. SEQ ID NO: 369 and SEQ ID NO: 526, respectively;
lvi. SEQ ID NO: 370 and SEQ ID NO: 527, respectively;
lvii. SEQ ID NO: 371 and SEQ ID NO: 528, respectively;
lviii. SEQ ID NO: 372 and SEQ ID NO: 529, respectively;
lix. SEQ ID NO: 373 and SEQ ID NO: 530, respectively;
lx. SEQ ID NO: 374 and SEQ ID NO: 531, respectively;
lxi. SEQ ID NO: 375 and SEQ ID NO: 532, respectively;
lxii. SEQ ID NO: 376 and SEQ ID NO: 533, respectively;
lxiii. SEQ ID NO: 377 and SEQ ID NO: 534, respectively;
lxiv. SEQ ID NO: 378 and SEQ ID NO: 535, respectively;
lxv. SEQ ID NO: 379 and SEQ ID NO: 536, respectively;
lxvi. SEQ ID NO: 380 and SEQ ID NO: 537, respectively;
lxvii. SEQ ID NO: 381 and SEQ ID NO: 538, respectively;
lxviii. SEQ ID NO: 382 and SEQ ID NO: 539, respectively;
lxix. SEQ ID NO: 383 and SEQ ID NO: 540, respectively;
lxx. SEQ ID NO: 384 and SEQ ID NO: 541, respectively;
lxxi. SEQ ID NO: 385 and SEQ ID NO: 542, respectively;
lxxii. SEQ ID NO: 386 and SEQ ID NO: 543, respectively;
lxxiii. SEQ ID NO: 387 and SEQ ID NO: 544, respectively;
lxxiv. SEQ ID NO: 388 and SEQ ID NO: 545, respectively;
lxxv. SEQ ID NO: 389 and SEQ ID NO: 546, respectively;

lxxvi. SEQ ID NO: 390 and SEQ ID NO: 547, respectively;
lxxvii. SEQ ID NO: 391 and SEQ ID NO: 548, respectively;
lxxviii. SEQ ID NO: 392 and SEQ ID NO: 549, respectively;
lxxix. SEQ ID NO: 393 and SEQ ID NO: 550, respectively;
lxxx. SEQ ID NO: 394 and SEQ ID NO: 551, respectively;
lxxxi. SEQ ID NO: 395 and SEQ ID NO: 552, respectively;
lxxxii. SEQ ID NO: 396 and SEQ ID NO: 553, respectively;
lxxxiii. SEQ ID NO: 397 and SEQ ID NO: 554, respectively;
lxxxiv. SEQ ID NO: 398 and SEQ ID NO: 555, respectively;
lxxxv. SEQ ID NO: 399 and SEQ ID NO: 556, respectively;
lxxxvi. SEQ ID NO: 400 and SEQ ID NO: 557, respectively;
lxxxvii. SEQ ID NO: 401 and SEQ ID NO: 558, respectively;
lxxxviii. SEQ ID NO: 402 and SEQ ID NO: 559, respectively;
lxxxix. SEQ ID NO: 403 and SEQ ID NO: 560, respectively;
xc. SEQ ID NO: 404 and SEQ ID NO: 561, respectively;
xci. SEQ ID NO: 405 and SEQ ID NO: 562, respectively;
xcii. SEQ ID NO: 406 and SEQ ID NO: 563, respectively;
xciii. SEQ ID NO: 407 and SEQ ID NO: 564, respectively;
xciv. SEQ ID NO: 408 and SEQ ID NO: 565, respectively;
xcv. SEQ ID NO: 409 and SEQ ID NO: 566, respectively;
xcvi. SEQ ID NO: 410 and SEQ ID NO: 567, respectively;
xcvii. SEQ ID NO: 411 and SEQ ID NO: 568, respectively;
xcviii. SEQ ID NO: 412 and SEQ ID NO: 569, respectively;
xcix. SEQ ID NO: 413 and SEQ ID NO: 570, respectively;
c. SEQ ID NO: 414 and SEQ ID NO: 571, respectively;
ci. SEQ ID NO: 415 and SEQ ID NO: 572, respectively;
cii. SEQ ID NO: 416 and SEQ ID NO: 573, respectively;
ciii. SEQ ID NO: 417 and SEQ ID NO: 574, respectively;
civ. SEQ ID NO: 418 and SEQ ID NO: 575, respectively;
cv. SEQ ID NO: 419 and SEQ ID NO: 576, respectively;
cvi. SEQ ID NO: 420 and SEQ ID NO: 577, respectively;
cvii. SEQ ID NO: 421 and SEQ ID NO: 578, respectively;
cviii. SEQ ID NO: 422 and SEQ ID NO: 579, respectively;
cix. SEQ ID NO: 423 and SEQ ID NO: 580, respectively;

