

**METHOD OF TREATING OR AMELIORATING METABOLIC DISORDERS USING
BINDING PROTEINS FOR GASTRIC INHIBITORY PEPTIDE RECEPTOR (GIPR)
IN COMBINATION WITH GLP-1 AGONISTS**

FIELD OF THE INVENTION

[0001] The present disclosure relates to the treatment or amelioration of a metabolic disorder, such as type 2 diabetes, elevated glucose levels, elevated insulin levels, obesity, non-alcoholic fatty liver disease, or cardiovascular diseases, using an antigen binding protein specific for the gastric inhibitory peptide receptor (GIPR).

BACKGROUND OF THE INVENTION

[0002] 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.

[0003] 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 patients while GLP-1's incretin effect remains intact (Nauck et al. J. Clin. Invest. 1993; 91:301-307).

[0004] 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.

[0005] GIPR knockout mice (*Gipr*^{-/-}) are resistant to high fat diet-induced weight gain and have improved insulin sensitivity and lipid profiles. (Yamada et al., *Diabetes*. 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).

[0006] Glucagon-like peptide-1 ("GLP-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 such as exenatide, liraglutide, dulaglutide have been developed and are now being used clinically to improve glycemic control in patients 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 patients (*Bioorg. Med. Chem. Lett* 2013, 23:4011-4018).

[0007] Collectively, these links to obesity and insulin resistance imply GIPR inhibition is a useful approach for therapeutic intervention, both as a monotherapy and in combination with GLP-1.

SUMMARY OF THE INVENTION

[0008] In one aspect, the present disclosure provides a method of treating a subject with a metabolic disorder, the method comprising administering to the subject a therapeutically effective amount of an antigen binding protein that specifically binds to a protein having an amino acid sequence having at least 90% amino acid sequence identity to an amino acid sequence of a GIPR. In one aspect the present invention is directed to a method of treating a subject with a metabolic disorder, the method comprising administering to the subject a therapeutically effective amount of a GLP-1 receptor agonist and a therapeutically effective amount of a GIPR antagonist that specifically binds to a protein having an amino acid sequence having at least 90% amino acid sequence identity to an amino acid sequence of a GIPR. In one embodiment, the metabolic disorder is a disorder of glucose metabolism. In

another embodiment, the glucose metabolism disorder comprises hyperglycemia and administering the antigen binding protein reduces plasma glucose. In another embodiment, the glucose metabolism disorder comprises hyperinsulinemia and administering the antigen binding protein reduces plasma insulin. In another embodiment, the glucose metabolism disorder comprises glucose intolerance and administering the antigen binding protein reduces increases glucose tolerance. In another embodiment, the glucose metabolism disorder comprises insulin resistance and administering the antigen binding protein reduces insulin resistance. In another embodiment, the glucose metabolism disorder comprises diabetes mellitus. In another embodiment, the subject is obese. In another embodiment, administering the antigen binding protein reduces body weight in an obese subject. In another embodiment, administering the antigen binding protein reduces body weight gain in an obese subject. In another embodiment, administering the antigen binding protein reduces fat mass in an obese subject. In another embodiment, the glucose metabolism disorder comprises insulin resistance and administering the antigen binding protein reduces insulin resistance in an obese subject. In another embodiment, administering the antigen binding protein reduces liver steatosis in an obese subject having increased liver steatosis. In another embodiment, administering the antigen binding protein reduces liver fat content in an obese subject having increased liver fat content.

[0009] In one aspect the present invention is directed to a method of treatment comprising administering to a subject a therapeutically effective amount of at least one GLP-1 receptor agonist in combination with administration of at least one GIPR antagonist which upon administration to a subject with symptoms of a metabolic disorder provides sustained beneficial effects.

[0010] In one embodiment, administration of at least one GLP-1 receptor agonist in combination with administration of at least one GIPR antagonist provides sustained beneficial effects of at least one symptom of a metabolic disorder.

[0011] In one embodiment, the therapeutically effective amounts of the GLP-1 receptor agonist and the GIPR antagonist are combined prior to administration to the subject.

[0012] In one embodiment, the therapeutically effective amounts of the GLP-1 receptor agonist and the GIPR antagonist are administered to the subject sequentially.

[0013] In one embodiment, the therapeutically effective amounts of a GLP-1 receptor agonist and a GIPR antagonist are synergistically effective amounts.

[0014] In one embodiment, the molar ratio of a GLP-1 receptor agonist to a GIPR antagonist is from about 1:1 to 1:110, 1:1 to 1:100, 1:1 to 1:75, 1:1 to 1:50, 1:1 to 1:25, 1:1 to 1:10, 1:1

to 1:5, and 1:1. In one embodiment, the molar ratio of a GIPR antagonist to a GLP-1 receptor agonist is from about 1:1 to 1:110, 1:1 to 1:100, 1:1 to 1:75, 1:1 to 1:50, 1:1 to 1:25, 1:1 to 1:10, and 1:1 to 1:5.

[0015] In one embodiment, the GLP-1 receptor agonist is used in combination with the GIPR antagonist at therapeutically effective molar ratios of between about 1:1.5 to 1:150, preferably 1:2 to 1:50.

[0016] In one embodiment, the GLP-1 receptor agonist and the GIPR antagonist are present in doses that are at least about 1.1 to 1.4, 1.5, 2, 3, 4, 5, 6, 7, 8, 9, or 10 fold lower than the doses of each compound alone required to treat a condition and/or disease.

[0017] In one embodiment, the GLP-1 receptor agonist is GLP-1(7-37) or a GLP-1(7-37) analog.

[0018] In one embodiment, the GLP-1 receptor agonist is selected from the group consisting of exenatide, liraglutide, lixisenatide, albiglutide, dulaglutide, semaglutide, and taspoglutide.

[0019] In one embodiment, the GLP-1 receptor agonist is selected from the group consisting of GLP-1(7-37) (SEQ ID NO: 1244); GLP-1(7-36)-NH₂ (SEQ ID NO: 1245); liraglutide; albiglutide; taspoglutide; dulaglutide, semaglutide; LY2428757; desamino-His⁷,Arg²⁶,Lys³⁴(N^ε-(γ-Glu(N-α-hexadecanoyl)))-GLP-1(7-37) (core peptide disclosed as SEQ ID NO: 1282); desamino-His⁷,Arg²⁶,Lys³⁴(N^ε-octanoyl)-GLP-1(7-37) (SEQ ID NO: 1283); Arg^{26,34},Lys³⁸(N^ε-(ω-carboxypentadecanoyl))-GLP-1(7-38) (SEQ ID NO: 1284); Arg^{26,34},Lys³⁶(N^ε-(γ-Glu(N-α-hexadecanoyl)))-GLP-1(7-36) (core peptide disclosed as SEQ ID NO: 1285); Aib^{8,35},Arg^{26,34},Phe³¹-GLP-1(7-36)) (SEQ ID NO: 1246); HXaa₈EGTFTSDVSSYLEXaa₂₂Xaa₂₃AAKEFIXaa₃₀WLXaa₃₃Xaa₃₄G Xaa₃₆Xaa₃₇; wherein Xaa₃ is A, V, or G; Xaa₂₂ is G, K, or E; Xaa₂₃ is Q or K; Xaa₃₀ is A or E; Xaa₃₃ is V or K; Xaa₃₄ is K, N, or R; Xaa₃₆ is R or G; and Xaa₃₇ is G, H, P, or absent (SEQ ID NO: 1247); Arg³⁴-GLP-1(7-37) (SEQ ID NO: 1248); Glu³⁰-GLP-1(7-37) (SEQ ID NO: 1249); Lys²²-GLP-1(7-37) (SEQ ID NO: 1250); Gly^{8,36},Glu²²-GLP-1(7-37) (SEQ ID NO: 1251); Val⁸,Glu²²,Gly³⁶-GLP-1(7-37) (SEQ ID NO: 1252); Gly^{8,36},Glu²²,Lys³³,Asn³⁴-GLP-1(7-37) (SEQ ID NO: 1253); Val⁸,Glu²²,Lys³³,Asn³⁴,Gly³⁶-GLP-1(7-37) (SEQ ID NO: 1254); Gly^{8,36},Glu²²,Pro³⁷-GLP-1(7-37) (SEQ ID NO: 1255); Val⁸,Glu²²,Gly³⁶Pro³⁷-GLP-1(7-37) (SEQ ID NO: 1256); Gly^{8,36},Glu²²,Lys³³, Asn³⁴,Pro³⁷-GLP-1(7-37) (SEQ ID NO: 1257); Val⁸,Glu²²,Lys³³,Asn³⁴,Gly³⁶,Pro³⁷-GLP-1(7-37) (SEQ ID NO: 1258); Gly^{8,36},Glu²²-GLP-1(7-36) (SEQ ID NO: 1259); Val⁸,Glu²²,Gly³⁶-GLP-1(7-36) (SEQ ID NO: 1260); Val⁸,Glu²²,Asn³⁴,Gly³⁶-GLP-1(7-36) (SEQ ID NO: 1261); and Gly^{8,36},Glu²²,Asn³⁴-GLP-1(7-36) (SEQ ID NO: 1262).

[0020] In another embodiment, the subject is a mammal. In another embodiment, the subject is human. In another embodiment, the GIPR is human GIPR. In another embodiment, the administering is by parenteral injection. In another embodiment, the administering is by subcutaneous injection.

[0021] In another aspect the present disclosure provides an antigen binding protein that specifically binds to a human GIPR polypeptide and inhibits activation of GIPR by GIP ligand. In one embodiment, the antigen binding protein inhibits GIP ligand binding to GIPR. In another embodiment, the antigen binding protein is a human antigen binding protein. In another embodiment, the antigen binding protein is a human antibody. In another embodiment, the antigen binding protein is a monoclonal antibody.

[0022] In another aspect, the present disclosure provides a pharmaceutical composition comprising at least one antigen binding protein according to any one of the foregoing embodiments.

[0023] In another aspect, the present disclosure provides a nucleic acid molecule encoding an antigen binding protein according to any one of the foregoing embodiments.

[0024] In another aspect, the present disclosure provides a vector comprising a nucleic acid molecule encoding an antigen binding protein according to any one of the foregoing embodiments.

[0025] In another aspect, the present disclosure provides a host cell comprising a nucleic acid molecule encoding an antigen binding protein according to any one of the foregoing embodiments or a vector comprising a nucleic acid molecule encoding an antigen binding protein according to any one of the foregoing embodiments. In another aspect the present disclosure provides an antigen binding protein that specifically binds to a human GIPR polypeptide expressed by the vector.

[0026] In another aspect, the present disclosure provides a method of making an antigen binding protein according to any one of the foregoing embodiments, the method comprising expressing the antigen binding protein in a host cell that secretes the antigen binding protein, and then purifying the antigen binding protein from the cell culture media. In another aspect the present disclosure provides an antigen binding protein that specifically binds to a human GIPR polypeptide purified from the host cell.

[0027] In another aspect, the present disclosure provides an antigen binding protein of any one of the foregoing embodiments or a pharmaceutical composition of any one of the foregoing embodiments for use in therapy.

DETAILED DESCRIPTION OF THE INVENTION

[0028] The present disclosure provides a method of treating a metabolic disorder, such as a disorder of glucose metabolism (e.g. Type 2 diabetes, elevated glucose levels, elevated insulin levels, dyslipidemia, metabolic syndrome (Syndrome X or insulin resistance syndrome), glucosuria, metabolic acidosis, Type 1 diabetes, obesity and conditions exacerbated by obesity) by blocking or interfering with the biological activity of GIP. In one embodiment, a therapeutically effective amount of an isolated human GIPR binding protein is administered to a subject in need thereof. Methods of administration and delivery are also provided.

[0029] Recombinant polypeptide and nucleic acid methods used herein, including in the Examples, are generally those set forth in Sambrook et al., *Molecular Cloning: A Laboratory Manual* (Cold Spring Harbor Laboratory Press, 1989) or *Current Protocols in Molecular Biology* (Ausubel et al., eds., Green Publishers Inc. and Wiley and Sons 1994), both of which are incorporated herein by reference for any purpose.

[0030] The section headings used herein are for organizational purposes only and are not to be construed as limiting the subject matter described.

[0031] 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.

[0032] Generally, nomenclatures used in connection with, and techniques of, cell and tissue culture, molecular biology, immunology, microbiology, genetics and protein and nucleic acid chemistry and hybridization described herein are those well-known and commonly used in the art. The methods and techniques of the present application are generally performed according to conventional methods well known in the art and as described in various general and more specific references that are cited and discussed throughout the present specification unless otherwise indicated. See, e.g., Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 3rd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (2001), Ausubel et al., *Current Protocols in Molecular Biology*, Greene Publishing Associates (1992), and Harlow and Lane *Antibodies: A Laboratory Manual* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1990), which are incorporated herein by reference. Enzymatic reactions and purification techniques are performed according to manufacturer's specifications, as commonly accomplished in the art or as described herein. The terminology

used in connection with, and the laboratory procedures and techniques of, analytical chemistry, synthetic organic chemistry, and medicinal and pharmaceutical chemistry described herein are those well-known and commonly used in the art. Standard techniques can be used for chemical syntheses, chemical analyses, pharmaceutical preparation, formulation, and delivery, and treatment of patients.

[0033] 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.

[0034] 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 may mean $\pm 1\%$.

[0035] Following convention, as used herein “a” and “an” mean “one or more” unless specifically indicated otherwise.

[0036] 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.

[0037] A “naturally occurring amino acid” is an amino acid that is encoded by the 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.

[0038] 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 -amino acids (such as piperidine-4-carboxylic acid) and the like.

[0039] 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. “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 lists 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), $N\alpha$ -methylcitrulline (NMeCit), $N\alpha$ -methylhomocitrulline ($N\alpha$ -MeHoCit), ornithine (Orn), $N\alpha$ -Methylornithine ($N\alpha$ -MeOrn or NMeOrn), sarcosine (Sar), homolysine (hLys or hK), homoarginine (hArg or hR), homoglutamine (hQ), $N\alpha$ -methylarginine (NMeR), $N\alpha$ -methylleucine ($N\alpha$ -MeL or NMeL), N-methylhomolysine (NMeHoK), $N\alpha$ -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 (Igl), para-iodophenylalanine (pI-Phe), para-aminophenylalanine (4AmP or 4-Amino-Phe), 4-guanidino phenylalanine (Guf), glycyllsine (abbreviated “K(N ϵ -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), $N\alpha$ -methyl valine (NMeVal), N- α -methyl leucine (NMeLeu), $N\alpha$ -methylnorleucine (NMeNle), cyclopentylglycine (Cpg), cyclohexylglycine (Chg), acetylgarginine (acetylarg), α , β -diaminopropionic 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, aminocaproic acid, aminoheptanoic acid, aminopimelic acid, desmosine, diaminopimelic acid, N-ethylglycine, N-ethylasparagine, 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.

[0040] The term “isolated nucleic acid molecule” refers to a single or double-stranded polymer of deoxyribonucleotide or ribonucleotide bases read from the 5' to the 3' end (e.g., a GIPR nucleic acid sequence provided herein), or an analog thereof, that has been separated from at least about 50 percent of polypeptides, peptides, lipids, carbohydrates, polynucleotides or other materials with which the nucleic acid is naturally found when total nucleic acid is isolated from the source cells. Preferably, an isolated nucleic acid molecule is substantially free from any other contaminating nucleic acid molecules or other molecules that are found in the natural environment of the nucleic acid that would interfere with its use in polypeptide production or its therapeutic, diagnostic, prophylactic or research use.

[0041] The term “isolated polypeptide” refers to a polypeptide (e.g., a GIPR polypeptide sequence provided herein or an antigen binding protein of the present invention) that has been separated from at least about 50 percent of polypeptides, peptides, lipids, carbohydrates, polynucleotides, or other materials with which the polypeptide is naturally found when isolated from a source cell. Preferably, the isolated polypeptide is substantially free from any other contaminating polypeptides or other contaminants that are found in its natural environment that would interfere with its therapeutic, diagnostic, prophylactic or research use.

[0042] The term “encoding” refers to a polynucleotide sequence encoding one or more amino acids. The term does not require a start or stop codon.

[0043] The terms “identical” and percent “identity,” in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same. “Percent identity” means the percent of identical residues between the amino acids or nucleotides in the compared molecules and is calculated based on the size of the smallest of the molecules being compared. For these calculations, gaps in alignments (if any) can be addressed by a particular mathematical model or computer program (i.e., an “algorithm”). Methods that can be used to calculate the identity of the aligned nucleic acids or polypeptides include those described in *Computational Molecular Biology*, (Lesk, A. M., ed.), (1988) New York: Oxford University Press; *Biocomputing Informatics and Genome Projects*, (Smith, D. W., ed.), 1993, New York: Academic Press; *Computer Analysis of Sequence Data, Part I*, (Griffin, A. M., and Griffin, H. G., eds.), 1994, New Jersey: Humana Press; von Heinje, G., (1987) *Sequence Analysis in Molecular Biology*, New York: Academic Press; *Sequence*

Analysis Primer, (Gribskov, M. and Devereux, J., eds.), 1991, New York: M. Stockton Press; and Carillo et al., (1988) SIAM J. Applied Math. 48:1073.

[0044] In calculating percent identity, the sequences being compared are aligned in a way that gives the largest match between the sequences. The computer program used to determine percent identity is the GCG program package, which includes GAP (Devereux et al., (1984) Nucl. Acid Res. 12:387; Genetics Computer Group, University of Wisconsin, Madison, WI). The computer algorithm GAP is used to align the two polypeptides or polynucleotides for which the percent sequence identity is to be determined. The sequences are aligned for optimal matching of their respective amino acid or nucleotide (the “matched span”, as determined by the algorithm). A gap opening penalty (which is calculated as 3x the average diagonal, wherein the “average diagonal” is the average of the diagonal of the comparison matrix being used; the “diagonal” is the score or number assigned to each perfect amino acid match by the particular comparison matrix) and a gap extension penalty (which is usually 1/10 times the gap opening penalty), as well as a comparison matrix such as PAM 250 or BLOSUM 62 are used in conjunction with the algorithm. In certain embodiments, a standard comparison matrix (see, Dayhoff et al., (1978) Atlas of Protein Sequence and Structure 5:345-352 for the PAM 250 comparison matrix; Henikoff et al., (1992) Proc. Natl. Acad. Sci. U.S.A. 89:10915-10919 for the BLOSUM 62 comparison matrix) is also used by the algorithm.

[0045] Recommended parameters for determining percent identity for polypeptides or nucleotide sequences using the GAP program are the following:

[0046] Algorithm: Needleman et al., 1970, J. Mol. Biol. 48:443-453;

[0047] Comparison matrix: BLOSUM 62 from Henikoff et al., 1992, supra;

[0048] Gap Penalty: 12 (but with no penalty for end gaps)

[0049] Gap Length Penalty: 4

[0050] Threshold of Similarity: 0

[0051] Certain alignment schemes for aligning two amino acid sequences can result in matching of only a short region of the two sequences, and this small aligned region can have very high sequence identity even though there is no significant relationship between the two full-length sequences. Accordingly, the selected alignment method (e.g., the GAP program) can be adjusted if so desired to result in an alignment that spans at least 50 contiguous amino acids of the target polypeptide.

[0052] The terms “GIPR polypeptide” and “GIPR protein” 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 GIPR protein). For purposes of this disclosure, the term “GIPR polypeptide” can be used interchangeably to refer to any full-length GIPR polypeptide, e.g., SEQ ID NO: 1201, which consists of 466 amino acid residues and which is encoded by the nucleotide sequence SEQ ID NO: 1202, or SEQ ID NO: 1203, which consists of 430 amino acid residues and which is encoded by the nucleic acid sequence SEQ ID NO: 1204, or SEQ ID NO: 1205, which consists of 493 amino acid residues and which is encoded by the nucleic acid sequence of SEQ ID NO: 1206, or SEQ ID NO: 1207, which consists of 460 amino acid residues and which is encoded by the nucleic acid sequence of SEQ ID NO: 1208, or SEQ ID NO: 1209, which consists of 230 amino acid residues and which is encoded by the nucleic acid sequence of SEQ ID NO: 1210.

[0053] The term “GIPR polypeptide” also encompasses a GIPR polypeptide in which a naturally occurring GIPR polypeptide sequence (e.g., SEQ ID NOs: 1201, 1203 or 1205) has been modified. Such modifications include, but are not limited to, one or more amino acid substitutions, including substitutions with non-naturally occurring amino acids non-naturally-occurring amino acid analogs and amino acid mimetics.

[0054] In various embodiments, a GIPR polypeptide comprises an amino acid sequence that is at least about 85 percent identical to a naturally-occurring GIPR polypeptide (e.g., SEQ ID NOs: 1201, 1203 or 1205). 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 NOs: 1201, 1203 or 1205). 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.

[0055] The terms “GIPR activity assay” (also referred to as a “GIPR functional assay”) means an assay that can be used to measure GIP or a GIP binding protein activity in a cellular setting. In one embodiment, the “activity” (or “functional”) assay can be a cAMP assay in GIPR expressing cells, in which GIP can induce cAMP signal, and the activity of a GIP/GIPR binding protein could be measured in the presence/absence of GIP ligand, in which IC₅₀/EC₅₀ and degree of inhibition/activation can be obtained (Biochemical and Biophysical Research Communications (2002) 290:1420–1426). In another embodiment, the “activity” (or “functional”) assay can be an insulin secretion assay in pancreatic beta cells, in which GIP can induce glucose-dependent insulin secretion, and the activity of a GIP/GIPR binding protein could be measured in the presence/absence of GIP ligand, in which

IC50/EC50 and degree of inhibition/activation can be obtained (Biochemical and Biophysical Research Communications (2002) 290:1420–1426).

[0056] The term “GIPR binding assay” means an assay that can be used to measure binding of GIP to GIPR. In one embodiment, “GIPR binding assay” can be an assay using FMAT or FACS that measures fluorescence-labeled GIP binding to GIPR expression cells, and GIP/GIPR binding protein’s activity can be measured for displacing fluorescence-labeled GIP binding to GIPR expression cells. In another embodiment, “GIPR binding assay” can be an assay that measures radioactive-labeled GIP binding to GIPR expression cells, and GIP/GIPR binding protein’s activity can be measured for displacing radioactive labeled GIP binding to GIPR expression cells (Biochimica et Biophysica Acta (2001) 1547:143-155).

[0057] The terms “GIP”, “Gastric inhibitory polypeptide”, “glucose-dependent insulintropic 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). For purposes of this disclosure, the term “GIP” can be used interchangeably to refer to any mature GIP polypeptide.

[0058] The 42 amino acid sequence of mature human GIP is:

[0059] Y A E G T F I S D Y S I A M D K I H Q Q D F V N W L L A Q K G K K N D W K H N I T Q (SEQ ID NO: 1211)

[0060] and is encoded by the DNA sequence:

[0061] t a t g c g g a a g g c a c c t t t a t t a g c g a t t a t a g c a t t g c g a t g g a t a a a a t
t c a t c a g c a g g a t t t t g t g a a c t g g c t g c t g g c g c a g a a a g g c a a a a a a a
a c g a t t g g a a a c a t a a c a t t a c c c a g (SEQ ID NO: 1212).

[0062] The 42 amino acid sequence of mature murine GIP is:

[0063] Y A E G T F I S D Y S I A M D K I R Q Q D F V N W L L A Q R G K K S D W K H N I T Q (SEQ ID NO: 1213)

[0064] and is encoded by the DNA sequence:

[0065] t a t g c g g a a g g c a c c t t t a t t a g c g a t t a t a g c a t t g c g a t g g a t a a a a t
t c g c c a g c a g g a t t t t g t g a a c t g g c t g c t g g c g c a g c g c g g c a a a a a a a
g c g a t t g g a a a c a t a a c a t t a c c c a g (SEQ ID NO: 1214).

[0066] The 42 amino acid sequence of mature rat GIP is:

[0067] Y A E G T F I S D Y S I A M D K I R Q Q D F V N W L L A Q K G K K N D W K H N L T Q (SEQ ID NO: 1215)

[0068] and is encoded by the DNA sequence:

[0069] tatgcggaag gcacctttat tagcgattat agcattgcga tggataaaat
tcgccagcag gattttgtga actggctgctg gcgcagaaag gcaaaaaaaaa
cgattggaaa cataacctga cccag (SEQ ID NO: 1216).

[0070] An “antigen binding protein” as used herein means any protein that specifically binds a specified target antigen, such as a GIPR polypeptide (e.g., a human GIPR polypeptide such as provided in SEQ ID NOs: 1201, 1203 or 1205). The term encompasses intact antibodies that comprise at least two full-length heavy chains and two full-length light chains, as well as derivatives, variants, fragments, and mutations thereof. Examples of antibody fragments include Fab, Fab', F(ab')₂, and Fv fragments. An antigen binding protein also includes domain antibodies such as nanobodies and scFvs as described further below.

[0071] In general, a GIPR antigen binding protein is said to “specifically bind” its target antigen GIPR when the antigen binding protein exhibits essentially background binding to non-GIPR molecules. An antigen binding protein that specifically binds GIPR may, however, cross-react with GIPR polypeptides from different species. Typically, a GIPR antigen binding protein specifically binds human GIPR when the dissociation constant (KD) is $\leq 10^{-7}$ M as measured via a surface plasma resonance technique (e.g., BIAcore, GE-Healthcare Uppsala, Sweden) or Kinetic Exclusion Assay (KinExA, Sapidyn, Boise, Idaho). A GIPR antigen binding protein specifically binds human GIPR with “high affinity” when the KD is $\leq 5 \times 10^{-9}$ M, and with “very high affinity” when the KD is $\leq 5 \times 10^{-10}$ M, as measured using methods described.

[0072] “Antigen binding region” means a protein, or a portion of a protein, that specifically binds a specified antigen. For example, that portion of an antigen binding protein that contains the amino acid residues that interact with an antigen and confer on the antigen binding protein its specificity and affinity for the antigen is referred to as “antigen binding region.” An antigen binding region typically includes one or more “complementary binding regions” (“CDRs”) of an immunoglobulin, single-chain immunoglobulin, or camelid antibody. Certain antigen binding regions also include one or more “framework” regions. A “CDR” is an amino acid sequence that contributes to antigen binding specificity and affinity. “Framework” regions can aid in maintaining the proper conformation of the CDRs to promote binding between the antigen binding region and an antigen.

[0073] A “recombinant protein”, including a recombinant GIPR antigen binding protein, is a protein made using recombinant techniques, i.e., through the expression of a recombinant

nucleic acid as described herein. Methods and techniques for the production of recombinant proteins are well known in the art.

[0074] The term “antibody” refers to an intact immunoglobulin of any isotype, or a fragment thereof that can compete with the intact antibody for specific binding to the target antigen, and includes, for instance, chimeric, humanized, fully human, and bispecific antibodies. An “antibody” as such is a species of an antigen binding protein. An intact antibody generally will comprise at least 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. The antigen binding proteins, antibodies, or binding fragments may be produced in hybridomas, by recombinant DNA techniques, or by enzymatic or chemical cleavage of intact antibodies.

[0075] The term “light chain” as used with respect to an antibody or fragments thereof includes a full-length light chain and fragments thereof having sufficient variable region sequence to confer binding specificity. A full-length light chain includes a variable region domain, VL, and a constant region domain, CL. The variable region domain of the light chain is at the amino-terminus of the polypeptide. Light chains include kappa chains and lambda chains.

[0076] The term “heavy chain” as used with respect to an antibody or fragment thereof includes a full-length heavy chain and fragments thereof having sufficient variable region sequence to confer binding specificity. A full-length heavy chain includes a variable region domain, VH, and three constant region domains, CH1, CH2, and CH3. The VH domain is at the amino-terminus of the polypeptide, and the CH domains are at the carboxyl-terminus, with the CH3 being closest to the carboxy-terminus of the polypeptide. Heavy chains may be of any isotype, including IgG (including IgG1, IgG2, IgG3 and IgG4 subtypes), IgA (including IgA1 and IgA2 subtypes), IgM and IgE.

[0077] The term “immunologically functional fragment” (or simply “fragment”) of an antibody or immunoglobulin chain (heavy or light chain), as used herein, is an antigen binding protein comprising 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 specifically binding to an antigen. Such fragments are biologically active in that they bind specifically to the target antigen and can compete with other antigen binding proteins, including intact antibodies, for specific binding to a given epitope.

[0078] These biologically active fragments may be produced by recombinant DNA techniques, or may be produced by enzymatic or chemical cleavage of antigen binding proteins, including intact antibodies. Immunologically functional immunoglobulin fragments include, but are not limited to, Fab, Fab', and F(ab')₂ fragments.

[0079] In another embodiment, Fvs, domain antibodies and scFvs, and may be derived from an antibody of the present invention.

[0080] It is contemplated further that a functional portion of the antigen binding proteins disclosed herein, for example, one or more CDRs, could be covalently bound to a second protein or to a small molecule to create a therapeutic agent directed to a particular target in the body, possessing bifunctional therapeutic properties, or having a prolonged serum half-life.

[0081] A "Fab fragment" is comprised of one light chain and the CH1 and variable regions of one heavy chain. The heavy chain of a Fab molecule cannot form a disulfide bond with another heavy chain molecule.

[0082] An "Fc" region contains two heavy chain fragments comprising the CH2 and CH3 domains of an antibody. The two heavy chain fragments are held together by two or more disulfide bonds and by hydrophobic interactions of the CH3 domains.

[0083] In certain embodiments, one or more amino acid modifications may be introduced into the Fc region of an antibody provided herein, thereby generating an Fc region variant. The Fc region variant may comprise a human Fc region sequence (e.g., a human IgG1, IgG2, IgG3 or IgG4 Fc region) comprising an amino acid modification (e.g. a substitution) at one or more amino acid positions.

[0084] In certain embodiments, the invention contemplates an antibody variant that possesses some but not all effector functions, which make it a desirable candidate for applications in which the half life of the antibody in vivo is important yet certain effector functions (such as complement and ADCC) are unnecessary or deleterious. In vitro and/or in vivo cytotoxicity assays can be conducted to confirm the reduction/depletion of CDC and/or ADCC activities. For example, Fc receptor (FcR) binding assays can be conducted to ensure that the antibody lacks Fc γ R binding (hence likely lacking ADCC activity), but retains FcRn binding ability. The primary cells for mediating ADCC, NK cells, express Fc γ RIII only, whereas monocytes express Fc γ RI, Fc γ RII and Fc γ RIII. FcR expression on hematopoietic cells is summarized in Table 3 on page 464 of Ravetch and Kinet, *Annu. Rev. Immunol.* 9:457-492 (1991). Non-limiting examples of in vitro assays to assess ADCC activity of a molecule of interest is described in U.S. Pat. No. 5,500,362 (see, e.g. Hellstrom, I. et al. *Proc. Nat'l Acad.*

Sci. USA 83:7059-7063 (1986)) and Hellstrom, I et al., Proc. Nat'l Acad. Sci. USA 82:1499-1502 (1985); 5,821,337 (see Bruggemann, M. et al., J. Exp. Med. 166:1351-1361 (1987)). Alternatively, non-radioactive assays methods may be employed (see, for example, ACTI.TM. non-radioactive cytotoxicity assay for flow cytometry (CellTechnology, Inc. Mountain View, Calif.; and CytoTox 96.RTM. non-radioactive cytotoxicity assay (Promega, Madison, Wis.). Useful effector cells for such assays include peripheral blood mononuclear cells (PBMC) and Natural Killer (NK) cells. Alternatively, or additionally, ADCC activity of the molecule of interest may be assessed in vivo, e.g., in a animal model such as that disclosed in Clynes et al. Proc. Nat'l Acad. Sci. USA 95:652-656 (1998). C1q binding assays may also be carried out to confirm that the antibody is unable to bind C1q and hence lacks CDC activity. See, e.g., C1q and C3c binding ELISA in WO 2006/029879 and WO 2005/100402. To assess complement activation, a CDC assay may be performed (see, for example, Gazzano-Santoro et al., J. Immunol. Methods 202:163 (1996); Cragg, M. S. et al., Blood 101:1045-1052 (2003); and Cragg, M. S. and M. J. Glennie, Blood 103:2738-2743 (2004)). FcRn binding and in vivo clearance/half life determinations can also be performed using methods known in the art (see, e.g., Petkova, S. B. et al., Int'l. Immunol. 18(12):1759-1769 (2006)).

[0085] In some embodiments, one or more amino acid modifications may be introduced into the Fc portion of the antibody provided herein in order to increase IgG binding to the neonatal Fc receptor. In certain embodiments, the antibody comprises the following three mutations according to EU numbering: M252Y, S254T, and T256E (the "YTE mutation") (U.S. Pat. No. 8,697,650; see also Dall'Acqua et al., Journal of Biological Chemistry 281(33):23514-23524 (2006). In certain embodiments, the YTE mutation does not affect the ability of the antibody to bind to its cognate antigen. In certain embodiments, the YTE mutation increases the antibody's serum half-life compared to the native (i.e., non-YTE mutant) antibody. In some embodiments, the YTE mutation increases the serum half-life of the antibody by 3-fold compared to the native (i.e., non-YTE mutant) antibody. In some embodiments, the YTE mutation increases the serum half-life of the antibody by 2-fold compared to the native (i.e., non-YTE mutant) antibody. In some embodiments, the YTE mutation increases the serum half-life of the antibody by 4-fold compared to the native (i.e., non-YTE mutant) antibody. In some embodiments, the YTE mutation increases the serum half-life of the antibody by at least 5-fold compared to the native (i.e., non-YTE mutant) antibody. In some embodiments, the YTE mutation increases the serum half-life of the antibody by at least 10-fold compared to the native (i.e., non-YTE mutant) antibody. See,

e.g., U.S. Pat. No. 8,697,650; see also Dall'Acqua et al., *Journal of Biological Chemistry* 281(33):23514-23524 (2006).

[0086] In certain embodiments, the YTE mutant provides a means to modulate antibody-dependent cell-mediated cytotoxicity (ADCC) activity of the antibody. In certain embodiments, the YTEO mutant provides a means to modulate ADCC activity of a humanized IgG antibody directed against a human antigen. See, e.g., U.S. Pat. No. 8,697,650; see also Dall'Acqua et al., *Journal of Biological Chemistry* 281(33):23514-23524 (2006). In certain embodiments, the YTE mutant allows the simultaneous modulation of serum half-life, tissue distribution, and antibody activity (e.g., the ADCC activity of an IgG antibody). See, e.g., U.S. Pat. No. 8,697,650; see also Dall'Acqua et al., *Journal of Biological Chemistry* 281(33):23514-23524 (2006).

[0087] Antibodies with reduced effector function include those with substitution of one or more of Fc region residues 238, 265, 269, 270, 297, 327 and 329 according to EU numbering (U.S. Pat. No. 6,737,056). Such Fc mutants include Fc mutants with substitutions at two or more of amino acid positions 265, 269, 270, 297 and 327 according to EU numbering, including the so-called "DANA" Fc mutant with substitution of residues 265 and 297 to alanine according to EU numbering (i.e., D265A and N297A according to EU numbering) (U.S. Pat. No. 7,332,581). In certain embodiments the Fc mutant comprises the following two amino acid substitutions: D265A and N297A. In certain embodiments the Fc mutant consists of the following two amino acid substitutions: D265A and N297A.

[0088] In certain embodiments, the proline at position 329 (EU numbering) (P329) of a wild-type human Fc region is substituted with glycine or arginine or an amino acid residue large enough to destroy the proline sandwich within the Fc/Fc γ receptor interface, that is formed between the P329 of the Fc and tryptophane residues W87 and W110 of Fc γ RIII (Sondermann et al.: *Nature* 406, 267-273 (20 Jul. 2000)). In a further embodiment, at least one further amino acid substitution in the Fc variant is S228P, E233P, L234A, L235A, L235E, N297A, N297D, or P331S and still in another embodiment said at least one further amino acid substitution is L234A and L235A of the human IgG1 Fc region or S228P and L235E of the human IgG4 Fc region, all according to EU numbering (U.S. Pat. No. 8,969,526 which is incorporated by reference in its entirety).

[0089] In certain embodiments, a polypeptide comprises the Fc variant of a wild-type human IgG Fc region wherein the polypeptide has P329 of the human IgG Fc region substituted with glycine and wherein the Fc variant comprises at least two further amino acid substitutions at L234A and L235A of the human IgG1 Fc region or S228P and L235E of the human IgG4 Fc

region, and wherein the residues are numbered according to the EU numbering (U.S. Pat. No. 8,969,526 which is incorporated by reference in its entirety). In certain embodiments, the polypeptide comprising the P329G, L234A and L235A (EU numbering) substitutions exhibit a reduced affinity to the human Fc.gamma.RIIIA and Fc.gamma.RIIA, for down-modulation of ADCC to at least 20% of the ADCC induced by the polypeptide comprising the wildtype human IgG Fc region, and/or for down-modulation of ADCP (U.S. Pat. No. 8,969,526 which is incorporated by reference in its entirety).

[0090] In a specific embodiment the polypeptide comprising an Fc variant of a wildtype human Fc polypeptide comprises a triple mutation: an amino acid substitution at position Pro329, a L234A and a L235A mutation according to EU numbering (P329/LALA) (U.S. Pat. No. 8,969,526 which is incorporated by reference in its entirety). In specific embodiments, the polypeptide comprises the following amino acid substitutions: P329G, L234A, and L235A according to EU numbering.

[0091] Certain antibody variants with improved or diminished binding to FcRs are described. (See, e.g., U.S. Pat. No. 6,737,056; WO 2004/056312, and Shields et al., J. Biol. Chem. 9(2): 6591-6604 (2001).)

[0092] In certain embodiments, an antibody variant comprises an Fc region with one or more amino acid substitutions which improve ADCC, e.g., substitutions at positions 298, 333, and/or 334 of the Fc region (EU numbering).

[0093] In some embodiments, alterations are made in the Fc region that result in altered (i. e., either improved or diminished) C1q binding and/or Complement Dependent Cytotoxicity (CDC), e.g., as described in U.S. Pat. No. 6,194,551, WO 99/51642, and Idusogie et al. J Immunol. 164: 4178-4184 (2000).

[0094] Antibodies with increased half lives and improved binding to the neonatal Fc receptor (FcRn), which is responsible for the transfer of maternal IgGs to the fetus (Guyer et al., J. Immunol. 117:587 (1976) and Kim et al., J. Immunol. 24:249 (1994)), are described in US2005/0014934A1 (Hinton et al.).

[0095] Those antibodies comprise an Fc region with one or more substitutions therein which improve binding of the Fc region to FcRn. Such Fc variants include those with substitutions at one or more of Fc region residues: 238, 256, 265, 272, 286, 303, 305, 307, 311, 312, 317, 340, 356, 360, 362, 376, 378, 380, 382, 413, 424 or 434, e.g., substitution of Fc region residue 434 (U.S. Pat. No. 7,371,826) according to EU numbering. See also Duncan & Winter, Nature 322:738-40 (1988); U.S. Pat. No. 5,648,260; U.S. Pat. No. 5,624,821; and WO 94/29351 concerning other examples of Fc region variants.

[0096] An “Fab' fragment” contains one light chain and a portion of one heavy chain that contains the VH domain and the CH1 domain and also the region between the CH1 and CH2 domains, such that an interchain disulfide bond can be formed between the two heavy chains of two Fab' fragments to form an F(ab')₂ molecule.

[0097] An “F(ab')₂ fragment” contains two light chains and two heavy chains containing a portion of the constant region between the CH1 and CH2 domains, such that an interchain disulfide bond is formed between the two heavy chains. A F(ab')₂ fragment thus is composed of two Fab' fragments that are held together by a disulfide bond between the two heavy chains.

[0098] The “Fv region” comprises the variable regions from both the heavy and light chains, but lacks the constant regions.

[0099] “Single chain antibodies” or “scFvs” are Fv molecules in which the heavy and light chain variable regions have been connected by a flexible linker to form a single polypeptide chain, which forms an antigen-binding region. scFvs are discussed in detail in International Patent Application Publication No. WO 88/01649 and United States Patent Nos. 4,946,778 and No. 5,260,203, the disclosures of which are incorporated by reference.

[0100] A “domain antibody” or “single chain immunoglobulin” is an immunologically functional immunoglobulin fragment containing only the variable region of a heavy chain or the variable region of a light chain. Examples of domain antibodies include Nanobodies®. In some instances, two or more VH regions are covalently joined with a peptide linker to create a bivalent domain antibody. The two VH regions of a bivalent domain antibody may target the same or different antigens.

[0101] A “bivalent antigen binding protein” or “bivalent antibody” comprises two antigen binding regions. In some instances, the two binding regions have the same antigen specificities. Bivalent antigen binding proteins and bivalent antibodies may be bispecific, see, *infra*.

[0102] A multispecific antigen binding protein” or “multispecific antibody” is one that targets more than one antigen or epitope.

[0103] A “bispecific,” “dual-specific” or “bifunctional” antigen binding protein or antibody is a hybrid antigen binding protein or antibody, respectively, having two different antigen binding sites. Bispecific antigen binding proteins and antibodies are a species of multispecific antigen binding protein or multispecific antibody and may be produced by a variety of methods including, but not limited to, fusion of hybridomas or linking of Fab' fragments. See, e.g., Songsivilai and Lachmann, 1990, Clin. Exp. Immunol. 79:315-321; Kostelny et al.,

1992, J. Immunol. 148:1547-1553. The two binding sites of a bispecific antigen binding protein or antibody will bind to two different epitopes, which may reside on the same or different protein targets.

[0104] The term “compete” when used in the context of antigen binding proteins (e.g., antibodies) means competition between antigen binding proteins is determined by an assay in which the antigen binding protein (e.g., antibody or immunologically functional fragment thereof) under test prevents or inhibits specific binding of a reference antigen binding protein to a common antigen (e.g., GIPR or a fragment thereof). Numerous types of competitive binding assays can be used, for example: solid phase direct or indirect radioimmunoassay (RIA), solid phase direct or indirect enzyme immunoassay (EIA), sandwich competition assay (see, e.g., Stahli et al., 1983, *Methods in Enzymology* 9:242-253); solid phase direct biotin-avidin EIA (see, e.g., Kirkland et al., 1986, *J. Immunol.* 137:3614-3619) solid phase direct labeled assay, solid phase direct labeled sandwich assay (see, e.g., Harlow and Lane, 1988, *Antibodies, A Laboratory Manual*, Cold Spring Harbor Press); solid phase direct label RIA using I-125 label (see, e.g., Morel et al., 1988, *Molec. Immunol.* 25:7-15); solid phase direct biotin-avidin EIA (see, e.g., Cheung, et al., 1990, *Virology* 176:546-552); and direct labeled RIA (Moldenhauer et al., 1990, *Scand. J. Immunol.* 32:77-82). Typically, such an assay involves the use of purified antigen bound to a solid surface or cells bearing either of these, an unlabeled test antigen binding protein and a labeled reference antigen binding protein. Competitive inhibition is measured by determining the amount of label bound to the solid surface or cells in the presence of the test antigen binding protein. Usually the test antigen binding protein is present in excess. Additional details regarding methods for determining competitive binding are provided in the examples herein. Usually, when a competing antigen binding protein is present in excess, it will inhibit specific binding of a reference antigen binding protein to a common antigen by at least 40%, 45%, 50%, 55%, 60%, 65%, 70% or 75%. In some instances, binding is inhibited by at least 80%, 85%, 90%, 95%, or 97% or more.

[0105] The term “antigen” refers to a molecule or a portion of a molecule capable of being bound by a selective binding agent, such as an antigen binding protein (including, e.g., an antibody), and additionally capable of being used in an animal to produce antibodies capable of binding to that antigen. An antigen may possess one or more epitopes that are capable of interacting with different antigen binding proteins, e.g., antibodies.

[0106] The term “epitope” is the portion of a molecule that is bound by an antigen binding protein (for example, an antibody). The term includes any determinant capable of specifically

binding to an antigen binding protein, such as an antibody. An epitope can be contiguous or non-contiguous (discontinuous) (e.g., in a polypeptide, amino acid residues that are not contiguous to one another in the polypeptide sequence but that within in context of the molecule are bound by the antigen binding protein). A conformational epitope is an epitope that exists within the conformation of an active protein but is not present in a denatured protein. In certain embodiments, epitopes may be mimetic in that they comprise a three dimensional structure that is similar to an epitope used to generate the antigen binding protein, yet comprise none or only some of the amino acid residues found in that epitope used to generate the antigen binding protein. Most often, epitopes reside on proteins, but in some instances may reside on other kinds of molecules, such as nucleic acids. Epitope determinants may include chemically active surface groupings of molecules such as amino acids, sugar side chains, phosphoryl or sulfonyl groups, and may have specific three dimensional structural characteristics, and/or specific charge characteristics. Generally, antigen binding proteins specific for a particular target antigen will preferentially recognize an epitope on the target antigen in a complex mixture of proteins and/or macromolecules.

[0107] As used herein, “substantially pure” means that the described species of molecule is the predominant species present, that is, on a molar basis it is more abundant than any other individual species in the same mixture. In certain embodiments, a substantially pure molecule is a composition wherein the object species comprises at least 50% (on a molar basis) of all macromolecular species present. In other embodiments, a substantially pure composition will comprise at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% of all macromolecular species present in the composition. In other embodiments, the object species is purified to essential homogeneity wherein contaminating species cannot be detected in the composition by conventional detection methods and thus the composition consists of a single detectable macromolecular species.

[0108] The term “treating” refers to any indicia of success in the treatment or amelioration of an injury, pathology or condition, including any objective or subjective parameter such as abatement; remission; diminishing of symptoms or making the injury, pathology or condition more tolerable to the patient; slowing in the rate of degeneration or decline; making the final point of degeneration less debilitating; improving a patient’s physical or mental well-being. The treatment or amelioration of symptoms can be based on objective or subjective parameters; including the results of a physical examination, neuropsychiatric exams, and/or a psychiatric evaluation. For example, certain methods presented herein successfully treat cardiovascular disease such as atherosclerosis by decreasing the incidence of cardiovascular

disease, causing remission of cardiovascular disease and/or ameliorating a symptom associated with cardiovascular disease.

[0109] An “effective amount” is generally an amount sufficient to reduce the severity and/or frequency of symptoms, eliminate the symptoms and/or underlying cause, prevent the occurrence of symptoms and/or their underlying cause, and/or improve or remediate the damage that results from or is associated with the disease state (e.g., diabetes, obesity, dyslipidemia, elevated glucose levels, elevated insulin levels or diabetic nephropathy). In some embodiments, the effective amount is a therapeutically effective amount or a prophylactically effective amount. A “therapeutically effective amount” is an amount sufficient to remedy a disease state (e.g. atherosclerosis) or symptoms, particularly a state or symptoms associated with the disease state, or otherwise prevent, hinder, retard or reverse the progression of the disease state or any other undesirable symptom associated with the disease in any way whatsoever. A “prophylactically effective amount” is an amount of a pharmaceutical composition that, when administered to a subject, will have the intended prophylactic effect, e.g., preventing or delaying the onset (or reoccurrence) of the disease state, or reducing the likelihood of the onset (or reoccurrence) of the disease state or associated symptoms. The full therapeutic or prophylactic effect does not necessarily occur by administration of one dose, and may occur only after administration of a series of doses. Thus, a therapeutically or prophylactically effective amount may be administered in one or more administrations.