cx. SEQ ID NO: 424 and SEQ ID NO: 581, respectively;
cxi. SEQ ID NO: 425 and SEQ ID NO: 582, respectively;
cxii. SEQ ID NO: 426 and SEQ ID NO: 583, respectively;
cxiii. SEQ ID NO: 427 and SEQ ID NO: 584, respectively;
cxiv. SEQ ID NO: 428 and SEQ ID NO: 585, respectively;
cxv. SEQ ID NO: 429 and SEQ ID NO: 586, respectively;
cxvi. SEQ ID NO: 430 and SEQ ID NO: 587, respectively;
cxvii. SEQ ID NO: 431 and SEQ ID NO: 588, respectively;
cxviii. SEQ ID NO: 432 and SEQ ID NO: 589, respectively;
cxix. SEQ ID NO: 433 and SEQ ID NO: 590, respectively;
cxx. SEQ ID NO: 434 and SEQ ID NO: 591, respectively;
cxxi. SEQ ID NO: 435 and SEQ ID NO: 592, respectively;
cxxii. SEQ ID NO: 436 and SEQ ID NO: 593, respectively;
cxxiii. SEQ ID NO: 437 and SEQ ID NO: 594, respectively;
cxxiv. SEQ ID NO: 438 and SEQ ID NO: 595, respectively;
cxxv. SEQ ID NO: 439 and SEQ ID NO: 596, respectively;
cxxvi. SEQ ID NO: 440 and SEQ ID NO: 597, respectively;
cxxvii. SEQ ID NO: 441 and SEQ ID NO: 598, respectively;
cxxviii. SEQ ID NO: 442 and SEQ ID NO: 599, respectively;
cxxix. SEQ ID NO: 443 and SEQ ID NO: 600, respectively;
cxxx. SEQ ID NO: 444 and SEQ ID NO: 601, respectively;
cxxxi. SEQ ID NO: 445 and SEQ ID NO: 602, respectively;
cxxxii. SEQ ID NO: 446 and SEQ ID NO: 603, respectively;
cxxxiii. SEQ ID NO: 447 and SEQ ID NO: 604, respectively;
cxxxiv. SEQ ID NO: 448 and SEQ ID NO: 605, respectively;
cxxxv. SEQ ID NO: 449 and SEQ ID NO: 606, respectively;
cxxxvi. SEQ ID NO: 450 and SEQ ID NO: 607, respectively;
cxxxvii. SEQ ID NO: 451 and SEQ ID NO: 608, respectively;
cxxxviii. SEQ ID NO: 452 and SEQ ID NO: 609, respectively;
cxxxix. SEQ ID NO: 453 and SEQ ID NO: 610, respectively;
cxl. SEQ ID NO: 454 and SEQ ID NO: 611, respectively;
cxli. SEQ ID NO: 455 and SEQ ID NO: 612, respectively;
cxlii. SEQ ID NO: 456 and SEQ ID NO: 613, respectively;
cxliii. SEQ ID NO: 457 and SEQ ID NO: 614, respectively;

cxliv. SEQ ID NO: 458 and SEQ ID NO: 615, respectively;
cxlv. SEQ ID NO: 459 and SEQ ID NO: 616, respectively;
cxlvi. SEQ ID NO: 460 and SEQ ID NO: 617, respectively;
cxlvii. SEQ ID NO: 461 and SEQ ID NO: 618, respectively;
cxlviii. SEQ ID NO: 462 and SEQ ID NO: 619, respectively;
cxlix. SEQ ID NO: 463 and SEQ ID NO: 620, respectively;
cl. SEQ ID NO: 464 and SEQ ID NO: 621, respectively;
cli. SEQ ID NO: 465 and SEQ ID NO: 622, respectively;
clii. SEQ ID NO: 466 and SEQ ID NO: 623, respectively;
cliii. SEQ ID NO: 467 and SEQ ID NO: 624, respectively;
cliv. SEQ ID NO: 468 and SEQ ID NO: 625, respectively;
clv. SEQ ID NO: 469 and SEQ ID NO: 626, respectively;
clvi. SEQ ID NO: 470 and SEQ ID NO: 627, respectively; and
clvii. SEQ ID NO: 471 and SEQ ID NO: 628, respectively,

wherein the antibody comprises one or more cysteine amino acid substitution(s) at one or more position(s) selected from 88 of the light chain, 384 of the heavy chain, or 487 of the heavy chain, according to AHo numbering.