[0110] The terms “therapeutically effective dose” and “therapeutically effective amount,” as used herein, means an amount of a GIPR binding protein that elicits a biological or medicinal response in a tissue system, animal, or human being sought by a researcher, physician, or other clinician, which includes alleviation or amelioration of the symptoms of the disease or disorder being treated, i.e., an amount of a GIPR binding protein that supports an observable level of one or more desired biological or medicinal response, for example lowering blood glucose, insulin, triglyceride, or cholesterol levels; reducing body weight; or improving glucose tolerance, energy expenditure, or insulin sensitivity.

[0111] The term “polynucleotide” or “nucleic acid” includes both single-stranded and double-stranded nucleotide polymers. The nucleotides comprising the polynucleotide can be ribonucleotides or deoxyribonucleotides or a modified form of either type of nucleotide. The modifications include base modifications such as bromouridine and inosine derivatives, ribose modifications such as 2',3'-dideoxyribose, and internucleotide linkage modifications

such as phosphorothioate, phosphorodithioate, phosphoroselenoate, phosphorodiselenoate, phosphoroanilothioate, phosphoraniladate and phosphoroamidate.

[0112] The term “oligonucleotide” means a polynucleotide comprising 200 or fewer nucleotides. In some embodiments, oligonucleotides are 10 to 60 bases in length. In other embodiments, oligonucleotides are 12, 13, 14, 15, 16, 17, 18, 19, or 20 to 40 nucleotides in length. Oligonucleotides may be single stranded or double stranded, e.g., for use in the construction of a mutant gene. Oligonucleotides may be sense or antisense oligonucleotides. An oligonucleotide can include a label, including a radiolabel, a fluorescent label, a hapten or an antigenic label, for detection assays. Oligonucleotides may be used, for example, as PCR primers, cloning primers or hybridization probes.

[0113] An “isolated nucleic acid molecule” means a DNA or RNA of genomic, mRNA, cDNA, or synthetic origin or some combination thereof which is not associated with all or a portion of a polynucleotide in which the isolated polynucleotide is found in nature, or is linked to a polynucleotide to which it is not linked in nature. For purposes of this disclosure, it should be understood that “a nucleic acid molecule comprising” a particular nucleotide sequence does not encompass intact chromosomes. Isolated nucleic acid molecules “comprising” specified nucleic acid sequences may include, in addition to the specified sequences, coding sequences for up to ten or even up to twenty other proteins or portions thereof, or may include operably linked regulatory sequences that control expression of the coding region of the recited nucleic acid sequences, and/or may include vector sequences.

[0114] Unless specified otherwise, the left-hand end of any single-stranded polynucleotide sequence discussed herein is the 5' end; the left-hand direction of double-stranded polynucleotide sequences is referred to as the 5' direction. The direction of 5' to 3' addition of nascent RNA transcripts is referred to as the transcription direction; sequence regions on the DNA strand having the same sequence as the RNA transcript that are 5' to the 5' end of the RNA transcript are referred to as “upstream sequences;” sequence regions on the DNA strand having the same sequence as the RNA transcript that are 3' to the 3' end of the RNA transcript are referred to as “downstream sequences.”

[0115] The term “control sequence” refers to a polynucleotide sequence that can affect the expression and processing of coding sequences to which it is ligated. The nature of such control sequences may depend upon the host organism. In particular embodiments, control sequences for prokaryotes may include a promoter, a ribosomal binding site, and a transcription termination sequence. For example, control sequences for eukaryotes may include promoters comprising one or a plurality of recognition sites for transcription factors,

transcription enhancer sequences, and transcription termination sequences. "Control sequences" can include leader sequences and/or fusion partner sequences.

[0116] The term "vector" means any molecule or entity (e.g., nucleic acid, plasmid, bacteriophage or virus) used to transfer protein coding information into a host cell.

[0117] The term "expression vector" or "expression construct" refers to a vector that is suitable for transformation of a host cell and contains nucleic acid sequences that direct and/or control (in conjunction with the host cell) expression of one or more heterologous coding regions operatively linked thereto. An expression construct may include, but is not limited to, sequences that affect or control transcription, translation, and, if introns are present, affect RNA splicing of a coding region operably linked thereto.

[0118] As used herein, "operably linked" means that the components to which the term is applied are in a relationship that allows them to carry out their inherent functions under suitable conditions. For example, a control sequence in a vector that is "operably linked" to a protein coding sequence is ligated thereto so that expression of the protein coding sequence is achieved under conditions compatible with the transcriptional activity of the control sequences.

[0119] The term "host cell" means a cell that has been transformed with a nucleic acid sequence and thereby expresses a gene of interest. The term includes the progeny of the parent cell, whether or not the progeny is identical in morphology or in genetic make-up to the original parent cell, so long as the gene of interest is present.

[0120] The terms "polypeptide" or "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms also apply to amino acid polymers in which one or more amino acid residues is an analog or mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers. The terms can also encompass amino acid polymers that have been modified, e.g., by the addition of carbohydrate residues to form glycoproteins, or phosphorylated. Polypeptides and proteins can be produced by a naturally-occurring and non-recombinant cell; or it is produced by a genetically-engineered or recombinant cell, and comprise molecules having the amino acid sequence of the native protein, or molecules having deletions from, additions to, and/or substitutions of one or more amino acids of the native sequence. The terms "polypeptide" and "protein" specifically encompass GIPR antigen binding proteins, antibodies, or sequences that have deletions from, additions to, and/or substitutions of one or more amino acids of an antigen-binding protein. The term "polypeptide fragment" refers to a polypeptide that has an amino-terminal deletion, a carboxyl-terminal deletion, and/or an internal deletion as

compared with the full-length protein. Such fragments may also contain modified amino acids as compared with the full-length protein. In certain embodiments, fragments are about five to 500 amino acids long. For example, fragments may be at least 5, 6, 8, 10, 14, 20, 50, 70, 100, 110, 150, 200, 250, 300, 350, 400, or 450 amino acids long. Useful polypeptide fragments include immunologically functional fragments of antibodies, including binding domains.

[0121] The term “isolated protein” means that a subject protein (1) is free of at least some other proteins with which it would normally be found, (2) is essentially free of other proteins from the same source, e.g., from the same species, (3) is expressed by a cell from a different species, (4) has been separated from at least about 50 percent of polynucleotides, lipids, carbohydrates, or other materials with which it is associated in nature, (5) is operably associated (by covalent or noncovalent interaction) with a polypeptide with which it is not associated in nature, or (6) does not occur in nature. Typically, an “isolated protein” constitutes at least about 5%, at least about 10%, at least about 25%, or at least about 50% of a given sample. Genomic DNA, cDNA, mRNA or other RNA, of synthetic origin, or any combination thereof may encode such an isolated protein. Preferably, the isolated protein is substantially free from proteins or polypeptides or other contaminants that are found in its natural environment that would interfere with its therapeutic, diagnostic, prophylactic, research or other use.

[0122] A “variant” of a polypeptide (e.g., an antigen binding protein such as an antibody) 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 another polypeptide sequence. Variants include fusion proteins.

[0123] A “derivative” of a polypeptide is a polypeptide (e.g., an antigen binding protein such as an antibody) that has been chemically modified in some manner distinct from insertion, deletion, or substitution variants, e.g., via conjugation to another chemical moiety.

[0124] The term “naturally occurring” as used throughout the specification in connection with biological materials such as polypeptides, nucleic acids, host cells, and the like, refers to materials which are found in nature.

[0125] A “subject” or “patient” as used herein can be any mammal. In a typical embodiment, the subject or patient is a human.

[0126] As disclosed herein, a GIPR polypeptide described by the instant disclosure can be engineered and/or produced using standard molecular biology methodology. In various examples, a nucleic acid sequence encoding a GIPR, which can comprise all or a portion of

SEQ ID NOs: 1203, 1203 or 1205, can be isolated and/or amplified from genomic DNA, or cDNA using appropriate oligonucleotide primers. Primers can be designed based on the nucleic and amino acid sequences provided herein according to standard (RT)-PCR amplification techniques. The amplified GIPR nucleic acid can then be cloned into a suitable vector and characterized by DNA sequence analysis.

[0127] Oligonucleotides for use as probes in isolating or amplifying all or a portion of the GIPR sequences provided herein can be designed and generated using standard synthetic techniques, e.g., automated DNA synthesis apparatus, or can be isolated from a longer sequence of DNA.

[0128] The 466 amino acid sequence of human GIPR is (Volz et al., FEBS Lett. 373:23-29 (1995); NCBI Reference Sequence: NP_0001555):

[0129] MTTSPILQLL LRLSLCGLLL QRAETGSKGQ TAGELYQRWE RYRRECQETL
 AAAEPPSGLA CNGSFDMYVC WDYAAPNATA RASCPWYLPW HHHVAAGFVL
 RQCGSDGQWG LWRDHTQCEN PEKNEAFLDQ RLILERLQVM YTVGYSLSLA
 TLLLALLILS LFRRLHCTRN YIHINLFTSF MLRAAAILSR DRLLPRPGPY
 LGDQALALWN QALAACRTAQ IVTQYCVGAN YTWLLVEGVY LHSLLVLVGG
 SEEGHFRYYL LLGWGAPALF VIPWVIVRYL YENTQCWERN EVKAIWWIIR
 TPILMTILIN FLIFIRILGI LLSKLRTRQM RCRDYRLRLA RSTLTIVPLL
 GVHEVVFAPV TEEQARGALR FAKLGFEIFL SSFQGFLVSV LYCFINKEVQ
 SEIRRGWHHC RLRRSLGEEQ RQLPERAFRA LPSGSGPGEV PTSRGLSSGT
 LPGPGNEASR ELESYC (SEQ ID NO: 1201)

[0130] and is encoded by the DNA sequence (NCBI Reference Sequence: NM_000164):

[0131] ggcagcggtg gcaggggctg caggagcaag tgaccaggag caggactggg
 gacaggcctg atcgccctg cacgaaccag acccttcgcc gccctcacga
 tgactacctc tccgatcctg cagctgctgc tgcggctctc actgtgcggg
 ctgctgctcc agagggcgga gacaggctct aaggggcaga cggcggggga
 gctgtaccag cgctgggaac ggtaccgcag ggagtgccag gagaccttgg
 cagccgcgga accgccttca ggcttcgcct gtaacgggtc cttegatatg
 tacgtctgct gggactatgc tgcacccaat gccactgcc gtgcgtcctg
 cccctggtac ctgccctggc accaccatgt ggctgcaggt ttcgtcctcc
 gccagtgtgg cagtgatggc caatggggac tttggagaga ccatacacia
 tgtgagaacc cagagaagaa tgaggccttt ctggaccaa ggctcatctt
 ggagcggttg caggatcatgt acactgtcgg ctactccctg tctctcgcca
 cactgctgct agccctgctc atcttgagtt tgttcaggcg gctacattgc

actagaaact atatccacat caacctgttc acgtctttca tgctgcgagc
 tgcggccatt ctgagccgag accgtctgct acctegacct ggcccctacc
 ttggggacca ggcccttgcg ctgtggaacc aggccctcgc tgccctgccgc
 acggcccaga tcgtgacca gtactgctg ggtgccaaact acacgtggct
 gctggtggag ggcgtctacc tgcacagtct cctggtgctc gtgggaggct
 ccgaggaggg ccacttcgc tactacctgc tcctcggctg gggggccccc
 gcgcttttcg tcattccctg ggtgatcgtc aggtacctgt acgagaacac
 gcagtgctgg gagcgcaacg aagtcaaggc ctttgggtgg attatacggg
 ccccatcct catgaccatc ttgattaatt tcctcatttt tatccgcatt
 cttggcattc tcctgtccaa gctgaggaca cggcaaatgc gctgccggga
 ttaccggctg aggtgggtc gctccacgct gacgctggtg cccctgctgg
 gtgtccacga ggtggtgttt gctcccgta cagaggaaca ggccgggggc
 gccctgcgct tcgccaagct cggctttgag atcttctca gctccttcca
 gggcttcctg gtcagcgtcc tctactgctt catcaacaag gaggtgcagt
 cggagatccg ccgtggctgg caccactgcc gcctgcgccg cagcctgggc
 gaggagcaac gccagctccc ggagcgcgcc ttccggggcc tgccctccgg
 ctccggcccc ggcgaggctc ccaccagccg cggcttgctc tcggggaccc
 tcccagggcc tgggaatgag gccagccggg agttggaaag ttactgctag
 ggggccccgat ccccggtgtc gttagcttag catggattta ttgagtcca
 actgctgcc agggccagta cggaggacgc tggggaaatg gtgaaggaaa
 cagaaaaaag gtccctgcc ttctggagat gacaactgag tggggaaaac
 agaccgtgaa cacaaaacat caagttccac acacgctatg gaatggttat
 gaaggggaagc gagaaggggg ctaggggtgg tctgggaggc gtctccaagg
 aggtgacact taagccatcc ccgaaagagg tgaaagagat cactttgggg
 agagctggag aacaggattc taggcggaag cgatagcata ggcaaaggcc
 cttgggcagg aaggcgtca gccttggtg gagtagaatt aagtcagagc
 caacagggtg ggagagacag agaagtgggc aggggcaccc aagttgggat
 ttcatctcag gtgcattgga gattcttagg agtgtctctt gggggttaata
 ttttattttt taaaaaatga ggat (SEQ ID NO: 1202).

[0132] A 430 amino acid isoform of human GIPR (isoform X1), predicted by automated computational analysis, has the sequence (NCBI Reference Sequence XP_005258790):

[0133] MTTSPILQLL LRLSLCGLLL QRAETGSKGQ TAGELYQRWE RYRRECQETL
 AAAEPPSVAA GFVLRQCGSD GQWGLWRDHT QCENPEKNEA FLDQRLILER
 LQVMYTVGYL LSLATLLLL LILSLFRRLH CTRNYIHINL FTSFMLRAAA

ILSRDRLLPR PGPYLGDQAL ALWNQALAAC RTAQIVTQYC VGANYTWLLV
 EGVYLHSLLV LVGGSEEGHF RYLLLLGWGA PALFVIPWVI VRYLYENTQC
 WERNEVKAIW WIIRTPILMT ILINFLIFIR ILGILLSKLR TRQMRCDYR
 LRLARSTLTL VPLLGVHEVV FAPVTEEQAR GALRFAKLGF EIFLSSFQGF
 LVSVLYCFIN KEVQSEIRRG WHHCRLRRSL GEEQRQLPER AFRALPSGSG
 PGEVPTSRGL SSGTLPGPGN EASRELESYC (SEQ ID NO: 1203)

[0134] and is encoded by the DNA sequence:

[0135] atgaccacca gcccgattct gcagctgctg ctgcgcctga gcctgtgcgg
 cctgctgctg cagcgcgcgg aaaccggcag caaaggccag accgcgggcg
 aactgtatca gcgctgggaa cgctatcgcc gcgaatgcca ggaaacctg
 gcggcggcgg aaccgccgag cgtggcggcg ggctttgtgc tgcgccagt
 cggcagcgat ggccagtggg gcctgtggcg cgatcatacc cagtgcgaaa
 acccgaaaa aaacgaagcg tttctggatc agcgcctgat tctggaacgc
 ctgcaggtga tgtataccgt gggctatagc ctgagcctgg cgacctgct
 gctggcgcctg ctgattctga gcctgtttcg ccgcctgcat tgcacctgca
 actatatcca tattaacctg tttaccagct ttatgctgcg cgcggcggcg
 attctgagcc gcgatcgct gctgccgcgc ccgggcccgt atctgggcga
 tcaggcgcctg gcgctgtgga accaggcgct ggcggcgtgc cgcaccgcgc
 agattgtgac ccagtattgc gtgggcgcga actataacctg gctgctggtg
 gaaggcgtgt atctgcatag cctgctggtg ctggtgggcg gcagcgaaga
 aggccatttt cgctattatc tgctgctggg ctggggcgcg ccggcgctgt
 ttgtgattcc gtgggtgatt gtgcgctatc tgtatgaaaa caccagtg
 tgggaacgca acgaagtga agcgatttgg tggattattc gcaccccgat
 tctgatgacc attctgatta actttctgat ttttattcgc attctgggca
 ttctgctgag caaactgcgc acccgccaga tgcgctgccg cgattatcgc
 ctgcgcctgg cgcgcagcac cctgacctg gtgccgctgc tgggcgtgca
 tgaagtgggtg tttgcgccgg tgaccgaaga acaggcgcgc ggcgcgctgc
 gctttgcgaa actgggcttt gaaatttttc tgagcagctt tcagggcttt
 ctggtgagcg tgctgtattg ctttattaac aaagaagtgc agagcgaaat
 tcgccgcggc tggcatcatt gccgcctgcg ccgcagcctg ggcgagaac
 agcgcagct gccggaacgc gcgtttcgcg cgctgccgag cggcagcggc
 ccgggcgaag tgccgaccag ccgcggcctg agcagcggca ccctgccggg
 cccgggcaac gaagcgagcc gcgaactgga aagctattgc (SEQ ID NO: 1204).

[0136] A 493 amino acid isoform of human GIPR, produced by alternative splicing, has the sequence (Gremlich et al., Diabetes 44:1202-8 (1995); UniProtKB Sequence Identifier: P48546-2):

[0137] MTTSPILQLL LRLSLCGLLL QRAETGSKGQ TAGELYQRWE RYRRECQETL
 AAAEPPSGLA CNGSFDMYVC WDYAAPNATA RASCPWYLPW HHHVAAGFVL
 RQCGSDGQWG LWRDHTQCEN PEKNEAFLDQ RLILERLQVM YTVGYSLSLA
 TLLLALLILS LFRRLHCTR N YIHINLFTSF MLRAAAILSR DRLLPRPGPY
 LGDQALALWN QALAACRTAQ IVTQYCVGAN YTWLLVEGVY LHSLLVLVGG
 SEEGHFRYYL LLGWGAPALF VIPWVIVRYL YENTQCWERN EVKAIWWIIR
 TPILMTILIN FLIFIRILGI LLSKLRTRQM RCRDYRLRLA RSTLTIVPLL
 GVHEVVFAPV TEEQARGALR FAKLGFEIFL SSFQGFVSV LYCFINKEVG
 RDPAAAPALW RRRGTAPPLS AIVSQVQSEI RRGWHHCRLR RSLGEEQRQL
 PERAFRALPS GSGPGEVPTS RGLSSGTLPG PGNEASRELE SYC (SEQ ID NO: 1205)

[0138] and is encoded by the DNA sequence:

[0139] atgaccacca gcccgattct gcagctgctg ctgcgccctga gcctgtgctg
 cctgctgctg cagcgcgctg aaaccggcag caaaggccag accgctggcg
 aactgtatca gcgctgggaa cgctatcgcc gcgaatgcca ggaaacctg
 gcggcgctg aaccgcccag cggcctggcg tgcaacggca gctttgatat
 gtatgtgtgc tgggattatg cggcgccgaa cgcgaccgag cgcgagct
 gcccgctgga tctgccgtgg catcatcatg tggcgccggg ctttgtgctg
 cgccagtgcg gcagcgatgg ccagtggggc ctgtggcgcg atcataccca
 gtgcgaaaac ccggaaaaaa acgaagcgtt tctggatcag cgctgattc
 tggaacgcct gcaggtgatg tataccgtgg gctatagcct gagcctggcg
 acctgctgc tggcgctgct gattctgagc ctgtttcgcc gcctgcattg
 caccgcaac tatattcata ttaacctgtt taccagcttt atgctgctg
 cggcgccgat tctgagccgc gatcgctgc tggcgccccc gggcccgat
 ctggcgatc aggcgctggc gctgtggaac caggcgctgg cggcgctgccc
 caccgctgag attgtgacct agtattgcgt gggcgccgaa tatacctggc
 tgctggtgga aggcgtgtat ctgcatagcc tgctggtgct ggtggcgccg
 agcgaagaag gccattttcg ctattatctg ctgctgggct gggcgccg
 ggcgctgttt gtgattccgt ggggtgattgt gcgctatctg tatgaaaaca
 ccagtgctg ggaacgcaac gaagtgaag cgatttggtg gattattcgc
 acccgcattc tgatgacct tctgattaac tttctgattt ttattcgc
 tctgggcatt ctgctgagca aactgcgcac ccgcccagatg cgctgcccgc

attatcgctt ggcctggcg cgcagcacc tgaccctggt gccgctgctg
 ggcgtgcatg aagtgggtgtt tgcgccggtg accgaagaac aggcgcgcgg
 cgcgctgcgc tttgcgaaac tgggctttga aatttttctg agcagctttc
 agggctttct ggtgagcgtg ctgtattgct ttattaacaa agaagtgggc
 cgcgatccgg cggcgggcgcc ggcgctgtgg cgcgcgcgcg gcaccgcgcc
 gccgctgagc gcgattgtga gccaggtgca gagcgaaatt cgcgcgggct
 ggcattcattg ccgcctgcgc cgcagcctgg gcgaagaaca gcgccagctg
 ccggaacgcg cgtttcgcgc gctgccgagc ggcagcggcc cgggcgaagt
 gccgaccagc cgcggcctga gcagcggcac cctgccgggc cggggcaacg
 aagcgagccg cgaactggaa agctattgct aa (SEQ ID NO: 1206)

[0140] The 460 amino acid sequence of murine GIPR is (NCBI Reference Sequence: NP_001074284; uniprotKB/Swiss-Prot Q0P543-1); see Vassilatis et al., PNAS USA 2003, 100:4903-4908.

[0141] MPLRLLLLLL WLWGLQWAET DSEGQTTTGE LYQRWEHYGQ ECQKMLETTE
 PPSGLACNGS FDMYACWNYT AANTTARVSC PWYLPWFRQV SAGFVFRQCG
 SDGQWGSWRD HTQCENPEKN GAFQDQTLIL ERLQIMYTVG YSLSLTTLIL
 ALLILSLFRR LHCTRNYYHM NLFTSFMLRA AAILTRDQLL PPLGPYTGDO
 APTPWNQALA ACRTAQIMTQ YCVGANYTWL LVEGVYLHHL LVIVGRSEKG
 HFRCYLLLGW GAPALFVIPW VIVRYLRENT QCWERNEVKA IWWIIRTPIL
 ITILINFLIF IRILGILVSK LRTRQMRCPD YRLRLARSTL TLVPLLGVHE
 VVFAPVTEEQ VEGSLRFAKL AFEIFLSSFQ GFLVSVLYCFINKEVQSEIRQ
 GWRHRRLRLS LQEQRP RP HQ ELAPRAVPLS SACREAAVGN ALPSGMLHVP
 GDEVLESYC (SEQ ID NO: 1207)

[0142] and is encoded by the DNA sequence (NCBI Reference Sequence: NM_001080815):

[0143] atgccgctgc gcctgctgct gctgctgctg tggctgtggg gcctgcagtg
 ggcggaaacc gatagcgaag gccagaccac caccggcgaa ctgtatcagc
 gctgggaaca ttatggccag gaatgccaga aaatgctgga aaccaccgaa
 ccgccgagcg gcctggcgtg caacggcagc tttgatatgt atgcgtgctg
 gaactatacc gcggcgaaca ccaccgcgcg cgtgagctgc ccgtggatc
 tgccgtggtt tcgccaggtg agcgcgggct ttgtgtttcg ccagtgcggc
 agcgatggcc agtggggcag ctggcgcgat cataccagc gcgaaaaccc
 ggaaaaaac ggcgcgtttc aggatcagac cctgattctg gaacgcctgc
 agattatgta taccgtgggc tatagcctga gcctgaccac cctgctgctg
 gcgctgctga ttctgagcct gtttcgccgc ctgcattgca cccgcaacta

tattcatatg aacctgttta ccagctttat gctgcgcgcg gcggcgattc
 tgaccgcga tcagctgctg ccgccgctgg gcccgtatac eggcgatcag
 gcgccgaccc cgtggaacca ggccgctggcg gcgtgccgca ccgcgcagat
 tatgaccag tattgcgtgg gcgcgaacta tacctggctg ctggtggaag
 gcgtgtatct gcatcatctg ctggtgattg tgggccgcag cgaaaaaggc
 cattttcgct gctatctgct gctgggctgg ggccgcgcgg cgctgtttgt
 gattccgtgg gtgattgtgc gctatctgcg cgaaaacacc cagtgtctggg
 aacgcaacga agtgaaagcg atttgggtga ttattcgac cccgattctg
 attaccattc tgattaactt tctgattttt attcgattc tgggcattct
 ggtgagcaaa ctgcgcaccc gccagatgcg ctgcccggat tatcgccctgc
 gcctggcgcg cagcacctg accctgggtgc cgctgctggg cgtgcatgaa
 gtggtgtttg cgccggtgac cgaagaacag gtggaaggca gcctgcgctt
 tgcgaaactg gcgtttgaaa tttttctgag cagctttcag ggctttctgg
 tgagcgtgct gtattgcttt attaacaaag aagtgcagag cgaaattcgc
 cagggctggc gccatcgccg cctgcgccctg agcctgcagg aacagcgccc
 gcgccgcgat caggaactgg cgccgcgcgc ggtgccgctg agcagcgctg
 gccgcgaagc ggccggtgggc aacgcgctgc cgagcggcat gctgcatgtg
 ccgggcgatg aagtgtctga aagctattgc taa (SEQ ID NO: 1208)

[0144] A 230 amino acid isoform of murine GIPR, produced by alternative splicing, has the sequence (Gerhard et al., Genome Res, 14:2121-2127 (2004); NCBI Reference Sequence: AAI20674):

[0145] MPLRLLLLLL WLWGLQWAET DSEGQTTTGE LYQRWEHYGQ ECQKMLETTE
 PPSGLACNGS FDMYACWNYT AANTTARVSC PWYLPWFRQV SAGFVFRQCG
 SDGQWGSWRD HTQCENPEKN GAFQDQTLIL ERLQIMYTVG YSLSLTTLIL
 ALLILSLFRR LHCTRNYIHM NLFTSFMLRA AAILTRDQLL PPLGPYTGDO
 APTPNQVLH RLLPGGTKTF PIYFRTFPHH (SEQ ID NO: 1209)

[0146] and is encoded by the DNA sequence:

[0147] atgccgctgc gcctgctgct gctgctgctg tggctgtggg gcctgcagtg
 ggccgaaacc gatagcgaag gccagaccac caccggcgaa ctgtatcagc
 gctgggaaca ttatggccag gaatgccaga aaatgctgga aaccaccgaa
 ccgccgagcg gcctggcgtg caacggcagc tttgatatgt atgcgtgctg
 gaactatacc gcggcgaaca ccaccgcgcg cgtgagctgc ccgtgggtatc
 tgccgtgggtt tcgccagggtg agcgcgggct ttgtgtttcg ccagtgcggc
 agcgatggcc agtggggcag ctggcgcat cataccagc gcgaaaaccc

ggaaaaaac ggcgcgtttc aggatcagac cctgattctg gaacgcctgc
 agattatgta taccgtgggc tatagcctga gcctgaccac cctgctgctg
 gcgctgctga ttctgagcct gtttcgccgc ctgcattgca cccgcaacta
 tattcatatg aacctgttta ccagctttat gctgcgcgcg gcggcgattc
 tgaccgcgca tcagctgctg ccgccgctgg gcccgtatac cggcgatcag
 gcgcccagacc cgtggaacca ggtgctgcat cgcctgctgc cgggcggcac
 caaaaccttt ccgatttatt ttcgcacctt tccgcatcat taa (SEQ ID NO: 1210).

[0148] As stated herein, the term “GIPR polypeptide” encompasses naturally occurring GIPR polypeptide sequences, e.g., human amino acid sequences SEQ ID NOs: 1201, 1203 or 1205. The term “GIPR polypeptide,” however, also encompasses polypeptides comprising an amino acid sequence that differs from the amino acid sequence of a naturally occurring GIPR polypeptide sequence, e.g., SEQ ID NOs: 1201, 1203 or 1205, by one or more amino acids, such that the sequence is at least 85% identical to SEQ ID NOs: 1201, 1203 or 1205. GIPR polypeptides can be generated by introducing one or more amino acid substitutions, either conservative or non-conservative and using naturally or non-naturally occurring amino acids, at particular positions of the GIPR polypeptide.

[0149] A “conservative amino acid substitution” can involve a substitution of a native amino acid residue (i.e., a residue found in a given position of the wild-type GIPR polypeptide sequence) with a nonnative residue (i.e., a residue that is not found in a given position of the wild-type GIPR polypeptide sequence) such that there is little or no effect on the polarity or charge of the amino acid residue at that position. Conservative amino acid substitutions also encompass non-naturally occurring amino acid residues that are typically incorporated by chemical peptide synthesis rather than by synthesis in biological systems. These include peptidomimetics, and other reversed or inverted forms of amino acid moieties.

[0150] Naturally occurring residues can be divided into classes based on common side chain properties:

[0151] (1) hydrophobic: norleucine, Met, Ala, Val, Leu, Ile;

[0152] (2) neutral hydrophilic: Cys, Ser, Thr;

[0153] (3) acidic: Asp, Glu;

[0154] (4) basic: Asn, Gln, His, Lys, Arg;

[0155] (5) residues that influence chain orientation: Gly, Pro; and

[0156] (6) aromatic: Trp, Tyr, Phe.

[0157] Additional groups of amino acids can also be formulated using the principles described in, e.g., Creighton (1984) PROTEINS: STRUCTURE AND MOLECULAR

PROPERTIES (2d Ed. 1993), W.H. Freeman and Company. In some instances it can be useful to further characterize substitutions based on two or more of such features (e.g., substitution with a “small polar” residue, such as a Thr residue, can represent a highly conservative substitution in an appropriate context).

[0158] Conservative substitutions can involve the exchange of a member of one of these classes for another member of the same class. Non-conservative substitutions can involve the exchange of a member of one of these classes for a member from another class.

[0159] Synthetic, rare, or modified amino acid residues having known similar physiochemical properties to those of an above-described grouping can be used as a “conservative” substitute for a particular amino acid residue in a sequence. For example, a D-Arg residue may serve as a substitute for a typical L-Arg residue. It also can be the case that a particular substitution can be described in terms of two or more of the above described classes (e.g., a substitution with a small and hydrophobic residue means substituting one amino acid with a residue(s) that is found in both of the above-described classes or other synthetic, rare, or modified residues that are known in the art to have similar physiochemical properties to such residues meeting both definitions).

[0160] Nucleic acid sequences encoding a GIPR polypeptide provided herein, including those degenerate to SEQ ID NOs: 1201, 1203 or 1205, and those encoding polypeptide variants of SEQ ID NOs: 1201, 1203 or 1205 form other aspects of the instant disclosure.

[0161] In order to express the GIPR nucleic acid sequences provided herein, the appropriate coding sequences, e.g., SEQ ID NOs: 1201, 1203 or 1205, can be cloned into a suitable vector and after introduction in a suitable host, the sequence can be expressed to produce the encoded polypeptide according to standard cloning and expression techniques, which are known in the art (e.g., as described in Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual* 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989). The invention also relates to such vectors comprising a nucleic acid sequence according to the invention.

[0162] A “vector” refers to a delivery vehicle that (a) promotes the expression of a polypeptide-encoding nucleic acid sequence; (b) promotes the production of the polypeptide therefrom; (c) promotes the transfection/transformation of target cells therewith; (d) promotes the replication of the nucleic acid sequence; (e) promotes stability of the nucleic acid; (f) promotes detection of the nucleic acid and/or transformed/transfected cells; and/or (g) otherwise imparts advantageous biological and/or physiochemical function to the polypeptide-encoding nucleic acid. A vector can be any suitable vector, including

chromosomal, non-chromosomal, and synthetic nucleic acid vectors (a nucleic acid sequence comprising a suitable set of expression control elements). Examples of such vectors include derivatives of SV40, bacterial plasmids, phage DNA, baculovirus, yeast plasmids, vectors derived from combinations of plasmids and phage DNA, and viral nucleic acid (RNA or DNA) vectors.

[0163] A recombinant expression vector can be designed for expression of a GIPR protein in prokaryotic (e.g., *E. coli*) or eukaryotic cells (e.g., insect cells, using baculovirus expression vectors, yeast cells, or mammalian cells). In one embodiment the host cell is a mammalian, non-human host cell. Representative host cells include those hosts typically used for cloning and expression, including *Escherichia coli* strains TOP10F', TOP10, DH10B, DH5a, HB101, W3110, BL21(DE3) and BL21 (DE3)pLysS, BLUESCRIPT (Stratagene), mammalian cell lines CHO, CHO-K1, HEK293, 293-EBNA pIN vectors (Van Heeke & Schuster, *J. Biol. Chem.* 264: 5503-5509 (1989); pET vectors (Novagen, Madison Wis.). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase and an *in vitro* translation system. Preferably, the vector contains a promoter upstream of the cloning site containing the nucleic acid sequence encoding the polypeptide. Examples of promoters, which can be switched on and off, include the lac promoter, the T7 promoter, the trc promoter, the tac promoter and the trp promoter.

[0164] Thus, provided herein are vectors comprising a nucleic acid sequence encoding GIPR that facilitate the expression of recombinant GIPR. In various embodiments, the vectors comprise an operably linked nucleotide sequence which regulates the expression of GIPR. A vector can comprise or be associated with any suitable promoter, enhancer, and other expression-facilitating elements. Examples of such elements include strong expression promoters (e.g., a human CMV IE promoter/enhancer, an RSV promoter, SV40 promoter, SL3-3 promoter, MMTV promoter, or HIV LTR promoter, EF1alpha promoter, CAG promoter), effective poly (A) termination sequences, an origin of replication for plasmid product in *E. coli*, an antibiotic resistance gene as a selectable marker, and/or a convenient cloning site (e.g., a polylinker). Vectors also can comprise an inducible promoter as opposed to a constitutive promoter such as CMV IE. In one aspect, a nucleic acid comprising a sequence encoding a GIPR polypeptide which is operatively linked to a tissue specific promoter which promotes expression of the sequence in a metabolically-relevant tissue, such as liver or pancreatic tissue is provided.

[0165] In another aspect of the instant disclosure, host cells comprising the GIPR nucleic acids and vectors disclosed herein are provided. In various embodiments, the vector or nucleic acid is integrated into the host cell genome, which in other embodiments the vector or nucleic acid is extra-chromosomal.

[0166] Recombinant cells, such as yeast, bacterial (e.g., *E. coli*), and mammalian cells (e.g., immortalized mammalian cells) comprising such a nucleic acid, vector, or combinations of either or both thereof are provided. In various embodiments cells comprising a non-integrated nucleic acid, such as a plasmid, cosmid, phagemid, or linear expression element, which comprises a sequence coding for expression of a GIPR polypeptide, are provided.

[0167] A vector comprising a nucleic acid sequence encoding a GIPR polypeptide provided herein can be introduced into a host cell by transformation or by transfection. Methods of transforming a cell with an expression vector are well known.

[0168] A GIPR-encoding nucleic acid can be positioned in and/or delivered to a host cell or host animal via a viral vector. Any suitable viral vector can be used in this capacity. A viral vector can comprise any number of viral polynucleotides, alone or in combination with one or more viral proteins, which facilitate delivery, replication, and/or expression of the nucleic acid of the invention in a desired host cell. The viral vector can be a polynucleotide comprising all or part of a viral genome, a viral protein/nucleic acid conjugate, a virus-like particle (VLP), or an intact virus particle comprising viral nucleic acids and a GIPR polypeptide-encoding nucleic acid. A viral particle viral vector can comprise a wild-type viral particle or a modified viral particle. The viral vector can be a vector which requires the presence of another vector or wild-type virus for replication and/or expression (e.g., a viral vector can be a helper-dependent virus), such as an adenoviral vector amplicon. Typically, such viral vectors consist of a wild-type viral particle, or a viral particle modified in its protein and/or nucleic acid content to increase transgene capacity or aid in transfection and/or expression of the nucleic acid (examples of such vectors include the herpes virus/AAV amplicons). Typically, a viral vector is similar to and/or derived from a virus that normally infects humans. Suitable viral vector particles in this respect, include, for example, adenoviral vector particles (including any virus of or derived from a virus of the adenoviridae), adeno-associated viral vector particles (AAV vector particles) or other parvoviruses and parvoviral vector particles, papillomaviral vector particles, flaviviral vectors, alphaviral vectors, herpes viral vectors, pox virus vectors, retroviral vectors, including lentiviral vectors.

[0169] A GIPR polypeptide expressed as described herein can be isolated using standard protein purification methods. A GIPR polypeptide can be isolated from a cell in which it

naturally expressed or it can be isolated from a cell that has been engineered to express GIPR, for example a cell that does not naturally express GIPR.

[0170] Protein purification methods that can be employed to isolate a GIPR polypeptide, as well as associated materials and reagents, are known in the art. Additional purification methods that may be useful for isolating a GIPR polypeptide can be found in references such as Bootcov MR, 1997, Proc. Natl. Acad. Sci. USA 94:11514-9, Fairlie WD, 2000, Gene 254: 67-76.

[0171] Antagonist antigen binding proteins that bind GIPR, including human GIPR (hGIPR) are provided herein. In one embodiment, the human GIPR has the sequence as such as set forth in SEQ ID NO: 1201. In another embodiment, the human GIPR has the sequence as such set forth in SEQ ID NO: 1203. In another embodiment, the human GIPR has the sequence as such set forth in SEQ ID NO: 1205.

[0172] The antigen binding proteins provided are polypeptides into which one or more complementary determining regions (CDRs), as described herein, are embedded and/or joined. In some antigen binding proteins, the CDRs are embedded into a "framework" region, which orients the CDR(s) such that the proper antigen binding properties of the CDR(s) are achieved. Certain antigen binding proteins described herein are antibodies or are derived from antibodies. In other antigen binding proteins, the CDR sequences are embedded in a different type of protein scaffold. The various structures are further described below.

[0173] The antigen binding proteins that are disclosed herein have a variety of utilities. The antigen binding proteins, for instance, are useful in specific binding assays, affinity purification of GIPR, and in screening assays to identify other antagonists of GIPR activity. Other uses for the antigen binding proteins include, for example, diagnosis of GIPR-associated diseases or conditions and screening assays to determine the presence or absence of GIPR. Given that the antigen binding proteins that are provided are antagonists, the GIPR antigen binding proteins have value in therapeutic methods in which it is useful to reduce weight gain, even while maintaining or increasing food intake, increasing % fat mass and increasing % lean mass, improving glucose tolerance, decreasing insulin levels, decreasing cholesterol and triglyceride levels. Accordingly, the antigen binding proteins have utility in the treatment and prevention of diabetes, e.g., type 2 diabetes, obesity, dyslipidemia, elevated glucose levels or elevated insulin levels.

[0174] A variety of selective binding agents useful for modulating the activity of GIPR are provided. These agents include, for instance, antigen binding proteins that contain an antigen binding domain (e.g., scFvs, domain antibodies, and polypeptides with an antigen binding

region) and specifically bind to a GIPR polypeptide, in particular human GIPR. Some of the agents, for example, are useful in enhancing the activity of GIPR, and can activate one or more activities associated with GIPR.

[0175] In general the antigen binding proteins that are provided typically comprise one or more CDRs as described herein (e.g., 1, 2, 3, 4, 5 or 6). In some instances, the antigen binding protein comprises (a) a polypeptide structure and (b) one or more CDRs that are inserted into and/or joined to the polypeptide structure. The polypeptide structure can take a variety of different forms. For example, it can be, or comprise, the framework of a naturally occurring antibody, or fragment or variant thereof, or may be completely synthetic in nature. Examples of various polypeptide structures are further described below.

[0176] In certain embodiments, the polypeptide structure of the antigen binding proteins is an antibody or is derived from an antibody. Accordingly, examples of certain antigen binding proteins that are provided include, but are not limited to, monoclonal antibodies, bispecific antibodies, minibodies, domain antibodies such as Nanobodies®, synthetic antibodies (sometimes referred to herein as "antibody mimetics"), chimeric antibodies, humanized antibodies, human antibodies, antibody fusions, and portions or fragments of each, respectively. In some instances, the antigen binding protein is an immunological fragment of a complete antibody (e.g., a Fab, a Fab', a F(ab')₂). In other instances the antigen binding protein is a scFv that uses CDRs from an antibody of the present invention.

[0177] The antigen binding proteins as provided herein specifically bind to a human GIPR. In a specific embodiment, the antigen binding protein specifically binds to human GIPR comprising or consisting of the amino acid sequence of SEQ ID NO: 1201. In a specific embodiment, the antigen binding protein specifically binds to human GIPR comprising or consisting of the amino acid sequence of SEQ ID NO: 1203. In a specific embodiment, the antigen binding protein specifically binds to human GIPR comprising or consisting of the amino acid sequence of SEQ ID NO: 1205.

[0178] The antigen binding proteins that are provided are antagonists and typically have one, two, three, four, five, six, seven or all eight of the following characteristics:

[0179] (a) ability to prevent or reduce binding of GIP to GIPR, where the levels can be measured, for example, by the methods such as radioactive- or fluorescence-labeled ligand binding study, or by the methods described herein (e.g. cAMP assay or other functional assays). The decrease can be at least 10, 25, 50, 100% or more relative to the pre-treatment levels of SEQ ID NO: 1201, 1203 or 1205 under comparable conditions.

[0180] (b) ability to decrease blood glucose;

- [0181] (c) ability to increase glucose tolerance;
- [0182] (d) ability to increase insulin sensitivity;
- [0183] (e) ability to decrease body weight or reduce body weight gain;
- [0184] (f) ability to decrease fat mass or decrease inflammation in fat tissue;
- [0185] (g) ability to decrease fasting insulin levels;
- [0186] (h) ability to decrease circulating cholesterol levels;
- [0187] (i) ability to decrease circulating triglyceride levels;
- [0188] (j) ability to decrease liver steatosis or reduce triglyceride level in liver;
- [0189] (k) ability to decrease AST, ALT, and/or ALP levels.
- [0190] In one embodiment, a GIPR antigen binding protein has one or more of the following activities:

[0191] (a) binds human GIPR such that KD is ≤ 200 nM, is ≤ 150 nM, is ≤ 100 nM, is ≤ 50 nM, is ≤ 10 nM, is ≤ 5 nM, is ≤ 2 nM, or is ≤ 1 nM, e.g., as measured via a surface plasma resonance or kinetic exclusion assay technique.

[0192] (b) has a half-life in human serum of at least 3 days;

[0193] Some antigen binding proteins that are provided have an on-rate (k_a) for GIPR of at least $10^4/M \times \text{seconds}$, at least $10^5/M \times \text{seconds}$, or at least $10^6/M \times \text{seconds}$ as measured, for instance, as described below. Certain antigen binding proteins that are provided have a slow dissociation rate or off-rate. Some antigen binding proteins, for instance, have a k_d (off-rate) of $1 \times 10^{-2} s^{-1}$, or $1 \times 10^{-3} s^{-1}$, or $1 \times 10^{-4} s^{-1}$, or $1 \times 10^{-5} s^{-1}$. In certain embodiments, the antigen binding protein has a KD (equilibrium binding affinity) of less than 25 pM, 50 pM, 100 pM, 500 pM, 1 nM, 5 nM, 10 nM, 25 nM or 50 nM.

[0194] Depending on the assay, the binding of an antigen binding protein to its target can also be measured as an EC_{50} (the concentration of antigen binding protein that gives a half-maximal response when bound to target). An EC_{50} for an anti-GIPR antigen binding protein of the present invention can be determined by incubating different concentrations of antigen binding protein with cells expressing GIPR. Anti-GIPR antigen binding proteins of the present invention can have EC_{50} s less 200 nM, 150 nM, 125 nM, 100 nM, 90 nM, 80 nM, 70 nM, 60 nM, 50 nM, 40 nM, or 30 nM.

[0195] An IC_{50} (the half maximal inhibitory concentration: a measure of the effectiveness of an antigen binding protein in inhibiting a specific biological or biochemical function) can also be used to measure the activity of anti-GIPR antigen binding protein. An IC_{50} can be measured using a functional assay. For example, such an assay can be used for the quantitative determination of cAMP in HEK 293T cells expressing the human GIPR or

cynomolgus monkey GIPR. GIP binding causes GIPR conformation change, stimulating the G protein to active adenylate cyclase resulting in cAMP production from ATP. Antibody binding to GIPR prevents GIP binding to GIPR with the result being less cAMP. This is measurable by a cAMP assay. Anti-GIPR antigen binding proteins of the present invention can have IC₅₀s less 200 nM, 150nM, 125 nM, 100 nM, 90 nM, 80 nM, 70 nM, 60 nM, 50 nM, 40 nM, 30 nM, 29 nM, 28 nM, 27 nM, 26 nM, 25 nM, 24 nM, 23 nM, 22 nM, 21 mM, 20 nM, 19 nM, 18 nM, 17 nM, 16 nM, 15 nM, 14 nM, 13 nM, 12 nM, 11 mM, 10 nM, 9 nM, 8 nM, 7 nM, 6 nM, 5 nM, 4 nM, 3 nM, 2 nM, or 1 nM.

[0196] In another aspect, an antigen-binding protein is provided having a half-life of at least one day in vitro or in vivo (e.g., when administered to a human subject). In one embodiment, the antigen binding protein has a half-life of at least three days. In various other embodiments, the antigen binding protein has a half-life of 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 40, 50, or 60 days or longer. In another embodiment, the antigen binding protein is derivatized or modified such that it has a longer half-life as compared to the underivatized or unmodified antibody. In another embodiment, the antigen binding protein contains point mutations to increase serum half-life. Further details regarding such mutant and derivatized forms are provided below.

[0197] Some of the antigen binding proteins that are provided have the structure typically associated with naturally occurring antibodies. The structural units of these antibodies typically comprise one or more tetramers, each composed of two identical couplets of polypeptide chains, though some species of mammals also produce antibodies having only a single heavy chain. In a typical antibody, each pair or couplet includes one full-length "light" chain (in certain embodiments, about 25 kDa) and one full-length "heavy" chain (in certain embodiments, about 50-70 kDa). Each individual immunoglobulin chain is composed of several "immunoglobulin domains", each consisting of roughly 90 to 110 amino acids and expressing a characteristic folding pattern. These domains are the basic units of which antibody polypeptides are composed. The amino-terminal portion of each chain typically includes a variable domain that is responsible for antigen recognition. The carboxy-terminal portion is more conserved evolutionarily than the other end of the chain and is referred to as the "constant region" or "C region". Human light chains generally are classified as kappa and lambda light chains, and each of these contains one variable domain and one constant domain. Heavy chains are typically classified as mu, delta, gamma, alpha, or epsilon chains, and these define the antibody's isotype as IgM, IgD, IgG, IgA, and IgE, respectively. IgG has several subtypes, including, but not limited to, IgG1, IgG2, IgG3, and IgG4. IgM subtypes

include IgM, and IgM2. IgA subtypes include IgA1 and IgA2. In humans, the IgA and IgD isotypes contain four heavy chains and four light chains; the IgG and IgE isotypes contain two heavy chains and two light chains; and the IgM isotype contains five heavy chains and five light chains. The heavy chain C region typically comprises one or more domains that may be responsible for effector function. The number of heavy chain constant region domains will depend on the isotype. IgG heavy chains, for example, each contain three C region domains known as CH1, CH2 and CH3. The antibodies that are provided can have any of these isotypes and subtypes. In certain embodiments, the GIPR antibody is of the IgG1, IgG2, or IgG4 subtype. The terms "GIPR antibody" and "anti-GIPR antibody" are used interchangeably throughout this application and figures. Both terms refer to an antibody that binds to GIPR.

[0198] In full-length light and heavy chains, the variable and constant regions are joined by a "J" region of about twelve or more amino acids, with the heavy chain also including a "D" region of about ten more amino acids. See, e.g. *Fundamental Immunology*, 2nd ed., Ch. 7 (Paul, W., ed.) 1989, New York: Raven Press (hereby incorporated by reference in its entirety for all purposes). The variable regions of each light/heavy chain pair typically form the antigen binding site.

[0199] For the antibodies provided herein, the 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/light chain pair mentioned above typically are aligned by the framework regions to form a structure that binds specifically with a specific epitope on GIPR. From N-terminal to C-terminal, naturally-occurring light and heavy chain variable regions both typically conform with the following order of these elements: FR1, CDR1, FR2, CDR2, FR3, CDR3 and FR4. A numbering system has been devised for assigning numbers to amino acids that occupy positions in each of these domains. This numbering system is defined in *Kabat Sequences of Proteins of Immunological Interest* (1987 and 1991, NIH, Bethesda, Md.), or Chothia & Lesk, 1987, *J. Mol. Biol.* 196:901-917; Chothia et al., 1989, *Nature* 342:878-883.

[0200] The sequence information for specific antibodies prepared and identified as described in the Examples below is summarized in TABLE 1. Thus, in an embodiment, an antigen binding protein is an antibody with the CDR, variable domain and light and heavy chain sequences as specified in one of the rows of TABLE 1.

[0201] 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 antibodies and fragments thereof of the present invention and are shown in TABLE 1. SEQ ID NOs have also been assigned to polynucleotides encoding the variable light chain, variable heavy chain, light chain, heavy chain, CDRL1, CDRL2, CDRL3, CDRH1, CDRH2, and CDRH3 sequences of the antibodies and fragments thereof of the present invention and are shown in TABLE 2. The antigen binding proteins of the present invention can be identified by SEQ ID NO, but also by construct name (e.g., 2C2.005) or identifier number (e.g., iPS:336175). The antigen binding proteins identified in Tables 1-5 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.

[0202] The various light chain and heavy chain variable regions provided herein are depicted in TABLE 3. 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.

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Table 1. Amino acid SEQ ID NOs.

Construct	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
2G10.303	723	724	963	964	4	5	6	364	365	366
2G10.304	727	728	967	968	10	11	12	370	371	372
2G10.323	731	732	971	972	16	17	18	376	377	378
2G10.309	735	736	975	976	22	23	24	382	383	384
2G10.316	739	740	979	980	28	29	30	388	389	390
2G10.604	743	744	983	984	34	35	36	394	395	396
2G10.609	747	748	987	988	40	41	42	400	401	402
2G10.603	751	752	991	992	46	47	48	406	407	408
2G10.318	755	756	995	996	52	53	54	412	413	414
2G10.324	759	760	999	1000	58	59	60	418	419	420
2G10.322	763	764	1003	1004	64	65	66	424	425	426
2G10.315	767	768	1007	1008	70	71	72	430	431	432
2G10.331	771	772	1011	1012	76	77	78	436	437	438
2G10.320	775	776	1015	1016	82	83	84	442	443	444
2G10.328	779	780	1019	1020	88	89	90	448	449	450
2G10.333	783	784	1023	1024	94	95	96	454	455	456
2G10.301	787	788	1027	1028	100	101	102	460	461	462
2G10.601	791	792	1031	1032	106	107	108	466	467	468
2G10.326	795	796	1035	1036	112	113	114	472	473	474
2G10.308	799	800	1039	1040	118	119	120	478	479	480
2G10.608	803	804	1043	1044	124	125	126	484	485	486
2G10.336	807	808	1047	1048	130	131	132	490	491	492
2G10.344	811	812	1051	1052	136	137	138	496	497	498
2G10.310	815	816	1055	1056	142	143	144	502	503	504
2G10.610	819	820	1059	1060	148	149	150	508	509	510
2G10.312	823	824	1063	1064	154	155	156	514	515	516
2G10.329	827	828	1067	1068	160	161	162	520	521	522
2G10.327	831	832	1071	1072	166	167	168	526	527	528
2G10.338	835	836	1075	1076	172	173	174	532	533	534
2G10.314	839	840	1079	1080	178	179	180	538	539	540
2G10.337	843	844	1083	1084	184	185	186	544	545	546
2G10.341	847	848	1087	1088	190	191	192	550	551	552
2G10.302	851	852	1091	1092	196	197	198	556	557	558
2G10.602	855	856	1095	1096	202	203	204	562	563	564
2G10.325	859	860	1099	1100	208	209	210	568	569	570

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2G10.343	863	864	1103	1104	214	215	216	574	575	576
2G10.313	867	868	1107	1108	220	221	222	580	581	582
2G10.317	871	872	1111	1112	226	227	228	586	587	588
2G10.311	875	876	1115	1116	232	233	234	592	593	594
2G10.306	879	880	1119	1120	238	239	240	598	599	600
2G10.606	883	884	1123	1124	244	245	246	604	605	606
2G10.347	887	888	1127	1128	250	251	252	610	611	612
2G10.348	891	892	1131	1132	256	257	258	616	617	618
2G10.346	895	896	1135	1136	262	263	264	622	623	624
2G10.647	899	900	1139	1140	268	269	270	628	629	630
2G10.649	903	904	1143	1144	274	275	276	634	635	636
2G10.305	907	908	1147	1148	280	281	282	640	641	642
2G10.605	911	912	1151	1152	286	287	288	646	647	648
2G10.340	915	916	1155	1156	292	293	294	652	653	654
2G10.334	919	920	1159	1160	298	299	300	658	659	660
2G10.339	923	924	1163	1164	304	305	306	664	665	666
2G10.307	927	928	1167	1168	310	311	312	670	671	672
2G10.607	931	932	1171	1172	316	317	318	676	677	678
2G10.321	935	936	1175	1176	322	323	324	682	683	684
2G10.342	939	940	1179	1180	328	329	330	688	689	690
2G10.319	943	944	1183	1184	334	335	336	694	695	696
2G10.332	947	948	1187	1188	340	341	342	700	701	702
2G10.345	951	952	1191	1192	346	347	348	706	707	708
2G10.335	955	956	1195	1196	352	353	354	712	713	714
2G10.330	959	960	1199	1200	358	359	360	718	719	720
iPS:529381	1286	1287	1288	1289	1290	1291	1292	1293	1294	1295
iPS:529382	1296	1297	1298	1299	1300	1301	1302	1303	1304	1305
iPS:529397	1306	1307	1308	1309	1310	1311	1312	1313	1314	1315
iPS:529399	1316	1317	1318	1319	1320	1321	1322	1323	1324	1325
iPS:529400	1326	1327	1328	1329	1330	1331	1332	1333	1334	1335
iPS:529403	1336	1337	1338	1339	1340	1341	1342	1343	1344	1345
iPS:529404	1346	1347	1348	1349	1350	1351	1352	1353	1354	1355
iPS:529405	1356	1357	1358	1359	1360	1361	1362	1363	1364	1365

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Table 2. Nucleic acid SEQ ID NOs.

Construct	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
2G10.303	721	722	961	962	1	2	3	361	362	363
2G10.304	725	726	965	966	7	8	9	367	368	369
2G10.323	729	730	969	970	13	14	15	373	374	375
2G10.309	733	734	973	974	19	20	21	379	380	381
2G10.316	737	738	977	978	25	26	27	385	386	387
2G10.604	741	742	981	982	31	32	33	391	392	393
2G10.609	745	746	985	986	37	38	39	397	398	399
2G10.603	749	750	989	990	43	44	45	403	404	405
2G10.318	753	754	993	994	49	50	51	409	410	411
2G10.324	757	758	997	998	55	56	57	415	416	417
2G10.322	761	762	1001	1002	61	62	63	421	422	423
2G10.315	765	766	1005	1006	67	68	69	427	428	429
2G10.331	769	770	1009	1010	73	74	75	433	434	435
2G10.320	773	774	1013	1014	79	80	81	439	440	441
2G10.328	777	778	1017	1018	85	86	87	445	446	447
2G10.333	781	782	1021	1022	91	92	93	451	452	453
2G10.301	785	786	1025	1026	97	98	99	457	458	459
2G10.601	789	790	1029	1030	103	104	105	463	464	465
2G10.326	793	794	1033	1034	109	110	111	469	470	471
2G10.308	797	798	1037	1038	115	116	117	475	476	477
2G10.608	801	802	1041	1042	121	122	123	481	482	483
2G10.336	805	806	1045	1046	127	128	129	487	488	489
2G10.344	809	810	1049	1050	133	134	135	493	494	495
2G10.310	813	814	1053	1054	139	140	141	499	500	501
2G10.610	817	818	1057	1058	145	146	147	505	506	507
2G10.312	821	822	1061	1062	151	152	153	511	512	513
2G10.329	825	826	1065	1066	157	158	159	517	518	519
2G10.327	829	830	1069	1070	163	164	165	523	524	525
2G10.338	833	834	1073	1074	169	170	171	529	530	531
2G10.314	837	838	1077	1078	175	176	177	535	536	537
2G10.337	841	842	1081	1082	181	182	183	541	542	543
2G10.341	845	846	1085	1086	187	188	189	547	548	549
2G10.302	849	850	1089	1090	193	194	195	553	554	555
2G10.602	853	854	1093	1094	199	200	201	559	560	561
2G10.325	857	858	1097	1098	205	206	207	565	566	567

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2G10.343	861	862	1101	1102	211	212	213	571	572	573
2G10.313	865	866	1105	1106	217	218	219	577	578	579
2G10.317	869	870	1109	1110	223	224	225	583	584	585
2G10.311	873	874	1113	1114	229	230	231	589	590	591
2G10.306	877	878	1117	1118	235	236	237	595	596	597
2G10.606	881	882	1121	1122	241	242	243	601	602	603
2G10.347	885	886	1125	1126	247	248	249	607	608	609
2G10.348	889	890	1129	1130	253	254	255	613	614	615
2G10.346	893	894	1133	1134	259	260	261	619	620	621
2G10.647	897	898	1137	1138	265	266	267	625	626	627
2G10.649	901	902	1141	1142	271	272	273	631	632	633
2G10.305	905	906	1145	1146	277	278	279	637	638	639
2G10.605	909	910	1149	1150	283	284	285	643	644	645
2G10.340	913	914	1153	1154	289	290	291	649	650	651
2G10.334	917	918	1157	1158	295	296	297	655	656	657
2G10.339	921	922	1161	1162	301	302	303	661	662	663
2G10.307	925	926	1165	1166	307	308	309	667	668	669
2G10.607	929	930	1169	1170	313	314	315	673	674	675
2G10.321	933	934	1173	1174	319	320	321	679	680	681
2G10.342	937	938	1177	1178	325	326	327	685	686	687
2G10.319	941	942	1181	1182	331	332	333	691	692	693
2G10.332	945	946	1185	1186	337	338	339	697	698	699
2G10.345	949	950	1189	1190	343	344	345	703	704	705
2G10.335	953	954	1193	1194	349	350	351	709	710	711
2G10.330	957	958	1197	1198	355	356	357	715	716	717
iPS:529381	1377	1378	1361	1362						
iPS:529382	1379	1380	1363	1364						
iPS:529397	1381	1382	1365	1366						
iPS:529399	1383	1384	1367	1368						
iPS:529400	1385	1386	1369	1370						
iPS:529403	1387	1388	1371	1372						
iPS:529404	1389	1390	1373	1374						
iPS:529405	1391	1392	1375	1376						

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Table 3. Exemplary Variable Light and Variable Heavy Regions: Nucleic Acid ("NA") and Amino Acid ("AA") Sequences

Ab	Type	LC V-region	HC V-region
2G10.303	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTGATAGACACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCCTCTCATC TACGAAGCAGCCACAGGCCACTGGTATCCAGC CAGGTTCAGTGGCAGTGGGTCTGGGACAGAGTTTCA TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTACAGCATATCAGAACTGGCCTCT CACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGGT CCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTCACTTCACTAATATATGGCATGCACGTG GGTCGCCAGGCTCCAGGCAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGTATGCAAGTGATAAATACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATTGGCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCACCGTGTCT TAGT
	AA	(SEQ ID NO: 721) EIVMTQSPATLSVSPGERATLSCRASQSVDRHLAWYQ QKPGQAPRLIYEAAATRAATGIPARFSGSGTEFTLTIS SLQSEDFAVYYCQQYQNWPLTFGGGKVEIK	(SEQ ID NO: 722) QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGEGLFWVAIIWFDASDKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDLAIFGVVVPD YWGQGTLVTVSS
	NA	(SEQ ID NO: 723) GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTAAACAGACACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCTCTCATC TACGAAGCAGCCACAGGGCCACTGGTATCCAGC CAGGTTCAGTGGCAGTGGGTCTGGGACAGAGTTTCA TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTACAGCATATCAGAACTGGCCTCT CACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	(SEQ ID NO: 724) CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGGT CCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTCACTTCACTAATATATGGCATGCACGTG GGTCGCCAGGCTCCAGGCAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGTATGCAAGTGATAAATACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATTGGCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCACCGTGTCT TAGT
2G10.304		(SEQ ID NO: 725)	(SEQ ID NO: 726)

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2G10.323	AA	EIVMTQSPATLSVSPGERATLSCRASQSVNRHLAWYQ QKPGQAPRLIYEAAATRAIGIPARFSGSGTEFTLTIS SLQSEDFAVYYCQQYQNWPLTFGGGTKVEIK (SEQ ID NO: 727)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDLAIFGVVVD YW'QGGLVTVSS (SEQ ID NO: 728)
	NA	GAAATAGTGATGACGCGAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTTCATAGACACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCCACCAGGCCACTGGTATCCAGC CAGGTTCAAGTGCCAGTGGGCTGGGACAGAGTTCCAC TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTACGAGTATCAGAACTGGCCTCT CACTTTCGGCGGAGGACCAAGGTGGAGATCAA (SEQ ID NO: 729)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCTGGAGGTCCCTGAGACTCTCCTGTCAGC ATCTGGATTACCTTCAGTAACATATGGCATGCAC GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGTATGCAAGTGAATAACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATTGGCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCACCGTGTCTC TAGT (SEQ ID NO: 730)
2G10.309	AA	EIVMTQSPATLSVSPGERATLSCRASQSVHRHLAWYQ QKPGQAPRLIYEAAATRAIGIPARFSGSGTEFTLTIS SLQSEDFAVYYCQQYQNWPLTFGGGTKVEIK (SEQ ID NO: 731)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDLAIFGVVVD YW'QGGLVTVSS (SEQ ID NO: 732)
	NA	GAAATAGTGATGACGCGAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTTCATAGACACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCCACCAGGCCACTGGTATCCAGC CAGGTTCAAGTGCCAGTGGGCTGGGACAGAGTTCCAC TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTACGAGTATCAGAACTGGCCTCT CACTTTCGGCGGAGGACCAAGGTGGAGATCAA (SEQ ID NO: 733)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTACCTTCAGTAACATATGGCATGCAC GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGTATGCAAGTGAATAACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATTGGCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCACCGTGTCTC TAGT (SEQ ID NO: 734)

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2C10.316	AA	EIVMTQSPATLSVSPGERATLSCRASQSVFRHLAWYQ QKPGQAPRLIYEAAATRAATGIPARFSGSGTEFTLTIS SLQSEDFAVYYCQYQNWPLTFGGGTKVEIK (SEQ ID NO: 735)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDLAIFGVVVD YW'QGGLVTVSS (SEQ ID NO: 736)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTTCAGACACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCCACCAGGCCACTGTATCCAGC CAGGTTCAAGTGCCAGTGGGCTGGGACAGAGTTCCAC TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTACAGCATCAGAACTGGCCTCT CACTTTCGGCGGAGGACCAAGGTGGAGATCAAA (SEQ ID NO: 737)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCTGGAGGTCCCTGAGACTCTCCTGTCAGC ATCTGGATTACCTTCAGTAACATATGGCATGACATG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGTATGCAAGTGATAAATACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATTGGCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCAACCGTGTCT TAGT (SEQ ID NO: 738)
2C10.604	AA	EIVMTQSPATLSVSPGERATLSCRASQSVFRHLAWYQ QKPGQAPRLIYEAAATRAATGIPARFSGSGTEFTLTIS SLQSEDFAVYYCQYQNWPLTFGGGTKVEIK (SEQ ID NO: 739)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDLAIFGVVVD YW'QGGLVTVSS (SEQ ID NO: 740)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTAAACAGACACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCCACCAGGCCACTGGTATCCCAGC CAGGTCAGTGGCAGTGGGCTGGGACAGAGTTCA CAGGTCAGTGGCAGTGGGCTGGGACAGAGTTCA CTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTG CAGTTTATTACTGTACAGCATCAGAACTGGCCTC TCACCTTCGGCGGAGGACCAAGGTGGAGATCAAA (SEQ ID NO: 741)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTACCTTCAGTAACATATGGCATGACATG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGTATGCAAGTGATAAATACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATTGGCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCAACCGTGTCT TAGT (SEQ ID NO: 742)

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2C10.609	AA	EIVMTQSPATLSVSPGERATLSCRASQSVNRHLAWYQ QKPGQAPRLLIYEAAATRAATGIPARVSGSGGTEFTLTIS SLQSEDFAVYYCQQYQNWPLTFGGGTKVEIK (SEQ ID NO: 743)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDLAIFGVVVPD YW'QGGLVTVSS (SEQ ID NO: 744)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTGAAAGACACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCACCCAGGGCCACTGGTATCCACG CAGGGTCAGTGGCAGTGGGTCTGGGACAGAGTTCA CTCTCACCATCAGCAGCCTGCAGTCTGAAAGATTTG CAGTTTATTACTGTACAGCATCAGAACTGGCCTC TCACTTTCGGCGGAGGACCAAGGTGGAGATCAAA (SEQ ID NO: 745)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCCTGGT CCAGCTGGAGGTCCCTGAGACTCTCCTGTCAGC ATCTGGATTACCTTCAGTAACATATGGCATGCAC GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGTATGCAAGTGAATAACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATTGGCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCAACCGTGTCT TAGT (SEQ ID NO: 746)
2C10.603	AA	EIVMTQSPATLSVSPGERATLSCRASQSVNRHLAWYQ QKPGQAPRLLIYEAAATRAATGIPARVSGSGGTEFTLTIS SLQSEDFAVYYCQQYQNWPLTFGGGTKVEIK (SEQ ID NO: 747)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDLAIFGVVVPD YW'QGGLVTVSS (SEQ ID NO: 748)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTGATAGACACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCACCCAGGGCCACTGGTATCCACG CAGGGTCAGTGGCAGTGGGTCTGGGACAGAGTTCA CAGGGTCAGTGGCAGTGGGTCTGGGACAGAGTTCA CTCTCACCATCAGCAGCCTGCAGTCTGAAAGATTTG CAGTTTATTACTGTACAGCATCAGAACTGGCCTC TCACTTTCGGCGGAGGACCAAGGTGGAGATCAAA (SEQ ID NO: 749)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCCTGGT CCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTACCTTCAGTAACATATGGCATGCAC GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGTATGCAAGTGAATAACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATTGGCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCAACCGTGTCT TAGT (SEQ ID NO: 750)

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2G10.318	AA	EIVMTQSPATLSVSPGERATLSCRASQSVDRHLAWYQ QKPGQAPRLIYEAAATRAATGIPARVSGSGGTEFTLTIS SLQSEDFAVYYCQYQNNWPLTFGGGKVEIK (SEQ ID NO: 751)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDLAIFGVVVPD YW'QGGLVTVSS (SEQ ID NO: 752)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTCTGAGTCACTTAGCCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCACCCAGGCCACTGGTATCCAGC CAGGTTCAAGTGCCAGTGGGCTGGGACAGAGTTCCAC TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTACAGCATATAACAAGTGGCCTCT CACTTTCGGCGGAGGACCAAGGTGGAGATCAA (SEQ ID NO: 753)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTACCTTCAGTAACTATGGCATGCATGG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGTATGCAAGTGATAAATACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATTGGCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCACCGTGTCTC TAGT (SEQ ID NO: 754)
2G10.324	AA	EIVMTQSPATLSVSPGERATLSCRASQSVLSHLAWYQ QKPGQAPRLIYEAAATRAATGIPARFSGSGGTEFTLTIS SLQSEDFAVYYCQYQNNWPLTFGGGKVEIK (SEQ ID NO: 755)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDLAIFGVVVPD YW'QGGLVTVSS (SEQ ID NO: 756)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTCTGAGTCACTTAGCCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCACCCAGGCCACTGGTATCCCAGC CAGGTTCAAGTGCCAGTGGGCTGGGACAGAGTTCCAC TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTACAGCATATAACAAGTGGCCTCT CACTTTCGGCGGAGGACCAAGGTGGAGATCAA (SEQ ID NO: 757)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTACCTTCAGTAACTATGGCATGCATG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGTATGCAAGTGATAAATACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATTGGCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCACCGTGTCTC TAGT (SEQ ID NO: 758)

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2G10.315	AA	EIVMTQSPATLSVSPGERATLSCRASQSVLSHLAWYQ QKPGQAPRLIYEAAATRAATGIPARFSGSGTEFTLTIS SLQSEDFAVYYCQYQNWPLTFGGGKVEIK (SEQ ID NO: 759)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADA VKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDLAIFGVVVPD YW'QGGLVTVSS (SEQ ID NO: 760)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTATGAGTCACTTAGCCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCACCCAGGGCCACTGGTATCCAGC CAGGTTCAGTGGCAGTGGTCTGGGACAGAGTTCCAC TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTACAGCATCAGAACTGGCCTCT CACTTTCGGCGGAGGGACCAAGGTGGAGATCAA (SEQ ID NO: 761)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTACCTTCAGTAACATATGGCATGCAC GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGTATGCAAGTGATAAATCT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATTGGCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCACCGTGTCTC TAGT (SEQ ID NO: 762)
2G10.322	AA	EIVMTQSPATLSVSPGERATLSCRASQSVMSHLAWYQ QKPGQAPRLIYEAAATRAATGIPARFSGSGTEFTLTIS SLQSEDFAVYYCQYQNWPLTFGGGKVEIK (SEQ ID NO: 763)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADA VKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDLAIFGVVVPD YW'QGGLVTVSS (SEQ ID NO: 764)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTCTGACGCACCTTAGCCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCACCCAGGGCCACTGGTATCCAGC CAGGTTCAGTGGCAGTGGTCTGGGACAGAGTTCCAC TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTACAGCATCAGAACTGGCCTCT CACTTTCGGCGGAGGGACCAAGGTGGAGATCAA (SEQ ID NO: 765)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTACCTTCAGTAACATATGGCATGCAC GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGTATGCAAGTGATAAATCT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATTGGCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCACCGTGTCTC TAGT (SEQ ID NO: 766)

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2G10.331	AA	EIVMTQSPATLSVSPGERATLSCRASQSVLTHLAWYQ QKPGQAPRLIYEAAATRAATGIPARFSGSGTEFTLTIS SLQSEDFAVYYCQYQNWPLTFGGGTKVEIK (SEQ ID NO: 767)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDLAIFGVVVD YW'QGGLVTVSS (SEQ ID NO: 768)
	NA	GAAATAGTGATGACGCGAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTGATCTGCACCTAGCCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCACCCAGGCCACTGGTATCCAGC CAGGTTCAAGTGCCAGTGGGCTGGGACAGAGTTCCAC TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTACAGCATATCAGAACTGGCCTCT CACTTTCGGCGGAGGACCAAGGTGGAGATCAA (SEQ ID NO: 769)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTACCTTCAGTAACATATGGCATGCATGG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAATGGG TGGCAGCTATATGGTTTGTATGCAAGTGAATAACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATTGGCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCAACCGTGTCTC TAGT (SEQ ID NO: 770)
2G10.320	AA	EIVMTQSPATLSVSPGERATLSCRASQSVDLHLAWYQ QKPGQAPRLIYEAAATRAATGIPARFSGSGTEFTLTIS SLQSEDFAVYYCQYQNWPLTFGGGTKVEIK (SEQ ID NO: 771)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDLAIFGVVVD YW'QGGLVTVSS (SEQ ID NO: 772)
	NA	GAAATAGTGATGACGCGAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTGAGCGAACACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCACCCAGGCCACTGGTATCCAGC CAGGTTCAAGTGCCAGTGGGCTGGGACAGAGTTCCAC TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTACAGCATATCAGAACTGGCCTCT CACTTTCGGCGGAGGACCAAGGTGGAGATCAA (SEQ ID NO: 773)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTACCTTCAGTAACATATGGCATGCATG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAATGGG TGGCAGCTATATGGTTTGTATGCAAGTGAATAACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATCTGGCGATTTTGGAGTGTCC CGACTACTGGGGCCAGGGAACCCCTGGTCAACCGTGTCTC TAGT (SEQ ID NO: 774)

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2G10.328	AA	EIVMTQSPATLSVSPGERATLSCRASQSVSEHLAWYQ QKPGQAPRLIYEAAATRAATGIPARFSGSGTEFTLTIS SLQSEDFAVYYCQYQNWPLTFGGGTKVEIK (SEQ ID NO: 775)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDLAIFGVVDPY WGQGTLVTVSS (SEQ ID NO: 776)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTAGCGAACAATTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCCACCAGGCCACTGGTATCCACG CAGGTTCAAGTGGCAGTGGTCTGGGACAGAGTTCCAC TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTACAGCATATCAGAACTGGCCTCT CACTTTCGGCGGAGGGACCAAGGTGGAGATCAA (SEQ ID NO: 777)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCTGGAGGTCCCTGAGACTCTCCTGTCAGC ATCTGGATTACCTTCAGTAACATATGGCATGCAC GGTCCGCCAGGCTCCAGCGAGGGGCTGGAATGGG TGGCAGCTATATGGTTTGTATGCAAGTGAATAACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATTGGCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCACCGTGTCTC TAGT (SEQ ID NO: 778)
2G10.333	AA	EIVMTQSPATLSVSPGERATLSCRASQSVSEHLAWYQ QKPGQAPRLIYEAAATRAATGIPARFSGSGTEFTLTIS SLQSEDFAVYYCQYQNWPLTFGGGTKVEIK (SEQ ID NO: 779)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDLAIFGVVDP YWQGTLVTVSS (SEQ ID NO: 780)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTAGCCGGCACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCCACCAGGCCACTGGTATCCCAGC CAGGTTCAAGTGGCAGTGGTCTGGGACAGAGTTCCAC TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTACAGCATATCAGAACTGGCCTCT CACTTTCGGCGGAGGGACCAAGGTGGAGATCAA (SEQ ID NO: 781)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTACCTTCAGTAACATATGGCATGCAC GGTCCGCCAGGCTCCAGCGAGGGGCTGGAATGGG TGGCAGCTATATGGTTTGTATGCAAGTGAATAACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATTGGCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCACCGTGTCTC TAGT (SEQ ID NO: 782)

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2C10.301	AA	EIVMTQSPATLSVSPGERATLSCRASQSVSRHLAWYQ QKPGQAPRLLIYEAAATRAATGIPARFSGSGTEFTLTIS SLQSEDFAVYYCQYQHWPLTFGGGKVEIK (SEQ ID NO: 783)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDLAIFGVVVD YW'QGGLVTVSS (SEQ ID NO: 784)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTTCAGCCACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCACCCAGGGCCACTGGTATCCAGC CAGGTTCAAGTGCCAGTGGGCTGGGACAGAGTTCCAC TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTACAGCATATCAGAACTGGCCTCT CACTTTCGGCGGAGGACCAAGGTGGAGATCAAA (SEQ ID NO: 785)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTACCTTCCAGAACTATGGCATGCACTG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGTATGCTGACAAATACT ATGCAGACGCCGTGAAGGCCGATTACCAATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATCTTGCATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCACCGTGTCT TAGT (SEQ ID NO: 786)
2C10.601	AA	EIVMTQSPATLSVSPGERATLSCRASQSVFSLAWYQQ KPGQAPRLLIYEAAATRAATGIPARFSGSGTEFTLTISL QSEDFAVYYCQYQNWPLTFGGGKVEIK (SEQ ID NO: 787)	QVQLVESGGGVVQPGRSLRLSCAASGFTFQNYGMHW VRQAPGELEWVAIIWFDASDKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDLAIFGVVVD YW'QGGLVTVSS (SEQ ID NO: 788)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTTCAGCCACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCACCCAGGGCCACTGGTATCCCAGC CAGGTCAGTGGCAGTGGGCTGGGACAGAGTTCA CTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTG CAGTTTATTACTGTACAGCATATCAGAACTGGCCTC TCACTTTCGGCGGAGGACCAAGGTGGAGATCAAA (SEQ ID NO: 789)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTACCTTCCAGAACTATGGCATGCACTG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGTATGCTGACAAATACT ATGCAGACGCCGTGAAGGGCCGATTACCAATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATCTTGCATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCACCGTGTCT TAGT (SEQ ID NO: 790)

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2C10.326	AA	EIVMTQSPATLSVSPGERATLSCRASQSVFSLHAWYQQ KPGQAPRLIYEAAATRAATGIPARVSGSGGTEFTLTIS LQSEDFAVYYCQQYQNWPLTFGGGKVEIK (SEQ ID NO: 791)	QVQLVESGGGVVQPGRSLRLSCAASGFTFQNYGMHW VRQAPGELEWVAIIWFDASDKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDLAIFGVVVPD YW'QGGLVTVSS (SEQ ID NO: 792)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTTCTGAGTCACTTAGCCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCACCCAGGCCACTGGTATCCAGC CAGGTTCAAGTGCCAGTGGGCTGGGACAGAGTTCCAC TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTACAGCATATCAGCAGTGGCCTCT CACTTTCGGCGGAGGACCAAGGTGGAGATCAA (SEQ ID NO: 793)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTCACTTCCAGAACTATGGCATGCACTG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGTATGCTGACAAATACT ATGCAGACGCCGTGAAGGCCGATTACCACTCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATCTGCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCAACCGTGTCTC TAGT
2C10.308	AA	EIVMTQSPATLSVSPGERATLSCRASQSVLSHLAWYQ QKPGQAPRLIYEAAATRAATGIPARFSGSGTEFTLTIS SLQSEDFAVYYCQQYQNWPLTFGGGKVEIK (SEQ ID NO: 795)	QVQLVESGGGVVQPGRSLRLSCAASGFTFQNYGMHW VRQAPGELEWVAIIWFDASDKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDLAIFGVVVPD YW'QGGLVTVSS (SEQ ID NO: 796)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTTTTCAGCCACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCACCCAGGCCACTGGTATCCCAGC CAGGTTCAAGTGCCAGTGGGCTGGGACAGAGTTCCAC TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTACAGCATATCAGCAGTGGCCTCT CACTTTCGGCGGAGGACCAAGGTGGAGATCAA (SEQ ID NO: 797)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTCACTTCCAGTAACTATGGCATGCACTG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGTATGCAAGTGATAAATACT ATGCAGACGCCGTGAAGGCCGATTACCACTCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATTGGCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCAACCGTGTCTC TAGT

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2C10.608	AA	EIVMTQSPATLSVSPGERATLSCRASQSVFSLHAWYQQ KPGQAPRLLIYEAAATRAATGIPARVSGSGTEFTLTISL QSEDFAVYQCQYQQWPLTFGGGKVEIK (SEQ ID NO: 799)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDLAIFGVVVD YW'QGGLVTVSS (SEQ ID NO: 800)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTTCAGCCACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCACCCAGGGCCACTGGTATCCAGC CAGGGTCAGTGCCAGTGGGTCTGGGACAGAGTTCA CTCTACCATCAGCAGCCTGCAGTCTGAAGATTTTG CAGTTTATTACTGTACAGCATATCAGCAGTGGCCTC TCACTTTCGGCGGAGGACCAAGGTGGAGATCAA (SEQ ID NO: 801)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCTGGAGGTCCCTGAGACTCTCCTGTCAGC ATCTGGATTACCTTCAGTAACATATGGCATGACATG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGTATGCAAGTGAATAACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATTGGCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCACCGTGTCT TAGT (SEQ ID NO: 802)
2C10.336	AA	EIVMTQSPATLSVSPGERATLSCRASQSVFSLHAWYQQ KPGQAPRLLIYEAAATRAATGIPARVSGSGTEFTLTISL LQSEDFAVYQCQYQQWPLTFGGGKVEIK (SEQ ID NO: 803)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDLAIFGVVVD YW'QGGLVTVSS (SEQ ID NO: 804)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTTCAGAGCCACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCACCCAGGGCCACTGGTATCCAGC CAGGTTCAGTGCCAGTGGGTCTGGGACAGAGTTTCA TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTACAGCATATCAGAACTGGCCTCT CACTTTCGGCGGAGGACCAAGGTGGAGATCAA (SEQ ID NO: 805)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTACCTTCAGTAACATATGGCATGACATG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGTATGCAAGTGAATAACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATATGGCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCACCGTGTCT TAGT (SEQ ID NO: 806)

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2G10.310	AA	EIVMTQSPATLSVSPGERATLSCRASQSVQSHLAWYQ QKPGQAPRLLIYEAAATRAATGIPARFSGSGTEFTLTIS SLQSEDFAVYYCQYQNWPLTFGGGKVEIK (SEQ ID NO: 807)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADA VKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDIAIFGVVPDY WGQGLVTVSS (SEQ ID NO: 808)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTAGTAGCCACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCACCCAGGCCACTGGTATCCAGC CAGGTTCAAGTGCCAGTGGGCTGGGACAGAGTTCCAC TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTACAGCATCAGCAGTGGCCTCT CACTTTCGGCGGAGGGACCAAGGTGGAGATCAA (SEQ ID NO: 809)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCTGGAGGTCCCTGAGACTCTCCTGTCAGC ATCTGGATTACCTTCAGTAACATATGGCATGACATG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGTATGCAAGTGAATAACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATATTCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCAACCGTGTCTC TAGT (SEQ ID NO: 810)
2G10.344	AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSHAWYQQ KPGQAPRLLIYEAAATRAATGIPARFSGSGTEFTLTISL QSEDFAVYYCQYQNWPLTFGGGKVEIK (SEQ ID NO: 811)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADA VKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDIAIFGVVPDY WGQGLVTVSS (SEQ ID NO: 812)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTTCACGCACCTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCACCCAGGCCACTGGTATCCCAGC CAGGTTCAAGTGCCAGTGGGCTGGGACAGAGTTCCAC TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTACAGCATCAGCAGTGGCCTCT CACTTTCGGCGGAGGGACCAAGGTGGAGATCAA (SEQ ID NO: 813)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTACCTTCAGTAACATATGGCATGACATG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGTATGCAAGTGAATAACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATTTGGCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCAACCGTGTCTC TAGT (SEQ ID NO: 814)

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2C10.610	AA	EIVMTQSPATLSVSPGERATLSCRASQSVFTHLAWYQ QKPGQAPRLIYEAAATRAATGIPARVSGSGTEFTLTIS SLQSEDFAVYYCQQYNWPLTFGGGKVEIK (SEQ ID NO: 815)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDLAIFGVVVD YW'QGGLVTVSS (SEQ ID NO: 816)
	NA	GAAATAGTGATGACGCGAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTTCACGCACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCACCCAGGGCCACTGGTATCCAGC CAGGGTCAGTGGCAGTGGGTCTGGGACAGAGTTCA CTCTCACCATCAGCAGCCTGCAGTCTGAAAGATTTTG CAGTTTATTACTGTACGAGTATAACAACCTGGCCTC TCACTTTCGGCGGAGGACCAAGGTGGAGATCAAA (SEQ ID NO: 817)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCCTGGAGGTCCCTGAGACTCTCCTGTCAGC ATCTGGATTACCTTCAGTAACATATGGCATGCACTG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGTATGCAAGTGATAAATACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATTGGCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCACCCGTGTC TAGT (SEQ ID NO: 818)
2C10.312	AA	EIVMTQSPATLSVSPGERATLSCRASQSVFTHLAWYQ QKPGQAPRLIYEAAATRAATGIPARVSGSGTEFTLTIS SLQSEDFAVYYCQQYNWPLTFGGGKVEIK (SEQ ID NO: 819)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDLAIFGVVVD YW'QGGLVTVSS (SEQ ID NO: 820)
	NA	GAAATAGTGATGACGCGAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTTCACGCACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCACCCAGGGCCACTGGTATCCAGC CAGGTTCAGTGGCAGTGGGTCTGGGACAGAGTTTCA TCTCACCATCAGCAGCCTGCAGTCTGAAAGATTTTG AGTTTATTACTGTACGAGTATAACAACCTGGCCTCT CACTTTCGGCGGAGGACCAAGGTGGAGATCAAA (SEQ ID NO: 821)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTACCTTCAGTAACATATGGCATGCACTG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGTATGCAAGTGATAAATACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATTGGCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCACCCGTGTC TAGT (SEQ ID NO: 822)

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2G10.327	AA	EIVMTQSPATLSVSPGERATLSCRASQSVFEHLAWYQ QKPGQAPRLIYEAAATRAIGIPARFSGSGTEFTLTIS SLQSEDFAVYYCQQYNWPLTFGGGTKVEIK (SEQ ID NO: 823)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDLAIFGVVVPD YW'QGGLVTVSS (SEQ ID NO: 824)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTGAACAGCACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCCACCAGGCCACTGGTATCCACG CAGGTTCAGTGGCAGTGGTCTGGGACAGAGTTCCAC TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTACAGCATATAACAAGTGGCCTCT CACTTTCGGCGGAGGACCAAGGTGGAGATCAA (SEQ ID NO: 825)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCCTGGT CCAGCTGGAGGTCCCTGAGACTCTCCTGTCAGC ATCTGGATTACCTTCAGTAACATATGGCATGACATG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGTATGCAAGTGAATAACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATTGGCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCACCCGTGTC TAGT (SEQ ID NO: 826)
2G10.329	AA	EIVMTQSPATLSVSPGERATLSCRASQSVFEHLAWYQ QKPGQAPRLIYEAAATRAIGIPARFSGSGTEFTLTIS SLQSEDFAVYYCQQYNWPLTFGGGTKVEIK (SEQ ID NO: 827)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDLAIFGVVVPD YW'QGGLVTVSS (SEQ ID NO: 828)
	NA	GAAATAGTGATGACGCAGTCTCCGGGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTATAGCCACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCCACCAGGGCCACTGGTATCCACG CAGGTTCAGTGGCAGTGGTCTGGGACAGAGTTCCAC TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTACAGCATATAACAAGTGGCCTCT CACTTTCGGCGGAGGACCAAGGTGGAGATCAA (SEQ ID NO: 829)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCCTGGT CCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTACCTTCAGTAACATATGGCATGACATG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGTATGCAAGTGAATAACT ATGCAGACGCCGTGAAGGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATTGGCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCACCCGTGTC TAGT (SEQ ID NO: 830)

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2G10.338	AA	EIVMTQSPATLSVSPGERATLSCRASQSVHSHLAWYQ QKPGQAPRLIYEAAATRAATGIPARFSGSGTEFTLTIS SLQSEDFAVYYCQQYNQWPLTFGGGKVEIK (SEQ ID NO: 831)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADA VKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDLAIFGVVVPD YW'QGGLVTVSS (SEQ ID NO: 832)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTTCATCATCACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCCACCAGGCCACTGGTATCCAGC CAGGTTCAGTGGCAGTGGTCTGGGACAGAGTTCCAC TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTACAGCATATAACAGTGGCCTCT CACTTTCCGGCGGAGGACCAAGGTGGAGATCAA (SEQ ID NO: 833)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGC GTGGT CCAGCTGGAGGTCCCTGAGACTCTCCTGTCAGC ATCTGGATTACCTTCAGTAACATATGGCATGCATGG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGTATGCAAGTGATAAATACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATTGGCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCACCGGTGTC TAGT (SEQ ID NO: 834)
2G10.314	AA	EIVMTQSPATLSVSPGERATLSCRASQSVHHHLAWYQ QKPGQAPRLIYEAAATRAATGIPARFSGSGTEFTLTIS SLQSEDFAVYYCQQYNQWPLTFGGGKVEIK (SEQ ID NO: 835)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADA VKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDLAIFGVVVPD YW'QGGLVTVSS (SEQ ID NO: 836)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTTCATAGCCACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCCACCAGGCCACTGGTATCCCAGC CAGGTTCAGTGGCAGTGGTCTGGGACAGAGTTCCAC TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTACAGCATATAACAGTGGCCTCT CACTTTCCGGCGGAGGACCAAGGTGGAGATCAA (SEQ ID NO: 837)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGC GTGGT CCAGCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTACCTTCAGTAACATATGGCATGCATG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGTATGCAAGTGATAAATACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATTGGCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCACCGGTGTC TAGT (SEQ ID NO: 838)

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2G10.337	AA	EIVMTQSPATLSVSPGERATLSCRASQSVHSHLAWYQ QKPGQAPRLIYEAAATRAATGIPARFSGSGTEFTLTIS SLQSEDFAVYYCQQYNQWPLTFGGGKVEIK (SEQ ID NO: 839)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDLAIFGVVVD YW'QGGLVTVSS (SEQ ID NO: 840)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTGATGTCAACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCACCCAGGCCACTGTATCCAGC CAGGTTCAAGTGCCAGTGGGTCTGGGACAGAGTTCCAC TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTACAGCATATAACAGTGGCCTCT CACTTTCCGGCGGAGGACCAAGGTGGAGATCAA (SEQ ID NO: 841)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCTGGAGGTCCCTGAGACTCTCCTGTCAGC ATCTGGATTACCTTCAGTAACATATGGCATGCATG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAATGGG TGGCAGCTATATGGTTTGTATGCAAGTGAATAACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATTGGCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCAACCGTGTCTC TAGT (SEQ ID NO: 842)
2G10.341	AA	EIVMTQSPATLSVSPGERATLSCRASQSVDNLAWYQ QKPGQAPRLIYEAAATRAATGIPARFSGSGTEFTLTIS SLQSEDFAVYYCQQYNQWPLTFGGGKVEIK (SEQ ID NO: 834)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDLAIFGVVVD YW'QGGLVTVSS (SEQ ID NO: 844)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTGATGTCCACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCACCCAGGCCACTGGTATCCCAGC CAGGTTCAAGTGCCAGTGGGTCTGGGACAGAGTTCCAC TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTACAGCATATAACAGTGGCCTCT CACTTTCCGGCGGAGGACCAAGGTGGAGATCAA (SEQ ID NO: 845)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTACCTTCAGTAACATATGGCATGCATG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAATGGG TGGCAGCTATATGGTTTGTATGCAAGTGAATAACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATTGGCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCAACCGTGTCTC TAGT (SEQ ID NO: 846)

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2C10.302	AA	EIVMTQSPATLSVSPGERATLSCRASQSVDFVHLAWYQ QKPGQAPRLIYEAAATRAATGIPARFSGSGTEFTLTIS SLQSEDFAVYYCQQYNQWPLTFGGGKVEIK (SEQ ID NO: 847)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADA VKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDLAIFGVVPD YW'QGTLVTVSS (SEQ ID NO: 848)
	NA	GAAATAGTGATGACGCGAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTITTTGAACACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCCACCAGGCCACTGGTATCCAGC CAGGTTCAGTGGCAGTGGGCTGGGACAGAGTTCCAC TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTACAGCATATAACAAGTGGCCTCT CACTTTCGGCGGAGGACCAAGGTGGAGATCAAA (SEQ ID NO: 849)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCCTGGAGGTCCCTGAGACTCTCCTGTCAGC ATCTGGATTACCTTCAGTAACATATGGCATGCACG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGTATGCAAGTGAATAACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATATTCGATTTTGGAGTGTTC CGACTACTGGGGCCAGGGAACCCCTGGTCAACCGTGTCTC TAGT (SEQ ID NO: 850)
2C10.602	AA	EIVMTQSPATLSVSPGERATLSCRASQSVFHEHLAWYQ QKPGQAPRLIYEAAATRAATGIPARFSGSGTEFTLTIS SLQSEDFAVYYCQQYNQWPLTFGGGKVEIK (SEQ ID NO: 851)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADA VKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDIAIFGVFPDY WGQTLVTVSS (SEQ ID NO: 852)
	NA	GAAATAGTGATGACGCGAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTITTTGAACACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCCACCAGGCCACTGGTATCCAGC CAGGTCAGTGGCAGTGGGCTGGGACAGAGTTCA CAGGTCAGTGGCAGTGGGCTGGGACAGAGTTCA CTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTG CAGTTTATTACTGTACAGCATATAACAAGTGGCCTC TCACCTTCGGCGGAGGACCAAGGTGGAGATCAAA (SEQ ID NO: 853)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTACCTTCAGTAACATATGGCATGCACG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGTATGCAAGTGAATAACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATATTCGATTTTGGAGTGTTC CGACTACTGGGGCCAGGGAACCCCTGGTCAACCGTGTCTC TAGT (SEQ ID NO: 854)