45. The conjugate molecule of claim 44, wherein the anti-GIPR antibody comprises the light chain and heavy chain of SEQ ID NO: 388 and SEQ ID NO: 545, respectively.

46. A conjugate molecule comprising:

an antagonist anti-glucose-dependent insulinotropic polypeptide receptor (GIPR) antibody, wherein the anti-GIPR antibody comprises:

a first and second light chain, each light chain comprising a CDRL1, a CDRL2, and a CDRL3 of SEQ ID NO: 702, SEQ ID NO: 859, and SEQ ID NO: 1016, respectively, and

a first and second heavy chain, each heavy chain comprising a CDRH1, a CDRH2, and a CDRH3 of SEQ ID NO: 1173, SEQ ID NO: 1330, and SEQ ID NO: 1487, respectively;

a first and second GLP-1 receptor agonist polypeptide, wherein each GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1579; and

a first and second peptide linker, wherein each peptide linker comprises the amino acid sequence of SEQ ID NO: 1592;

wherein the first GLP-1 receptor agonist polypeptide is conjugated, at its C-terminus via the first linker, to the first heavy chain of the anti-GIPR antibody at a cysteine residue at position 384 of the first heavy chain according to AHo numbering, and

wherein the second GLP-1 receptor agonist polypeptide is conjugated, at its C-terminus via the second linker, to the second heavy chain of the anti-GIPR antibody at a cysteine residue at position 384 of the second heavy chain according to AHo numbering.

47. The conjugate molecule of claim 46, wherein each light chain comprises a VL of SEQ ID NO: 74, and each heavy chain comprises a VH of SEQ ID NO: 231.

48. The conjugate molecule of claim 46, wherein each light chain comprises the amino acid sequence of SEQ ID NO: 388, and each heavy chain comprises the amino acid sequence of SEQ ID NO: 1571.

49. A conjugate molecule comprising:

an antagonist anti-glucose-dependent insulinotropic polypeptide receptor (GIPR) antibody, wherein the anti-GIPR antibody comprises:

a first and second light chain, each light chain comprising a CDRL1, a CDRL2, and a CDRL3 of SEQ ID NO: 702, SEQ ID NO: 859, and SEQ ID NO: 1016, respectively, and

a first and second heavy chain, each heavy chain comprising a CDRH1, a CDRH2, and a CDRH3 of SEQ ID NO: 1173, SEQ ID NO: 1330, and SEQ ID NO: 1487, respectively;

a first and second GLP-1 receptor agonist polypeptide, wherein each GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1580; and

a first and second peptide linker, wherein each peptide linker comprises the amino acid sequence of SEQ ID NO: 1591;

wherein the first GLP-1 receptor agonist polypeptide is conjugated, at its C-terminus via the first linker, to the first heavy chain of the anti-GIPR antibody at a cysteine residue at position 384 of the first heavy chain according to AHo numbering, and

wherein the second GLP-1 receptor agonist polypeptide is conjugated, at its C-terminus via the second linker, to the second heavy chain of the anti-GIPR antibody at a cysteine residue at position 384 of the second heavy chain according to AHo numbering.

50. The conjugate molecule of claim 49, wherein each light chain comprises a VL of SEQ ID NO: 74, and each heavy chain comprises a VH of SEQ ID NO: 231.

51. The conjugate molecule of claim 49, wherein each light chain comprises the amino acid sequence of SEQ ID NO: 388, and each heavy chain comprises the amino acid sequence of SEQ ID NO: 1571.

52. A conjugate molecule comprising:

an antagonist anti-glucose-dependent insulinotropic polypeptide receptor (GIPR) antibody, wherein the anti-GIPR antibody comprises:

a first and second light chain, each light chain comprising a CDRL1, a CDRL2, and a CDRL3 of SEQ ID NO: 702, SEQ ID NO: 859, and SEQ ID NO: 1016, respectively, and

a first and second heavy chain, each heavy chain comprising a CDRH1, a CDRH2, and a CDRH3 of SEQ ID NO: 1173, SEQ ID NO: 1330, and SEQ ID NO: 1487, respectively;

a first and second GLP-1 receptor agonist polypeptide, wherein each GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1581; and

a first and second peptide linker, wherein each peptide linker comprises the amino acid sequence of SEQ ID NO: 1586;

wherein the first GLP-1 receptor agonist polypeptide is conjugated, at its C-terminus via the first linker, to the first heavy chain of the anti-GIPR antibody at a cysteine residue at position 384 of the first heavy chain according to AHo numbering, and

wherein the second GLP-1 receptor agonist polypeptide is conjugated, at its C-terminus via the second linker, to the second heavy chain of the anti-GIPR antibody at a cysteine residue at position 384 of the second heavy chain according to AHo numbering.