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2G10.343	AA	EIVMTQSPATLSVSPGERATLSCRASQSVFEHLAWYQ QKPGQAPRLIYEAAATRAATGIPARVSGSGGTEFTLTIS SLQSEDFAVYYCQQYNWPLTFGGGKVEIK (SEQ ID NO: 855)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADA VKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDIAIFGVVDPY WGQGLVTVSS (SEQ ID NO: 856)
	NA	GAAATAGTGATGACGCGAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTTCGAAACACTTAGCCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCCACCAGGCCACTGGTATCCAGC CAGGTTCAGTGGCAGTGGGTCTGGGACAGAGTTCCAC TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTACGAGTATAACAGTGGCCTCT CACTTTCGGCGGAGGGACCAAGGTGGAGATCAA (SEQ ID NO: 857)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTACCTTCAGTAACATATGGCATGCACTG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAATGGG TGGCAGCTATATGGTTTGTATGCAAGTGAATAACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATATTCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCACCCGTGTC TAGT (SEQ ID NO: 858)
2G10.325	AA	EIVMTQSPATLSVSPGERATLSCRASQSVFEHLAWYQ QKPGQAPRLIYEAAATRAATGIPARFSGSGGTEFTLTIS SLQSEDFAVYYCQQYNQWPLTFGGGKVEIK (SEQ ID NO: 859)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADA VKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDIAIFGVVDPY WGQGLVTVSS (SEQ ID NO: 860)
	NA	GAAATAGTGATGACGCGAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTTCGAAACACTTAGCCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCCACCAGGCCACTGGTATCCAGC CAGGTTCAGTGGCAGTGGGTCTGGGACAGAGTTCCAC TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTACGAGTATAACAGTGGCCTCT CACTTTCGGCGGAGGGACCAAGGTGGAGATCAA (SEQ ID NO: 861)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTACCTTCAGTAACATATGGCATGCACTG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAATGGG TGGCAGCTATATGGTTTGTATGCAAGTGAATAACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATATTCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCACCCGTGTC TAGT (SEQ ID NO: 862)

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2G10.317	AA	EIVMTQSPATLSVSPGERATLSCRASQSVLEHLAWYQ QKPGQAPRLLIYEAAATRAATGIPARFSGSGTEFTLTIS SLQSEDFAVYYCQQYNQWPLTFGGGKVEIK (SEQ ID NO: 863)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADA VKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDIAIFGVFPDY WGQGLVTVSS (SEQ ID NO: 864)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTGATAGACACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCCACCAGGCCACTGGTATCCAGC CAGGTTCAAGTGGCAGTGGGCTGGGACAGAGTTCCAC TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTACAGCATATAACAGTGGCCTCT CACTTTCCGGCGGAGGACCAAGGTGGAGATCAAA (SEQ ID NO: 865)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCTGGAGGTCCCTGAGACTCTCCTGTCAGC ATCTGGATTACCTTCAGTAACATATGGCATGCATG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAATGGG TGGCAGCTATATGGTTTGTATGCAAGTGAATAACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATATTCGATTTTGGAGTGTTC CGACTACTGGGGCCAGGGAACCCCTGGTCAACCGTGTCTC TAGT (SEQ ID NO: 866)
2G10.313	AA	EIVMTQSPATLSVSPGERATLSCRASQSVDRHLAWYQ QKPGQAPRLLIYEAAATRAATGIPARFSGSGTEFTLTIS SLQSEDFAVYYCQQYNQWPLTFGGGKVEIK (SEQ ID NO: 867)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADA VKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDIAIFGVFPDY WGQGLVTVSS (SEQ ID NO: 868)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTAAACCGGCACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCCACCAGGGCCACTGGTATCCCAGC CAGGTTCAAGTGGCAGTGGGCTGGGACAGAGTTCCAC TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTACAGCATATAACAGTGGCCTCT CACTTTCCGGCGGAGGACCAAGGTGGAGATCAAA (SEQ ID NO: 869)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTACCTTCAGTAACATATGGCATGCATG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAATGGG TGGCAGCTATATGGTTTGTATGCAAGTGAATAACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATATTCGATTTTGGAGTGTTC CGACTACTGGGGCCAGGGAACCCCTGGTCAACCGTGTCTC TAGT (SEQ ID NO: 870)

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2C10.311	AA	EIVMTQSPATLSVSPGERATLSCRASQSVNRHLAWYQ QKPGQAPRLIYEAAATRAATGIPARFSGSGTEFTLTIS SLQSEDFAVYYCQYQQWPLTFGGGKVEIK (SEQ ID NO: 871)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADA VKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDIAIFGVFPDY WGQGLVTVSS (SEQ ID NO: 872)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTTAACGTACACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACCAGCAGCCACCAGGCCACTGGTATCCAGCC AGTTTCAGTGGCAGTGGGTCTGGACAGAGTTCACT CTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCA GTTTATTACTGTCAGCAGTATAACAGTGGCCTCTC ACTTTCGGCGGAGGACCAAGGTGGAGATCAAA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTACCTTCAGTAACATATGGCATGACATG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGTATGCAAGTGAATAACT ATGCAGACGCCGTGAAGGCCGATTCAACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTTATTA CTGTGCGAGAGATATTCGATTTTGGAGTGTTC CGACTACTGGGGCCAGGGAACCCCTGGTCAACCGTGTCT TAGT (SEQ ID NO: 874)
2C10.306	AA	EIVMTQSPATLSVSPGERATLSCRASQSVNVHLAWYQ QKPGQAPRLIYQAATRAATGIPARFSGSGTEFTLTIS SLQSEDFAVYYCQYQQWPLTFGGGKVEIK (SEQ ID NO: 875)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADA VKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDIAIFGVFPDY WGQGLVTVSS (SEQ ID NO: 876)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTTCTGACGCACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCCACCAGGGCCACTGGTATCCCAGC CAGGTTCAAGTGGCAGTGGGTCTGGGACAGAGTTCAC TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTCAGCAGTATCAGAACTGGCCTCT CACTTTCGGCGGAGGACCAAGGTGGAGATCAAA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTACCTTCAGTAACATATGGCATGACATG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGTATGCAAGTGAATAACT ATGCAGACGCCGTGAAGGCCGATTCAACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTTATTA CTGTGCGAGAGATATTCGATTTTGGAGTGTACCC CGACTACTGGGGCCAGGGAACCCCTGGTCAACCGTGTCT TAGT (SEQ ID NO: 878)

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2C10.606	AA	EIVMTQSPATLSVSPGERATLSCRASQSVLTHLAWYQ QKPGQAPRLIYEAAATRAATGIPARVSGSGTEFTLTIS SLQSEDFAVYYCQYQNWPLTFGGGKVEIK (SEQ ID NO: 879)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADA VKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDIAIFGVIPDY WGQGLVTVSS (SEQ ID NO: 880)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTCTGAGCCACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCCACCAGGCCACTGGTATCCAGC CAGGGTCAGTGGCAGTGGTCTGGGACAGAGTTCA CTCTCACCATCAGCAGCCTGCAGTCTGAAAGATTTTG CAGTTTATTACTGTACAGCATATCAGAACTGGCCTC TCACTTTCGGCGGAGGACCAAGGTGGAGATCAAA (SEQ ID NO: 881)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTACCTTCAGTAACATATGGCATGACG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGATGCAAGTGATAAATACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATATTCGATTTTGGAGTGATCCC CGACTACTGGGGCCAGGGAACCCCTGGTCACCGTGTCT TAGT (SEQ ID NO: 882)
2C10.347	AA	EIVMTQSPATLSVSPGERATLSCRASQSVLTHLAWYQ QKPGQAPRLIYEAAATRAATGIPARVSGSGTEFTLTIS SLQSEDFAVYYCQYQNWPLTFGGGKVEIK (SEQ ID NO: 883)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADA VKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDIAIFGVIPDY WGQGLVTVSS (SEQ ID NO: 884)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTAGCAGCAACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TATGGTGCAGCCACCAGGGCCACTGGTATCCCAGCC AGGTTCACTGGCAGTGGGTCTGGGACAGAGTTCAC CTCACCATCAGCAGCCTGCAGTCTGAAAGATTTTGA GTTTATTACTGCAGCAGTATAATAACTGGGCTCTC ACTTTCGGCGGAGGACCAAGGTGGAGATCAAA (SEQ ID NO: 885)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTACCTTCAGTAACATATGGCATGACG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGATGCAAGTGATAAATACT ATGCAGACGCCGTGAAGGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATTTGGCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCACCGTGTCT TAGT (SEQ ID NO: 886)

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2C10.346	AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQ KPGQAPRLIYGAATRAATGIPARFSGSGTEFTLTIS LQSEDFAVYYCQQYNWPLTFGGGKVEIK (SEQ ID NO: 887)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDLAIFGVVDP YW'QGTLTVSS (SEQ ID NO: 888)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTAGCAGCAACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGTCCTCAGGCTCCTCATC TATGGTGCAGCCACAGGGCCACTGGTATCCAGCC AGTTTCAGTGGCAGTGGGTCTGGACAGAGTTCACT CTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCA GTTTATTACTGTCAGCAGTATAATACTGGCCTCTC ACTTTCGGCGGAGGACCAAGGTGGAGATCAAA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTACCTTCAGTAACATATGGCATGCATG GGTCCGCCAGGTCCTCAGCGAGGGGCTGGAATGGG TGGCAGCTATATGGTTTGTATGCAAGTGAATAACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATCAGGCGATTTTGGAGTGGTCCC CGATTACTGGGGCCAGGGAACCCCTGGTCAACCGTGTCT TAGT (SEQ ID NO: 890)
2C10.348	AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQ KPGQAPRLIYGAATRAATGIPARFSGSGTEFTLTIS LQSEDFAVYYCQQYNWPLTFGGGKVEIK (SEQ ID NO: 889)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDQAIIFGVVDP YW'QGTLTVSS (SEQ ID NO: 892)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTAGCAGCAACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGTCCTCAGGCTCCTCATC TATGGTGCAGCCACAGGGCCACTGGTATCCAGCC AGTTTCAGTGGCAGTGGGTCTGGACAGAGTTCACT CTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCA GTTTATTACTGTCAGCAGTATAATACTGGCCTCTC ACTTTCGGCGGAGGACCAAGGTGGAGATCAAA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTACCTTCAGTAACATATGGCATGCATG GGTCCGCCAGGTCCTCAGCGAGGGGCTGGAATGGG TGGCAGCTATATGGTTTGTATGCAAGTGAATAACT ATGCAGACGCCGTGAAGGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATATTCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCAACCGTGTCT TAGT (SEQ ID NO: 894)

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2C10.649	AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLA WYQQ KPGQAPRLIYGAATRA TGI PARFSGSGTEFTLTIS LQSEDFAVYYCQQYNWPLTFGGG TKVEIK (SEQ ID NO: 895)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDIAIFGVVDPY WGQGTLVTVSS (SEQ ID NO: 896)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTAGCAGCAACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TATGGTGCAGCCACAGGGCCACTGGTATCCAGCC AGGGTCAGTGGCAGTGGGTCTGGGACAGAGTTTCA TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTACAGCATATAA TAACTGGCCTCT CACTTTCGGCGGAGGACCAAGGTGGAGATCAAA (SEQ ID NO: 897)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCTGGAGGTCCCTGAGACTCTCCTGTCAGC ATCTGGATTACCTTCAGTAACATATGGCATGCATG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAATGGG TGGCAGCTATATGGTTTGTATGCAAGTGAATAACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATTGGCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCACCGTGTCT TAGT (SEQ ID NO: 898)
2C10.649	AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLA WYQQ KPGQAPRLIYGAATRA TGI PARVSGSGTEFTLTIS LQSEDFAVYYCQQYNWPLTFGGG TKVEIK (SEQ ID NO: 899)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDLAIFGVVDP YWQGTLVTVSS (SEQ ID NO: 900)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTAGCAGCAACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TATGAAGCAGCCACAGGGCCACTGGTATCCCAGCC AGGGTCAGTGGCAGTGGGTCTGGGACAGAGTTTCA TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTACAGCATATAA TAACTGGCCTCT CACTTTCGGCGGAGGACCAAGGTGGAGATCAAA (SEQ ID NO: 901)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTACCTTCAGTAACATATGGCATGCATG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAATGGG TGGCAGCTATATGGTTTGTATGCAAGTGAATAACT ATGCAGACGCCGTGAAGGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATCAGGCGATTTTGGAGTGGTCCC CGATTACTGGGGCCAGGGAACCCCTGGTCACCGTGTCT TAGT (SEQ ID NO: 902)

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2C10.305	AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQ KPGQAPRLIYEAAATRAATGIPARVSGSGGTEFTLTIS LQSEDFAVYYCQQYNWPLTFGGGKVEIK (SEQ ID NO: 903)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDQAIFGVVVPD YW'QGGLVTVSS (SEQ ID NO: 904)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTGATGTTAACTTAGCCGTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACAACGCAGCCACCAGGCCACTGGTATCCAGCC AGGTTCAAGTGGCAGTGGGTCTGGACAGAGTTCACT CTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCA GTTTATTACTGTCAGCAGTATCAGAACTGGCCCTC ACTTTCGGCGGAGGACCAAGGTGGAGATCAAA (SEQ ID NO: 905)	CAGGTGCAGCTGCTGGAGTCTGGGGGAGGCGTGGT CCAGCTGGAGGTCCCTGAGACTCTCCTGTCAGC ATCTGGATTACCTTCAGTAACATATGGCATGCATGG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGATGCAAGTGATAAATACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATTGGCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCACCGTGTCTC TAGT (SEQ ID NO: 906)
2C10.605	AA	EIVMTQSPATLSVSPGERATLSCRASQSVVDVNLAWYQ QKPGQAPRLIYNAAATRAATGIPARFSGSGTEFTLTIS SLQSEDFAVYYCQQYNWPLTFGGGKVEIK (SEQ ID NO: 907)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDLAIFGVVVPD YW'QGGLVTVSS (SEQ ID NO: 908)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTGATGTTAACTTAGCCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACAACGCAGCCACCAGGCCACTGGTATCCAGCC AGGTTCAAGTGGCAGTGGGTCTGGACAGAGTTCACT CTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCA GTTTATTACTGTCAGCAGTATCAGAACTGGCCCTC CACTTTCGGCGGAGGACCAAGGTGGAGATCAAA (SEQ ID NO: 909)	CAGGTGCAGCTGCTGGAGTCTGGGGGAGGCGTGGT CCAGCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTACCTTCAGTAACATATGGCATGCATG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGATGCAAGTGATAAATACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATTGGCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCACCGTGTCTC TAGT (SEQ ID NO: 910)

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2C10.334	AA	EIVMTQSPATLSVSPGERATLSCRASQSVVDVNLAWYQ QKPGQAPRLLIYNAAATRAATGIPARVSGSGSGTEFTLTIS SLQSEDFAVYYCQYQNWPLTFGGGKVEIK (SEQ ID NO: 911)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADA VKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDLAIFGVVDPD YW'QGTLVTVSS (SEQ ID NO: 912)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTTCATAGGAACCTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACAACGCAGCCACCAGGCCACTGGTATCCAGCC AGGTTCAAGTGCCAGTGGGTCTGGACAGAGTTCACT CTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCA GTTTATTACTGTACGAGTATCAGAACTGGCCTCTC ACTTTCGGCGGAGGACCAAGGTGGAGATCAAA (SEQ ID NO: 913)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCTGGAGGTCCCTGAGACTCTCCTGTCAGC ATCTGGATTACCTTCAGTAACATATGGCATGCACTG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGATGCAAGTGATAAATACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATATGCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCACCGTGTCT TAGT (SEQ ID NO: 914)
2C10.340	AA	EIVMTQSPATLSVSPGERATLSCRASQSVHTNLAWYQ QKPGQAPRLLIYNAAATRAATGIPARFSGSGSGTEFTLTIS SLQSEDFAVYYCQYQNWPLTFGGGKVEIK (SEQ ID NO: 915)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADA VKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDIAIFGVVDPD WGQTLVTVSS (SEQ ID NO: 916)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTAACTGAACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACCAGGCAGCCACCAGGCCACTGGTATCCCAGCC AGGTTCAAGTGCCAGTGGGTCTGGGACAGAGTTCACT CTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCA GTTTATTACTGTACGAGTATAACCAAGTGGCCTCTC ACTTTCGGCGGAGGACCAAGGTGGAGATCAAA (SEQ ID NO: 917)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTACCTTCAGTAACATATGGCATGCACTG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGATGCAAGTGATAAATACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATTTGGCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCACCGTGTCT TAGT (SEQ ID NO: 918)

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2G10.339	AA	EIVMTQSPATLSVSPGERATLSCRASQSVNLSLAWYQ QKPGQAPRLLIYQAAATRAATGIPARFSGSGTEFTLTIS SLQSEDFAVYYCQQYNQWPLTFGGGKVEIK (SEQ ID NO: 919)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADA VKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDLAIFGVVDPD YW'QGTLVTVSS (SEQ ID NO: 920)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTTCAGAACTTAGCCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACCAGCAGCCACCAGGCCACTGGTATCCAGCC AGTTTCAGTGGCAGTGGGTCTGGACAGAGTTCACT CTCACCATCAGCAGCCTGCAGTCTGAAGATTTGCA GTTTATTACTGTCAGCAGTATAACAGTGGCCTCTC ACTTTCGGCGGAGGACCAAGGTGGAGATCAAA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTACCTTCAGTAACATATGGCATGCATGG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGATGCAAGTGATAAATACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATATTCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCACCGTGTCTC TAGT
2G10.307	AA	EIVMTQSPATLSVSPGERATLSCRASQSVFQNLAWYQ QKPGQAPRLLIYQAAATRAATGIPARFSGSGTEFTLTIS SLQSEDFAVYYCQQYNQWPLTFGGGKVEIK (SEQ ID NO: 921)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDASDKYYADA VKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDIAIFGVVDPD WGQTLVTVSS (SEQ ID NO: 924)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTGATAGACACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCCACCAGGGCCACTGGTATCCCAGC CAGGTTCAAGTGGCAGTGGGTCTGGGACAGAGTTCAC TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTCAGCAGTATAACAGTGGCCTCT CACTTTCGGCGGAGGACCAAGGTGGAGATCAAA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTACCTTCAGAACTATGGCATGCATG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGATGCGTACGGTAAATACT ATGCAGACGCCGTGAAGGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATCAGACGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCACCGTGTCTC TAGT

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2G10.607	AA	EIVMTQSPATLSVSPGERATLSCRASQSVDRHLAWYQ QKPGQAPRLIYEAAATRAATGIPARVSGSGTEFTLTIS SLQSEDFAVYYCQQYNQWPLTFGGGKVEIK (SEQ ID NO: 927)	QVQLVESGGGVVQPGRSLRLSCAASGFTTFQNYGMHW VRQAPGELEWVAIIWFDAYGKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDQTIFGVVVD YW'QGGLVTVSS (SEQ ID NO: 928)
	NA	GAAATAGTGATGACGCGAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTGATAGACACTTACGCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCACCCAGGGCCACTGGTATCCAGC CAGGGTCAGTGGCAGTGGGTCTGGGACAGAGTTCA CTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTG CAGTTTATTACTGTACGAGTATAACAGTGGCCTC TCACTTTCGGCGGAGGACCAAGGTGGAGATCAAA (SEQ ID NO: 929)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTACCTTCCAGAACTATGGCATGCGACTG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGTATGCGTACGGTAAATCT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATCAGACGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCACCGTGTCTC TAGT (SEQ ID NO: 930)
2G10.321	AA	EIVMTQSPATLSVSPGERATLSCRASQSVDRHLAWYQ QKPGQAPRLIYEAAATRAATGIPARVSGSGTEFTLTIS SLQSEDFAVYYCQQYNQWPLTFGGGKVEIK (SEQ ID NO: 931)	QVQLVESGGGVVQPGRSLRLSCAASGFTTFQNYGMHW VRQAPGELEWVAIIWFDAYGKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDQTIFGVVVD YW'QGGLVTVSS (SEQ ID NO: 932)
	NA	GAAATAGTGATGACGCGAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTAAACGGCACTTACGCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCACCCAGGGCCACTGGTATCCCAGC CAGGTTCAGTGGCAGTGGGTCTGGGACAGAGTTCAC TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTACGAGTATAACCAAGTGGCCTCT CACTTTCGGCGGAGGACCAAGGTGGAGATCAAA (SEQ ID NO: 933)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTACCTTCCAGAACTATGGCATGCGACTG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGTATGCGTACGGTAAATCT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATAAGACGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCACCGTGTCTC TAGT (SEQ ID NO: 934)

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2G10.319	NA	EIVMTQSPATLSVSPGERATLSCRASQSVNRHLAWYQ QKPGQAPRLIYEAAATRAIGIPARFSGSGTEFTLTIS SLQSEDFAVYYCQQYNQWPLTFGGGKVEIK (SEQ ID NO: 935)	QVQLVESGGGVVQPGRSLRLSCAASGFTFQNYGMHW VRQAPGELEWVAIWFDAYGKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDKTIFFGVVVD YW'QGGLVTVSS (SEQ ID NO: 936)
		GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTGAAAGACACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCCACCAGGCCACTGGTATCCAGC CAGGTTCAAGTGCCAGTGGGCTGGGACAGAGTTCCAC TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTACAGCATATCAGCAGTGGCCTCT CACTTTCGGCGGAGGACCAAGGTGGAGATCAAA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTACCTTCCAGAACTATGGCATGCACTG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGTATGCTACGGTAAATACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATAAGACGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCAACCGTGTCTC TAGT
2G10.342	AA	EIVMTQSPATLSVSPGERATLSCRASQSVNRHLAWYQ QKPGQAPRLIYEAAATRAIGIPARFSGSGTEFTLTIS SLQSEDFAVYYCQQYNQWPLTFGGGKVEIK (SEQ ID NO: 937)	QVQLVESGGGVVQPGRSLRLSCAASGFTFQNYGMHW VRQAPGELEWVAIWFDAYGKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDKTIFFGVVVD YW'QGGLVTVSS (SEQ ID NO: 938)
		GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTGAAAGACACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCCACCAGGCCACTGGTATCCAGC CAGGTTCAAGTGCCAGTGGGCTGGGACAGAGTTCCAC TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTACAGCATATCAGCAGTGGCCTCT CACTTTCGGCGGAGGACCAAGGTGGAGATCAAA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTACCTTCCAGTAACATATGGCATGCACTG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGTATGCTACGGTAAATACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATAAGACGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCAACCGTGTCTC TAGT
2G10.319	NA	EIVMTQSPATLSVSPGERATLSCRASQSVNRHLAWYQ QKPGQAPRLIYEAAATRAIGIPARFSGSGTEFTLTIS SLQSEDFAVYYCQQYNQWPLTFGGGKVEIK (SEQ ID NO: 939)	QVQLVESGGGVVQPGRSLRLSCAASGFTFQNYGMHW VRQAPGELEWVAIWFDAYGKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDKTIFFGVVVD YW'QGGLVTVSS (SEQ ID NO: 940)
		GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTGAAAGACACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCCACCAGGCCACTGGTATCCAGC CAGGTTCAAGTGCCAGTGGGCTGGGACAGAGTTCCAC TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTACAGCATATCAGAACTGGCCTCT CACTTTCGGCGGAGGACCAAGGTGGAGATCAAA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTACCTTCCAGTAACATATGGCATGCACTG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGTATGCTACGGTAAATACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATAAGACGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCAACCGTGTCTC TAGT

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2G10.332	AA	EIVMTQSPATLSVSPGERATLSCRASQSVFRHLAWYQ QKPGQAPRLLIYEAAATRAATGIPARFSGSGTEFTLTIS SLQSEDFAVYYCQYQNNWPLTFGGGTKVEIK (SEQ ID NO: 943)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGELEWVAIIWFDAYKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDKTIFFGVVVD YW'QGGLVTVSS (SEQ ID NO: 944)
	NA	GAAATAGTGATGACGCGAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTCTGAGTCACTTAGCCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCCACCAGGCCACTGGTATCCAGC CAGGTTCAAGTGGCAGTGGGCTGGGACAGAGTTCCAC TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTACGAGTATAACAAGTGGCCTCT CACTTTCGGCGGAGGACCAAGGTGGAGATCAAA (SEQ ID NO: 945)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTCACTTCCAGAACTATGGCATGCGACTG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGTATGCTACGACAAATACT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATAAGTCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCACCGTGTCTC TAGT (SEQ ID NO: 946)
2G10.345	AA	EIVMTQSPATLSVSPGERATLSCRASQSVLSHLAWYQ QKPGQAPRLLIYEAAATRAATGIPARFSGSGTEFTLTIS SLQSEDFAVYYCQYQNNWPLTFGGGTKVEIK (SEQ ID NO: 947)	QVQLVESGGGVVQPGRSLRLSCAASGFTFQNYGMHW VRQAPGELEWVAIIWFDAYKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDKSIFFGVVVD YW'QGGLVTVSS (SEQ ID NO: 948)
	NA	GAAATAGTGATGACGCGAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTAAACAGACACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCCACCAGGGCCACTGGTATCCCAGC CAGGTTCAAGTGGCAGTGGGCTGGGACAGAGTTCCAC TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTACGAGTATAACAAGTGGCCTCT CACTTTCGGCGGAGGACCAAGGTGGAGATCAAA (SEQ ID NO: 949)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTCACTTCCAGAACTATGGCATGCGACTG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGTATGCTACGACAAATACT ATGCAGACGCCGTGAAGGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATAAGTCGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCACCGTGTCTC TAGT (SEQ ID NO: 950)

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2C10.330	AA	EIVMTQSPATLSVSPGERATLSCRASQSVNRHLAWYQ QKPGQAPRLIYEAAATRAATGIPARFSGSGTEFTLTIS SLQSEDFAVYYCQQYNQWPLTFGGGTKVEIK (SEQ ID NO: 951)	QVQLVESGGGVVQPGRSLRLSCAASGFTTFQNYGMHW VRQAPGELEWVAIIWFDAYDKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDKSIKIFGVVVD YWGQGTLVTVSS (SEQ ID NO: 952)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTACAGCCACCTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACGAAGCAGCCACCAGGCCACTGGTATCCACG CAGGTTCAAGTGGCAGTGGGCTGGGACAGAGTTCCAC TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC AGTTTATTACTGTACAGCATATAACAGTGGCCTCT CACTTTCGGCGGAGGACCAAGGTGGAGATCAAA (SEQ ID NO: 953)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTACCTTCCAGAACTATGGCATGCACTG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGTATGCGGCTTTCAAAATCT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATCTCGGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCAACCGTGTCT TAGT (SEQ ID NO: 954)
2C10.335	AA	EIVMTQSPATLSVSPGERATLSCRASQSVTSHLAWYQ QKPGQAPRLIYEAAATRAATGIPARFSGSGTEFTLTIS SLQSEDFAVYYCQQYNQWPLTFGGGTKVEIK (SEQ ID NO: 955)	QVQLVESGGGVVQPGRSLRLSCAASGFTTFQNYGMHW VRQAPGELEWVAIIWFDAYDKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDLAIFGVVVD YWGQGTLVTVSS (SEQ ID NO: 956)
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG GCCAGTCAGAGTGTATCAGCACTTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATC TACCAGGCAGCCACCAGGCCACTGGTATCCCAGCC AGGTTCAAGTGGCAGTGGGCTGGGACAGAGTTCACT CTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC GTTTATTACTGTACAGCATATCAGAACTGGCCTCTC ACTTTCGGCGGAGGACCAAGGTGGAGATCAAA (SEQ ID NO: 957)	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGT CCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGC ATCTGGATTACCTTCCAGAACTATGGCATGCACTG GGTCCGCCAGGCTCCAGCGAGGGGCTGGAGTGGG TGGCAGCTATATGGTTTGTATGCGGCTTTCAAAATCT ATGCAGACGCCGTGAAGGCCGATTACCATCTCCA GAGACAACTCCAAGAACACGCTGTATCTGCAAAATG AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATCTCGGATTTTGGAGTGGTCCC CGACTACTGGGGCCAGGGAACCCCTGGTCAACCGTGTCT TAGT (SEQ ID NO: 958)

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	AA	EIVMTQSPATLSVSPGERATLSCRASQSVSDQHLAWYQ QKPGQAPRLLIYQAATRAATGIPARFSGSGTEFTLTIS SLQSEDFAVYYCQYQNWPLTFGGGKVEIK (SEQ ID NO: 959)	QVQLVESGGGVVQPGRSLRLSCAASGFTFQNYGMHW VRQAPGEGLWVAIWFDAAFKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDLAIFGVVDP YW'GQGTLTVSS (SEQ ID NO: 960)
		ATGGACATGAGGGTGCCCGCTCAGCTCCTGGGGCTC CTGCTGTGTGGCTGAGAGGTGCGCGCTGTGAAATC GTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCT CCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAG TCAGAGTGTAGCGAACACTTACCTGTGTACAGCA GAAACCTGGCCAGGCTCCAGGCTCCTCATCTACGA AGCAGCCACCAGGGCCACTGGTATCCAGCCAGGTT CAGTGGCAGTGGTCTGGGACAGAGTTCACCTCAC CATCAGCAGCCTGCAGTCTGAAGATTGTCAGTT	ATGGACATGAGGGTGCCCGCTCAGCTCCTGGGGCTC CTGCTGTGTGGCTGAGAGGTGCGCGCTGTGAAATC GTGATGACGCAGTCTCCAGCCACCCTGTGTGTCT CCAGGGGAAAGAGCCACCCTCTCCTGCAGCCATCTGG ATTCACCTTCAGTAACATATGGCATGCATGGGTCCG CCAGGCTCCAGGCGAGGGGCTGGAGTGGGTGGCAG CTATCTGTTTGTATGCAAGTGATAAATACTATGCAG ACGCCGTGAAGGGCCGATTACCATCTCCAGAGAC AATCCCAAGAACACGCTGTATCTGCAATGAACAG CCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGC GAGA
!PS:529381	NA	(SEQ ID NO: 1377)	(SEQ ID NO: 1378)
	AA	EIVMTQSPATLSVSPGERATLSCRASQSVSEHLAWYQ QKPGQAPRLLIYEAAATRAATGIPARFSGSGTEFTLTIS SLQSEDFAVYYCQYQNWPLTFGGGKVEIK (SEQ ID NO: 1086)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGEGLWVAIWFDASDKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDLAIFGVIPDY WGQGTLLTVSS (SEQ ID NO: 1287)
!PS:529382	NA	ATGGACATGAGGGTGCCCGCTCAGCTCCTGGGGCTC CTGCTGTGTGGCTGAGAGGTGCGCGCTGTGAAATC GTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCT CCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAG TCAGAGTGTAGCAGCAACTTACCTGTGTACAGCA GAAACCTGGCCAGGCTCCAGGCTCCTCATCTATGG TGCAGCCACCAGGGCCACTGGTATCCAGCCAGGTT CAGTGGCAGTGGTCTGGGACAGAGTTCACCTCAC CATCAGCAGCCTGCAGTCTGAAGATTGTCAGTT	ATGGACATGAGGGTGCCCGCTCAGCTCCTGGGGCTC CTGCTGTGTGGCTGAGAGGTGCGCGCTGTGAAATC CAGCTGGTGGAGTCTGGGGGAGGCGGTGCTCCAGCC TGGGAGGTCCCTGAGACTCTCCTGTGCGAGCATCTGG ATTCACCTTCAGTAACATATGGCATGCATGGGTCCG CCAGGCTCCAGGCGAGGGGCTGGAGTGGGTGGCAG CTATCTGTTTGTATGCAAGTGATAAATACTATGCAG ACGCCGTGAAGGGCCGATTACCATCTCCAGAGAC AATCCCAAGAACACGCTGTATCTGCAATGAACAG CCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGC GAGA
	AA	(SEQ ID NO: 1379)	(SEQ ID NO: 1380)
	AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQ KPGQAPRLLIYGAATRAATGIPARFSGSGTEFTLTIS	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHW VRQAPGEGLWVAIWFDASDKYYADAVKGRFTISR

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IP:529397		LQSEDFAVYQCQYNNWPLTFGGGKVEIK (SEQ ID NO: 1296)	DNSKNTLYQMNSLRAEDTAVYYCARDIAIFGVVPDY WGQGLVTVSS (SEQ ID NO: 1297)
	NA	ATGGACATGAGGGTGCCCGCTCAGCTCCTGGGGCTC CTGCTGCTGTGGCTGAGAGGTGCGCGCTGTGAAATC GTGCTGACGCACTCTCCAGCCACCCTGTCTGTCT CCAGGGAAAGAGCCACCCTCTCTGCAAGGGCCAG TCAGAGTGTAGCAGCACTTAGCCTGGTACCAGCA GAAACCTGGCAGGCTCCAGGCTCCTCATCTATGG TGCAGCCACCAGGGCCACTGGTATCCAGAGAGGTT CAGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCAC CATCAGCAGGCTGGAGCCTGAAGATTTTGCAGTT	ATGGACATGAGGGTGCCCGCTCAGCTCCTGGGGCTC CTGCTGCTGTGGCTGAGAGGTGCGCGCTGTGAGGTG CAGCTGGTGGAGTCTGGGGGAGGCGTGTCCAGCC TGGAGGTCCTTGAGACTCTCCTGTGTCAGCATCTGG ATTCACTTCAGTAACATATGGCATGCACTGGGTCCG CCAGGCTCCAGCGAGGGGCTGGAGTGGTGGCCAG CTATCTGTTTGTGCAAGTGAATAAATACTATGCAG ACGCCGTGAAGGGCCGATTCAACCATCTCCAGAGAC AACTCCAAGAAACACGCTGTATCTGCAAAATGAACAG CCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGC GAGA
	AA	(SEQ ID NO: 1381) EIVLTQSPATLSLSPGERATLSCRASQSVSSNLAWYQQ KPGQAPRLIYGAATRAATGIPDRFSGSGTEFTLTISR LEPEDEFAVYQCQYNNWPLTFGGGKVEIK	(SEQ ID NO: 1382) QVQLVESGGGVVQPGRLRLSCAASGFTFSNYGMHW VRQAPGEGLWVAIWFDASDKYYADA VKGRFTISR DNSKNTLYQMNSLRAEDTAVYYCARDQAIFGVVPD YWGGGLVTVSS
IP:529399		(SEQ ID NO: 1306) ATGGACATGAGGGTGCCCGCTCAGCTCCTGGGGCTC CTGCTGCTGTGGCTGAGAGGTGCGCGCTGTGAAATC GTGCTGACGCACTCTCCAGCCACCCTGTCTGTCT CCAGGGAAAGAGCCACCCTCTCTGCAAGGGCCAG TCAGAGTGTAGCAGCACTTAGCCTGGTACCAGCA GAAACCTGGCAGGCTCCAGGCTCCTCATCTACGA AGCAGCCACCAGGGCCACTGGTATCCAGACAGGT TCAGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCA CCATCAGCAGGCTGGAGCCTGAAGATTTTGCAGTT	(SEQ ID NO: 1307) ATGGACATGAGGGTGCCCGCTCAGCTCCTGGGGCTC CTGCTGCTGTGGCTGAGAGGTGCGCGCTGTGAGGTG CAGCTGGTGGAGTCTGGGGGAGGCGTGTCCAGCC TGGAGGTCCTTGAGACTCTCCTGTGTCAGCATCTGG ATTCACTTCAGTAACATATGGCATGCACTGGGTCCG CCAGGCTCCAGCGAGGGGCTGGAGTGGTGGCCAG CTATCTGTTTGTGCAAGTGAATAAATACTATGCAG ACGCCGTGAAGGGCCGATTCAACCATCTCCAGAGAC AACTCCAAGAAACACGCTGTATCTGCAAAATGAACAG CCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGC GAGA
	NA	(SEQ ID NO: 1383) EIVLTQSPATLSLSPGERATLSCRASQSVSEHLAWYQQ KPGQAPRLIYEAAATRAATGIPDRFSGSGTEFTLTISR LEPEDEFAVYQCQYQNNWPLTFGGGKVEIK	(SEQ ID NO: 1384) QVQLVESGGGVVQPGRLRLSCAASGFTFSNYGMHW VRQAPGEGLWVAIWFDASDKYYADA VKGRFTISR DNSKNTLYQMNSLRAEDTAVYYCARDLAIFGVIPDY WGQGLVTVSS
	AA		

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IP:5293400	NA	(SEQ ID NO: 1316) ATGGACATGAGGGTGCCCGCTCAGCTCCTGGGGCTC CTGCTGCTGTGGCTGAGAGGTGCGCGCTGTGAAATC GTGCTGACGCACTCCAGCCACCCTGTCTGTCT CCAGGGAAAGAGCCACCCTCTCTGCAGGGCCAG TCAGAGTTAGCAGCAACTTAGCTGCTACACGCA GAAACCTGGCAGGCTCCAGGCTCCTCATCTATGG TGCAGCCACAGGGCCACTGGTATCCAGACAGGTT CAGTGGCAGTGGTCTGGGACAGAGTTCACTCTAC CATCAGCAGGCTGGAGCCTGAAGATTTTGCAGTT	(SEQ ID NO: 1317) ATGGACATGAGGGTGCCCGCTCAGCTCCTGGGGCTC CTGCTGCTGTGGCTGAGAGGTGCGCGCTGTGAGGTG CAGTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCC TGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGG ATTACCTTCAGTAACATATGGCATGCACTGGTCCG CCAGGCTCCAGGAGGGGCTGGAGTGGTGGCAG CTATCTGTTTGTATGCAAGTATAAATACTATGCAG ACGCCGTGAAGGGCCGATTCACTCCTCCAGAGAC AATCCAAAGAACACGCTGTATCTGCAATGAACAG CCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGC GAGA
		(SEQ ID NO: 1385) EIVLTQSPATLSLSPGERATLSRASQSVSSNLAWYQQ KPGQAPRLIYGAATRAATGIPDRFSGSGTEFTLTISR LEPEDFAVYYCQQYNWPLTFGGGKVEIK	(SEQ ID NO: 1386) QVQLVESGGGVVQPGRLRLSCAASGFTFSNYGMHW VRQAPGEGLWVAAIWFDAADSKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDIAIFGVVVDY WQGQGLVTVSS
	NA	(SEQ ID NO: 1326) ATGGACATGAGGGTGCCCGCTCAGCTCCTGGGGCTC CTGCTGCTGTGGCTGAGAGGTGCGCGCTGTGAAATC GTGCTGACGCACTCCAGCCACCCTGTCTGTCT CCAGGGAAAGAGCCACCCTCTCTGCAGGGCCAG TCAGAGTTGATGCTGCACTTAGCTGGTACCAGCA GAAACCTGGCAGGCTCCAGGCTCCTCATCTACGA AGCAGCCACAGGGCCACTGGTATCCAGACAGGT TCAGTGGCAGTGGTCTGGGACAGAGTTCACTCTCA CCATCAGCAGGCTGGAGCCTGAAGATTTTGCAGTT	(SEQ ID NO: 1327) ATGGACATGAGGGTGCCCGCTCAGCTCCTGGGGCTC CTGCTGCTGTGGCTGAGAGGTGCGCGCTGTGAGGTG CAGTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCC TGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGG ATTACCTTCAGTAACATATGGCATGCACTGGTCCG CCAGGCTCCAGGAGGGGCTGGAGTGGTGGCAG CTATCTGTTTGTATGCAAGTATAAATACTATGCAG ACGCCGTGAAGGGCCGATTCACTCCTCCAGAGAC AATCCAAAGAACACGCTGTATCTGCAATGAACAG CCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGC GAGA
IP:5293403	AA	(SEQ ID NO: 1387) EIVLTQSPATLSLSPGERATLSRASQSVDLHLAWYQQ KPGQAPRLIYEAATRAATGIPDRFSGSGTEFTLTISR LEPEDFAVYYCQQYNWPLTFGGGKVEIK	(SEQ ID NO: 1388) QVQLVESGGGVVQPGRLRLSCAASGFTFSNYGMHW VRQAPGEGLWVAAIWFDAADSKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDIAIFGVVVDY YWQGQGLVTVSS
		(SEQ ID NO: 1336) ATGGACATGAGGGTGCCCGCTCAGCTCCTGGGGCTC	(SEQ ID NO: 1337) ATGGACATGAGGGTGCCCGCTCAGCTCCTGGGGCTC
	NA		

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IP:529405		CTGCTGCTGTGGCTGAGAGGTGCGCGCTGTGAAATC GTGCTGACGCAGTCTCCAGCCACCTGCTCTGTCT CCAGGGAAAGAGCCACCCTCTCTGCAGGGCCAG TCAGAGTGTAACTGAACCTAGCCTGGTACCAGCA GAAACCTGGCCAGGCTCCAGGCTCCTCATCTACCA GGCAGCCACAGGGCCACTGGTATCCAGACAGGT TCAGTGGCAGTGGGTCTGGGACAGAGTTCACCTCA CCATCAGCAGGCTGGAGCCTGAAGATTTTGCAGTT (SEQ ID NO: 1389)	CTGCTGCTGTGGCTGAGAGGTGCGCGCTGTGAGGTG CAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCC TGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGG ATTCACCTTCAGTAACCTATGGCATGCATGGGTCCG CCAGGCTCCAGCGGAGGGGCTGGAGTGGGTGGCAG CTATCTGTTTGTATGCAAGTGAATAAATACTATGAG ACGCCGTGAAGGGCCGATTACCATCTCCAGAGAC AACTCCAAGAACCGCTGTATCTGCAAAATGAACAG CCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGC GAGA (SEQ ID NO: 1390)
	AA	EIVLTQSPATLSLSPGERATLSRASQSVNINLAWYQQ KPGQAPRLIYQAATRAATGIPDRFSGSGTEFTLTISR LEPEDFAVYYCQYNQWPLTFGGGTKVEIK (SEQ ID NO: 1346)	QVQLVESGGGVVQPGRSRLSCAASGFTFSNYGMHW VRQAPGEGLWVAIWFDAADSKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDLAIFGVVVD YWGQGLTVTVSS (SEQ ID NO: 1347)
	NA	ATGGACATGAGGGTGCCCGCTCAGCTCCTGGGGCTC CTGCTGCTGTGGCTGAGAGGTGCGCGCTGTGAAATC GTGCTGACGCAGTCTCCAGCCACCCTGCTCTGTCT CCAGGGAAAGAGCCACCCTCTCTGCAGGGCCAG TCAGAGTGTTCAGCCACTTAGCCTGGTACCAGCA GAAACCTGGCAGGCTCCAGGCTCCTCATCTACGA AGCAGCCACAGGGCCACTGGTATCCAGACAGGT TCAGTGGCAGTGGGTCTGGGACAGAGTTCACCTCA CCATCAGCAGGCTGGAGCCTGAAGATTTTGCAGTT (SEQ ID NO: 1391)	ATGGACATGAGGGTGCCCGCTCAGCTCCTGGGGCTC CTGCTGCTGTGGCTGAGAGGTGCGCGCTGTGAGGTG CAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCC TGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGG ATTCACCTTCAGAACTATGGCATGCACTGGGTCCG CCAGGCTCCAGCGGAGGGGCTGGAGTGGGTGGCAG CTATCTGTTTGTATGCGTCTGACAAATACTATGCAG ACGCCGTGAAGGGCCGATTACCATCTCCAGAGAC AACTCCAAGAACCGCTGTATCTGCAAAATGAACAG CCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGC GAGA (SEQ ID NO: 1392)
	AA	EIVLTQSPATLSLSPGERATLSRASQSVFSLAWYQQ KPGQAPRLIYEAATRAATGIPDRFSGSGTEFTLTISR LEPEDFAVYYCQYNQWPLTFGGGTKVEIK (SEQ ID NO: 1356)	QVQLVESGGGVVQPGRSRLSCAASGFTFQNYGMHW VRQAPGEGLWVAIWFDAADSKYYADAVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARDLAIFGVVVD YWGQGLTVTVSS (SEQ ID NO: 1357)

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Table 4. Exemplary CDR1, CDR2, CDR3, CDRH1, CDRH2, and CDRH3 Nucleic Acid ("NA") and Amino Acid ("AA") Sequences

Table 4A. Exemplary CDR1, CDR2, and CDR3 Nucleic Acid ("NA") and Amino Acid ("AA") Sequences

Ab	Type	CDR1	CDR2	CDR3
2G10.303	NA	AGGGCCAGTCAGAGTGTGATAG ACACTTAGCC	GAAGCAGCCACCAGGGCCACT	CAGCAGTATCAGAACTGGCCTCT CACT
		(SEQ ID NO: 1)	(SEQ ID NO: 2)	(SEQ ID NO: 3)
	AA	RASQSVDRHLA	EAATRA	QQYQNWPLT
2G10.304		(SEQ ID NO: 4)	(SEQ ID NO: 5)	(SEQ ID NO: 6)
	NA	AGGGCCAGTCAGAGTGTAAACAG ACACTTAGCC	GAAGCAGCCACCAGGGCCACT	CAGCAGTATCAGAACTGGCCTCT CACT
		(SEQ ID NO: 7)	(SEQ ID NO: 8)	(SEQ ID NO: 9)
2G10.323	AA	RASQSVNRHLA	EAATRA	QQYQNWPLT
		(SEQ ID NO: 10)	(SEQ ID NO: 11)	(SEQ ID NO: 12)
	NA	AGGGCCAGTCAGAGTGTTCATAG ACACTTAGCC	GAAGCAGCCACCAGGGCCACT	CAGCAGTATCAGAACTGGCCTCT CACT
2G10.309		(SEQ ID NO: 13)	(SEQ ID NO: 14)	(SEQ ID NO: 15)
	AA	RASQSVHRHLA	EAATRA	QQYQNWPLT
		(SEQ ID NO: 16)	(SEQ ID NO: 17)	(SEQ ID NO: 18)
2G10.316	NA	AGGGCCAGTCAGAGTGTGAAAG ACACTTAGCC	GAAGCAGCCACCAGGGCCACT	CAGCAGTATCAGAACTGGCCTCT CACT
		(SEQ ID NO: 19)	(SEQ ID NO: 20)	(SEQ ID NO: 21)
	AA	RASQSVRHLA	EAATRA	QQYQNWPLT
2G10.316		(SEQ ID NO: 22)	(SEQ ID NO: 23)	(SEQ ID NO: 24)
	NA	AGGGCCAGTCAGAGTGTTCACAG ACACTTAGCC	GAAGCAGCCACCAGGGCCACT	CAGCAGTATCAGAACTGGCCTCT CACT
		(SEQ ID NO: 25)	(SEQ ID NO: 26)	(SEQ ID NO: 27)
2G10.316	AA	RASQSVRHLA	EAATRA	QQYQNWPLT
		(SEQ ID NO: 28)	(SEQ ID NO: 29)	(SEQ ID NO: 30)

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2G10.604	NA	AGGCCAGTCAGAGTGTTAACAG ACACTTAGCC	GAAAGCAGCCACCAGGGCCACT	CAGCAGTATCAGAACTGGCCTCT CACT
	AA	(SEQ ID NO: 31) RASQSVNRHLA	(SEQ ID NO: 32) EAATRAT	(SEQ ID NO: 33) QQYQNWPLT
2G10.609	NA	(SEQ ID NO: 34) AGGCCAGTCAGAGTGTTGAAAG ACACTTAGCC	(SEQ ID NO: 35) GAAAGCAGCCACCAGGGCCACT	(SEQ ID NO: 36) CAGCAGTATCAGAACTGGCCTCT CACT
	AA	(SEQ ID NO: 37) RASQSVNRHLA	(SEQ ID NO: 38) EAATRAT	(SEQ ID NO: 39) QQYQNWPLT
2G10.603	NA	(SEQ ID NO: 40) AGGCCAGTCAGAGTGTTGATAG ACACTTAGCC	(SEQ ID NO: 41) GAAAGCAGCCACCAGGGCCACT	(SEQ ID NO: 42) CAGCAGTATCAGAACTGGCCTCT CACT
	AA	(SEQ ID NO: 43) RASQSVDRHLA	(SEQ ID NO: 44) EAATRAT	(SEQ ID NO: 45) QQYQNWPLT
2G10.318	NA	(SEQ ID NO: 46) AGGCCAGTCAGAGTGTTCTGAG TCACTTAGCC	(SEQ ID NO: 47) GAAAGCAGCCACCAGGGCCACT	(SEQ ID NO: 48) CAGCAGTATAACAACCTGGCCTCT CACT
	AA	(SEQ ID NO: 49) RASQSVLSHLA	(SEQ ID NO: 50) EAATRAT	(SEQ ID NO: 51) QQYQNWPLT
2G10.324	NA	(SEQ ID NO: 52) AGGCCAGTCAGAGTGTTCTGAG TCACTTAGCC	(SEQ ID NO: 53) GAAAGCAGCCACCAGGGCCACT	(SEQ ID NO: 54) CAGCAGTATCAGAACTGGCCTCT CACT
	AA	(SEQ ID NO: 55) RASQSVLSHLA	(SEQ ID NO: 56) EAATRAT	(SEQ ID NO: 57) QQYQNWPLT
2G10.322	NA	(SEQ ID NO: 58) AGGCCAGTCAGAGTGTTATGAG TCACTTAGCC	(SEQ ID NO: 59) GAAAGCAGCCACCAGGGCCACT	(SEQ ID NO: 60) CAGCAGTATCAGAACTGGCCTCT CACT
	AA	(SEQ ID NO: 61) RASQSVMSHLA	(SEQ ID NO: 62) EAATRAT	(SEQ ID NO: 63) QQYQNWPLT
2G10.322	NA	(SEQ ID NO: 64) AGGCCAGTCAGAGTGTTCTGAC GCACTTAGCC	(SEQ ID NO: 65) GAAAGCAGCCACCAGGGCCACT	(SEQ ID NO: 66) CAGCAGTATCAGAACTGGCCTCT CACT
	AA	(SEQ ID NO: 64) AGGCCAGTCAGAGTGTTCTGAC GCACTTAGCC	(SEQ ID NO: 65) GAAAGCAGCCACCAGGGCCACT	(SEQ ID NO: 66) CAGCAGTATCAGAACTGGCCTCT CACT

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	AA	(SEQ ID NO: 67)	(SEQ ID NO: 68)	(SEQ ID NO: 69)
		RASQSVLTHLA	EAATRAT	QQYQNWPLT
2G10.331	NA	(SEQ ID NO: 70)	(SEQ ID NO: 71)	(SEQ ID NO: 72)
		AGGGCCAGTCAGAGTGTTGATCT GCACTTAGCC	GAAGCAGCCACCAGGGCCACT	CAGCAGTATCAGAACTGGCCTCT CACT
AA	AA	(SEQ ID NO: 73)	(SEQ ID NO: 74)	(SEQ ID NO: 75)
		RASQSVDLHLA	EAATRAT	QQYQNWPLT
2G10.320	NA	(SEQ ID NO: 76)	(SEQ ID NO: 77)	(SEQ ID NO: 78)
		AGGGCCAGTCAGAGTGTTAGCGA ACACTTAGCC	GAAGCAGCCACCAGGGCCACT	CAGCAGTATCAGAACTGGCCTCT CACT
AA	AA	(SEQ ID NO: 79)	(SEQ ID NO: 80)	(SEQ ID NO: 81)
		RASQSVSEHLA	EAATRAT	QQYQNWPLT
2G10.328	NA	(SEQ ID NO: 82)	(SEQ ID NO: 83)	(SEQ ID NO: 84)
		AGGGCCAGTCAGAGTGTTAGCGA ACACTTAGCC	GAAGCAGCCACCAGGGCCACT	CAGCAGTATCAGAACTGGCCTCT CACT
AA	AA	(SEQ ID NO: 85)	(SEQ ID NO: 86)	(SEQ ID NO: 87)
		RASQSVSEHLA	EAATRAT	QQYQNWPLT
2G10.333	NA	(SEQ ID NO: 88)	(SEQ ID NO: 89)	(SEQ ID NO: 90)
		AGGGCCAGTCAGAGTGTTAGCCG GCACTTAGCC	GAAGCAGCCACCAGGGCCACT	CAGCAGTATCAGAACTGGCCTCT CACT
AA	AA	(SEQ ID NO: 91)	(SEQ ID NO: 92)	(SEQ ID NO: 93)
		RASQSVSRHLA	EAATRAT	QQYQHWPLT
2G10.301	NA	(SEQ ID NO: 94)	(SEQ ID NO: 95)	(SEQ ID NO: 11)
		AGGGCCAGTCAGAGTGTTTCAG CCACTTAGCC	GAAGCAGCCACCAGGGCCACT	CAGCAGTATCAGAACTGGCCTCT CACT
AA	AA	(SEQ ID NO: 97)	(SEQ ID NO: 98)	(SEQ ID NO: 99)
		RASQSVFHLA	EAATRAT	QQYQNWPLT
2G10.601	NA	(SEQ ID NO: 100)	(SEQ ID NO: 101)	(SEQ ID NO: 102)
		AGGGCCAGTCAGAGTGTTTCAG CCACTTAGCC	GAAGCAGCCACCAGGGCCACT	CAGCAGTATCAGAACTGGCCTCT CACT
AA	AA	(SEQ ID NO: 103)	(SEQ ID NO: 104)	(SEQ ID NO: 105)
		RASQSVFHLA	EAATRAT	QQYQNWPLT

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2G10.326	NA	(SEQ ID NO: 106) AGGGCCAGTCAGAGTGTTCTGAG TCACTTAGCC	(SEQ ID NO: 107) GAAGCAGCCACCAGGGCCACT	(SEQ ID NO: 108) CAGCAGTATCAGCAGTGGCCTCT CACT
	AA	(SEQ ID NO: 109) RASQSVLSHLA (SEQ ID NO: 112) AGGGCCAGTCAGAGTGTTTTCAG CCACTTAGCC	(SEQ ID NO: 110) EAATRAT (SEQ ID NO: 113) GAAGCAGCCACCAGGGCCACT	(SEQ ID NO: 111) QQYQQWPLT (SEQ ID NO: 114) CAGCAGTATCAGCAGTGGCCTCT CACT
2G10.308	NA	(SEQ ID NO: 115) RASQSVFSLA	(SEQ ID NO: 116) EAATRAT	(SEQ ID NO: 117) QQYQQWPLT
	AA	(SEQ ID NO: 118) AGGGCCAGTCAGAGTGTTTTCAG CCACTTAGCC	(SEQ ID NO: 119) GAAGCAGCCACCAGGGCCACT	(SEQ ID NO: 120) CAGCAGTATCAGCAGTGGCCTCT CACT
2G10.608	NA	(SEQ ID NO: 121) RASQSVFSLA	(SEQ ID NO: 122) EAATRAT	(SEQ ID NO: 123) QQYQQWPLT
	AA	(SEQ ID NO: 124) AGGGCCAGTCAGAGTGTTTTCAG CCACTTAGCC	(SEQ ID NO: 125) GAAGCAGCCACCAGGGCCACT	(SEQ ID NO: 126) CAGCAGTATCAGAACTGGCCTCT CACT
2G10.336	NA	(SEQ ID NO: 127) RASQSVQSHLA	(SEQ ID NO: 128) EAATRAT	(SEQ ID NO: 129) QQYQNWPLT
	AA	(SEQ ID NO: 130) AGGGCCAGTCAGAGTGTTAGTAG CCACTTAGCC	(SEQ ID NO: 131) GAAGCAGCCACCAGGGCCACT	(SEQ ID NO: 132) CAGCAGTATCAGCAGTGGCCTCT CACT
2G10.344	NA	(SEQ ID NO: 133) RASQSVSSH LA	(SEQ ID NO: 134) EAATRAT	(SEQ ID NO: 135) QQYQQWPLT
	AA	(SEQ ID NO: 136) AGGGCCAGTCAGAGTGTTTTCAG GCACCTTAGCC	(SEQ ID NO: 137) GAAGCAGCCACCAGGGCCACT	(SEQ ID NO: 138) CAGCAGTATAACAACACTGGCCTCT CACT
2G10.310	NA	(SEQ ID NO: 139) RASQSVFTHLA	(SEQ ID NO: 140) EAATRAT	(SEQ ID NO: 141) QQYNNWPLT
	AA	(SEQ ID NO: 142) (SEQ ID NO: 143)	(SEQ ID NO: 143) (SEQ ID NO: 144)	(SEQ ID NO: 144)

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2G10.610	NA	AGGCCAGTCAGAGTGTTCAC GCACTTAGCC	GAAAGCAGCCACCAGGGCCACT	CAGCAGTATAACAAGTGGCCTCT CACT
	AA	(SEQ ID NO: 145) RASQSVFHLA	(SEQ ID NO: 146) EAATRAT	(SEQ ID NO: 147) QQYNNWPLT
2G10.312	NA	(SEQ ID NO: 148) AGGCCAGTCAGAGTGTTCATGA CACTTAGCC	(SEQ ID NO: 149) GAAAGCAGCCACCAGGGCCACT	(SEQ ID NO: 150) CAGCAGTATAACAAGTGGCCTCT CACT
	AA	(SEQ ID NO: 151) RASQSVFEHLA	(SEQ ID NO: 152) EAATRAT	(SEQ ID NO: 153) QQYNNWPLT
2G10.329	NA	(SEQ ID NO: 154) AGGCCAGTCAGAGTGTTCATGAACA GCACTTAGCC	(SEQ ID NO: 155) GAAAGCAGCCACCAGGGCCACT	(SEQ ID NO: 156) CAGCAGTATAACAAGTGGCCTCT CACT
	AA	(SEQ ID NO: 157) RASQSVFHLA	(SEQ ID NO: 158) EAATRAT	(SEQ ID NO: 159) QQYNNWPLT
2G10.327	NA	(SEQ ID NO: 160) AGGCCAGTCAGAGTGTTCATAG CCACTTAGCC	(SEQ ID NO: 161) GAAAGCAGCCACCAGGGCCACT	(SEQ ID NO: 162) CAGCAGTATAACAAGTGGCCTCT CACT
	AA	(SEQ ID NO: 163) RASQSVHHLA	(SEQ ID NO: 164) EAATRAT	(SEQ ID NO: 165) QQYNNWPLT
2G10.338	NA	(SEQ ID NO: 166) AGGCCAGTCAGAGTGTTCATCA TCACTTAGCC	(SEQ ID NO: 167) GAAAGCAGCCACCAGGGCCACT	(SEQ ID NO: 168) CAGCAGTATAACAAGTGGCCTCT CACT
	AA	(SEQ ID NO: 169) RASQSVHHLA	(SEQ ID NO: 170) EAATRAT	(SEQ ID NO: 171) QQYNNWPLT
2G10.314	NA	(SEQ ID NO: 172) AGGCCAGTCAGAGTGTTCATAG CACTTAGCC	(SEQ ID NO: 173) GAAAGCAGCCACCAGGGCCACT	(SEQ ID NO: 174) CAGCAGTATAACAAGTGGCCTCT CACT
	AA	(SEQ ID NO: 175) RASQSVHHLA	(SEQ ID NO: 176) EAATRAT	(SEQ ID NO: 177) QQYNNWPLT
2G10.326	NA	(SEQ ID NO: 178) AGGCCAGTCAGAGTGTTCATGT CACTTAGCC	(SEQ ID NO: 179) GAAAGCAGCCACCAGGGCCACT	(SEQ ID NO: 180) CAGCAGTATAACAAGTGGCCTCT CACT

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2G10.341	AA	(SEQ ID NO: 181) RASQSDVNLA	(SEQ ID NO: 182) EAATRAT	(SEQ ID NO: 183) QQYNQWPLT
	NA	(SEQ ID NO: 184) AGGGCCAGTCAGAGTGTTGATGT CCACTTAGCC	(SEQ ID NO: 185) GAAGCAGCCACCAGGGCCACT	(SEQ ID NO: 186) CAGCAGTATAACCACTGGCCTCT CACT
2G10.302	AA	(SEQ ID NO: 187) RASQSDVHLA	(SEQ ID NO: 188) EAATRAT	(SEQ ID NO: 189) QQYNQWPLT
	NA	(SEQ ID NO: 190) AGGGCCAGTCAGAGTGTTTGTGA ACACTTAGCC	(SEQ ID NO: 191) GAAGCAGCCACCAGGGCCACT	(SEQ ID NO: 192) CAGCAGTATAACCACTGGCCTCT CACT
2G10.602	AA	(SEQ ID NO: 193) RASQSVFEHLA	(SEQ ID NO: 194) EAATRAT	(SEQ ID NO: 195) QQYNNWPLT
	NA	(SEQ ID NO: 196) AGGGCCAGTCAGAGTGTTTGTGA ACACTTAGCC	(SEQ ID NO: 197) GAAGCAGCCACCAGGGCCACT	(SEQ ID NO: 198) CAGCAGTATAACCACTGGCCTCT CACT
2G10.325	AA	(SEQ ID NO: 199) RASQSVFEHLA	(SEQ ID NO: 200) EAATRAT	(SEQ ID NO: 201) QQYNNWPLT
	NA	(SEQ ID NO: 202) AGGGCCAGTCAGAGTGTTTGTGA ACACTTAGCC	(SEQ ID NO: 203) GAAGCAGCCACCAGGGCCACT	(SEQ ID NO: 204) CAGCAGTATAACCACTGGCCTCT CACT
2G10.343	AA	(SEQ ID NO: 205) RASQSVFEHLA	(SEQ ID NO: 206) EAATRAT	(SEQ ID NO: 207) QQYNQWPLT
	NA	(SEQ ID NO: 208) AGGGCCAGTCAGAGTGTTCTGGA ACACTTAGCC	(SEQ ID NO: 209) GAAGCAGCCACCAGGGCCACT	(SEQ ID NO: 210) CAGCAGTATAACCACTGGCCTCT CACT
2G10.313	AA	(SEQ ID NO: 211) RASQSVLEHLA	(SEQ ID NO: 212) EAATRAT	(SEQ ID NO: 213) QQYNNWPLT
	NA	(SEQ ID NO: 214) AGGGCCAGTCAGAGTGTTGATAG ACACTTAGCC	(SEQ ID NO: 215) GAAGCAGCCACCAGGGCCACT	(SEQ ID NO: 216) CAGCAGTATAACCACTGGCCTCT CACT
2G10.313	AA	(SEQ ID NO: 217) RASQSDVDRHLA	(SEQ ID NO: 218) EAATRAT	(SEQ ID NO: 219) QQYNQWPLT

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2G10.317	NA	(SEQ ID NO: 220) AGGGCCAGTCAGAGTGTTAAACCG GCACTTAGCC	(SEQ ID NO: 221) GAAGCAGCCACCAGGGCCACT	(SEQ ID NO: 222) CAGCAGTATCAGCAGTGGCCTCT CACT
	AA	(SEQ ID NO: 223) RASQSVNRHLA	(SEQ ID NO: 224) EAATRA	(SEQ ID NO: 225) QQYQWPLT
2G10.311	NA	(SEQ ID NO: 226) AGGGCCAGTCAGAGTGTTAAACGT ACACTTAGCC	(SEQ ID NO: 227) CAGGCAGCCACCAGGGCCACT	(SEQ ID NO: 228) CAGCAGTATAACCACTGGCCTCT CACT
	AA	(SEQ ID NO: 229) RASQSVNVHLA	(SEQ ID NO: 230) QAATRA	(SEQ ID NO: 231) QQYNQWPLT
2G10.306	NA	(SEQ ID NO: 232) AGGGCCAGTCAGAGTGTTCTGAC GCACTTAGCC	(SEQ ID NO: 233) GAAGCAGCCACCAGGGCCACT	(SEQ ID NO: 234) CAGCAGTATCAGAACTGGCCTCT CACT
	AA	(SEQ ID NO: 235) RASQSVLTHLA	(SEQ ID NO: 236) EAATRA	(SEQ ID NO: 237) QQYQWPLT
2G10.606	NA	(SEQ ID NO: 238) AGGGCCAGTCAGAGTGTTCTGAC GCACTTAGCC	(SEQ ID NO: 239) GAAGCAGCCACCAGGGCCACT	(SEQ ID NO: 240) CAGCAGTATCAGAACTGGCCTCT CACT
	AA	(SEQ ID NO: 241) RASQSVLTHLA	(SEQ ID NO: 242) EAATRA	(SEQ ID NO: 243) QQYQWPLT
2G10.347	NA	(SEQ ID NO: 244) AGGGCCAGTCAGAGTGTTAGCAG CAACTTAGCC	(SEQ ID NO: 245) GGTGCAGCCACCAGGGCCACT	(SEQ ID NO: 246) CAGCAGTATAATACTGGCCTCT CACT
	AA	(SEQ ID NO: 247) RASQSVSSNLA	(SEQ ID NO: 248) GAATRA	(SEQ ID NO: 249) QQYNNWPLT
2G10.348	NA	(SEQ ID NO: 250) AGGGCCAGTCAGAGTGTTAGCAG CAACTTAGCC	(SEQ ID NO: 251) GGTGCAGCCACCAGGGCCACT	(SEQ ID NO: 252) CAGCAGTATAATACTGGCCTCT CACT
	AA	(SEQ ID NO: 253) RASQSVSSNLA	(SEQ ID NO: 254) GAATRA	(SEQ ID NO: 255) QQYNNWPLT
		(SEQ ID NO: 256)	(SEQ ID NO: 257)	(SEQ ID NO: 258)

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2G10.346	NA	AGGCCAGTCAGAGTGTTAGCAG CAACTTAGCC	GGTGACGCCACCGGGCCACT	CAGCAGTATAATAACTGGCCTCT CACT
	AA	(SEQ ID NO: 259) RASQSVSSNLA	(SEQ ID NO: 260) GAATRAT	(SEQ ID NO: 261) QQYNNWPLT
2G10.647	NA	(SEQ ID NO: 262) AGGCCAGTCAGAGTGTTAGCAG CAACTTAGCC	(SEQ ID NO: 263) GGTGACGCCACCGGGCCACT	(SEQ ID NO: 264) CAGCAGTATAATAACTGGCCTCT CACT
	AA	(SEQ ID NO: 265) RASQSVSSNLA	(SEQ ID NO: 266) GAATRAT	(SEQ ID NO: 267) QQYNNWPLT
2G10.649	NA	(SEQ ID NO: 268) AGGCCAGTCAGAGTGTTAGCAG CAACTTAGCC	(SEQ ID NO: 269) GAATRAT	(SEQ ID NO: 270) CAGCAGTATAATAACTGGCCTCT CACT
	AA	(SEQ ID NO: 271) RASQSVSSNLA	(SEQ ID NO: 272) EAATRAT	(SEQ ID NO: 273) QQYNNWPLT
2G10.305	NA	(SEQ ID NO: 274) AGGCCAGTCAGAGTGTTGATGT TAACTTAGCC	(SEQ ID NO: 275) AAGCAGCCACCGGGCCACT	(SEQ ID NO: 276) CAGCAGTATCAGAACTGGCCTCT CACT
	AA	(SEQ ID NO: 277) RASQSVSVNLA	(SEQ ID NO: 278) NAATRAT	(SEQ ID NO: 279) QQYQNWPLT
2G10.605	NA	(SEQ ID NO: 280) AGGCCAGTCAGAGTGTTGATGT TAACTTAGCC	(SEQ ID NO: 281) AAGCAGCCACCGGGCCACT	(SEQ ID NO: 282) CAGCAGTATCAGAACTGGCCTCT CACT
	AA	(SEQ ID NO: 283) RASQSVSVNLA	(SEQ ID NO: 284) NAATRAT	(SEQ ID NO: 285) QQYQNWPLT
2G10.340	NA	(SEQ ID NO: 286) AGGCCAGTCAGAGTGTTTCATAC GAACCTTAGCC	(SEQ ID NO: 287) AAGCAGCCACCGGGCCACT	(SEQ ID NO: 288) CAGCAGTATCAGAACTGGCCTCT CACT
	AA	(SEQ ID NO: 289) RASQSVHTNLA	(SEQ ID NO: 290) NAATRAT	(SEQ ID NO: 291) QQYQNWPLT
2G10.340	NA	(SEQ ID NO: 292) AGGCCAGTCAGAGTGTTAACCT GAACCTTAGCC	(SEQ ID NO: 293) CAGCAGCCACCGGGCCACT	(SEQ ID NO: 294) CAGCAGTATAACCAGTGGCCTCT CACT

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2G10.339	AA	(SEQ ID NO: 295) RASQSVNLNLA	(SEQ ID NO: 296) QAATRAT	(SEQ ID NO: 297) QQYNQWPLT
	NA	(SEQ ID NO: 298) AGGGCCAGTCAGAGTGTTTCCA GAACCTTAGCC	(SEQ ID NO: 299) CAGGCAGCCACCAGGGCCACT	(SEQ ID NO: 300) CAGCAGTATAACCAAGTGGCCTCT CACT
2G10.307	AA	(SEQ ID NO: 301) RASQSVFNLA	(SEQ ID NO: 302) QAATRAT	(SEQ ID NO: 303) QQYNQWPLT
	NA	(SEQ ID NO: 304) AGGGCCAGTCAGAGTGTTGATAG ACACTTAGCC	(SEQ ID NO: 305) GAAGCAGCCACCAGGGCCACT	(SEQ ID NO: 306) CAGCAGTATAACCAAGTGGCCTCT CACT
2G10.607	AA	(SEQ ID NO: 307) RASQSVDRHLA	(SEQ ID NO: 308) EAATRAT	(SEQ ID NO: 309) QQYNQWPLT
	NA	(SEQ ID NO: 310) AGGGCCAGTCAGAGTGTTGATAG ACACTTAGCC	(SEQ ID NO: 311) GAAGCAGCCACCAGGGCCACT	(SEQ ID NO: 312) CAGCAGTATAACCAAGTGGCCTCT CACT
2G10.321	AA	(SEQ ID NO: 313) RASQSVDRHLA	(SEQ ID NO: 314) EAATRAT	(SEQ ID NO: 315) QQYNQWPLT
	NA	(SEQ ID NO: 316) AGGGCCAGTCAGAGTGTTAACCG GCACCTTAGCC	(SEQ ID NO: 317) GAAGCAGCCACCAGGGCCACT	(SEQ ID NO: 318) CAGCAGTATAACCAAGTGGCCTCT CACT
2G10.342	AA	(SEQ ID NO: 319) RASQSVNRHLA	(SEQ ID NO: 320) EAATRAT	(SEQ ID NO: 321) QQYNQWPLT
	NA	(SEQ ID NO: 322) AGGGCCAGTCAGAGTGTTGAAAG ACACTTAGCC	(SEQ ID NO: 323) GAAGCAGCCACCAGGGCCACT	(SEQ ID NO: 324) CAGCAGTATCAGCAGTGGCCTCT CACT
2G10.319	AA	(SEQ ID NO: 325) RASQSVRHLA	(SEQ ID NO: 326) EAATRAT	(SEQ ID NO: 327) QQYQQWPLT
	NA	(SEQ ID NO: 328) AGGGCCAGTCAGAGTGTTTTCAG ACACTTAGCC	(SEQ ID NO: 329) GAAGCAGCCACCAGGGCCACT	(SEQ ID NO: 330) CAGCAGTATCAGAACTGGCCTCT CACT
2G10.319	AA	(SEQ ID NO: 331) RASQSVFRHLA	(SEQ ID NO: 332) EAATRAT	(SEQ ID NO: 333) QQYNQWPLT

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2G10.332	NA	(SEQ ID NO: 334) AGGGCCAGTCAGAGTGTCTTGAG TCACCTTAGCC	(SEQ ID NO: 335) GAAGCAGCCACCAGGGCCACT	(SEQ ID NO: 336) CAGCAGTATAACAACCTGGCCTCT CACT
	AA	(SEQ ID NO: 337) RASQSVLSHLA	(SEQ ID NO: 338) EAATRAT	(SEQ ID NO: 339) QQYNNWPLT
2G10.345	NA	(SEQ ID NO: 340) AGGGCCAGTCAGAGTGTTAACAG ACACTTAGCC	(SEQ ID NO: 341) GAAGCAGCCACCAGGGCCACT	(SEQ ID NO: 342) CAGCAGTATAACAACCTGGCCTCT CACT
	AA	(SEQ ID NO: 343) RASQSVNRHLA	(SEQ ID NO: 344) EAATRAT	(SEQ ID NO: 345) QQYNNWPLT
2G10.335	NA	(SEQ ID NO: 346) AGGGCCAGTCAGAGTGTACCAG CCACTTAGCC	(SEQ ID NO: 347) GAAGCAGCCACCAGGGCCACT	(SEQ ID NO: 348) CAGCAGTATAACAACCTGGCCTCT CACT
	AA	(SEQ ID NO: 349) RASQSVTSHLA	(SEQ ID NO: 350) EAATRAT	(SEQ ID NO: 351) QQYNQWPLT
2G10.330	NA	(SEQ ID NO: 352) AGGGCCAGTCAGAGTGTGATCA GCACCTTAGCC	(SEQ ID NO: 353) CAGGCAGCCACCAGGGCCACT	(SEQ ID NO: 354) CAGCAGTATCAGAACTGGCCTCT CACT
	AA	(SEQ ID NO: 355) RASQSVQHLA	(SEQ ID NO: 356) QAATRAT	(SEQ ID NO: 357) QQYNNWPLT
iPS:529381	AA	RASQSVSEHLA (SEQ ID NO: 1290)	EAATRAT (SEQ ID NO: 1291)	QQYNNWPLT (SEQ ID NO: 1292)
	AA	RASQSVSSNLA (SEQ ID NO: 1300)	GAATRAT (SEQ ID NO: 1301)	QQYNNWPLT (SEQ ID NO: 1302)
iPS:529397	AA	RASQSVSSNLA (SEQ ID NO: 1310)	GAATRAT (SEQ ID NO: 1311)	QQYNNWPLT (SEQ ID NO: 1312)
	AA	RASQSVSEHLA (SEQ ID NO: 1320)	EAATRAT (SEQ ID NO: 1321)	QQYNNWPLT (SEQ ID NO: 1322)
iPS:529400	AA	RASQSVSSNLA (SEQ ID NO: 1330)	GAATRAT (SEQ ID NO: 1331)	QQYNNWPLT (SEQ ID NO: 1332)

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IPS:529403	AA	RASQSVDLHLA	EAAATTRAT	QYQNWPLT
		(SEQ ID NO: 1340)		(SEQ ID NO: 1342)
IPS:529404	AA	RASQSVNLNLA	QAAATTRAT	QYQNWPLT
		(SEQ ID NO: 1350)		(SEQ ID NO: 1352)
IPS:529405	AA	RASQSVFSLA	EAAATTRAT	QYQNWPLT
		(SEQ ID NO: 1360)		(SEQ ID NO: 1362)

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Table 4B. Exemplary CDRH1, CDRH2, and CDRH3 Nucleotide and Amino Acid Sequences

Ab	Type	CDRH1	CDRH2	CDRH3
2G10.303	NA	AACATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGGC	GATTGGCGATTTTGGAGTGGT CCCCGACTAC
		(SEQ ID NO: 361)	(SEQ ID NO: 362)	(SEQ ID NO: 363)
	AA	NYGMH	AIWFDASDKYYADAVKG	DLAIFGVVPDY
2G10.304		(SEQ ID NO: 364)	(SEQ ID NO: 365)	(SEQ ID NO: 366)
	NA	AACATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGGC	GATTGGCGATTTTGGAGTGGT CCCCGACTAC
		(SEQ ID NO: 367)	(SEQ ID NO: 368)	(SEQ ID NO: 369)
2G10.323	AA	NYGMH	AIWFDASDKYYADAVKG	DLAIFGVVPDY
		(SEQ ID NO: 370)	(SEQ ID NO: 371)	(SEQ ID NO: 372)
	NA	AACATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGGC	GATTGGCGATTTTGGAGTGGT CCCCGACTAC
2G10.329		(SEQ ID NO: 373)	(SEQ ID NO: 374)	(SEQ ID NO: 375)
	AA	NYGMH	AIWFDASDKYYADAVKG	DLAIFGVVPDY
		(SEQ ID NO: 376)	(SEQ ID NO: 377)	(SEQ ID NO: 378)
2G10.309	NA	AACATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGGC	GATTGGCGATTTTGGAGTGGT CCCCGACTAC
		(SEQ ID NO: 379)	(SEQ ID NO: 380)	(SEQ ID NO: 381)
	AA	NYGMH	AIWFDASDKYYADAVKG	DLAIFGVVPDY
2G10.31		(SEQ ID NO: 382)	(SEQ ID NO: 383)	(SEQ ID NO: 384)
	NA	AACATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGGC	GATTGGCGATTTTGGAGTGGT CCCCGACTAC
		(SEQ ID NO: 385)	(SEQ ID NO: 386)	(SEQ ID NO: 387)

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2G10.604	AA	NYGMH (SEQ ID NO: 388)	AIWFDASDKYYADAVKG (SEQ ID NO: 389)	DLAIFGVVPDY (SEQ ID NO: 390)
	NA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGGC	GATTGGCGATTTTGGAGTGGT CCCCGACTAC
2G10.609	AA	(SEQ ID NO: 391)	(SEQ ID NO: 392)	(SEQ ID NO: 393)
	NA	NYGMH (SEQ ID NO: 394)	AIWFDASDKYYADAVKG (SEQ ID NO: 395)	DLAIFGVVPDY (SEQ ID NO: 396)
2G10.603	AA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGGC	GATTGGCGATTTTGGAGTGGT CCCCGACTAC
	NA	(SEQ ID NO: 397)	(SEQ ID NO: 398)	(SEQ ID NO: 399)
2G10.318	AA	NYGMH (SEQ ID NO: 400)	AIWFDASDKYYADAVKG (SEQ ID NO: 401)	DLAIFGVVPDY (SEQ ID NO: 402)
	NA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGGC	GATTGGCGATTTTGGAGTGGT CCCCGACTAC
2G10.324	AA	(SEQ ID NO: 403)	(SEQ ID NO: 404)	(SEQ ID NO: 405)
	NA	NYGMH (SEQ ID NO: 406)	AIWFDASDKYYADAVKG (SEQ ID NO: 407)	DLAIFGVVPDY (SEQ ID NO: 408)
2G10.318	AA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGGC	GATTGGCGATTTTGGAGTGGT CCCCGACTAC
	NA	(SEQ ID NO: 409)	(SEQ ID NO: 410)	(SEQ ID NO: 411)
2G10.324	AA	NYGMH (SEQ ID NO: 412)	AIWFDASDKYYADAVKG (SEQ ID NO: 413)	DLAIFGVVPDY (SEQ ID NO: 414)
	NA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGGC	GATTGGCGATTTTGGAGTGGT CCCCGACTAC
2G10.324	AA	(SEQ ID NO: 415)	(SEQ ID NO: 416)	(SEQ ID NO: 417)
	NA	NYGMH (SEQ ID NO: 418)	AIWFDASDKYYADAVKG (SEQ ID NO: 419)	DLAIFGVVPDY (SEQ ID NO: 420)

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2G10.322	NA	AACATATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGC	GATTTGGCGATTTTGGAGTGGT CCCCGACTAC
	AA	(SEQ ID NO: 421) NYGMH (SEQ ID NO: 424)	(SEQ ID NO: 422) AIWFDASDKYYADAVKG (SEQ ID NO: 425)	(SEQ ID NO: 423) DLAIFGVVPDY (SEQ ID NO: 426)
2G10.315	NA	AACATATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGC	GATTTGGCGATTTTGGAGTGGT CCCCGACTAC
	AA	(SEQ ID NO: 427) NYGMH (SEQ ID NO: 430)	(SEQ ID NO: 428) AIWFDASDKYYADAVKG (SEQ ID NO: 431)	(SEQ ID NO: 429) DLAIFGVVPDY (SEQ ID NO: 432)
2G10.331	NA	AACATATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGC	GATTTGGCGATTTTGGAGTGGT CCCCGACTAC
	AA	(SEQ ID NO: 433) NYGMH (SEQ ID NO: 436)	(SEQ ID NO: 434) AIWFDASDKYYADAVKG (SEQ ID NO: 437)	(SEQ ID NO: 435) DLAIFGVVPDY (SEQ ID NO: 438)
2G10.320	NA	AACATATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGC	GATCTGGCGATTTTGGAGTGGT TCCCGACTAC
	AA	(SEQ ID NO: 439) NYGMH (SEQ ID NO: 442)	(SEQ ID NO: 440) AIWFDASDKYYADAVKG (SEQ ID NO: 443)	(SEQ ID NO: 441) DLAIFGVIPDY (SEQ ID NO: 444)
2G10.328	NA	AACATATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGC	GATTTGGCGATTTTGGAGTGGT CCCCGACTAC
	AA	(SEQ ID NO: 445) NYGMH (SEQ ID NO: 448)	(SEQ ID NO: 446) AIWFDASDKYYADAVKG (SEQ ID NO: 449)	(SEQ ID NO: 447) DLAIFGVVPDY (SEQ ID NO: 450)
2G10.33	NA	AACATATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGC	GATTTGGCGATTTTGGAGTGGT CCCCGACTAC
		(SEQ ID NO: 451)	(SEQ ID NO: 452)	(SEQ ID NO: 453)

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2G10.301	AA	NYGMH (SEQ ID NO: 454)	AIWFDASDKYYADAVKG (SEQ ID NO: 455)	DLAIFGVVPDY (SEQ ID NO: 456)
	NA	AACTATGGCATGCAC	GCTATATGGTTTGATGCGTCTGA CAAATACTATGCAGACGCCGTGA AGGGC	GATCTTGC GATTTTGGAGTGGT CCCCGACTAC
2G10.601	AA	(SEQ ID NO: 457)	(SEQ ID NO: 458)	(SEQ ID NO: 459)
	NA	NYGMH (SEQ ID NO: 460)	AIWFDASDKYYADAVKG (SEQ ID NO: 461)	DLAIFGVVPDY (SEQ ID NO: 462)
2G10.326	AA	AACTATGGCATGCAC	GCTATATGGTTTGATGCGTCTGA CAAATACTATGCAGACGCCGTGA AGGGC	GATCTTGC GATTTTGGAGTGGT CCCCGACTAC
	NA	(SEQ ID NO: 463)	(SEQ ID NO: 464)	(SEQ ID NO: 465)
2G10.326	AA	NYGMH (SEQ ID NO: 466)	AIWFDASDKYYADAVKG (SEQ ID NO: 467)	DLAIFGVVPDY (SEQ ID NO: 468)
	NA	AACTATGGCATGCAC	GCTATATGGTTTGATGCGTCTGA CAAATACTATGCAGACGCCGTGA AGGGC	GATCTTGC GATTTTGGAGTGGT CCCCGACTAC
2G10.308	AA	(SEQ ID NO: 469)	(SEQ ID NO: 470)	(SEQ ID NO: 471)
	NA	NYGMH (SEQ ID NO: 472)	AIWFDASDKYYADAVKG (SEQ ID NO: 473)	DLAIFGVVPDY (SEQ ID NO: 474)
2G10.608	AA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGGC	GATTTGGCGATTTTGGAGTGGT CCCCGACTAC
	NA	(SEQ ID NO: 475)	(SEQ ID NO: 476)	(SEQ ID NO: 477)
2G10.608	AA	NYGMH (SEQ ID NO: 478)	AIWFDASDKYYADAVKG (SEQ ID NO: 479)	DLAIFGVVPDY (SEQ ID NO: 480)
	NA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGGC	GATTTGGCGATTTTGGAGTGGT CCCCGACTAC
2G10.608	AA	(SEQ ID NO: 481)	(SEQ ID NO: 482)	(SEQ ID NO: 483)
	NA	NYGMH (SEQ ID NO: 484)	AIWFDASDKYYADAVKG (SEQ ID NO: 485)	DLAIFGVVPDY (SEQ ID NO: 486)

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2G10.336	NA	AACATATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGC	GATATTGCGATTTTGGAGTGGT CCCCGACTAC
	AA	(SEQ ID NO: 487) NYGMH (SEQ ID NO: 490)	(SEQ ID NO: 488) AIWFDASDKYYADAVKG (SEQ ID NO: 491)	(SEQ ID NO: 489) DIAIFGVVPDY (SEQ ID NO: 492)
2G10.344	NA	AACATATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGC	GATATTGCGATTTTGGAGTGGT CCCCGACTAC
	AA	(SEQ ID NO: 493) NYGMH (SEQ ID NO: 496)	(SEQ ID NO: 494) AIWFDASDKYYADAVKG (SEQ ID NO: 497)	(SEQ ID NO: 495) DIAIFGVVPDY (SEQ ID NO: 498)
2G10.310	NA	AACATATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGC	GATTGGCGATTTTGGAGTGGT CCCCGACTAC
	AA	(SEQ ID NO: 499) NYGMH (SEQ ID NO: 502)	(SEQ ID NO: 500) AIWFDASDKYYADAVKG (SEQ ID NO: 503)	(SEQ ID NO: 501) DLAIFGVVPDY (SEQ ID NO: 504)
2G10.610	NA	AACATATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGC	GATTGGCGATTTTGGAGTGGT CCCCGACTAC
	AA	(SEQ ID NO: 505) NYGMH (SEQ ID NO: 508)	(SEQ ID NO: 506) AIWFDASDKYYADAVKG (SEQ ID NO: 509)	(SEQ ID NO: 507) DLAIFGVVPDY (SEQ ID NO: 510)
2G10.312	NA	AACATATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGC	GATTGGCGATTTTGGAGTGGT CCCCGACTAC
	AA	(SEQ ID NO: 511) NYGMH (SEQ ID NO: 514)	(SEQ ID NO: 512) AIWFDASDKYYADAVKG (SEQ ID NO: 515)	(SEQ ID NO: 513) DLAIFGVVPDY (SEQ ID NO: 516)
2G10.32	NA	AACATATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGC	GATTGGCGATTTTGGAGTGGT CCCCGACTAC
	AA	(SEQ ID NO: 517) NYGMH (SEQ ID NO: 518)	(SEQ ID NO: 519) DLAIFGVVPDY (SEQ ID NO: 520)	(SEQ ID NO: 521) DLAIFGVVPDY (SEQ ID NO: 522)

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2G10.327	AA	NYGMH (SEQ ID NO: 520)	AIWFDASDKYYADAVKG (SEQ ID NO: 521)	DLAIFGVVPDY (SEQ ID NO: 522)
	NA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGGC	GATTTGGCGATTTTGGAGTGGT CCCCGACTAC
2G10.338	AA	(SEQ ID NO: 523)	(SEQ ID NO: 524)	(SEQ ID NO: 525)
	NA	NYGMH (SEQ ID NO: 526)	AIWFDASDKYYADAVKG (SEQ ID NO: 527)	DLAIFGVVPDY (SEQ ID NO: 528)
2G10.314	AA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGGC	GATTTGGCGATTTTGGAGTGGT CCCCGACTAC
	NA	(SEQ ID NO: 529)	(SEQ ID NO: 530)	(SEQ ID NO: 531)
2G10.337	AA	NYGMH (SEQ ID NO: 532)	AIWFDASDKYYADAVKG (SEQ ID NO: 533)	DLAIFGVVPDY (SEQ ID NO: 534)
	NA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGGC	GATTTGGCGATTTTGGAGTGGT CCCCGACTAC
2G10.341	AA	(SEQ ID NO: 535)	(SEQ ID NO: 536)	(SEQ ID NO: 537)
	NA	NYGMH (SEQ ID NO: 538)	AIWFDASDKYYADAVKG (SEQ ID NO: 539)	DLAIFGVVPDY (SEQ ID NO: 540)
2G10.337	AA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGGC	GATTTGGCGATTTTGGAGTGGT CCCCGACTAC
	NA	(SEQ ID NO: 541)	(SEQ ID NO: 542)	(SEQ ID NO: 543)
2G10.341	AA	NYGMH (SEQ ID NO: 544)	AIWFDASDKYYADAVKG (SEQ ID NO: 545)	DLAIFGVVPDY (SEQ ID NO: 546)
	NA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGGC	GATTTGGCGATTTTGGAGTGGT CCCCGACTAC
2G10.341	AA	(SEQ ID NO: 547)	(SEQ ID NO: 548)	(SEQ ID NO: 549)
	NA	NYGMH (SEQ ID NO: 550)	AIWFDASDKYYADAVKG (SEQ ID NO: 551)	DLAIFGVVPDY (SEQ ID NO: 552)

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2G10.302	NA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGC	GATATTGCGATTTTGGAGTGTTT CCCGACTAC
	AA	(SEQ ID NO: 553) NYGMH (SEQ ID NO: 556) AACTATGGCATGCAC	(SEQ ID NO: 554) AIWFDASDKYYADAVKG (SEQ ID NO: 557) GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGC	(SEQ ID NO: 555) DIAIFGVFPDY (SEQ ID NO: 558) GATATTGCGATTTTGGAGTGTTT CCCGACTAC
2G10.602	NA	(SEQ ID NO: 559) NYGMH (SEQ ID NO: 562) AACTATGGCATGCAC	(SEQ ID NO: 560) AIWFDASDKYYADAVKG (SEQ ID NO: 563) GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGC	(SEQ ID NO: 561) DIAIFGVFPDY (SEQ ID NO: 564) GATATTGCGATTTTGGAGTGTTT CCCGACTAC
	AA	(SEQ ID NO: 565) NYGMH (SEQ ID NO: 568) AACTATGGCATGCAC	(SEQ ID NO: 566) AIWFDASDKYYADAVKG (SEQ ID NO: 569) GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGC	(SEQ ID NO: 567) DIAIFGVFPDY (SEQ ID NO: 570) GATATTGCGATTTTGGAGTGTTT CCCGACTAC
2G10.325	NA	(SEQ ID NO: 571) NYGMH (SEQ ID NO: 574) AACTATGGCATGCAC	(SEQ ID NO: 572) AIWFDASDKYYADAVKG (SEQ ID NO: 575) GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGC	(SEQ ID NO: 573) DIAIFGVFPDY (SEQ ID NO: 576) GATATTGCGATTTTGGAGTGTTT CCCGACTAC
	AA	(SEQ ID NO: 577) NYGMH (SEQ ID NO: 580) AACTATGGCATGCAC	(SEQ ID NO: 578) AIWFDASDKYYADAVKG (SEQ ID NO: 581) GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGC	(SEQ ID NO: 579) DIAIFGVFPDY (SEQ ID NO: 582) GATATTGCGATTTTGGAGTGTTT CCCGACTAC
2G10.313	NA	(SEQ ID NO: 583) NYGMH (SEQ ID NO: 586) AACTATGGCATGCAC	(SEQ ID NO: 584) AIWFDASDKYYADAVKG (SEQ ID NO: 587) GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGC	(SEQ ID NO: 585) DIAIFGVFPDY (SEQ ID NO: 588) GATATTGCGATTTTGGAGTGTTT CCCGACTAC
	AA	(SEQ ID NO: 589) NYGMH (SEQ ID NO: 592) AACTATGGCATGCAC	(SEQ ID NO: 590) AIWFDASDKYYADAVKG (SEQ ID NO: 593) GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGC	(SEQ ID NO: 591) DIAIFGVFPDY (SEQ ID NO: 594) GATATTGCGATTTTGGAGTGTTT CCCGACTAC
2G10.31	NA	(SEQ ID NO: 595) NYGMH (SEQ ID NO: 598) AACTATGGCATGCAC	(SEQ ID NO: 596) AIWFDASDKYYADAVKG (SEQ ID NO: 599) GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGC	(SEQ ID NO: 597) DIAIFGVFPDY (SEQ ID NO: 600) GATATTGCGATTTTGGAGTGTTT CCCGACTAC
	AA	(SEQ ID NO: 601) NYGMH (SEQ ID NO: 604) AACTATGGCATGCAC	(SEQ ID NO: 602) AIWFDASDKYYADAVKG (SEQ ID NO: 605) GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGC	(SEQ ID NO: 603) DIAIFGVFPDY (SEQ ID NO: 606) GATATTGCGATTTTGGAGTGTTT CCCGACTAC

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2G10.311	AA	NYGMH (SEQ ID NO: 586)	AIWFDASDKYYADAVKG (SEQ ID NO: 587)	DIAIFGVFPDY (SEQ ID NO: 588)
	NA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGGC	GATATTGCGATTTTGGAGTGGT CCCCGACTAC
2G10.306	AA	(SEQ ID NO: 589)	(SEQ ID NO: 590)	(SEQ ID NO: 591)
	NA	NYGMH (SEQ ID NO: 592)	AIWFDASDKYYADAVKG (SEQ ID NO: 593)	DIAIFGVFPDY (SEQ ID NO: 594)
2G10.606	AA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGGC	GATATTGCGATTTTGGAGTGGT CCCCGACTAC
	NA	(SEQ ID NO: 595)	(SEQ ID NO: 596)	(SEQ ID NO: 597)
2G10.606	AA	NYGMH (SEQ ID NO: 598)	AIWFDASDKYYADAVKG (SEQ ID NO: 599)	DIAIFGVFPDY (SEQ ID NO: 600)
	NA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGGC	GATATTGCGATTTTGGAGTGGT CCCCGACTAC
2G10.347	AA	(SEQ ID NO: 601)	(SEQ ID NO: 602)	(SEQ ID NO: 603)
	NA	NYGMH (SEQ ID NO: 604)	AIWFDASDKYYADAVKG (SEQ ID NO: 605)	DIAIFGVFPDY (SEQ ID NO: 606)
2G10.348	AA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGGC	GATTTGGCGATTTTGGAGTGGT CCCCGACTAC
	NA	(SEQ ID NO: 607)	(SEQ ID NO: 608)	(SEQ ID NO: 609)
2G10.348	AA	NYGMH (SEQ ID NO: 610)	AIWFDASDKYYADAVKG (SEQ ID NO: 611)	DIAIFGVFPDY (SEQ ID NO: 612)
	NA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGGC	GATCAGCGATTTTGGAGTGGT CCCCGACTAC
2G10.348	AA	(SEQ ID NO: 613)	(SEQ ID NO: 614)	(SEQ ID NO: 615)
	NA	NYGMH (SEQ ID NO: 616)	AIWFDASDKYYADAVKG (SEQ ID NO: 617)	DIAIFGVFPDY (SEQ ID NO: 618)