53. The conjugate molecule of claim 52, wherein each light chain comprises a VL of SEQ ID NO: 74, and each heavy chain comprises a VH of SEQ ID NO: 231.

54. The conjugate molecule of claim 52, wherein each light chain comprises the amino acid sequence of SEQ ID NO: 388, and each heavy chain comprises the amino acid sequence of SEQ ID NO: 1571.

55. A conjugate molecule comprising:

an antagonist anti-glucose-dependent insulinotropic polypeptide receptor (GIPR) antibody, wherein the anti-GIPR antibody comprises:

a first and second light chain, each light chain comprising a CDRL1, a CDRL2, and a CDRL3 of SEQ ID NO: 702, SEQ ID NO: 859, and SEQ ID NO: 1016, respectively, and

a first and second heavy chain, each heavy chain comprising a CDRH1, a CDRH2, and a CDRH3 of SEQ ID NO: 1173, SEQ ID NO: 1330, and SEQ ID NO: 1487, respectively;

a first and second GLP-1 receptor agonist polypeptide, wherein each GLP-1 receptor agonist polypeptide comprises the amino acid sequence of SEQ ID NO: 1581; and

a first and second peptide linker, wherein each peptide linker comprises the amino acid sequence of SEQ ID NO: 1585;

wherein the first GLP-1 receptor agonist polypeptide is conjugated, at its C-terminus via the first linker, to the first heavy chain of the anti-GIPR antibody at a cysteine residue at position 275 of the first heavy chain, and

wherein the second GLP-1 receptor agonist polypeptide is conjugated, at its C-terminus via the second linker, to the second heavy chain of the anti-GIPR antibody at a cysteine residue at position 275 of the second heavy chain.

56. The conjugate molecule of claim 55, wherein each light chain comprises a VL of SEQ ID NO: 74, and each heavy chain comprises a VH of SEQ ID NO: 231.

57. The conjugate molecule of claim 55, wherein each light chain comprises the amino acid sequence of SEQ ID NO: 388, and each heavy chain comprises the amino acid sequence of SEQ ID NO: 1571.

58. A pharmaceutical composition comprising:

a GLP-1 receptor agonist polypeptide of any one of claims 1 to 10, the molecule of any one of claims 11 to 16, or the conjugate molecule of any one of claims 17 to 57; and

a pharmaceutically acceptable excipient.

59. A method of reducing body weight and/or food intake in a subject in need thereof, the method comprising:

administering the GLP-1 receptor agonist polypeptide of any one of claims 1 to 10, the molecule of any one of claims 11 to 16, the conjugate molecule of any one of claims 17 to 57, or the pharmaceutical composition of claim 58 to the subject.

60. A method of treating obesity or an obesity related condition in a subject in need thereof, the method comprising:

administering, to the subject, the GLP-1 receptor agonist polypeptide of any one of claims 1 to 10, the molecule of any one of claims 11 to 16, the conjugate molecule of any one of claims 17 to 57, or the pharmaceutical composition of claim 58.

61. The method of claim 60, wherein the obesity related condition is selected from the group consisting of sleep apnea, dyslipidemia, atherosclerotic cardiovascular disease, heart failure, hypertension, chronic kidney failure, and metabolic dysfunction-associated steatohepatitis.

62. A method of treating type 2 diabetes or a type 2 diabetes related condition in a subject in need thereof, the method comprising:

administering, to the subject, the GLP-1 receptor agonist polypeptide of any one of claims 1 to 10, the molecule of any one of claims 11 to 17, the conjugate molecule of any one of claims 17 to 57, or the pharmaceutical composition of claim 58.

63. The method of claim 62, wherein the type 2 diabetes related conditions is selected from the group consisting of hypertension, high blood sugar, diabetic kidney disease, and diabetic kidney failure.

64. The GLP-1 receptor agonist polypeptide of any one of claims 1 to 10, the molecule of any one of claims 11 to 16, or the conjugate molecule of any one of claims 17 to 57 for use as a medicament.