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2G10.346	NA	AACATATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGC	(SEQ ID NO: 619)	(SEQ ID NO: 620)	(SEQ ID NO: 621)	GATATTGCGATTTTGGAGTGGT CCCCGACTAC
	AA	NYGMH	AIWFDASDKYYADAVKG	(SEQ ID NO: 622)	(SEQ ID NO: 623)	DIAIFGVVPDY	
2G10.647	NA	AACATATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGC	(SEQ ID NO: 625)	(SEQ ID NO: 626)	(SEQ ID NO: 627)	GATTTGGCGATTTTGGAGTGGT CCCCGACTAC
	AA	NYGMH	AIWFDASDKYYADAVKG	(SEQ ID NO: 628)	(SEQ ID NO: 629)	DLAIFGVVPDY	
2G10.649	NA	AACATATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGC	(SEQ ID NO: 631)	(SEQ ID NO: 632)	(SEQ ID NO: 633)	GATCAGGCGATTTTGGAGTGGT CCCCGATTAC
	AA	NYGMH	AIWFDASDKYYADAVKG	(SEQ ID NO: 634)	(SEQ ID NO: 635)	DQAIFGVVPDY	
2G10.305	NA	AACATATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGC	(SEQ ID NO: 637)	(SEQ ID NO: 638)	(SEQ ID NO: 639)	GATTTGGCGATTTTGGAGTGGT CCCCGACTAC
	AA	NYGMH	AIWFDASDKYYADAVKG	(SEQ ID NO: 640)	(SEQ ID NO: 641)	DLAIFGVVPDY	
2G10.605	NA	AACATATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGC	(SEQ ID NO: 643)	(SEQ ID NO: 644)	(SEQ ID NO: 645)	GATTTGGCGATTTTGGAGTGGT CCCCGACTAC
	AA	NYGMH	AIWFDASDKYYADAVKG	(SEQ ID NO: 646)	(SEQ ID NO: 647)	DLAIFGVVPDY	
2G10.34	NA	AACATATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGC	(SEQ ID NO: 649)	(SEQ ID NO: 650)	(SEQ ID NO: 651)	GATATTGCGATTTTGGAGTGGT CCCCGACTAC

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2G10.334	AA	NYGMH (SEQ ID NO: 652)	AIWFDASDKYYADAVKG (SEQ ID NO: 653)	DIAIFGVVPDY (SEQ ID NO: 654)
	NA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGGC	GATTTGGCGATTTTGGAGTGGT CCCCGACTAC
2G10.339	AA	(SEQ ID NO: 655)	(SEQ ID NO: 656)	(SEQ ID NO: 657)
	NA	NYGMH (SEQ ID NO: 658)	AIWFDASDKYYADAVKG (SEQ ID NO: 659)	DLAIFGVVPDY (SEQ ID NO: 660)
2G10.307	AA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTGA TAAATACTATGCAGACGCCGTGA AGGGC	GATATTGCGATTTTGGAGTGGT CCCCGACTAC
	NA	(SEQ ID NO: 661)	(SEQ ID NO: 662)	(SEQ ID NO: 663)
2G10.607	AA	NYGMH (SEQ ID NO: 664)	AIWFDASDKYYADAVKG (SEQ ID NO: 665)	DIAIFGVVPDY (SEQ ID NO: 666)
	NA	AACTATGGCATGCAC	GCTATATGGTTTGATGCGTACGG TAAATACTATGCAGACGCCGTGA AGGGC	GATCAGACGATTTTGGAGTGGT CCCCGACTAC
2G10.321	AA	(SEQ ID NO: 667)	(SEQ ID NO: 668)	(SEQ ID NO: 669)
	NA	NYGMH (SEQ ID NO: 670)	AIWFDAYGKYYADAVKG (SEQ ID NO: 671)	DQTIFGVVPDY (SEQ ID NO: 672)
2G10.607	AA	AACTATGGCATGCAC	GCTATATGGTTTGATGCGTACGG TAAATACTATGCAGACGCCGTGA AGGGC	GATCAGACGATTTTGGAGTGGT CCCCGACTAC
	NA	(SEQ ID NO: 673)	(SEQ ID NO: 674)	(SEQ ID NO: 675)
2G10.321	AA	NYGMH (SEQ ID NO: 676)	AIWFDAYGKYYADAVKG (SEQ ID NO: 677)	DQTIFGVVPDY (SEQ ID NO: 678)
	NA	AACTATGGCATGCAC	GCTATATGGTTTGATGCGTACGG TAAATACTATGCAGACGCCGTGA AGGGC	GATAAGACGATTTTGGAGTGGT CCCCGACTAC
2G10.321	AA	(SEQ ID NO: 679)	(SEQ ID NO: 680)	(SEQ ID NO: 681)
	NA	NYGMH (SEQ ID NO: 682)	AIWFDAYGKYYADAVKG (SEQ ID NO: 683)	DKTIFGVVPDY (SEQ ID NO: 684)

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2G10.342	NA	AACATATGGCATGCAC	GCTATATGGTTTGATGCGTACGG TAAATACTATGCAGACGCCGTGA AGGC	(SEQ ID NO: 685)	(SEQ ID NO: 686)	(SEQ ID NO: 687)	GATAAGACGATTTTGGAGTGGT CCCCGACTAC
	AA			NYGMH	AIWFDAYGKYYADAVKG	DKTIFGVVPDY	
2G10.319	NA	AACATATGGCATGCAC	GCTATATGGTTTGATGCGTACGG TAAATACTATGCAGACGCCGTGA AGGC	(SEQ ID NO: 688)	(SEQ ID NO: 689)	(SEQ ID NO: 690)	GATAAGACGATTTTGGAGTGGT CCCCGACTAC
	AA			NYGMH	AIWFDAYGKYYADAVKG	DKTIFGVVPDY	
2G10.332	NA	AACATATGGCATGCAC	GCTATATGGTTTGATGCGTACGA CAAATACTATGCAGACGCCGTGA AGGC	(SEQ ID NO: 691)	(SEQ ID NO: 692)	(SEQ ID NO: 693)	GATAAGTCGATTTTGGAGTGGT CCCCGACTAC
	AA			NYGMH	AIWFDAYDKYYADAVKG	DKSIFGVVPDY	
2G10.345	NA	AACATATGGCATGCAC	GCTATATGGTTTGATGCGTACGA CAAATACTATGCAGACGCCGTGA AGGC	(SEQ ID NO: 697)	(SEQ ID NO: 698)	(SEQ ID NO: 699)	GATAAGTCGATTTTGGAGTGGT CCCCGACTAC
	AA			NYGMH	AIWFDAYDKYYADAVKG	DKSIFGVVPDY	
2G10.335	NA	AACATATGGCATGCAC	GCTATATGGTTTGATGCGTACGA CAAATACTATGCAGACGCCGTGA AGGC	(SEQ ID NO: 700)	(SEQ ID NO: 701)	(SEQ ID NO: 702)	GATAAGTCGATTTTGGAGTGGT CCCCGACTAC
	AA			NYGMH	AIWFDAYDKYYADAVKG	DKSIFGVVPDY	
2G10.333	NA	AACATATGGCATGCAC	GCTATATGGTTTGATGCGTACGA CAAATACTATGCAGACGCCGTGA AGGC	(SEQ ID NO: 703)	(SEQ ID NO: 704)	(SEQ ID NO: 705)	GATCTCGCGATTTTGGAGTGGT CCCCGACTAC
	AA			NYGMH	AIWFDAYDKYYADAVKG	DLAIFGVVPDY	
2G10.33	NA	AACATATGGCATGCAC	GCTATATGGTTTGATGCGGCTTT CAAATACTATGCAGACGCCGTGA AGGC	(SEQ ID NO: 712)	(SEQ ID NO: 713)	(SEQ ID NO: 714)	GATCTCGCGATTTTGGAGTGGT CCCCGACTAC
	NA			(SEQ ID NO: 715)	(SEQ ID NO: 716)	(SEQ ID NO: 717)	

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	AA	NYGMH (SEQ ID NO: 718)		AIWFDAAFKYYADAVKG (SEQ ID NO: 719)		DLAIFGVVPDY (SEQ ID NO: 720)
		NYGMH (SEQ ID NO: 1293)	NYGMH (SEQ ID NO: 1294)	AIWFDASDKYYADAVKG (SEQ ID NO: 1295)	DLAIFGVVPDY (SEQ ID NO: 1296)	
IPS:529381	AA	NYGMH (SEQ ID NO: 1303)	NYGMH (SEQ ID NO: 1304)	AIWFDASDKYYADAVKG (SEQ ID NO: 1305)	DQALFGVVPDY (SEQ ID NO: 1306)	
IPS:529382	AA	NYGMH (SEQ ID NO: 1313)	NYGMH (SEQ ID NO: 1314)	AIWFDASDKYYADAVKG (SEQ ID NO: 1315)	DLAIFGVVPDY (SEQ ID NO: 1316)	
IPS:529397	AA	NYGMH (SEQ ID NO: 1323)	NYGMH (SEQ ID NO: 1324)	AIWFDASDKYYADAVKG (SEQ ID NO: 1325)	DLAIFGVVPDY (SEQ ID NO: 1326)	
IPS:529399	AA	NYGMH (SEQ ID NO: 1333)	NYGMH (SEQ ID NO: 1334)	AIWFDASDKYYADAVKG (SEQ ID NO: 1335)	DLAIFGVVPDY (SEQ ID NO: 1336)	
IPS:529400	AA	NYGMH (SEQ ID NO: 1343)	NYGMH (SEQ ID NO: 1344)	AIWFDASDKYYADAVKG (SEQ ID NO: 1345)	DLAIFGVVPDY (SEQ ID NO: 1346)	
IPS:529403	AA	NYGMH (SEQ ID NO: 1353)	NYGMH (SEQ ID NO: 1354)	AIWFDASDKYYADAVKG (SEQ ID NO: 1355)	DLAIFGVVPDY (SEQ ID NO: 1356)	
IPS:529404	AA	NYGMH (SEQ ID NO: 1363)	NYGMH (SEQ ID NO: 1364)	AIWFDASDKYYADAVKG (SEQ ID NO: 1365)	DLAIFGVVPDY (SEQ ID NO: 1366)	

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Table 5. Exemplary Light and Heavy Chain Nucleic Acid (“NA”) and Amino Acid (“AA”) Sequences

Ab	Description	Type	LC	HC
2G10.303	[hu anti- <huGIPR> 2G10.303 VK3 (1-236) VLJ::huKLC -CL + [Unknown anti- <huGIPR> 2G10.610 VH3 (1-472) VHJ::huIgG1 zSEFL2-2 (mAb); LMR ID: SS- 26180	NA	GAAATAGTGATGACGCAGTCT CCAGCCACCCTGTCTGTGTCT CCAGGGAAAGAGCCACCCT CTCCTGACGGCCAGTCAGAG TGTTGATAGACACTTAGCCTG GTACCAGCAGAAACCTGGCC AGGCTCCAGGCTCCTCATCT ACGAAGCAGCCACCAGGGCC ACTGGTATCCAGCCAGGTTTC AGTGGCAGTGGGTCTGGGAC AGAGTTCAC'TCTCACCATCAG CAGCCTGCAGTCTGAAGATT TGCAGTTTATTACTGTTCAGCA GTATCAGAACTGGCTCTCAC TTTCGGCGAGGGACCAAGGT GGAGATCAAAACGAACGGTGG CTGCACCATCTGTCTTCATCTT CCCGCCATCTGATGAGCAGTT GAAATCTGGAAC'TGCCCTGT TGTGTGCTGCTGAATAACTT CTATCCACAGAGAGGCCAAAG TACAGTGGAAAGTGGATAAC GCCCTCCAATCGGGTAACTCC CAGGAGAGTGTACACAGAGCA GGACAGCAAGGACAGCACCT ACAGCCTCAGCAGCACCTGA CGCTGAGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCAACCATCAGGG CCTGAGCTCGCCGTCACAA GAGCTTCAACAGGGGAGAGT GT	CAGGTGCAGCTGGTGGAGTCTGGGGAGGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCAGTAACTATGGCATGCAC'TGGGTCCGCCAGGCTCCA GGCGAGGGCTGGAGTGGTGGCAGCTATATGTTTGTATGC AAGTGATAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAAC'TCCAAGAACACGGCTGTATCTGCAA ATGAACAGCCTGAGAGCCGAGACACGGCTGTGTATTACTG TGGAGAGATTGGCGATTTTGGAGTGGTCCCGACTACT GGGGCCAGGGAACCTGGTCAACCGTGTCTAGTGCCTCCACC AAGGGCCCATCGGTCTTCCCTTGGCACCC'TCCTCCAAGAG CACCTCTGGGGCACAGCGGCCCTGGGCTGCCGTGGTCAAGG ACTACTTCCCGAACC'GGTGACGGTGTCTGTGAAC'TCAGGC GCCCTGACAGCGGTGCACACCTTCCCGGCTGTCTCTACA GTCTCTAGCACTCTACTCCCTCAGCAGCGGTGGTGAACCTGC CCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTG AATCACAAAGCCAGCAACACCAAGTGGACAAAGAAAGTTG AGCCAAATCTTGTGACAAAC'TCACATGCCCACCGTGC CCAGCACCTGAAC'TCCTGGGGGACCGTCACTCTTCTCTTC CCCCAAACCCAAAGACACCC'CATGATCTCCCGGACCCC TGAGGTCAACATGCGTGGTGGTGGACGTGAGCCACGAAGACC CTGAGGTCAAAGTTCAACTGTTACGTGGACGGCGTGGAGGTG CATATGCCAAGACAAGCCGTGGGAGGAGCAGTACGGCA GCACGTACC'TTGGTTCAGCTCAGCTCCTCACCCTGCAACAG GACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTGTCCA ACAAAGCCCTCCAGCCCCCATCGAGAAACCATCTCCAAA GCCAAAGGGCAGCCCCGAGAACCAAGGTGTACACCTGGCC CCCATCCGGGAGGAGATGACCAAGAACCAAGGTCAAGCTG ACCTGCCCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGT GGAGTGGGAGGACAATGGGACGCCGGAAGAACTACAAG ACCAGCCTCCCGTGTGTGGACTCCGACGGCTCTCTTCTCTC TATAGCAAGCTCACCGTGGACAAAGCAGGTTGGCAGCAGG GGAAACGTCTTCTCATGTCTCCGTGATGCATGAGGCTCTGCAC

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2G10.304	[hu anti- <huGIPR> 2G10.304 VK3 (1-236) VL]:huKLC -CL + [Unknown anti- <huGIPR> 2G10.610 VH3 (1-472) VH]:huIgG1 zSEFL2-2 (mAb); LMR ID: SS- 26181	NA	AA	(SEQ ID NO: 12) EIVMTQSPATLSVSPGERATLS CRASQSVDRHLAWYQQKPGQ APRLIYEAAATRAATGIPARFSGS GSQTEFTLTISLSQSEDFAVYYC QQYQNWPLTFGGGKVEIKRT VAAPSVFIFFPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSSTYS LSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC	(SEQ ID NO: 13) AACCCTACACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAA A
				(SEQ ID NO: 14) GAAATAGTGATGACGCAGTCT CCAGCCACCTGTCTGTGTCT CCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAG TGTTAACAGACACTTAGCCTG GTACCAGAGAAACCTGGCC AGGCTCCAGGCTCCTCATCT ACGAAGCAGCCACCAGGGCC ACTGGTATCCAGCCAGGTTTC AGTGGCAGTGGTCTGGGAC AGAGTTCACCTCACCATCAG CAGCCTGCAGTCTGAAAGATT TGCAAGTTTATTACTGTACGCA GTATCAGAACTGGCTCTCAC TTTCGGCGGAGGACCAAGGT GGAGATCAACGAAACGGTGG CTGCACCATCTGTCTTCATCTT CCCGCCATCTGATGACAGTT GAAATCTGGAACAGCCCTCTGT TGTGTGCTGCTGAATAACTT CTATCCAGAGAGGCGCAAG	(SEQ ID NO: 15) CAGGTGCAGTGGTGGAGTCTGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCAGTAACTATGGCATGCACCTGGTCCGCCAGGCTCA GGCGAGGGCTGGAGTGGTGGCAGCTATATGGTTTGATGC AAGTGATAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAACCTCAAGAACACGCTGTATCTGCAA ATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTG TGGAGAGATTGGCGATTTTGGAGTGGTCCCGACTACT GGGGCAGGGAACCTGGTCAACGCTGTCTAGTGCCTCCACC AAGGGCCCATCGGTCTTCCCTCCCTGGCACCTCTCCCAAGAG CACCTTGGGGGCACAGGGCCCTGGGTGGCTGGTCAAGG ACTACTTCCCGAACCAGGTGACGGTGTGTGGAACCTCAGGC GCCCTGACAGCGCGTGCACACCTTCCCGGCTGTCTTACA GTCTCTAGGACTCTACTCCCTCAGCAGCGTGGTGAACCGTGC CCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTG AATCACAAAGCCAGCAACACCAAGGTGGACAAAGAAAGTTG AGCCAAATCTTGTACAAATCAACATGCCCACCGTGC CCAGCAGCTGAACCTCTGGGGGAGCGTCAAGTCTTCTCTTC CCCCAAAACCCAGGACACCTCATGATCTCCCGGACCCC TGAGGTACATGCTGTGGTGGACGTGAGCCACGAAGACC CTGAGGTCAAGTTCAACTGTTACGTGACGCGCGTGGAGGTG

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2G10.323	[hu anti- <huGIPR> 2G10.323 VK3 (1-236) VLJ::huKLC -CL + [Unknown anti- <huGIPR> 2G10.610]	NA	TACAGTGGAAGGTGGATAAC GCCCTCCAATCGGGTAACTCC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCTCAGCAGCACCTGA CGTGAGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCAACCATCAGGG CCTGAGCTCGCCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT	CATAATGCCAAGACAAAGCCGTGCGAGGAGCAGTACGGCA GCACGTACCGTTGCTCAGCTCTCACCCTCTGCACCCAG GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTGTCCA ACAAAGCCCTCCAGCCCCATCGAGAAACCACTCTCCAAA GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCTGCC CCCATCCCGGGAGGAGATGACCAAGAACCCAGGTACGCCTG ACCTGCCCTGGTCAAGGCTTCTATCCCAGCGACATCGCCGT GGAGTGGGAGGACAATGGGCGCCGAGAACAACTACAAG ACCAAGCTCCCGTCTGGACTCCGACGGCTCTCTTCTCCTC TATAGCAAGCTACCCGTGGACAAAGCAGGTGGCAGCAGG GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC AACCACTACACGCAGAAAGACCTCTCCCTGTCTCCGGGTAA A
			(SEQ ID NO: 16)	(SEQ ID NO: 17)
			EIVMTQSPATLSVSPGERATLS CRASQSVNRHLAWYQQKPGQ APRLIYEATRATGIPARFSGS GSGTEFTLTISLSQSEDFAVVYC QQYQNWPLTFGGGKVEIKRT VAAPSVFIPIPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDYTS LSSTLTLSKADYEEKHKVYACE VTHQGLSSPVTKSFNRGEC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAIWFDASDKYYADA VKGRFTISRDN SKNTLYLQ MNSLR AEDTAVYYCARDLAIFGVDPDYWGQGLVTVSSASTK GPSVFPLAPSSKSTSGGTAALGLCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCTCPCPAPELGGPSVFLPPKPKDITL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSYRCVSVLTIVLHQDWLNGKEYCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHREALHNHYTQKSLSLSPGK
2G10.323	[hu anti- <huGIPR> 2G10.323 VK3 (1-236) VLJ::huKLC -CL + [Unknown anti- <huGIPR> 2G10.610]	NA	(SEQ ID NO: 18)	(SEQ ID NO: 19)
			GAAATAGTGATGACGCAGTCT CCAGCCACCCTGTCTGTGTCT CCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAG TGTTCTATAGACACTTAGCCTG GTACCAGCAGAAACCTGGCC AGGCTCCCAGGCTCCTCATCT ACGAAGCAGCCACCAAGGGCC ACTGGTATCCCAAGCCAGGTTC AGTGCGAGTGGGTCTGGGAC	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCAGTAACTATGGCATGCACCTGGTCCGCCAGGTCCA GGCGAGGGCTGGAGTGGTGGCAGCTATATGGTTTGTATGC AAGTGATAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCATCTCCAGAGCAACTCCAAGAACACGCTGTATCTGCAA ATGAACAGCTGAGACGCCGAGGACACGGCTGTGTATTACTG TGCAGAGATTGGCGATTTTGGAGTGGTCCCCGACTACT GGGGCCAGGAAACCTGGTACCCCTGTCTAGTGCCTCCACC AAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCTCTCCAAGAG
			(SEQ ID NO: 16)	(SEQ ID NO: 17)

AA

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		(SEQ ID NO: 22)	(SEQ ID NO: 23)
		GAAATAGTGATGACGCAGTCT CCAGCCACCCTGTCTGTGTCT CCAGGGAAAGAGCCACCCT CTCTGCAGGGCCAGTCAGAG TGTTGAAAGACACTTAGCCTG GTACCAGCAAAACCTGGCC AGGCTCCAGGCTCCTCATCT ACGAAGCAGCCACCAGGGCC ACTGGTATCCAGCCAGGTTT AGTGGCAGTGGGTCTGGGAC AGAGTTCACTCTACCATCAG CAGCCTGCAGTCTGAAGATT TGCAGTTTATTACTGTACGAC GTATCAGAACTGGCTCTCAC TTTCGGCGGAGGACCAAGGT GGAGATCAAAACGAACGGTGG CTGCACCATCTGTCTTCATCTT CCCGCCATCTGATGAGCAGTT GAAATCTGGAACCTGCCTCTGT TGTGTGCTGCTGAATAACTT CTATCCAGAGAGGCCAAAG TACAGTGGAAGGTGGATAAC GCCCTCCAATCGGTTAACTCC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCTCAGCAGCACCCCTGA CGCTGAGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT	CAGGTGCAGCTGGTGGAGTCTGGGGAGGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTCTGTGAGCATCTGGATTCA CCTTCAGTAACATATGGCATGCACCTGGTCCGCCAGGCTCCA GGCGAGGGGTGGAGTGGGTGGCAGCTATATAGGTTTGATGC AAGTGATAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAACCTCAAGAACACGCTGTATCTGCAA ATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTG TGCAGAGATTGGCGATTTTGGAGTGGTCCCCGACTACT GGGGCCAAGGAACCTTGGTCAACCGTGTCTAGTGCCTCCACC AAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAG CACCTCTGGGGCACACGGCCCTGGGCTGCCCTGGTCAAGG ACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGC GCCCTGACAGCGGTGCACACCTTCCCGGTGTCTCTCTACA GTCTCAGGACTCTACTCCTCAGCAGCGTGGTGACCGTGC CCTCCAGCAGCTTGGCACCCAGACCTACATCTGCAACGTG AATCAAAAGCCACGAAACACCAAGGTGGACAAGAAAGTTG AGCCAAATCTTGTGACAAACCTCACACATGCCACCGTGC CCAGCACCTGAACCTCTGGGGGACCGTCACTTCTCTCTTC CCCCAAACCCCAAGGACACCTTCATGATCTCCCGGACCCC TGAGGTACATGCTGTGGTGGACGTGAGCCACGAAGACC CTGAGGTCAAGTTCAACTGGTACGTGACGGCGGTGGAGGTG CATAATGCCAAGACAAGCCGTGCGAGGAGCAGTACGGCA GCACGTACCGTTGCGTCAAGCTCCTCACCGTCTCTGCACCAG GACTGGCTGAATGGCAAGGAGTACAAGTGCAGGTGTCCA ACAAAGCCCTCCAGGCCCATCGAGAAACCATCTCCAAA GCCAAAGGGCAGCCCCGAGAACCAAGGTGTACACCCCTGCC CCCATCCCGGGAGGAGATGACCAAGAACCCAGGTCAACCTG ACCTGCCGTGGTCAAAGGCTTCTATCCAGCGACATCGCCGT GGAGTGGGAGAGCAATGGGCAAGCCGGAGAACCACTACAAG ACCACGCCCTCCCGTGTGGACTCCGACGGCTCTCTTCTCCTC TATAGCAAGCTCACCGTGGACAAAGACAGCAGGTGGCAGCAGG GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC AACCCTACACGCAGAAAGAGCCTCTCTCCCTGTCTCCGGGTAA A
		(SEQ ID NO: 24)	(SEQ ID NO: 25)

2G10.309

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		AA	EIVMTQSPATLSVSPGERATLS CRASQSVVERHLAWYQKPGQ APRLIYEAAATRAATGIPARFSGS GSGTEFTLTISLQSEDFAVYYC QQYQNWPFTFGGKVEIKRT VAAPSFIPIPPSDEQLKSGTASV VCLLNNFYPREAKVQWQVDN ALQSGNSQESVTEQDSKDYSTYS LSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC	QVQLVESGGGVQVQGRSLRLSCAASGFTFSNRYGMHWVRQAP GEGLEWVAIWFDAADSKYYADA VKGRFTISRDN SKNTLYLQ MNSLRAEDTAVYYCARDLAIFGVVPDYWQGTLVTSSASTK GPSV/FPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTPVSSSLGTQTYICNVNHPKPSN TKVDKVEPKSCDKTHTCPPCPAPELLGGPSVFLPPKPKDITL MISRTPEYTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTI SKAKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHREALHNHYTQKSLSLSPGK
	[hu anti- <huGIPR> 2G10.316 VK3 (1-236) VL]:huKLC -CL + [Unknown anti- <huGIPR> 2G10.610 VH3 (1-472) VH]:huIgG1 zSEFL2-2 (mAb); LMR ID: SS- 26193	NA	(SEQ ID NO: 26) GAAATAGTGATGACGCAGTCT CCAGCCACCCTGTCTGTGTCT CCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAG TGTTTTCAGACACTTAGCCTG GTACAGCAGAAACCTGGCC AGGCTCCCAGGCTCCTCATCT ACGAAGCAGCCACCAGGGCC ACTGGTATCCAGCCAGGTTC AGTGGCAGTGGGTCTGGGAC AGAGTTCACCTCACCATCAG CAGCCTGCAGTCTGAAGATT TGCAGTTTATTACTGTACGA GTATCAGAACTGGCCTCTCAC TTTCGGCGGAGGGACCAAGGT GGAGATCAAACGAACGGTGG CTGCACCATCTGTCTCATCTT CCCGCCATCTGATGAGCAGTT GAAATCTGGAACCTGCCCTGT TGTGTGCTGCTGAATAACTT CTATCCCAGAGAGGCCAAAG TACAGTGGAAAGGTGGATAAC GCCCTCCAATCGGGTAACTCC CAGGAGAGTGTACAGAGCA	(SEQ ID NO: 27) CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCAGTAATACTATGGCATGCACCTGGTCCGCCAGGCTCCA GGCGAGGGCTGGAGTGGTGGCAGCTATATGGTTTGATGC AAGTGATAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAACCTCCAGAACACGCTGTATCTGCAA ATGAACAGCTGAGAGCCGAGACACGGCTGTGTATTACTG TGGGAGAGATTTGGCGATTTTGGAGTGGTCCCGGACTACT GGGGCCAGGAACCTGGTCAACCGTGTAGTGCCTCCACC AAGGGCCATCGGTCTTCCCTTGGCACCCTCCCTCCAGAG CACTCTGGGGGCACAGCGCCCTGGGCTGCCGTGTCAGG ACTACTTCCCGAACCGGTGACGGTGTGCTGGAACCTCAGGC GCCCTGACCAGCGCGTGCACACCTTCCCGGCTGTCTACA GTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAACCTGC CCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTG AATCAACAGCCAGCAACACCAAGGTGGACAAGAAAGTTG AGCCCAAATCTGTGACAAACTCACATGCCACCCGTGC CCAGCACCTGAACCTCTGGGGGACCGTCAGTCTTCCCTTC CCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCC TGAGGTACATGCTGGTGGTGGACGTGAGCCACGAAGACC CTGAGGTCAAGTTCAACTGGTACGTGGACGGCTGGAGGTG CATAATGCCAAGACAAGCCGTGCGGAGGAGCAGTACGGCA GCACGTACCGTTGCGTCAAGCTCTCACCCTGCTGACCCAG GACTGGCTGAATGGCAAGGAGTACAAAGTGCAAGGTGTCCA

2G10.316

A-2164-WO-PCT

2G10.604	[hu anti- <huGIPR> 2G10.604 VK3 (1-236) VLj::huKLC -CL + [Unknown anti- <huGIPR> 2G10.610 VH3 (1-472) VHj::huIgG1 zSEFL2-2	NA	GGACAGCAAGGACAGCACCT ACAGCCTCAGCAGCACCTGA CGCTGAGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT	ACAAAGCCCTCCAGCCCCCATCGAGAAACCATCTCCAAA GCCAAAGGCGCCCGGAGAACACAGGTGTACACCTGCCC CCCATCCCGGAGGATGACCAAGAACAGGTACGCTG ACCTGCTGGTCAAAGGCTTCTATCCAGCGACATCGCGGT GGAGTGGGAGAGCAATGGGACGCCGAGAAACTACAAG ACCACGCTCCCTGCTGGAGTCCGACGGCTCTCTTCTCTC TATAGCAAGCTACCCGTGGACAAAGCAGGTGGCAGCAGG GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC AACCCTACACGACAGAGAGCCTCTCCCTGTCTCCGGGTAA A
			(SEQ ID NO: 28) EIVMTQSPATLSVSPGERATLS CRASQSVFRHLAWYQQKPGQA PRLLIYEAAATRAATGIPARFSGS SGTEFTLTISLSQSEDFAVYYCQ QYQNWPLTFGGGTKEIKRTV AAPSVEIFPPSDEQLKSGTASVV CLLNIFYPREAKVQWVKVDNAL QSGNSQESVTEQDSKDSYSL STLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC	(SEQ ID NO: 29) QVQLVESGGGVQPGRSLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAIWFDASDKYYADA VKGRFTISRDN SKNTLYLQ MNSLRAEDTAVYYCARDLAIFGVVPDYWGQGLVTVSSASTK GPSVFPLAPSSKTSGGTAALGLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHPKPSN TKVDKKVEPKSCDKTHTCPCPAPEL LGGPSVFLFPKPKDTL MISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHREALHNHYTQKSLSLSPGK
			(SEQ ID NO: 30) GAAATAGTGATGACGCAGTCT CCAGCCACCCTGTCTGTGTCT CCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAG TGTTAACAGACACTTAGCCTG GTACCAGCAGAAACCTGGCC AGGCTCCAGGCTCCTCATCT ACGAAAGAGCCACCAGGGCC ACTGGTATCCAGCCAGGGTIC AGTGGCAGTGGGTCTGGGAC AGAGTTCACTCTCACCATCAG CAGCCTGCAGTCTGAAGATT TGCAGTTTATTAAGTTCAGCA	(SEQ ID NO: 31) CAGGTGACAGTGGTGGAGTCTGGGGAGGCGGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCAGTAACTATGGCATGCACCTGGTCCGCCAGGCTCCA GGCGAGGGCTGGAGTGGTGGCAGCTATATGGTTTGATGC AAGTGATAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAACCTCAAGAACACGCTGTATCTGCAA ATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTG TGGAGAGATTGGCGATTTTGGAGTGGTCCCGACTACT GGGGCCAGGAACCTTGTGACCGTGTAGTGCCTCCACC AAGGGCCCATCGGTCTTCCCTCCCTGGCACCCCTCTCCCAAGAG CACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGG ACTACTTCCCGCAACCGGTGACGGTGTGTGGAACCTCAGGC GCCGTGACACGCGGCGTGCACACCTTCCCGGCTGTCTCTACA

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	(mAb); LMR ID: SS- 26229	GTATCAGAACTGGCCTCTCAC TTTCGGCGGAGGGAACCAAGGT GGAGATCAAAACGAACGGTGG CTGCACCATCTGTCTTCATCTT CCCGCCATCTGATGAGCAGTT GAAATCTGGAACCTGCTCTGT TGTGTGCTGCTGAATAACTT CTATCCAGAGAGGCCAAAG TACAGTGGAAGGTGGATAAC GCCCTCCAAATCGGGTAACCTC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCTCAGCAGCACCTGA CGTGAGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCAACCATCAGGG CCTGAGCTCGCCCGTCACAAA GAGCTTCAACACAGGGGAGAGT GT	GTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGC CCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTG AATCACAAGCCAGCAACCAAGGTGGACAAAGAAAGTTG AGCCCAATCTTGTGACAAACTCACATGCCCCACCGTGC CCAGCACCTGAACCTCTGGGGGACCGCTAGTCTTCTCTTC CCCCAAACCCAGACACCTCATGATCTCCCGGACCCC TGAGGTACATGCTGGTGGTGGAGTGGAGCCAGCAAGACC CTGAGGTCAAGTTCAACTGTAAGTGGAGCGCGTGGAGGTG CATAATGCCAAGACAAAGCGTGGGAGGAGCAGTACGGCA GCACGTACCGTTGCTCAGCTCCTCACCCTCTGCACCCAG GACTGGCTGAATGGCAAGGATACAAAGTCAAGGTGTCCA ACAAAGCCCTCCAGCCCCATCGAGAAACCATCTCCAAA GCCAAAGGCGAGCCCGAGAACACAGGTGTACACCTGCC CCCATCCCGGAGGAGATGACCAAGAACCCAGGTACGCTG ACCTGCTGGTCAAGGCTTCTATCCAGCGACATCGCCGT GGAGTGGGAGCAATGGGCGCCGAGCAACAACTACAAG ACCACGCTCCCGTCTGGACTCCGACGGCTCTTCTTCTC TATAGCAAGCTACCGTGGACAAAGCAGGTGGCAGCAGG GGAACGTCTTCTCATGCTCCGTGATGATGAGGTCTTGCAC AACCACACACGCAAGAGCCCTCTCCCTGTCTCCGGGTAA A
		(SEQ ID NO: 32) EIVMTQSPATLSVSPGERATLS CRASQSVNRHLAWYQQKPGQ APRLIYEAAATRAATGIPARVSGS GSGTEFTLTISLSQSEDFAVVYC QQYQNWPLTFGGGKVEIKRT VAAPSVFIPPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKSTYS LSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC	(SEQ ID NO: 33) QVQLVESGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAIWFDASDKYYADA VKGRFTISRDNKNTLYLQ MNSLRAEDTAVYYCARDLAIFGVVPDYWGQGTLVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHSTCPPELAPPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHREALHNYTQKSLSLSPGK
AA		(SEQ ID NO: 34) GAAATAGTGATGACGCAGTCT CCAGCCACCCTGTCTGTGTCT	(SEQ ID NO: 35) CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGTCAGCATCTGGATTCA
	[hu anti- <huGIPR>	NA	

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2G10.609 VK3 (1-236) VLJ::huKLC -CL + [Unknown anti- <huGIPR> 2G10.610 VH3 (1-472) VHJ::huIgG1 zSEFL2-2 (mAb); LMR ID: SS- 26234	CCAGGGGAAAGAGCCACCCT CTCTGCAGGGCCAGTCAGAG TGTTGAAAGACACTTAGCCTG GTACCAGCAGAAACCTGGCC AGGCTCCAGGCTCCTCATCT ACGAAAGAGCCACCAGGGCC ACTGGTATCCAGCCAGGGTC AGTGGCAGTGGTCTGGGAC AGAGTTCACTCTCACCATCAG CAGCCTGCAGTCTGAAGATT TGCAGTTTATTACTGTCAGCA GTATCAGAACTGGCCTCTCAC TTTCGGCGGAGGACCAAGGT GGAGATCAAAAGAACGGTGG CTGCACCATCTGTCTTCATCTT CCCGCCATCTGATGAGCAGTT GAAATCTGGAAGTGCCTCTGT TGTGTGCTGTCTGAATAACTT CTATCCCAGAGAGGCCAAAG TACAGTGGAAAGGTGGATAAC GCCCTCCAATCGGGTAACTCC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCTCAGCAGCACCCCTGA CGCTGAGCAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCAACCATCAGGG CCTGAGCTCGCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT	CCTTCAGTAACTATGGCATGCACTGGGTCCGCCAGGCTCCA GGCGAGGGCTGGAGTGGGTGGCAGCTATATGGTTTGATGC AAGTGATAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAACCTCCAAGAACACGGCTGTATCTGCAA ATGAACAGCTGAGAGCCGAGGACACGGCTGTGTATTACTG TGGAGAGATTGGCGATTGGTGGTGGTCCCGACTACT GGGGCCAGGGAACCTGGTACCGGTGTCTAGTGCCTCCACC AAGGGCCCATCGGTCTTCCCCCTGGACCCCTCCCAAGAG CACCTCTGGGGCACAGCGGCCCTGGGCTGCCGTGGTCAAGG ACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGC GGCCTGACACGCGCGTGCACACTTCCCGGTGTCTTACA GTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAACCGTGC CCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTG AATCAAGCCCAAGCAACCAAGGTGGACAAAGAAAGTTG AGCCCAATCTTGTGACAAAACCTACACATGGCCACCGTGC CCAGCACCTGAACCTCTGGGGGACCGTCACTCTTCTCTTC CCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCC TGAGGTACATCGTGTGGTGGACGTGAGCCACGAAGACC CTGAGGTCAAGTTCAACTGTACGTGGACGGCGTGGAGGTG CATAATGCCAAGACAAGCCGTGCGAGGAGCAGTACGGCA GCACGTACCGTTGCGTACGCTCCTCACCGTCTTGCACCA GACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTGTCCA ACAAAGCCCTCCAGCCCCATCGAGAAACCATCTCCAAA GCCAAAGGGCAGCCCCGAGAACCAACAGGTGACACCCCTGCC CCCATCCCGGAGGAGATGACCAAGAACAGGTACGCTG ACCTGCCTGGTCAAGGCTTCTATCCAGCGACATCGCGT GGAGTGGGAGAGCAATGGGCAAGCGGAGAAACAACATAAAG ACCAGCCCTCCGTGCTGGACTCCGACGGCTCTTCTCTCTC TATAGCAAGCTCACCGTGGACAAAGCAGGTGGCAGCAGG GGAACGTCTTCTCATGCTCCGTGATGATGAGGCTCTGCAC AACCACTACACGCAAGAGACCTCTCCCTGTCTCCGGGTAA A
	(SEQ ID NO: 36) EIVMTQSPATLSVSPGERATLS CRASQSVVERHLAWYQKPGQ APRLIYEAAATRAITGIPARVSGS	(SEQ ID NO: 37) QVQLVESGGGVVQPRSLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAIWFDASDKYYADA VKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCARDLAIFGVVDPYWGQGTLVTVSSASTK

AA

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		<p>GSGETFTLTISLSQSEDAFVYYC QQYQNWPLTFGGGKVEIKRT VAAPSVFIPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKSDSYS LSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC</p>	<p>GPSVFPLAPSSKTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPCPAPELGGPSVFLPPKPKDNL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYSGTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPRPEQVYVLPPLPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHAEALHNHYTQKSLSLSPGK</p>
		<p>(SEQ ID NO: 38)</p> <p>GAAATAGTGATGACGCAGTCT CCAGCCACCTGTCTGTGTCT CCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAG TGTGTATAGACACTTAGCCTG GTACCAGCAGAAACCTGGCC AGGCTCCAGGCTCCTCATCT ACGAAGCAGCCACCAGGGCC ACTGGTATCCAGCCAGGGTC AGTGGCAGTGGGTCTGGGAC AGAGTTCACTCTCACCATCAG CAGCCTGCAGTCTGAAGATT TGCAGTTTATTACTGTGAGCA GTATCAGAACTGGCCTCTCAC TTTCGGCGGAGGGACCAAGGT GGAGATCAAAACGAACGGTGG CTGCACCATCTGTCTTCATCT CCCGCCATCTGATGAGCAGTT GAAATCTGGAACCTGGCTCTGT TGTGTGCTGCTGAATACTT CTATCCCAGAGAGGCCAAAG TACAGTGGAAAGTGGATAAC GCCCTCCAAATCGGGTAACTCC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCCTCAGCAGCACCTGA CGCTGAGCAAAAGCAGACTAC</p>	<p>(SEQ ID NO: 39)</p> <p>CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGGTCCAGCC TGGGAGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCACTAATATGGCATGCACCTGGTCCGCCAGGTCCA GCGAGGGGCTGGAGTGGTGGCAGCTATATGTTTGTATGC AAGTGATAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCACTCCAGAGACAACCTCAAGAACACGCTGTATCTGCAA ATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTG TGCAGAGATTGTGGCATTTTGGAGTGGTCCCCGACTACT GGGGCCAGGAACCTGGTCAACGCTGTCTAGTGCCTCCACC AAGGGCCATCGGTCTTCCCCCTGGCACCCCTCTTCCAAGAG CACTCTGGGGGCACAGCGCCCTGGCTGGCTGGTCAAGG ACTACTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGC GCGCTGACCAGCGGCTGCACACCTTCCCGCTGTCTTACA GTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAACCGTGC CCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTG AATCACAAGCCAGCAACACCAAGGTGGACAAAGAAAGTTG AGCCCAAATCTGTGACAAACTCACACATGCCACCCGCTGC CCAGCACCTGAACCTCTGGGGGACCGTCAAGTCTTCTCTTC CCCCCAAACCCAAAGGACACCTTCAATGATCTCCCGGACCCC TGAGGTCACTGCTGGTGGTGGACGCTGAGGCCACGAAGACC CTGAGGTCAAGTCAACTGTAACGTGACGCGCTGGAGGTG CATAATGCCAAGACAAACCGCTGCGAGGAGCAGTACCGCA GCACGTACCGTGGTCACTGCTCCTCACCCTCTGCAACAG GACTGGCTGAATGGCAAGGAGTACAAAGTGAAGGTGTCCA ACAAAGCCCTCCAGCCCCCATCGAAGAAACCATCTCCAAA GCGCAAAGGGCAGCCCCGAGAACCCACAGGTGTACACCTGCC CCCATCCCGGGAGGAGATGACCAAGAACCAAGGTCAAGCTG</p>
2G10.603	<p>[hu anti- <huGIPR> 2G10.603 VL]:huKLC -CL + [Unknown anti- <huGIPR> 2G10.610 VH3 (1-472) VHJ::huIgG1 zSEFL2-2 (mAb): LMR ID: SS- 26228</p>	NA	

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		GAGAAACACAAAGTCTACGC CTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT	(SEQ ID NO: 40) EIVMTQSPATLSVSPGERATLS CRASQSVDRHLAWYQQKPGQ APRLIYEAAATRAATGIPARVSGS GSGTEFTLTSSLSQSEDFAVYYC QQYQNWPFLTGGGKVEIKRT VAAPSFIFFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDYSTYS LSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC	(SEQ ID NO: 41) QVQLVESGGGVQPRSLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAIAIFDASDKYYADA VKGRFTISRDN SKNTLYLQ MNSLRAEDTAVYYCARDLAI FGVVPDYWQQGTLVTVSSASTK GPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHCTCPPELPGPSVFLPFPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHREALHNYTQKSLSPGK	ACCTGCCTGGTCAAGGCTTCTATCCAGCGACATCGCCGT GGAGTGGGAGAGCAATGGGCA GCCGGAGAAACA ACTACAAG ACCACGCTCCCTGCTGGACTCCGACGGCTCTTCTTCTCTC TATAGCAAGCTCACCGTGGACAAAGACAGGTGGCAGCAGG GGAACGTCTTCTCATGCTCGGTGATGATGAGGCTCTGCAC AACCACTACACGCAAGAGAGCCTCTCCCTGTCTCCGGGTAA A
	AA			(SEQ ID NO: 42) GAAATAGTGATGACGCAGTCT CCAGCCACCTGTCTGTGTCT CCAGGGGAAAGAGCCACCCT CTCTGCA GGGCCAGTCAGAG TGTTCTGAGTCACTTAGCCTG GTACCAGCAGAAACCTGGCC AGGCTCCAGGCTCCTCATCT ACGAAAGCAGCCACCAGGGCC ACTGGTATCCCA GCCAGGTTC AGTGCAAGTGGTCTGGGAC AGAGTTCACCTCACCATCAG CAGCCTGCAGTCTGAAGATT TGCAGTTTATTACTGTCAGCA GTATAACAACCTGGCTCTCAC TTTCGGCGGAGGACCAAGGT GGAGATCAAAACGAAACGGTGG	(SEQ ID NO: 43) CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCAGTAACTATGGCATGCAC TGGGTCCGCCAGGCTCCA GGCAGGGCTGGAGTGGTGCGAGCTATATGGTTTGATGC AAGTGATAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCATCTCCAGAGACA ACTCCAAGAACACGCTGTATCTGCAA ATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTG TGGAGAGATTTGGCGATTTTGGAGTGGTCCCCGACTACT GGGGCCAGGAAACCTGGTCACTGTGTCTAGTGCCTCCACC AAGGGCCCATCGGTCTTCCCCCTGGCACCTCTCTCCAAGAG CACCTCTGGGGGCACAGCGGCTTGGGTGCTGCTGGA ACTCAGGC ACTACTTCCCCGAACCGGTGACGGTGTGCTGGA ACTCAGGC GGCCTGACACGCGGTGCACACTTCCCGGCTGTCTCTACA GTCTCAGGACTCTACTCCCTCAGCAGCGGTGTTGACCGTGC CCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTG AATCAACAAGCCCAAGCAACCAAGGTGGACAAAGAAAGTTG
2G10.318	[hu anti- <huGIPR> 2G10.318 VK3 (1-236) VL]:huKLC -CL + [Unknown anti- <huGIPR> 2G10.610 VH3 (1-472) VH]:huIgG1 zSEFL2-2 (mAb); LMR ID: SS- 26195	NA			

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2G10.324	hu anti- <huGIPR> 2G10.324 VK3 (1-236) VLj::huKLC	NA	CTGCACCATCTGTCTTCATCTT CCCGCCATCTGATGAGAGTT GAAATCTGGAACCTGCTCTGT TGTGTGCTGCTGAATACTT CTATCCAGAGAGGCCAAAG TACAGTGGAAAGTGGATAAC GCCCTCCAATCGGGTAACCTC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCTCAGCAGCACCTGA CGCTGAGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCAACCATCAGGG CCTGAGCTCGCCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT	AGCCAAATCTTGTGACAAAACTCACACATGCCACCGTGC CCAGCACCTGAACCTCTGGGGGACCGTCAGTCTTCTCTTC CCCCAAACCCAAAGACACCTCATGATCTCCCGGACCCC TGAGGTACATGCTGTGTGGACGTGAGCCACGAAGACC CTGAGGTCAAGTCAACTGCTACGTGACGCGGTGGAGGTG CATATGCCAAAGAAAGCCGTGCGAGGAGCAGTACGGCA GCACGTACCGTTCGCTCAGCTCTCACCCGTCTGCACAG GACTGGCTGAATGGCAAGGAGTACAAGTCAAGGTGTCCA ACAAAGCCCTCCAGCCCCATCGAGAAACCACTCTCCAAA GCCAAAGGCGAGCCCGAGAACACAGGTGTACACCTGCC CCCATCCCGGGAGGAGATGACCAAGAACAGGTACAGCTG ACCTGCTGTGTCAAAGGCTTCTATCCAGCGACATCGCCGT GGAGTGGAGAGCAATGGCGAGCCGAGAACAACTACAAG ACCAAGCTCCCTGCTGCTGACTCCGACGGCTCTTCTCTC TATAGCAAGCTACCGTGGACAAAGCAGGTGGCAGCAGG GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC AACCACCTACAGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAA A
			(SEQ ID NO: 44) EIVMTQSPATLSVSPGERATLS CRASQSVLSHLAWYQQKPGQA PRLLIYEAAATRAATGIPARFSGS SGTEFTLTISLQSEDFAVYYCQ QYNNWPLTFGGGKVEIKRTV AAPSVFIFPPSDEQLKSGTASVV CLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSYSL STLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC	(SEQ ID NO: 45) QVQLVESGGGVVQGRSLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAIWFDASDKYYADAVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYCARDLAIFGVVPDYWGQGLVTVSSASTK GPSVFLAPSSKTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPETCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSYRCVSVLTVLHQDWLNKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHREALHNYHTQKSLSPGK
			(SEQ ID NO: 46) GAAATAGTGATGACGCAGTCT CCAGCCACCCTGTCTGTGTCT CCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAG TGTTCTGAGTCACTTAGCCTG	(SEQ ID NO: 47) CAGGTGAGTGGAGTCTGGGGAGGCGGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCAGTAACCTATGGCATGCATGGTCCGCCAGGCTCCA GGCGAGGGGCTGGAGTGGGTGGCAGCTATATGGTTTGATGC AAGTGATAAATACTATATGCAGACGCCGTGAAGGGGCCGATTCA

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-CL + [Unknown anti- <huGIPR> 2G10.610 VH3 (1-472) VH]::huIgG1 zSEFL2-2 (mAb); LMR ID: SS- 26201	GTACCAGCAGAAACCTGGCC AGGCTCCAGGCTCCTCATCT ACGAAGCAGCCACCAGGGCC ACTGGTATCCAGCCAGGTTT AGTGGCAGTGGGTCTGGGAC AGAGTTCACTCTACCATCAG CAGCTTCAGTCTGAAGATT TGCAGTTTATTACTGTCAGCA GTATCAGAACTGGCTCTCAC TTTCGGCGGAGGACCAAGTT GGAGATCAAACGAACGGTGG CTGCACCATCTGTCTTCATCTT CCCGCATCTGATGAGCAGTT GAAATCTGGAACCTGCCCTCTGT TGTGTGCTGCTGAATAACTT CTATCCAGAGAGGCCAAAG TACAGTGGAAGTGGATAAC GCCCTCCAAATCGGGTAACTCC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCTCAGCAGCACCCCTGA CGCTGAGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT	CCATCTCCAGAGACAACCTCCAAGAACACGCTGTATCTGCAAA ATGAACAGCTGAGAGCCGAGGACACGGCTGTGTATTACTG TGGAGAGATTTGGCGATTTTGGAGTGGTCCCCGACTACT GGGGCCAGGAACCTGGTCAACCGTGTCTAGTGCCTCCACC AAGGGCCATCGGTCTTCCCCTGGCACCTCTCTCCAAGAG CACTCTGGGGCACACAGGCCCTGGGCTGCCTGGTCAAGG ACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGC GCCCTGACCAGCGGTGCACACCTTCCCCGGTGTCTCTACA GTCTCAGGACTCTACTCCCTCAGCAGCTGGTGTGACCGTGC CCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTG AATCACAAGCCAGCAACACCAAGGTGGACAAGAAAGTTG AGCCCAATCTTGTGACAAACTCACATGCCCCACCGTGC CCAGCACCTGAACCTCTGGGGGACCGTCACTCTCTCTCTTC CCCCAAACCCAAAGGACACCTCATGATCTCCCGGACCCC TGAGGTACATGCTGGTGTGGACGTGAGCCACGAAGACC CTGAGGTCAAGTTCAACTGTCAGTGGACGGCTGGAGGTG CATAATGCCAAGACAAGCCGTCGCGAGGAGCAGTACGGCA GCACGTACCGTTGCTCAGCTCTCAACGCTCTGCACCCAG GACTGGTGAATGGCAAGGATCAAAGTCAAGTGAAGGTGTCCA ACAAAGCCCTCCAGCCCCATCGAGAAACCATCTCCAAA GCCAAAGGCAGCCCGAGAACCAACAGGTGTACACCTGCC CCCATCCGGGAGGAGATGACCAAGAACCCAGGTACGCTG ACCTGCTGTCAAAGGCTTCTATCCACGACATCGCCGT GGAGTGGAGACCAATGGGCGACCCGAGAACAACTACAAG ACCACGCTCCCGTCTGACTCCGACGGCTCTCTCTCTCCTC TATAGCAAGCTCACCGTGGACAAAGAGCAGGTGGCAGCAGG GGAACTCTTCTCATGTCTCCGTGATGCATGAGGCTCTGCAC AACCACTACAGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAA A
	(SEQ ID NO: 48) EIVMTQSPATLSVSPGERATLS CRASQSVLSHLAWYQQKPGQA PRLIYEAAATRAIGPARFSGSG SGTEFTLTISLQSEDFAVYYCQ QYQNWPPLTFGGGTKEIKRTV AAPSVFIFPPSDEOLKSGTASVV	(SEQ ID NO: 49) QVQLVESGGGVVQPRSLRLSCAASGFTFSNYGMHWRQAP GEGLEWVAIWFDASDKYYADA VKGRFTISRDNKNTLYLQ MNSLRAEDTAVYYCARDLAIFGVVPDYWGQGTLVTVSSASTK GPSVFPLAPSSKTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCTPCCPAPELLGGPSVFLFPKPKDITL
AA		

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		CLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSYSL STLTLISKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC	(SEQ ID NO: 50)	MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSYRCVSLVTLVHLQDWLNKEYKCKVSNKALPAPIEKTI SKAKGPQPREQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSGSFFLYSKLTVDKSRWQQGN VFSCSVMHLEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 51)	CAGGTGCAGTGGTGGAGTCTGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTCAGTAACTATGGCATGCTGCTGGTCCGCCAGGCTCCA GGCGAGGGCTGGAGTGGTGGCAGCTATATGGTTTGATGC AAGTATAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAACCTCAAGAACACGCTGTATCTGCAA ATGAACAGCCTGAGAGCCGAGGACACGGCTGTATTACTG TGGAGAGATTGGCGATTTTGGAGTGGTCCCGACTACT GGGCCAGGGAACCTGGTACCGTGTCTAGTGCCTCCACC AAGGGCCCATCGTCTTCCCTCCGACCTCTCCCAAGAG CACCTTGGGGGACAGCGGCCCTGGGCTGCCTGGTCAAGG ACTACTCCCGAACCGGTGACGGTGTGTGGAACCTCAGGC GCCCTGACAGCGCGTGCACACTTCCCGGCTGTCTACA GTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAACCGTGC CCTCAGCAGCTTGGCACCCAGACCTACATCTGCAACGTG AATCACAGCCAGCAACACCAAGGTGGACAAAGAAAGTTG AGCCAAATCTTGTGACAAACTCACATGCCACCGTGC CCAGCACCTGAATCTCTGGGGGACCGTCACTCTCTCTTTC CCCCAAACCCAGGACACCTCATGATCTCCCGGACCCC TGAGGTCACTGCTGGTGGTGGACGTGAGCCACGAAGACC CTGAGGTCAAGTTCACTGTGTGACGGCGGTGGAGGTG CATATGCCAAGACAAGCCGTGGGAGGAGCAGTACGGCA GCACGTACCGTTCGTGCTGCTCCTCCTCCTGCTGACCCAG GACTGGCTGAATGGCAAGGAGTACAAGTCAAGGTGTCCA ACAAAGCCCTCCAGCCCTCCATCGAGAAACCATCTCCAAA GCCAAAGGCGACCCGAGAACCAAGGTGTACACCTGCC CCATCCCGGGAGGAGTACCAAGAACAGGTGACGCTG ACCTGCCTGGTCAAGGCTTCTATCCAGCGACATCGCCGT GGAGTGGGAGGACAATGGGACGCCGAGAAACATACAAG ACCAGCCTCCCGTGTGTGACTCCGACGGCTCTCTCTCTCTC
2G10.322	[hu anti- <huGIPR> 2G10.322 VK3 (1-236) VLJ::huKLC -CL + [Unknown anti- <huGIPR> 2G10.610 VH3 (1-472) VHJ::huIgG1 zSEFL2-2 (mAb); LMR ID: SS- 26199	NA		

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			GAGCTTCAACAGGGGAGAGT GT	(SEQ ID NO: 52) EIVMTQSPATLSVSPGERATLS CRASQVMSHLAWYQKPGQ APRLIYEAAATRAATGIPARFSGS GSGTEFTLTISLQSEDFAVVYC QQYQNWPLTFGGGKVEIKRT VAAPSVFIPIPPSDEQLKSGTASV VCLLNFFYPREAKVQWKVDN ALQSGNSQESVTEQDSKSDSTYS LSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC	(SEQ ID NO: 53) QVQLVESGGVVQPGRSRLRSCAASGFTFSNYGMHWVVRQAP GEGLEWVAIWFDASDKYYADA VKGRFTISRDN SKNTLYLQ MNSLRAEDTAVYYCARDLAIFGVVPDYWQGGLTVTVSSASTK GPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLPPKPKDITL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHREALHNHYTQKSLSLSPGK	TATAGCAAGCTCACCGTGGACAAAGACAGGTGGCAGCAGG GGAACGTCTTCTCATGCTCGTGATGCATGAGGCTCTGCAC AACCACTACACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAA A
	AA			(SEQ ID NO: 54) GAAATAGTGATGACGCAGTCT CCAGCCACCCTGTCTGTGTCT CCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAG TGTCTGACGCACCTTAGCCTG GTACCAGCAGAAACCTGGCC AGGCTCCAGGGCTCCTCATCT ACGAAGCAGCCACCAGGGCC ACTGGTATCCAGCCAGGTTC AGTGGCAGTGGGTCTGGGAC AGAGTTCACTCTCACCATCAG CAGCCTGCAGTCTGAAGATT TGCAGTTTATTACTGTCAGCA GTATCAGAACTGGCTCTCAC TTTCGGCGGAGGGACCAAGGT GGAGATCAAAACGAACGGTGG CTGCACCATCTGTCTCATCTT CCCGCCATCTGATGAGCAGT GAAATCTGGAACTGCCCTCTGT	(SEQ ID NO: 55) CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCAGTAACATAAGCATGCACCTGGTCCGCCAGGCTCCA GGCAGGGGCTGGAGTGGGTGGCAGCTATATGGTTTGTATGC AAGTGATAAATACTATGCAGACGCCGTGAAGGCCGATTCA CCATCTCCAGAGACAACCTCCAAGAACACGCTGTATCTGCAA ATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTG TGGAGAGATTTGGCGATTTTGGAGTGGTCCCCGACTACT GGGGCCAGGAACCTGGTACCGTGTCTAGTGCCTCCACC AAGGGCCATCGGTCTTCCCTGGCACCTCTCCCAAGAG CACTCTGGGGGCACAGCGCCCTGGGCTGCCCTGGTCAAGG ACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGC GCCCTGACCAGCGGTGCACACTTCCCGGTGTCTCTACA GTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAACCGTGC CCTCCAGACTTGGGACCCAGACCTACATCTGCAACGTG AATCAACAAGCCAGCAACCAAGGTGGACAAAGAAAGTTG AGCCCAAATCTGTGACAAACTCACATGCCCCACCGTGC CCAGCACCTGAACCTGGGGGACCGTCACTGTCTCCCTTC CCCCCAAAACCCCAAGGACACCCCTCATGATCTCCCGGACCCC	
2G10.315	[hu anti- <huGIPR> 2G10.306 VK3 (1-236) VLj]:huKLC -CL + [Unknown anti- <huGIPR> 2G10.610 VH3 (1-472) VHj]:huIgG1 zSEFL2-2 (mAb); LMR ID: SS- 26192	NA				

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		TGTGTGCTGCTGAATAACTT CTATCCAGAGAGGCCAAAG TACAGTGGAAAGGTGGATAAC GCCCTCCAAATCGGTAACCTC CAGGAGAGTGTACAGAGCA GGACAGCAAAGGACAGCACCT ACAGCTCAGCAGCACCTTGA CGCTGAGCAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCACCCATCAGGG CCTGAGCTGCCCCGTCACAA GAGCTTCAACAGGGGAGAGT GT	TGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACC CTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTG CATAATGCCAAGACAAAGCCGTGCGAGGAGCAGTACGGCA GCACGTACCGTTGCGTACGCTCTCACCCTCCTGCACACG GACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTGTCCA ACAAAGCCTCCACGCCCTATCGAGAAACCAACTCTCCAAA GCCAAAGGACGCCCCGAGAACCAAGGTGTACACCTGCC CCCATCCGGGAGGAGATGACCAAGAACCAAGGTACAGCTG ACCTGCCTGGTCAAGGCTTCTATCCAGCGACATCGCGT GGAGTGGGAGACAATGGGACGCCGAGAACCAACTACAAG ACCACGCTCCCGTCTGGACTCCGACGGCTCCTTCTTCTC TATAGCAAGCTCACCGTGGACAAAGACAGGTGGCAGCAGG GGAACGTCTTCTCATGCTCCGTGATGATGAGGCTCTGCAC AACCACTACACGACGAAGAGCCTCTCCCTGTCTCCGGGTAA A
	AA	(SEQ ID NO: 56) EIVMTQSPATLSVSPGERATLS CRASQSVLTHLAWYQQKPGQA PRLIYEAAATRAIGIPARFSGS SGTEFTLTISLQSEDFAVYYCQ QYQNWPLTFGGGTKVEIKRTV AAPSVFIFPPSDEQLKSGTASVV CLLNNFYPREAKVQWVKVDNAL QSGNSQESVTEQDSKDSYSL STLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC	(SEQ ID NO: 57) QVQLVESGGGVVQPRSLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAIWFDASDKYYADAVKGRFTISRDNKNTLYLQ MNSLRAEDTAVYYCARDLAIQVVDYWGQGLTVTVSSASTK GPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHKPSN TKVDKKEPKSCDKTHCTPPCAPPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCYSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTI SKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQKSLSLSPGK
2G10.331	NA	(SEQ ID NO: 58) GAAATAGTGATGACGCAGTCT CCAGCCACCCTGTCTGTGTCT CCAGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAAGAG TGTTGATCTGCACCTTAGCCTG GTACCAGCAGAAACCTGGCC AGGCTCCAGGCTCCTCATCT ACGAAGCAGCCACCAAGGCC	(SEQ ID NO: 59) CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCAGTAACATATGGCATGCTGCTGGTCCGCCAGGCTCCA GGCAGGGGTGGAGTGGGTGGCAGCTATATGGTTTGTATGC AAGTGATAAATACTATGCAGACGCCGTGAAGGCCGATTCA CCATCTCCAGAGACAACCTCAAGAACACAGCTGTATCTGCAA ATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTG TGCGAGAGATTGGCGATTTTGGAGTGGTCCCCGACTACT

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<p><huGIPR> 2G10.610 VH3 (1-472) VHJ::huIgG1 zSEFL2-2 (mAb); LMR ID: SS- 26208</p>	<p>ACTGGTATCCAGCCAGGTTC AGTGGCAGTGGGTCTGGGAC AGAGTTCACTCTACCATCAG CAGCCTGCAGTCTGAAGATT TGCAGTTTATTACTGTCAGCA GTATCAGAACTGGCCTCTCAC TTTCGGCGGAGGGACCAAGGT GGAGATCAACGAAACGGTGG CTGCACCATCTGTCTTCATCTT CCCGCCATCTGATGAGCAGTT GAAATCTGGAACCTGCTCTGT TGTGTGCTGCTGAATACTT CTATCCAGAGAGGCCAAAG TACAGTGGAAGGTGGATAAC GCCCTCCAATCGGGTAAGTCC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCCTCAGCAGCACCCCTGA CGCTGAGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCAACCATCAGGG CCTGAGCTCGCCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT</p>	<p>GGGGCCAGGAAACCCCTGGTCAACCGTGTCTAGTGCCTCCACC AAGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAG CACCTCTGGGGGCACAGCGGCCCTGGCTGCCCTGGTCAAGG ACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGC GCCCTGACCAGCGGTGACACCTTCCCGCTGTCTCTACA TGCTCAGAGCTCTACTCCCTCAGCAGCGTGGTGAACCGTGC CTCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTG AATCAACAAGCCAGCAACCAAGGTGGACAAAGAAAGTTG AGCCCAATCTGTGACAAACTCACACATGCCACCCACCGTGC CCAGCACCTGAACCTCTGGGGGACCGTCAAGTCTTCTCTTC CCCCAAACCCAAAGACACCTCATGATCTCCCGGACCCC TGAGGTACATGCTGGTGGTGGACGTGAGCCACGAAGACC CTGAGGTCAAGTCAACTGTAAGTGGTACGTGGCGGTGGAGGTG CATATGCCAAGACAAACCGCTGCGAGGAGCAGTACGGCA GCACGTACCGTGGTGCAGCTCCTCAGCTCCTGCAACAG GACTGGCTGAATGGCAAGGATCAAGTCAAGTCAAGGTGTCCA ACAAAGCCCTCCAGCCCCATCGAGAAACCACTCTCCAAA GCCAAAGGGCAGCCCCGAGAACCAAGGTGTACACCCCTGCC CCCATCCCGGAGGAGATGACCAAGAACCAAGGTCAAGCTG ACCTGCTGGTCAAGGCTTCTATCCAGCGACATCGCCGT GGAGTGGGAGACAATGGGACGCCGAGAACAACTACAAG ACCAAGCCTCCGCTGTGGACTCCGACGGCTCTTCTCTC TATAGCAAGTCAACCGTGGACAAAGCAGGTGGCAGCAGG GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC AACCCTACACGCAGAAAGACGCTCTCCCTGTCTCCGGGTAA A</p>
AA	<p>(SEQ ID NO: 60) EIVMTQSPATLSVSPGERATLS CRASQSVDLHLAWYQQKPGQ APRLIYEAAATRAATGIPARFSGS GSGTEFTLTISLSQSEDFAVVYC QQYQNWPLTFGGGKVEIKRT VAAPSVFIAPPDEQLKSGTASV VCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSYS LSSTLTLSKADYEKHKVYACE</p>	<p>(SEQ ID NO: 61) QVQLVESGGGVQPGRLSLRSCAASGFTFSNYGMHWVRQAP GEGLEWVAIWFDASDKYYADA VKGRFTISRDN SKNTLYLQ MNSLR AEDTAVYYCARDLAIFGVVPDYWGQGLVTVSSASTK GPSVFPLAPSSKTSGGTAALGLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN HKPSN TKVDKKVEPKSCDKTHTCPCPAPELLGGPSVFLPPKPKD TL MISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSYRCVSLTVLHODWLNKEYCKVSNKALPAPIEKTI SKAKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGFYPSDIAV</p>

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			VTHQGLSSPVTKSFNRGEC	EWESNGQPENNYKTTTPVVLDSGDSFFLYSKLTVDKSRWQQGN VFSCSVMHREALHNHYTQKSLSLSPGK
			(SEQ ID NO: 62)	(SEQ ID NO: 63)
			GAAATAGTGATGACGCAGTCT CCAGCCACCCTGTCTGTGTCT CCAGGGAAAGAGCCACCCT CTCCTGCAGGGCAGTCAGAG TGTTAGCGAACAATTAGCCTG GTACCAGCAGAAACCTGGCC AGGCTCCAGGCTCCTCATCT ACGAAGCAGCCACCAGGGCC ACTGGTATCCAGCCAGGTTC AGTGGCAGTGGTCTGGGAC AGAGTTCAC'TCACCATCAG CAGCCTGCAGTCTGAAGATT TGCAGTTTATTACTGTCAGCA GTATCAGAACTGGCTCTCAC TTTCGGCGGAGGACCAAGGT GGAGATCAAACGAACGGTGG CTGCACCATCTGTCTTCATCT CCCGCCATCTGATGAGCAGTT GAAATCTGGAACCTGCCCTGT TGTGTGCTGTGTAATAACTT CTATCCAGAGAGGCCAAAG TACAGTGGAAGGTGGATAAC GCCCTCCAATCGGGTAACTCC CAGGAGAGTGTACAGAGCA GGACAGCAAAGGACAGCACCT ACAGCCTCAGCAGCACCCCTGA CGCTGAGCAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCAGTAACTATGGCATGCACTGGGTCCGCCAGGCTCCA GGCGAGGGCTGGAGTGGTGGCAGCTATATGGTTTGTATGC AAGTGATAAATACTATGCAGAGCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAATCCAGAACAACGCTGTATCTGCAA ATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTG TGGAGAGATCTGGCAGATTTTGGAGTGAATCCCGACTACT GGGGCCAGGGAACCTGGTCAACCTGTCTAGTGCCTCCACC AAGGGCCCATCGGTCTTCCCTTGGCACCCTCC'TCCAAGAG CACCTCTGGGGCACAGCGGCCCTGGGCTGCCGTGTCGAAGG ACTACTTCCCGCAACCGGTGACGGTGTCTGTGGAAC'TCAAGGC GCCCTGACCAAGCGGTGTGCACACTTCCCGGTGTCTTACA GTCTCAGGACTCTACTCCCTCAGCAGCGTGTGAGCCGTGC CCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTG AATCAAGCCCAAGCAACCAAGGTGGACAAAGAAAGTTG AGCCCAAATCTTGTGACAAAAC'TCACATGCCCACCGTGC CCAGCACCTGAACCTCTGGGGGACCGTCACTTCTCTTTC CCCCAAAACCCAAAGGACACCCCTCATGATCTCCCGGACCCC TGAGTCAACATGCTGGTGGTGGACGTGAGCCACGAAGACC CTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTG CATAATGCCAAGACAAGCCGTGCGAGGAGCAGTACGGCA GCACGTACCCTGCGTCAAGCTCCTCACCGTCTTGCACCAAG GACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTGTCCA ACAAAGCCCTCCAGCCCCCTCAGAAACCAATCTCCAAA GCCAAAGGGCAGCCCCGAGAACCAACAGGTACACCCCTGCC CCCATCCCGGGAGGAGATGACCAAGAACAGGTCAAGCTG ACCTGCCCTGGTCAAGGCTTCTATCCAGCGACATCGCGGT GGAGTGGGAGAGCAATGGGCAAGCGGAGAACAACTACAAG ACCACGCTCCCGTGTGGAGTCCGACGGCTCTTCTTCTC TATAGCAAGCTCACCGTGGACAAAGCAGGTGGCAGCAGC GGAACGTCTTCTCATGTCCGTGATGATGAGGCTCTGCAC AACCACTACAGCAGCAAGAGCCCTCTCCCTGTCTCCGGGTAA
2G10.320	[hu anti- <huGIPR> 2G10.320 VK3 (1-236) VL]:huKLC -CL + [hu anti- <huGIPR> 2G10.320 VH3 (1-472) VH]:huIgG1 zSEFL2-2 (mAb); LMR ID: SS- 26197	NA		

[illegible]

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		<p>GCCCTCCAAATCGGGTAACTCC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCCTCAGCAGCACCCCTGA CGTGAGCAAAAGCAGACTAC GAGAAACACAAGTCTACGC CTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT</p>	<p>GCACGTACCGTTGCGTCAGCGTCTCACCCTGCTGCAACGACCGAG GACTGGTGAATGGCAAAGGAGTACAAAGTGCAAGGTGTCCA ACAAAGCCCTCCAGCCCCATCGAGAAACCATCTCTCCAAA GCCAAAGGCGAGCCCCGAGAACACAGGTGTACACCCCTGCC CCATCCCGGAGGAGATGACCAAGAACAGGTCAGCTAGCCTG ACTGCTGGTCAAAGGCTTCTATCCACGACATCGCCGT GGAGTGGGAGAGCAATGGGCGACCCGAGAACAACTACAAG ACCACGCTCCCGTCTGGACTCCGACGGCTCTTCTTCTCCTC TATAGCAAGCTCACCCTGGACAAAGACAGGTGGCAGCAGG GGAACGTCTTCTCATGCTCCGTGATGATGAGGCTCTGCAC AACCACTACACGCAGAAAGCCCTCTCCCTGTCTCCGGGTAA A</p>	
	AA	<p>(SEQ ID NO: 68) EIVMTQSPATLSVSPGERATLS CRASQSVSEHLAWYQOKPGQA PRLIYEAAATRAATGIPARFSGS SGTEFTLTISLSQSEDFAVYYCQ QYQNWPLTFGGGKVEIKRTV AAPSVFIFPPSDEQLKSGTASVV CLLNFFYPREAKVQWVKVDNAL QSGNSQESVTEQDSKDSYSL STLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC</p>	<p>(SEQ ID NO: 69) QVQLVESGGGVQPGRSRLRSCAASGFTFSNYGMHWVRQAP GEGLEWVAIWFDASDKYYADA VKGRFTISRDNKNTLYLQ MNSLRAEDTAVYYCARDLAIFGVVPDYWQGTLVTYSSASTK GPSVFPPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTI SKAKGQPREPVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQKSLSLSPGK</p>	
2G10.333	[hu anti- <huGIPR> 2G10.333 VK3 (1-236) VL]:huKLC -CL + [Unknown anti- <huGIPR> 2G10.610 VH3 (1-472)]	NA	<p>(SEQ ID NO: 70) GAAATAGTGATGACGCAGTCT CCAGCCACCTGTCTGTGTCT CCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAG TGTTAGCCGGCACCTAGCCTG GTACCAGCAGAAACCTGGCC AGGCTCCAGGCTCCTCATCT ACGAAGCAGCCACCAAGGCC ACTGGTATCCAGCCAGGTT AGTGGCAGTGGGTCTGGGAC AGAGTTCACTCTACCATCAG</p>	<p>(SEQ ID NO: 71) CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGACGATCTGGATTCA CCTTCAGTAACATATGGCATGCATGGTCCGCCAGGCTCCA GGCGAGGGCTGGAGTGGTGGCAGCTATATGGTTTGTATGC AAGTGATAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAACCTCAAGAACACGCTGTATCTGCAA ATGAACAGCTGAGAGCCGACGACACGGCTGTGTATTACTG TGGCAGAGATTTGGCGATTTTGGAGTGGTCCCGGACTACT GGGGCCAGGAACCCCTGGTACCGGTGTCTAGTCCCTCCACC AAGGGCCCATCGGTCTTCCCTTGGCACCCCTCTCCCAAGAG CACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGG</p>

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<p>VHJ::hulgG1 zSEFL2-2 (mAb); LMR ID: SS- 26210</p>	<p>CAGCCTGCAGTCTGAAGATT TGAGTTTATTACTGTGAGCA GTATCAGCACTGGCCTCTCAC TTTCGGCGGAGGACCAAGGT GGAGATCAAAACGAACGGTGG CTGACCATCTGTCTTCATCTT CCGCCATCTGATGAGCAGTT GAAATCTGGAATGCCCTCTGT TGTGTGCTGCTGAATAACTT CTATCCAGAGAGGCCAAAG TACAGTGGAAAGGTGGATAAC GCCCTCCAATCGGGTAACCTC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCCTCAGCAGCACCTGA CGCTGAGCAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT</p>	<p>ACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGC GCCCTGACAGCGGCTGCACACCTTCCCGGTGTCTCTACA GTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGC CCTCAGCAGCTTGGCACCCAGACCTACATCTGCAACGTG AATCAACAGCCAGCAACACCAAGTGGACAAAGAAAGTTG AGCCAAATCTTGTGACAAACCTACACATGCCACCGTGC CCAGCACCTGAACCTCTGGGGGACCGTACGTCTTCTCTTC CCCCAAACCCAGGACACCTCATGATCTCCCGGACCCC TGAGGTACATGCTGTGTGGTGGACGTGAGCCACGAAGACC CTGAGGTCAAGTTCAACTGCTACGTGACGGCTGGAGGTG CATAATGCCAAGCAAAAGCTGGGAGGAGCAGTACGGCA GCACGTACCGTTGCTGCTCAGCGTCTCACCCTCTGCACCA GACTGGCTGAATGCCAAGGAGTACAAGTGAAGGTGTCCA ACAAAGCCCTCCAGCCCCCATCGAGAAACCATCTCCAAA GCCAAAGGGCAGCCCGAGAACACAGGTGTACACCTGCC CCCATCCCGGAGGAGTACCAAGAACACAGGTACAGCTG ACCTGCCTGGTCAAGGCTTCTATCCAGCGACATCGCCGT GGAGTGGGAGAGCAATGGGACCCGAGAAACACTACAAG ACCACGCTCCCTGCTGCTGAGTCCGACGGCTCTTCTCTCTC TATAGCAAGCTCACCGTGGACAAAGCAGGTGGCAGCAGG GGAACGCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC AACCACTACACGCAAGAGAGCCTCTCCCTGTCTCCCGGTAA A</p>
	<p>(SEQ ID NO: 72)</p> <p>AA</p>	<p>(SEQ ID NO: 73)</p> <p>QVQLVESGGGVQGRSLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAIWFDASDKYYADAVKGRFTISRDNKNTLYLQ MNSLRAEDTAVYCARDLAIFGVVPDYWGQGLVTVSSASTK GPSVFPPLAPSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHPN TKVDKKVEPKSCDKTHTCPCPAPELGGPSVFLPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHAEALHNHYTQKSLSLSPGK</p> <p>(SEQ ID NO: 75)</p>
	<p>(SEQ ID NO: 74)</p>	

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<p>2G10.301</p> <p>[hu anti- <huGIPR> 2G10.301 VK3 (1-236) VLJ::huKLC -CL + [hu anti- <huGIPR> 2G10.301 VH3 (1-472) VHJ::huIgG1 zSEFL2-2 (mAb); LMR ID: SS- 26178</p>	<p>NA</p>	<p>GAAATAGTGATGACGCAGTCT CCAGCCACCCTGTCTGTGTCT CCAGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAG TGTTTCAGCCACTTAGCCTG GTACCAGCAGAAACCTGGCC AGGTCCTCCAGGCTCCTCATCT ACGAAGCAGCCACCAGGGCC ACTGGTATCCAGCCAGGTTTC AGTGGCAGTGGGTCTGGGAC AGAGTTCACTCTCACCATCAG CAGCCTGCAGTCTGAAGATT TGCAGTTTATTACTGTACGCA GTATCAGAACTGGCCTCTCAC TTTCGGCGGAGGGACCAAGGT GGAGATCAACGAAACGGTGG CTGCACCATCTGTCTTCATCTT CCCGCCATCTGATGAGCAGTT GAAATCTGGAACCTGCTCTGT TGTGTGCTGTGAATAACTT CTATCCCAGAGAGGCCAAAG TACAGTGGAAGTGGATAAC GCCCTCCAATCGGGTAACCTC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCCTCAGCAGCACCTGA CGCTGAGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT</p>	<p>CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCC TGGGAGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCCAGAACTATGGCATGCACTGGTCCGCCAGGCTCCA GGCGAGGGCTGGAGTGGTGGCAGCTATATGTTTGTATGC GTCTGACAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCAATCTCCAGAGACAACCTCAAGAACACGCTGTATCTGCAA ATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTG TGCAGAGATCTTGCATTTTGGATTTGGAGTGTCCCCGACTACTG GGCCAGGGAACCTGTCTACCGTGTCTAGTGCCTCCACCA AGGGCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGC ACCTCTGGGGGCACAGGGCCCTGGGCTGGCTGGTCAAGGA CTACTTCCCCGAACCCGTGACGGTGTCTGGAACCTCAGGCG CCCTGACCAGCGGCGTGCACACCTTCCGGCTGTCTCTACAG TCCTCAGGACTCTACTCCCTCAGCAGCTGTGTGACCGTGCCC TCCAGCAGCTTGGGACCCAGACCTACATCTGCAACCTGAA TCACAAGCCAGCAACCAAGGTGGACAAAGAAAGTTGAG CCCAATCTTGTGACAAACTCACACATGCCACCGTGCCC AGCACCTGAACCTCTGGGGGACCGTCACTCTCTCTCCC CCCAAAACCAAGAACACCTCATGATCTCCCGGACCCCTG AGTGCACATGCTGTGTGGTGGACGTGAGCCACGAAGACCT GAGGTCAAGTTCAACTGGTACGTGACGGCGTGGAGGTGCA TAATGCCAAGACAAGCCGTGGGAGGAGCAGTACGGCAGC ACGTACCGTTCGCTCAGCTCTCACCCTGTGCACCAAGGA CTGGCTGAATGGCAAGGAGTACAAGTGCAGAGGTGTCCAACA AAGCCCTCCAGCCCCCATCGAGAAACCATCTCCAAGCC AAAGGGCAGCCCCGAGAACCCAGGTGTACACCTTGCCCCC ATCCCGGAGGAGATGACCAAGAACCAAGGTACGCTGACCT GCCGTGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAG TGGGAGAGCAATGGCAGCCGAGAACAACTACAAGACCA CGCTCCCGTGTGGACTCCGACGGCTCTCTCTCTCTATA GCAGCTCACCTGGCAAGAGCAGGTGGCAGCAGGGGAA CGTCTTCTCATGCTCCGTGATGAGGTGAGGCTCTGCACAAACA CTACAGCAGAGAGCCCTCTCCCTGTCTCCGGGTAAA</p>
		<p>(SEQ ID NO: 76)</p> <p>EIVMTQSPATLSVSPGERATLS CRASQSVFSLAWYQQKPGQA</p>	<p>(SEQ ID NO: 77)</p> <p>QVQLVESGGGVQPGRSRLSCAASGFTFQNYGMHWVRQAP GEGLEWVAIWFDASDKYYADA VKGRFTISRDNKNTLYLQ</p>

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		<p>PRLLIYEAAATRAATGIPARFSGG SGTEFTLTISLSQSEDFAVYYCQ QYQNWPLTFGGGKVEIKRTV AAPSVEIFPPSDEQLKSGTASVV CLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSYSTSL STLTLSKADYEHKHKVYACEVT HQGLSSPVTKSFNRGEC</p>	<p>MNSLRAEDTAVYYCARDLAIFGVVPDYWGQGLVTVSSASTK GPSVFLPAPSSKTSGGTAALGGLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQYICNVNHNKPSN TKVDKKVEPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSYTRCVSLTVLHQLDNLNKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSGFFLYSKLTVDKSRWQQGN VFSCSVMHREALHNYHTQKSLSLSPGK</p>
		(SEQ ID NO: 78)	(SEQ ID NO: 79)
<p>Ihu anti- <huGIPR> 2G10.601 VK3 (1-236) VL]:huKLC -CL + Ihu anti- <huGIPR> 2G10.301 VH3 (1-472) VHJ::huIgG1 zSEFL2-2 (mAb): LMR ID: SS- 26226</p>	NA	<p>GAAATAGTGATGACGCAGTCT CCAGCCACCCTGTCTGTGTCT CCAGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAG TGTTTTAGCCACTTAGCCTG GTACCAGCAGAAACCTGGCC AGGCTCCAGGCTCCTCATCT ACGAAGCAGCCACCAGGGCC ACTGGTATCCAGCCAGGGTIC AGTGGCAGTGGGTCTGGGAC AGAGTTCACCTCACCATCAG CAGCCTGCAGTCTGAAGATT TGCAAGTTTATTACTGTACGCA GTATCAGAACTGGCTCTCAC TTTCGGCGGAGGACCAAGGT GGAGATCAAAACGAACGGTGG CTGCACCATCTGTCTTCATCTT CCCGCCATCTGATGAGCAGTT GAAATCTGGAACCTGCCCTGT TGTGTGCTGCTGAATAACTT CTATCCACAGAGAGGCCAAAG TACAGTGGAAGGTGGATAAC GCCCTCCAATCGGGTAACCTC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCCTCAGCAGCACCCCTGA</p>	<p>CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCCAGAACTATGGCATGCCTGGTCCGCCAGGCTCCA GGCGAGGGCTGGAGTGGTGGCAGCTATATGGTTTGATGC GTCTGACAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAACCTCAAGACACGCTGTATCTGCAA ATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTG TGCAGAGATCTTGCAGATTTTGGAGTGTCTCCCGACTACTG GGCCAGGGAACCTGTCTACCGTGTCTAGTGCCTCCACCA AGGGCCCATCGGTCTTCCCTGGCACCCCTCCTCCAGAGC ACCTCTGGGGCACACGGCCCTGGCTGCCCTGGTCAAGGA CTACTTCCCGAACCGGTGACGGTGTCTGTGAACCTCAGCG CCCTGACCAGCGCGTGCACACCTTCCCGGTGTCTCTACAG TCCTCAGGACTACTCTCTCAGCAGCGTGGTGACCGTGCCC TCCAGCAGCTTGGCACCCAGACCTACATCTGCAACGTGAA TCACAAGCCAGCAACACCAAGGTGGACAAAGAAAGTTGAG CCCAATCTTGTGACAAACTCACACATGCCACCGTGCCC AGCACCTGAACCTCTGGGGGACCGTCAAGTCTTCTTCCC CCCAAAACCCAGGACACCTCATGATCTCCCGGACCCCTG AGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCT GAGGTCAAGTCAACTGTTACGTGAGCGGTGGAGGTGCA TAATGCCAAGACAAAGCGTGGAGGAGCAGTACGGCAGC ACGTACCTTGGTCAAGCTCTCACCCTCTGCAACCCAGGA CTGGCTGAATGGCAAGGATACAACTGCAAGGTGTCCACAA AAGCCCTCCAGCCCCCATCGAGAAACCATCTCCAAAGCC AAGGGCAGCCCCCGAGAACCAAGGTGTACACCTTGCCCCC</p>

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		AA	CGCTGAGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT (SEQ ID NO: 80)	ATCCCGGAGGAGATGACCAAGAACAGGTCAGCCTGACCT GGCTGTGTCAAAGGCTTCTATCCACGACATCGCCGTGGAG TGGGAGAGCAATGGCAGCCGGAGAACAACTACAAGACCA CGCTCCCGTGTGACTCCGACGGCTCTTCTTCTCTCTATA GCAAGCTCACCGTGGACAAAGCAGGTGGCAGCAGGGAA CGTCTTCTCATGCTCCGTGATGATGAGGCTCTGCACAACCA CTACAGCAGAGAAGCCTCTCCCTGTCTCCGGGTAAA (SEQ ID NO: 81)
			EIVMTQSPATLSVSPGERATLS CRASQSVFSLAWYQQKPGQA PRLIYEAAATRAITGIPARVSGS SGTEFTLTISLQSEDFAVYYCQ QYQNWPLTFGGGTKEIKRTV AAPSVFIFPPSDEQLKSGTASVV CLLNNFYPREAKVQWQKVDNAL QSGNSQESVTEQDSKDSYSL STLTLSKADYEKHKVYACEVT HQGLSPVTKSFNRGEC (SEQ ID NO: 82)	QVQLVESGGGVVQPGSRSLRLSCAASGFTFQNYGMHWVRQAP GEGLEWVAIAIFDASDKYYADA VKGRFTISRDN SKNTLYLQ MNSLRAEDTAVYYCARDLAI FGVVPDYWQQGTLVTYSSASTK GPSVFP LAPSSKTSGGT AALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHCTCPPEL LGGPSVFLPFPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTPPVLDSGFFLYSKLTVDKSRWQQGN VFSCSVMH EALHNHYTQKSLSPGK (SEQ ID NO: 83)
2G10.326	[hu anti- <huGIPR> 2G10.326 VK3 (1-236) VL]:huKLC -CL + [hu anti- <huGIPR> 2G10.301 VH3 (1-472) VH]:huIgG1 zSEFL2-2 (mAb); LMR ID: SS- 26203	NA	GAAATAGTGATGACGCAGTCT CCAGCCACCTGTCTGTGTCT CCAGGGGAAAGAGCCACCCT CTCCTGCAAGGCCAGTCAGAG TGTTCTGAGTCACTTAGCCTG GTACCAGCAGAAACCTGGCC AGGTCCAGGCTCCTCATCT ACGAAAGCAGCCACCAGGGCC ACTGGTATCCAGCCAGGTTT AGTGCAAGTGGTCTGGGAC AGAGTTCACCTCACCATCAG CAGCCTGCAGTCTGAAGATT TGCAGTTTATTACTGTCAGCA GTATCAGCAGTGGCTCTCAC TTTCGGCGGAGGACCAAGGT GGAGATCAAAACGAAACGGTGG (SEQ ID NO: 84)	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGGTGGTCCAGCC TGGGAGGTCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCCAGAACTATGGCATGCACTGGTCCGCCAGGCTCCA GGCAGGGGCTGGAGTGGTGGCAGCTATATGGTTTGATGC GTCTGACAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAACCTCAAGAACACGCTGTATCTGCAA ATGAACAGCTGAGAGCCGAGGACACGGCTGTGTATTACTG TGGAGAGATCTTGCAGATTTTGGAGTGGTCCCGACTACTG GGGCCAGGGAACCTGGTCAACCGTGTCTAGTGCCTCCACCA AGGGCCCATCGTCTTCCCCCTGGCACCTCTCTCCAAAGC ACCTTGGGGGACAGCGGCCCTGGGCTGCCTGGTCAAGGA CTACTTCCCGCAACCGGTGACGGTGTGTGGAACTCAAGCG CCCTGACAGCGGGCTGCACACCTTCCCGGCTGTCTCTACAG TCCTCAGGACTCTACTCCCTCAGCAGCGGTGGTACCGTGCCC TCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTGAA TCACAAGCCCAAGCAACACCAAGGTGTGACAAAGAAAGTTGAG (SEQ ID NO: 85)

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2G10.308	Ihu anti- <huGIPR> 2G10.308 VK3 (1-236) VLJ::huKLC -CL +	NA	CTGCACCATCTGTCTTCATCTT CCCGCCATCTGATGAGCAGTT GAAATCTGGAACCTGCTCTGT TGTGTGCTGCTGAATACTT CTATCCAGAGAGGCCAAG TACAGTGGAAGGTGGATAAC GCCCTCCAATCGGGTAACCTC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCTCAGCAGCACCTGA CGCTGAGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCAACCATCAGGG CCTGAGCTCGCCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT	CCCAATCTTGTGACAAAACTCACATGCCCACCGTGCCC AGCACTGAACCTCTGGGGGACCGTCAGTCTTCTTCCC CCCAAAACCAAGACACCTCATGATCTCCCGGACCCCTG AGGTCACATGCGTGTGTGACGTGAGCCACGAAGACCT GAGGTCAAGTTCAACTGGTACGTGAGCGGTGAGGTGCA TAATGCCAAGCAAAAGCCGTGGAGGACGAGTACGGCAGC AGTACCGTGTGCTGACGCTCTCACCGTCTGCACCCAGGA CTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTGTCCAACA AAGCCCTCCAGCCCCATCGAGAAACCATCTCCAAGCC AAAGGCAGCCCCGAGAACACACAGGTGTACACCTGCCCCC ATCCGGGAGGAGATGACCAAGAACAGGTGACGCTGACCT GCCGTGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAG TGGGAGAGCAATGGCAGCCGAGAACAACTACAAGACCA CGCTCCCGTGTGCTGACTCCGACGGCTCTTCTTCTCTATA GCAAGCTCACCGTGGACAAGACAGGTGGCAGCAGGGGAA CGTCTTCTCATGCTCCGTGATGATGAGGCTCTGCACAACA CTACACGCAAGAGACCTCTCCCTGTCTCCGGGTAAA (SEQ ID NO: 85)
			EIVMTQSPATLSVSPGERATLS CRASQSVLSHLAWYQQKPGQA PRLIYEATRATGIPARFSGS SGTEFTLTISLQSEDFAVYYCQ QYQQWPLTFGGGKVEIKRTV AAPSVFIPTPSDEQLKSGTASVV CLLNFFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSYSL STLTLSKADYEEKHKVYACEVT HQGLSSPVTKSFNRGEC (SEQ ID NO: 84)	QVQLVESGGVVQPGRSLRLSCAASGFTFNQYGMHWVRQAP GEGLEWVAIWFDASDKYYADA VKGRFTISRDNKNTLYLQ MNSLRAEDTAVYYCARDLAIFGVVPDYWGQGLVTVSSASTK GPSVFLAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLPPKPKDNL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVNMEALHNHYTQKSLSLSPGK (SEQ ID NO: 87)
2G10.308	Ihu anti- <huGIPR> 2G10.308 VK3 (1-236) VLJ::huKLC -CL +	NA	AA	QVQLVESGGVVQPGRSLRLSCAASGFTFNQYGMHWVRQAP GEGLEWVAIWFDASDKYYADA VKGRFTISRDNKNTLYLQ MNSLRAEDTAVYYCARDLAIFGVVPDYWGQGLVTVSSASTK GPSVFLAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLPPKPKDNL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVNMEALHNHYTQKSLSLSPGK (SEQ ID NO: 87)
			GT	QVQLVESGGVVQPGRSLRLSCAASGFTFNQYGMHWVRQAP GEGLEWVAIWFDASDKYYADA VKGRFTISRDNKNTLYLQ MNSLRAEDTAVYYCARDLAIFGVVPDYWGQGLVTVSSASTK GPSVFLAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLPPKPKDNL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVNMEALHNHYTQKSLSLSPGK (SEQ ID NO: 87)

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[Unknown anti- <huGIPR> 2G10.610 VH3 (1-472) VH1::huIgG1 zSEFL2-2 (mAb); LMR ID: SS- 26185	AGGTCCACGAGCTCTCTCATCT ACGAAGCAGCCACAGGGCC ACTGGTATCCAGCCAGGTTC AGTGGCAGTGGTCTGGGAC AGAGTTCACCTCACCATCAG CAGCCTGCAGTCTGAAGATT TGCAGTTTATTACTGTACGA GTATCAGCAGTGGCTCTCAC TTTCGGCGGAGGACCAAGGT GGAGATCAAAACGAACGGTGG CTGCACCATCTGTCTTCATCTT CCCGCCATCTGATGACAGTT GAAATCTGGAACCTGCCCTGT TGTGTGCTGTGTAATAACTT CTATCCAGAGAGGCCAAAG TACAGTGAAGGTGGATAAC GCCCTCAAATCGGGTAACTCC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCTCAGCAGCACCCCTGA CGCTGAGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT	ATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTG TGGAGAGATTTGGCGATTTTGGAGTGGTCCCCGACTACT GGGGCCAGGAAACCTGGTACCGTGTCTAGTGCCTCCACC AAGGGCCCATCGTCTTCCCCCTGGCACCTTCTCCAAAGAG CACCTCTGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGG ACTACTTCCCCGAACCGGTGACGGTGTCTGGAAACTCAGGC GGCCTGACCAAGCGGTGCACACTTCCCGGCTGTCTCTACA GTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGTGACCGTGC CCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTG AATCAAGCCCAAGCAACCAAGGTGGACAAAGAAAGTTG AGCCCAATCTTGTGACAAAACCTCACACATGGCCACCGTGC CCAGCACCTGAACCTCTGGGGGACCGTCACTCTTCTCTTC CCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCC TGAGGTCACATCGTGTGTGGACGTGAGCCACGAAAGACC CTGAGGTCAAGTTCAACTGCTGACGTGGACGGCTGGAGGTG CATAATGCCAAGCAAAAGCCGTGCGAGGAGCAGTACGGCA GCACGTACCGTTGCGTCAAGTCTCACCCTGCAACCAAG GACTGGCTGAATGGCAAGGAGTCAAGTGCAGGTGTCTCA ACAAAGCCCTCCAGCCCCATCGAGAAACCATCTCCAAA GCCAAAGGCGACCCCGAGAACCAACAGGTACACCCCTGCC CCCATCCGGGAGGAGATGACCAAGAACCAAGTCAAGCTG ACCTGCTGTGTCAAAGGCTTCTATCCAGCGACATCGCGT GGAGTGGGAGAGCAATGGGCAAGCCGAGAAACAACATAAG ACCACGCTCCCGTGTGCTGACTCCGACGGCTCTTCTCCTC TATAGCAAGCTCACCGTGGACAAAGCAGGTGGCAGCAGG GGAACGTCTTCTCATGCTCCGTGATGATGAGGCTCTGCAC AACCACTACAGCAGAAAGAGCCCTCTCCCTGTCTCCGGGTAA A
	(SEQ ID NO: 88) EIVMTQSPATLSVSPGERATLS CRASQSVFSLAWYQKPGQA PRLIYEAAATRAIGPARFSGS SGTEFTLTISLQSEDFAVYQC QYQQWPLTFGGGKVEIKRTV AAPSVFIFPPSDEQLKSGTASV CLLNFFYPREAKVQWKVDNAL	(SEQ ID NO: 89) QVQLVESGGGVVQPGRSRLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAAIWFDADSKYYADA VKGRFTISRDN SKNTLYLQ MNSLRAEDTAVYYCARDLAI FGVVPDYWGQGLTVTVSSASTK GPSVFPLAPSSKSTSGGTAA LGLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE

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		QSGNSQESVTEQDSKSDSTYSLS STLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC		(SEQ ID NO: 90) GAAATAGTGATGACGCGAGTCT CCAGCCACCTGTCTGTGTCT CCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAG TGTTTTCAGCCACTTAGCCTG GTACGACGAGAAACCTGGCC AGGCTCCAGGCTCCTCATCT ACGAAAGCAGCCACCAGGGCC ACTGGTATCCAGCCAGGGTC AGTGGCAGTGGGTCTGGGAC AGAGTTCACCTCACCATCAG CAGCCTGCAGTCTGAAGATT TGCAGTTTATTACTGTCAGCA GTATCAGCAGTGGCTCTCAC TTTCGGCGGAGGACCAAGGT GGAGATCAACGAAACGGTGG CTGCACCATCTGTCTTCATCT CCCGCATCTGATGAGCAGTT GAAATCTGGAACCTGGCTCTGT TGTGTGCTGCTGAATAACTT CTATCCCAGAGAGGCCAAAG TACAGTGGAAAGTGGATAAC GCCCTCCAATCGGGTAACTCC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCCTCAGCAGCACCTGA CGCTGAGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCAACCATCAGGG CCTGAGCTCGCCCGTCACAA GAGCTTCAACAGGGGAGAGT		EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMEALHNHYTQKSLSLSPGK (SEQ ID NO: 91) CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCAGTAACATAGGCATGCACCTGGTCCGCCAGGCTCCA GGCGAGGGCTGGAGTGGTGGCAGCTATATGTTTGTATGC AAGTGATAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAACCTCAAGAACACGCTGTATCTGCAA ATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTG TGCAGAGATTGGCGATTGTTTGGAGTGGTCCCCGACTACT GGGGCCAGGAAACCTGGTCAACCGTGTCTAGTCCCTCCACC AAGGCCCATCGTCTTCCCCCTGGCACCTCTCTCCAAGAG CACCTCTGGGGGCACAGCGGCCCTGGGTGCCCTGCTCAAG ACTACTTCCCCGAACCGGTGACGGTGTGCTGGAACCTCAGGC GCCCTGACCAGCGGTGCACACCTTCCCGGTGCTCTCTACA GTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAACCTGCG CCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCCAACGTG AATCACAAGCCAGCAACACCAAGGTGGACAAAGAAAGTTG AGCCAAATCTTGTGACAAACCTCACACATGCCACCGCTGC CCAGCACCTGAACTCTCTGGGGGACCGTCAAGTCTTCTCTTC CCCCAAACCCCAAGGACACCTCATGATCTCCCGGACCC TGAGGTACATGCTGTGTGGTGGACCTGAGCCACGAAGACC CTGAGGTCAAGTTCAACTGTAACGTGACGCGCGCTGGAGGTG CATAATGCCAAGACAAGCCGTGCGAGGAGCAGTACGGCA GCACGTACCGTGGTCAAGGTCTCACCCTCTGCAACCCAG GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTGTCCA ACAAAGCCCTCCAGCCCCATCGAGAAACCACTCTCCAAA GCCAAAGGGCAGCCCGAGAACCCAGGTGTACACCCCTGCC CCCATCCCGGGAGAGATGACCAAGAACCCAGGTCAAGCTG ACCTGCCCTGGTCAAAAGCTTCTATCCAGCGACATCGCCGT GGAGTGGGAGAGCAATGGGCAAGCGGAGCAACAACTACAAG ACCACGCTCCCGTGTGACTCCGACGGCTCTCTTCTCTC TATAGCAAGCTCACCGTGGACAAAGAGCGAGTGGCAGCAGG
	[hu anti- <huGIPR> 2G10.608 VK3 (1-236) VLj::huKLC -CL + [Unknown anti- <huGIPR> 2G10.610 VH3 (1-472) VHj::huIgG1 zSEFL2-2 (mAb); LMR ID: SS- 26233	NA				

2G10.608

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2G10.336			GT	GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC AACCACTACAGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAA A
		AA	(SEQ ID NO: 92) EIVMTQSPATLSVSPGERATLS CRASQSFSLAWYQQKPGQA PRLIYEAAATRAITGIPARVSGS SGTEFTLTISLQSEDFAVYQC QYQQWPLTFGGGKVEIKRTV AAPSVFIFPPSDEQLKSGTASVV CLLNNFYPREAKVQWVKVDNAL QSGNSQESVTEQDSKDSYSL STLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC	(SEQ ID NO: 93) QVQLVESGGGVQPGRLSLRLSAAAGFTFSNYGMHWVRQAP GEGLEWVAIAWFDASDKYYADA VKGRFTISRDN SKNTLYLQ MNSLRAEDTAVYCARDLAI FGVV PDYWGQGLTVTVSSASTK GPSVFLPAPSSKTSGGTAA LGLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN HKPSN TKVDKKVEPKSCDKTHTCPCPAPELLGGPSVFLPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTI SKAKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPVLDSDSGSFFLYSKLTVDKSRWQQGN VFSCSVMH EALHNHYTQKSLSPGK
	[hu anti- <huGIPR> 2G10.336 VK3 (1-236) VLJ]:huKLC -CL + [hu anti- <huGIPR> 2G10.325 VH3 (1-472) VHJ]:huIgG1 zSEFL2-2 (mAb); LMR ID: SS- 26213	NA	(SEQ ID NO: 94) GAAATAGTGATGACGCAGTCT CCAGCCACCTGTCTGTGTCT CCAGGGAAAGAGCCACCCT CTCCTGCAAGGCCAGTCAGAG TGTTTCAGAGCCACTTAGCCTG GTACCAGCAGAAACCTGGCC AGGCTCCAGGCTCCTCATCT ACGAAGCAGCCACCAGGGCC ACTGGTATCCCAAGCCAGGTTC AGTGCACTGGGCTCTGGGAC AGAGTTCAC'TCACCATCAG CAGCCTGCAGTCTGAAGATT TGCAGTTTATTACTGTGAGCA GTATCAGAACTGGCTCTCAC TTTCGGCGGAGGACCAAGGT GGAGATCAAACGACCGGTGG CTGCACCATCTGTCTTCATCTT CCCGCCATCTGATGAGCAGTT GAAATCTGGAACCTGCCCTGT TGTTGCTCTGCTGAATAACTT	(SEQ ID NO: 95) CAGGTGCAGCTGGTGAGTCTGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCAGTAACTATGGCATGCATGGGTCCGCCAGGCTCCA GGCAGGGGCTGGAGTGGTGCGAGCTATATGGTTTGATGC AAGTGATAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAACCTCAAGAACACGCTGTATCTGCAA ATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTG TGGAGAGATAATTGCGATTTTGGAGTGGTCCCCGACTACT GGGGCCAGGAAACCTGGTCAACGTGTCTAGTGCCTCCACC AAGGGCCCATCGGTCTTCCCCCTGGCACCTCTCTCCAAAG CACCTCTGGGGGCACAGCGCCCTGGGCTGCCCTGGTCAAGG ACTACTTCCCCGAACCGGTGACGGTGTGCGTGGAACTCAGGC GCCC TGACCAGCGCGTGCACACTTCCCGGCTGTCTACA GTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGC CCTCCAGCAGCTTGGCACCCAGACCTACATCTGCAACGTTG AATCAAGCCAGCAACCAAGGTGGACAAAGAAAGTTG AGCCCAAATCTTGTGACAAACATCACATGCCCACCGTGC CCAGCACCTGAACCTCTGGGGGACCGTCAGTCTTCCCTTC CCCCAAAACCCAAAGGACACCTCATGATCTCCCGGACCCC TGAGGTCACATGCGTGGTGGTGGACCTGAGCCACGAAGACC

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2G10.344	hu anti- <huGIPR> 2G10.344 VK3 (1-236) VLJ::huKLC -CL + hu anti- <huGIPR> 2G10.325	NA	CTATCCAGAGAGGCCAAAG TACAGTGGAAGGTGGATAAC GCCCTCCAATCGGGTAACTCC CAGGAGAGTGTCACAGAGCA GGACAGCAAGGACAGCACCT ACAGCCTCAGCAGCACCTGA CGCTGAGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT	CTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTG CATAATGCCAAGACAAAAGCCGTGGCAGGAGCAGTACGGCA GCACGTACCGTTCGCTCAGCGTCTCACCCTCTGCACAG GACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTGTCCA ACAAAGCCCTCCAGCCCCATCGAGAAACCATCTCCAAA GCCAAAGGGCAGCCCGAGACACAGGTGTACACCCCTGCC CCCATCCCGGGAGGAGATGACCAAGAACCCAGGTACGCTG ACCTGCTGGTCAAGGCTTCTATCCAGCGACATCGCCGT GGAGTGGGAGAGCAATGGGACGCCGGAACAACACTACAAG ACCACGCTCCCGTCTGGACTCCGACGGCTCTCTTCTCCTC TATAGCAAGCTCACCCTGGACAAAGCAGGTGGCAGCAGG GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC AACCACCTACACGCAAGAGACCTCTCCCTGTCTCCCGGTAA A
			(SEQ ID NO: 96) EIVMTQSPATLSVSPGERATLS CRASQSVQSHLAWYQQKPGQ APRLIYEAAATRAITGIPARFSGS GSGTEFTLTISLSQSEDFAVYYC QQYQNWPLTFGGGKVEIKRT VAAPSVFIFFPSDEQLKSGTASV VCLLNIFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSYIS LSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC	(SEQ ID NO: 97) QVQLVESGGGVQPGRSRLRSCAASGFTFSNYGMHWVRQAP GEGLEWVAIWFDAADKYADAVKGRFTISRDNKNTLYLQ MNSLRAREDYVYCARDIAIFGVPDYWGQGLVTVSSASTK GPSVFLAPSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVFSSSLGTQYICNVNHPKPSN TKVDKKVEPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSYRCVSVLTIVLHQLDNLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHREALHNYHTQKSLSPGK
			(SEQ ID NO: 98) GAAATAGTGATGACGCAGTCT CCAGCCACCCTGTCTGTGTCT CCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAG TGTTAGTAGCCACTTAGCCTG GTACCAGCAGAAACCTGGCC AGGCTCCAGGCTCCTCATCT ACGAAGCAGCCACCAAGGGCC ACTGGTATCCCAAGCCAGGTTC	(SEQ ID NO: 99) CAGGTGCAGTGGTGGAGTCTGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCAGTAACTATGGCATGCACCTGGTCCGCCAGGCTCCA GGCGAGGGCTGGAGTGGTGGCAGCTATATGGTTTGATGC AAGTGATAAATACTATGCAGACGCCGTGAAGGGGCCGATTCA CCATCTCCAGAGACAACCTCAAGAACACGCTGTATCTGCAA ATGAACAGCCTGAGAGCCGACACGCTGTGTATTACTG TGGAGAGATATTGCGATTTTGGAGTGGTCCCCGACTACT GGGGCCAGGGAACCCCTGGTCAACCGTGTCTAGTGCCTCCACC

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<p>VH3 (1-472) VHJ::huIgG1 zSEFL2-2 (mAb); LMR ID: SS- 26221</p>	<p>AGTGGCAGTGGGTCTGGGAC AGAGTTCACTCTACCATCAG CAGCTGCAGTCTGAAGATT TGCAGTTTATTACTGTCAGCA GTATCAGCAGTGGCTCTCAC TTTCGGCGGAGGACCAAGGT GGAGATCAACGAAACGGTGG CTGCACCATCTGTCTTCACTT CCGCCATCTGATGAGCAGTT GAAATCTGGAACGTGCTCTGT TGTGTGCTGTGTAATAACTT CTATCCCAGAGAGGCCAAAG TACAGTGGAAGGTGGATAAC GCCCTCCAAATCGGGTAACTC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCTCAGCAGCACCCCTGA CGTGAGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCAACCATCAGGG CCTGAGCTCGCCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT</p>	<p>AAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAAGAG CACTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGG ACTACTTCCCCGAACCGGTGACGGTGTGCTGGAACCTCAGGC GCCCTGACACAGCGGTGACACCTTCCCCGGCTGTCTCTACA GTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGCTGC CCTCCAGCAGCTTGGGACACAGACCTACATCTGCAACGTG AATCAACAAGCCAGCAACACCAAGGTGGACAAAGATTG AGCCCAATCTGTGACAAACTCACATGACCATGCCACCGTGC CCAGCACCTGAACCTCTGGGGGACCGTCACTCTTCTCTTC CCCCAAACCCAAAGGACACCTCTATCTCCCGGACCCC TGAGGTACATGCTGGTGGTGGACGTGAGCCACGAAGACC CTGAGGTCAAGTTCACTGACGTGACGCGGTGGAGGTG CATAATGCCAAGACAAAGCGTGGCAGGAGCAGTACGGCA GCACGTACCGTTCGTCAGCAGTCTACCGTCTGCAACCAG GACTGGTGAATGGCAAGGAGTACAAGTCAAGGTGTCCA ACAAAGCCCTCCAGCCCCATCGAGAAACCATCTCCAAA GCCAAAGGCGACCCCGAGAACACAGGTGTACACCTGCC CCCATCCCGGAGGAGATGACCAAGAACCCAGGTCAAGCTG ACCTGCTGTGTCAAAGGCTTCTATCCAGCGACATCGCGT GGAGTGGGAGAGCAATGGGCGACCCGAGAACAACTACAAG ACCACGCTCCCGTCTGAGTCCGACGCGCTCTCTCTCTC TATAGCAAGTCAACCGTGGACAAAGCAGGTGGCAGCAGG GGAACGTCTTCTCATGCTCCGTGATGATGAGGTCTTGCAC AACCACTACACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAA A</p>
	<p>(SEQ ID NO: 100)</p> <p>EIVMTQSPATLSVSPGERATLS CRASQSVSSHLAWYQQKPGQA PRLIYEAAATRAIGIPARFSGS SGTEFTLTISLQSEDFAVYYCQ QYQQWPLTFGGGKVEIKRTV AAPSVFIFPPSDEQLKSGTASVV CLLNFFYPREAKVQW/KVDNAL QSGNSQESVTEQDSKDSSTYSLS STLTLSKADYVEKHKVYACEVT HQGLSSPVTKSFNRGEC</p>	<p>(SEQ ID NO: 101)</p> <p>QVQLVESGGGVQPGRSLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAIWFDASDKYYADA VKGRFTISRDNKNTLYLQ MNSLRAEDTAVYYCARDIAIFGVVDPYWGQGLVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPPCPAPPELLGGPSVFLPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGN</p>

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		(SEQ ID NO: 102)	(SEQ ID NO: 103)	VFSCSVMEALHNHYTQKSLSLSPGK
		GAAATAGTGATGAGGCAGTCT CCAGCCACCCTGTCTGTGTCT CCAGGGAAAGAGCCACCCT CTCCTGAGGGCCAGTCAGAG TGTTTTCACGCACCTTAGCCTG GTACCAGAGAAACCTGGCC AGGCTCCAGGCTCCTCATCT ACGAAGCAGCCACCAGGGCC ACTGTATCCCAGCCAGGTTTC AGTGGCAGTGGGTCTGGGAC AGAGTTCACTCTACCATCAG CAGCCTGCAGTCTGAAGATT TGCAGTTTATTACTGTACGA GTATAACAACTGGCTCTCAC TTTCGGCGGAGGACCAAGGT GGAGATCAACGAACGGTGG CTGCACCATCTGTCTTCATCT CCCGCCATCTGATGAGCAGTT GAAATCTGGAACCTGCCCTGT TGTGTGCTGTCTGAATAACT CTATCCCAGAGAGGCCAAAG TACAGTGGAAAGGTGGATAAC GCCCTCCAATCGGGTAACTCC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCCTCAGCAGCACCCCTGA CGCTGAGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCACAA GAGCTTCAACAGGGGAGAGT GT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCAGTAACATATGGCATGCACCTGGGTCCGCCAGGCTCCA GGCGAGGGCTGGAGTGGGTGGCAGCTATATGTTTGTATGC AAGTGATAAATACTATGCAGACGCCGTGAAGGCCGATTCA CCATCTCCAGAGACAACCTCAAGACAACGCTGTATCTGCAA ATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTG TGCAGAGATTGGCGATTTTGGAGTGGTCCCCGACTACT GGGGCCAGGGAACCTGTGTCACCGTGTCTAGTGCCTCCACC AAGGGCCCATCGGTCTTCCCCCTGGCACCTCTCTCCAAAGAG CACCTCTGGGGCACACGGGCCCTGGGTGCCCTGGTCAAGG ACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGC GCCCTGACAGCGGCTGTGCACACCTTCCCGGTGTCTCTACA GTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGTGACCGTGC CCTCCAGCAGCTTGGGACCCAGCACCTACATCTGCAACGTG AATCAACAAGCCAGCAACACCAAGGTGGACAAAGAAAGTTG AGCCAAATCTTGTGACAAACTCACATGCCACCGCTGC CCAGCACCTGAACCTCTGGGGGACCGTCAAGTCTTCTCTTTC CCCCAAACCCAAAGACACCTCATGATCTCCCGGACCCC TGAGGTACATGCTGTGGTGGTGACGTGAGCCACGAAGACCC CTGAGGTCAAGTTCAACTGTACGTGACGGCGGTGGAGGTG CATAAATGCCAAGACAAGCCGTGCGAGGAGCAGTACGGCA GCAGTACCGTTGCTCAGCGTCTCACCGTCTCTGCACCAAG GACTGGTGAATGGCAAGGATGCAAGTGCAGAGTGTCCA ACAAAGCCCTCCAGCCCCATCGAGAAACCATCTCCAAA GCCAAAGGACGCCCGAGAACCAAGGTGTACACCTGCC CCCATCCGGGAGGAGATGACCAAGAACCAAGTCAAGCCTG ACCTGCCCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGT GGAGTGGGAGAGCAATGGGACGCCGGAGAACCACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCTCTTCTCTC TATAGCAAGCTCACCGTGGACAAAGAGCAGGTGGCAGCAGG GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC AACCCTACAGCAGAAAGACCTCTCCCTGTCTCCGGGTAA A	
			NA	
	[hu anti- <huGIPR> 2G10.310 VK3 (1-236) VL]:huKLC -CL + [Unknown anti- <huGIPR> 2G10.610 VH3 (1-472) VH]:huIgG1 zSEFL2-2 (mAb); LMR ID: SS- 26187			

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			(SEQ ID NO: 104) EIVMTQSPATLSVSPGERATLS CRASQSVFTHLAWYQQKPGQA PRLIYEAAATRAATGIPARFSGS SGTEFTLTISLQSEDFAVYYCQ QYNNWPLTFGGGTKEIKRTV AAPSVFIFPPSDEQLKSGTASVV CLLNFFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSYSL STLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC	(SEQ ID NO: 105) QVQLVESGGGVQPGRLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAIWFDASDKYYADA VKGRFTISRDN SKNTLYLQ MNSLRAEDTAVYYCARDLAIFGVDPDYWGQGLTVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTPVSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHSTCPPELAPPELLGGPSVFLFPPKPKDITL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHREALHNYHTQKSLSLSPGK
			(SEQ ID NO: 106) GAAATAGTGATGACGCAGTCT CCAGCCACCCTGTCTGTGTCT CCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAG TGTTTTCACGCACCTTAGCCTG GTACCAGCAGAAACCTGGCC AGGCTCCCAGGCTCCTCATCT ACGAAGCAGCCACCAGGGCC ACTGGTATCCCAGCCAGGGTC AGTGCGAGTGGGTCTGGGAC AGAGTTCACTCTCACCATCAG CAGCCTGCAGTCTGAAGATT TGCAGTTTATTACTGTACGA GTATAACAACCTGGCCTCTCAC TTTCGGCGGAGGGACCAAGGT GGAGATCAAAACGAACGGTGG CTGCACCATCTGTCTTCATCT CCCAGCATCTGATGAGCAGTT GAAATCTGGAACCTGCTCTGT TGTGTGCTGCTGAATAACTT CTATCCCAGAGAGGCCAAAG TACAGTGAAGAGTGGATAAC GCCCTCCAAATCGGGTAACCTC	(SEQ ID NO: 107) CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCAGTAACCTATGGCATGCACCTGGTCCGCCAGGTTCCA GGCGAGGGCTGGAGTGGTGGCAGCTATATGGTTTGATGC AAGTGATAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAACCTCAAGAACACGCTGTATCTGCAA ATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTG TGGAGAGATTGGCGATTTTGGAGTGGTCCCCGACTACT GGGGCCAGGAAACCTGGTCAACCGTGTCTAGTGCCTCCACC AAGGCCCATCGGTCTTCCCCCTGGCACCTCTCTCCAAGAG CAGCTCTGGGGGCAACGCGCCCTGGGCTGGCTGGTCAAGG ACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGC GCCCTGACCAGCGCGTGCACACCTTCCCCGCTGTCTTACA GTCTCTAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGC CCTCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTG AATCACAAGCCAGCAACACCAAGGTGGACAAAGAAAGTTG AGCCCAATCTTGTGACAAACTCACATGCCCCACCGTGC CCAGCACCTGAACCTCTGGGGGACCGTCACTCTCTCTTC CCCCCAAAACCAAGGACACCTCATATCTCTCCGGACCCC TGAGGTACATGCGTGGTGGACCTGAGCCACGAAGACC CTGAGGTCAAGTTCAACTGGTACGTGGACGCGGTGGAGGTG CATAATGCCAAGCAAAAGCCGTGCGAGGAGCAGTACGGCA GCACGTACCGTTGCGTCAAGCTCTCAACCGTCTGCAACCAAG

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		CAGGAGAGTGTCACAGAGCA GGACAGCAAGGACAGCACCT ACAGCTCAGCAGCACCCCTGA CGCTGAGCAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCAACCCATCAGGG CCTGAGCTCGCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT	(SEQ ID NO: 108)	(SEQ ID NO: 109)	GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTGTCCA ACAAAGCCCTCCAGCCCTCCATCGAGAAACCATCTCCAAA GCCAAAGGGCAGCCCGAGAACACAGGTGTACACCCCTGCC CCCATCCGGGAGGAGATGACCAAGAACAGGTACGCCTG ACCTGCCTGGTCAAGGCTTCTATCCAGCGACATCGCGT GGAGTGGGAGAGCAATGGGACGCCGAGAAACAACATAAAG ACCAGCCCTCCCTGCTGGACTCCGACGGCTCTTCTTCTCTC TATAGCAAGCTCACCCTGGACAAAGCAGGTGGCAGCAGG GGAACGTCTTCTATGCTCCGTGATGATGAGGCTCTGCAC AACCACTACACGACAGAGAGCCTCTCCCTGTCTCCGGGTAA A
	AA	EIVMTQSPATLSVSPGERATLS CRASQSVFTHLAWYQQKPGQA PRLIYEAAATRAITGIPARVSGS SGTEFTLTISLQSEDFAVYYCQ QYNNWPLTFGGGKVEIKRTV AAPSFIFFPPSDEQLKSGTASVV CLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSYSL STLTLSKADYEKHKVYACEVT HQLSLSPVTKSFNRGEC	(SEQ ID NO: 110)	(SEQ ID NO: 111)	QVQLVESGGGVVQPRSLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAAIWFDASDKYYADAVKGRFTISRDNKNTLYLQ MNSLRAEDTAVYYCARDLAIFGVVDPYWGQGLTVTVSSASTK GPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKHTHTCPCPAPELGGPSVFLPFPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHREALHNYTQKSLSPGK
2G10.312	[hu anti- <huGIPR> 2G10.302 VK3 (1-236) VL]:huKLC -CL + [Unknown anti- <huGIPR> 2G10.610 VH3 (1-472) VH]:huIgG1	NA	(SEQ ID NO: 110)	(SEQ ID NO: 111)	GAAATAGTGATGACGCAGTCT CCAGCCACCTGTCTGTGTCT CCAGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAG TGTTTTTGAACACTTAGCCTG GTACCAGCAGAAACCTGGCC AGGC'TCCAGGCTCCTCATCT ACGAAAGCAGCCACAGGGCC ACTGGTATCCCAGCCAGGTTT AGTGCGAGTGGGCTGGGAC AGAGTCACTCTCACCATCAG CAGCCTGCAGTCTGAAGATT
			(SEQ ID NO: 110)	(SEQ ID NO: 111)	CAGGTGCAGTGGTGGAGTCTGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCAGTAACTATGGCATGCACTGGGTCCGCCAGGCTCCA GGCAGGGGTGGAGTGGTGGCAGCTATATGGTTTGATGC AAGTGATAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAACCTCAAGAACACGCTGTATCTGCAA ATGAACAGCTGAGAGCCGAGGACACGGCTGTGTATTACTG TGGAGAGATTGGCGATTCTTGGAGTGGTCCCGACTACT GGGGCCAGGGAACCTGGTACCGTGTCTAGTGCCTCCACC AAGGGCCCATCGTCTTCCCTCCCTGGCAGCTCTCCCAAGAG CACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGG ACTACTTCCCCGAAACCGGTGACGGTGTGTGGAACTCAGGC

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<p>zSEFL2-2 (mAb); LMR ID: SS- 26189</p>		<p>TGCAGTTTATTACTGTACGCA GTATAACAACTGGCTCTCAC TTTCGGCGGAGGACCAAGGT GGAGATCAACACGAACGGTGG CTGCACCATCTGTCTTCATCTT CCCGCATCTGATGAGCAGTT GAAATCTGGAACCTGCTCTGT TGTGTGCTGTCTGAATACTT CTATCCAGAGAGGCCAAAG TACAGTGGAAAGGTGGATAAC GCCCTCCAAATCGGGTAATCC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCTCAGCAGCACCCCTGA CGCTGAGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCAACCATCAGGG CCTGAGCTCGCCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT</p>	<p>GCCCTGACCAGCGGCGTGACACCTTCCCGGCTGTCTCTACA GTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGC CCTCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTG AATCAACAAGCCAGCAACACCAAGGTGGACAAAGAAAGTTG AGCCCAATCTGTGACAAACTCACACATGCCACCGTGC CCAGCACCTGAATCTGGGGGACCGTCACTTCTCTCTTC CCCCAAACCCAGGACACCTCATGATCTCCCGGACCCC TGAGGTACATGCTGTGTGGACGTGAGCCACGAAGACC CTGAGGTCAAGTCACTGACGTGACGCGGTGGAGGTG CATATGCCAAGACAAAGCCGTGCGAGGAGCAGTACGGCA GCACGTACCGTGGTCAAGCTCTCACCCTCTGCAACAG GACTGGCTGAATGGCAAGGATACAAAGTCAAGGTGTCCA ACAAAGCCCTCCAGCCCCATCGAGAAACCATCTCCAAA GCCAAAGGCGCCCGGAGAACACAGGTGTACACCCCTGCC CCCATCCCGGAGGAGATGACCAAGAACAGGTACAGCTG ACCTGCTGTGCAAGGCTTCTATCCAGCGACATCGCCGT GGAGTGGGAGAGCAATGGGACGCCGAGAACAACTACAAG ACCAAGCTCCGCTGCTGAGTCCGACGGCTCTCTCTCTC TATAGCAAGTCAAGCTGAGCAAGAGCAGGTGGCAGCAGG GGAACGTCTCTCATGCTCCGTGATGCATGAGGCTCTGCAC AACCCTACACGCAAGAGACCTCTCCCTGTCTCCGGGTAA A</p>
	AA	<p>(SEQ ID NO: 112) EIVMTQSPATLSVSPGERATLS CRASQSVFEHLAWYQQKPGQA PRLLIYEAATRAATGIPARFSGS SGTEFTLTISLSQSEDFAVYYCQ QYNNWPLTFGGGKVEIKRTV AAPSVFIPTPSDEQLKSGTASVV CLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSYSL STLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC</p>	<p>(SEQ ID NO: 113) QVQLVESGGGVVQPRSLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAIWFDASDKYYADA VKGRFTISRDN SKNTLYLQ MNSLRAEDTAVYYCARDLAIFGVVDPYWGQGLVTVSSASTK GPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTL MISRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSYRCSVLTVLHODWLNKGKEYCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHAEALHNHYTQKSLSLSPGK</p>
<p>hu anti-</p>	NA	<p>(SEQ ID NO: 114) GAAATAGTGATGACGCAGTCT</p>	<p>(SEQ ID NO: 115) CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGGTGGTCCAGCC</p>

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<p><huGIPR> 2G10.329 VK3 (1-236) VLJ::huKLC -CL + [Unknown anti- <huGIPR> 2G10.610 VH3 (1-472) VHJ::huIgG1 zSEFL2-2 (mAb); LMR ID: SS- 26206</p>	AA	<p>CCAGCCACCTGTCTGTGTCT CCAGGGAAAGAGCCACCCT CTCTGCAGGGCCAGTCAGAG TGTGAAACAGCACTTAGCCTG GTACCAGCAAAACCTGGCC AGGCTCCAGGCTCCTCATCT ACGAAGCAGCCACCAAGGCC ACTGGTATCCAGCCAGGTT AGTGGCAGTGGTCTGGGAC AGAGTTCACTCTCACCATCAG CAGCTGCAGTCTGAAGATT TGCAGTTTATTACTGTCAGCA GTATAACAACCTGGCCTCTCAC TTTCGGCGGAGGGAACCAAGGT GGAGATCAAAACGAACGGTGG CTGCACCATCTGTCTTCATCTT CCCGCCATCTGATGAGCAGTT GAAATCTGGAACCTGCCCTCTGT TGTGTGCTGTGCTGAATAACTT CTATCCCAGAGAGGCCAAAG TACAGTGGAAGGTGGATAAC GCCCTCCAATCGGGTAACTCC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCTCAGCAGCACCCCTGA CGCTGAGCAAAAGCAGACTAC GAGAAACACAAAAGTCTACGC CTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT</p>	<p>TGGGAGGTCCCTGAGACTCTCTCTGTGTCAGCATCTGGATTCA CCTTCAGTAACTATGGCATGCATGGTCCGCCAGGCTCCA GGCGAGGGCTGGAGTGGGTGGCAGCTATATGGTTTGTATGC AAGTGATAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAACCTCAAGAACACGCTGTATCTGCAA ATGAACAGCTGAGAGCCGACAGCACGGCTGTGTATTACTG TGGGAGAGATTTGGCGATTTTGGAGTGGTCCCGACTACT GGGGCCAGGAACCTTGGTACCGCTGTCTAGTGCCTCCACC AAGGGCCCATCGGTCTTCCCTTGGCACCTTCTCCCAAGAG CACCTCTGGGGGCACAGCGGCCCTGGGCTGCCGTGTCAAAGG ACTACTTCCCGGAACCGGTGACGGTGTGCTGGAACCTCAGGC GCCCTGACCAGCGCGTGCACACTTCCCGGCTGTCTCTACA GTCTCAGGACTCTACTCCCTCAGCAGCTGGTGAACCTGTC CCTCCAGCAGCTTGGGACCCAGACCTTACATCTGCAACCTG AATCAAGCCAGCAACCAAGGTGGACAAAGAAAGTTG AGCCAAATCTGTGACAAACTCACACATGCCACCCGTGC CCAGCACCTGAACCTCTGGGGGACCGTCAGTCTTCTCTTC CCCCAAACCCAAAGGACACCTCATGATCTCCCGACCC TGAGGTACATGCTGTGTGGACGTGAGCCACGAAGACC CTGAGGTCAAGTTCAACTGTAAGTACGTGGACGGCTGGAGGTG CATAATGCCAAGACAAGCCGTGCGAGGAGCAGTACGGCA GCACGTACCGTTGCGTCAGCTCCTCACCTCTGCACCCAG GACTGGTGAATGGCAAGGAGTACAAGTGAAGGTGTCCA ACAAAGCCCTCCAGCCCCCATCGAGAAACCATCTCCAAA GCCAAAGGCGACCCCGAGAACACAGGTGTACACCTGCC CCCATCCCGGAGGAGATGACCAAGAACCCAGGTACGCTG ACCTGCTGTGTCAAAGGCTTCTATCCAGCGACATCGCCGT GGAGTGGGAGAGCAATGGGCGACCCGGAGAACAACTACAAG ACCACGCTCCCGTCTGTGACTCCGACGGCTCTTCTCTCTC TATAGCAAGCTCACCGTGGACAAAGCAGGTGGCAGCAGG GGAACGTCTTCTCATGCTCCGTGATGATGAGGCTCTGCAC AACCACTACAGCAGAAAGACCTCTCCCTGTCTCCGGGTAA A</p>
		<p>(SEQ ID NO: 116) EIVMTQSPATLSVSPGERATLS CRASQSVETHLAWYQQKPGQ</p>	<p>(SEQ ID NO: 117) QVQLVSGGVPQGRSLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAIWFDASDKYYADA VKGRFTISRDNKNTLYLQ</p>

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		APRLIYEAAATRATGIPARFSGS GSGTEFTLTISLSQSEDFAVYYC QQYNNWPLTFGGGKVEIKRT VAAPSVFIFFPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSYVS LSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC (SEQ ID NO: 118)	MNSLRAEDTAVYYCARDLAIFGVVPDYWGQGLVTVSSASTK GPSVFLAPSSKTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSYRVTCVSLTVLHQLDNLNKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSGSEFFLYSKLTVDKSRWQQGN VFSCSVMHREALHNYHTQKSLSLSPGK (SEQ ID NO: 119)
[hu anti- <huGIPR> 2G10.327 VK3 (1-236) VL]:huKLC -CL + [Unknown anti- <huGIPR> 2G10.610 VH3 (1-472) VH]:huIgG1 zSEFL2-2 (mAb); LMR ID: SS- 26204	NA	GAAATAGTGATGACGCAGTCT CCGCCACCCGTGTCTGTGTCT CCAGGGAAAGAGCCACCCT CTCCTGACGGCCAGTCAGAG TGTTCTATAGCCACTTAGCCTG GTACCAGCAGAAACCTGGCC AGGCTCCAGGCTCCTCATCT ACGAAGCAGCCACCAGGGCC ACTGGTATCCAGCCAGGTTC AGTGGCAGTGGGTCTGGGAC AGAGTTCAC'TCACCATCAG CAGCCTGCAGTCTGAAGATT TGCAAGTTTATTACTGTACGCA GTATAACCAAGTGGCTCTCAC TTTCGGCGGAGGACCAAGGT GGAGATCAAAACGAACGGTGG CTGCACCATCTGTCTTCATCTT CCCGCCATCTGATGAGCAGTT GAAATCTGGAAC'TGCCCTGT TGTGTGCTGCTGAATAACTT CTATCCACAGAGAGGCCAAAG TACAGTGGAAAGGTGGATAAC GCCCTCCAATCGGGTAACCC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCCTCAGCAGCACCCCTGA	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTCAGTAAC'TATGGCATGCAC'TGGTCCGCCAGGCTCCA GGCGAGGGCTGGAGTGGTGGCAGCTATATGGTTTGATGC AAGTGATAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAAC'TCCAAGACACGCTGTATCTGCAA ATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTG TGGAGAGATTGGCGATTTTGGAGTGGTCCCGACTACT GGGGCAGGAACCTGGTCAACGCTGTAGTGCCTCCACC AAGGGCCCATCGGTCTTCCCTCCGACCCCTCCTCCAAGAG CACCTTGGGGCACACGGGCCCTGGGCTGCCCTGGTCAAGG ACTACTCCCGGAACCGGTGACGGTGTGTTGGAAC'TCAGGC GCCCTGACAGCGCGTGCACACCTTCCCGGCTGTCTTACA GTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAACCGTGC CCTCAGCAGCTTGGCACCCAGACCTACATCTGCAACGTG AATCACAAAGCCAGCAACACCAAGGTGGACAAGAAAGTTG AGCCAAATCTTGTGACAAAC'TCACACATGCCACCGTGC CCAGCCTGAAC'TCCTGGGGGACCGTCAAGTCTTCTCTTC CCCCAAACCCAAAGACACCCCTCATGATCTCCCGGACCCC TGAGGTACATCGGTGGTGGACGTGAGCCACGAAGACC CTGAGGTCAAGTCAACTGTACGTGACGGCGTGGAGGTG CATAATGCCAAGACAAGCGTGGAGGAGCAGTACGGCA GCACGTACCGTTCGCTCAGCGTCTCACCGCTCTGCACCA GACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTGTCCA ACAAAGCCCTCCAGCCCCCATCGAGAAACCATCTCCAAA GCCAAAGGGCAGCCCCGAGAACCAAGGTGTACACCTGCC

2G10.327

A-2164-WO-PCT

2G10.338	[hu anti- <huGIPR> 2G10.338 VK3 (1-236) VL]:huKLC -CL + [Unknown anti- <huGIPR> 2G10.610 VH3 (1-472) VH1]:huIgG1 zSEFL2-2 (mAb); LMR ID: SS-	AA	CGCTGAGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT	CCCATCCCGGAGGAGATGACCAAGAACCAAGGTCAGCCTG ACCTGCCTGGTCAAGGCTTCTATCCAGCGACATCGCCGT GGAGTGGGAGAGCAATGGGCGAGCCGAGAACAACTACAAG ACCACGCTCCCGTCTGGACTCCGACGGCTCTTCTTCTC TATAGCAAGCTACCGTGGACAAAGCAGGTGGCAGCAGG GGAACGTCTTCTCATGCTCCGTGATGATGAGGCTCTGCAC AACCACTACAGCAGAAAGAGCCCTCTCCCTGTCTCCGGGTAA A
			(SEQ ID NO: 120) EIVMTQSPATLSVSPGERATLS CRASQSVHSLAWYQKPGQ APRLIYEAAATRAATGIPARFSGS GSGTEFTLTISLQSEDFAVYYC QQYNQWPLTFGGGKVEIKRT VAAPSFIPIPPSDEQLKSGTASV VCLLNFIYPREAKVQWKVDN ALQSGNSQESVTEQDSKDYTS LSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC	(SEQ ID NO: 121) QVQLVESGGGVQPGRSRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAIWFDASDKYYADA VKGRFTISRDN SKNTLYLQ MNSLRAEDTAVYYCARDLAIFGVDPDYWGQGLVTVSSASTK GPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHPKPSN TKVDKKVEPKSCDKTHSTCPPEPAPELLGGPSVFLPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 122) GAAATAGTGATGACGCAGTCT CCAGCCACCTGTCTGTGTCT CCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAG TGTTTCATCATCACTTAGCCTG GTACCAGCAGAAACCTGGCC AGGCTCCAGGCTCCTCATCT ACGAAAGCAGCCACCAAGGCC ACTGGTATCCAGCCAGGTTC AGTGGCAGTGGGTCTGGGAC AGAGTTCACTTCAACATCAG CAGCCTGCAGTCTGAAGATT TGCAGTTTATTACTGTACAGTA GTATAACCAAGTGGCCTCTCAC TTTCGGCGGAGGGACCAAGGT	(SEQ ID NO: 123) CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCAGTA ACTATGGCATGC ACTGGTCCGCCAGGCTCCA GGCAGGGGCTGGAGTGGGTGGCAGCTATATGGTTTGTATGC AAGTGATAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAACCTCAAGAACACGCTGTATCTGCAA ATGAACAGCCTGAGAGCCGAGACACGGCTGTGTATTACTG TGGGAGAGATTTGGCGATTTTGGAGTGTCCCCGACTACT GGGGCCAGGAACCTGGTCAACCGTGTAGTGCCTCCACC AAGGGCCCATCGGTCTCCCGCTGGCACCTCTCCCAAGAG CACTCTGGGGGACACAGCGCCCTGGGCTGCCTGTCACAGG ACTACTTCCCCGAACCGGTGACGGTGTGCTGGA ACTCAGGC GCCCTGACCAAGCGGTGACACCTTCCCGGCTGTCTCTACA GTCTCTAGGACTCTACTCCCTCAGCAGCGTGGTGTGACCGTGC CCTCCAGCAGCTTGGGCAACCCAGACCTTACATCTGCAACGCTG

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26215		GGAGATCAAAACGAACGGTGG CTGCACCATCTGTCTTCATCTT CCCGCCATCTGATGAGCAGTT GAAATCTGGAACCTGCCTCTGT TGTTGCTGCTGAATAACTT CTATCCAGAGAGGCCAAAG TACAGTGGAAAGTGGATAAC GCCCTCAAATCGGTAACTCC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCTCAGCAGCACCTGA CGCTGAGCAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT	AATCACAAGCCAGCAACACCAAGGTGGACAAAGAAAGTTG AGCCAAATCTTGTGACAAAACCTACACATGCCACCGTGC CCAGCACCTGAATCTCTGGGGGACCGTCACTTCTCTCTTC CCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCC TGAGGTACATGCTGTGTGGTGGACGTGAGCCACGAAGACC CTGAGTCAAGTTCAACTGTTAGTGGACGGCTGGAGGTG CATAATGCCAAGACAAAGCCCTGCGAGGAGCAGTACGGCA GCACGTACCTGCTGCTGACGTCCTCACCTGCTCGCACGAG GACTGGTGAATGGCAAGGAGTACAAGTGAAGGTGTCCA ACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAA GCCAAAGGCAAGCCCGAGAACCAAGGTGTACACCTGCC CCATCCCGGAGGAGATGACCAAGAACCAAGGTCAAGCTG ACCTGCCTGGTCAAGGCTTCTATCCAGCGACATCGCCGT GGAGTGGGAGAGCAATGGGACGCCGAGAACCAACTACAAG ACCAGCTCCCTGCTGCTGAGATCCGACGGCTCTTCTTCTC TATAGCAAGCTCACCTGGACAAAGCAGAGTGGCAGCAGG GGAACGTCTTCTCATGCTCCGTGATGATGAGGCTCTGCAC AACCACTACACGCAAGAGAGCTCTCCCTGCTCCCGGTAA A	
	AA	(SEQ ID NO: 124) EIVMTQSPATLSVSPGERATLS CRASQSVHHHLAWYQQKPGQ APRLIYEAAATRAATGIPARFSGS GSGTEFTLTISLQSEDFAVYYC QQYNQWPLTFGGGTGKVEIKRT VAAPSVFIFFPSDEQLKSGTASV VCLLNFFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSSTYS LSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC	(SEQ ID NO: 125) QVQLVESGGGVQPGRLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAIWFDASDKYVADAVKGRFTISRDNKNTLYLQ MNSLRAEDTAVYYCARDLAIFFGVVDYWGQGLTVTVSSASTK GPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCTPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQKSLSLSPGK	
261031	hu anti- <huGIPR> 2G10.314 VK3 (1-236)	NA	(SEQ ID NO: 126) GAAATAGTGATGACGCAGTCT CCAGCCACCCTGTCTGTGTCT CCAGGGAAAGAGCCACCCT CTCTGCAGGGCCAGTCAGAG	(SEQ ID NO: 127) CAGGTGCAGTGGTGGAGTCTGGGGGAGGCGGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCAGTAACTATGGCATGCACCTGGGTCCGCAAGCTCCA GGCAGGGGCTGGAGTGGGTGGCAGCTATATGGTTTGTATGC

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		VAAPSVFIFFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKSDSTYS LSSTLTLKADYKHKVYACE VTHQGLSSPVTKSFNRGEC	(SEQ ID NO: 130)	TKVDKKVEPKSCDKTHTCTPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSYRCVSLVTLVHQDLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPPVLDSGSFFLYSKLTVDKSRWQQGN VFSCSVMHREALHNYTQKSLSPGK
			(SEQ ID NO: 131)	CAGGTGCAGTGGTGGAGTCTGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCAGTAACTATGGCATGCACTGGGTCCGCCAGGCTCCA GGCGAGGGCTGGAGTGGTGGCAGCTATATGGTTTGATGC AAGTGATAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAACCTCAAGAACAACGCTGTATCTGCAA ATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTG TGGAGAGATTGGCGATTTTGGAGTGGTCCCCGACTACT GGGGCCAAGGAACCTGGTACCGTGTCTAGTGCCTCCACC AAGGGCCCATCGGTCTTCCCCCTGGCACCTCTCCCAAGAG CACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGG ACTACTTCCCCGAACCGGTGACGGTGTGTGGAACCTCAGGC GGCCTGACCAGCGCGTGCACACCTTCCCGGCTGTCTTACA GTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAACCGTGC CCTCCAGCAGCTTGGCACCCAGACCTACATCTGCAACCGTG AATCAAGCCCAAGCAACCAAGGTGGACAAAGAAAGTTG AGCCCAAATCTTGTGACAAACTCACACATGCCACCGTGC CCAGCACCTGAACCTCTGGGGGACCGTCACTCTTCTCTTC CCCCAAAACCCAAAGACACCTCATGATCTCCCGGACCCC TGAGGTACATCGGTGGTGGTGGACGTGAGCCACGAAGACC CTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTG CATAATGCCAAGACAAGCCGTGCGAGGAGCAGTACGGCA GCACGTACCGTTGCGTACGCTCCTCACCGTCTTGCACCAAG GACTGGTGAATGGCAAGGAGTACAAGTGAAGGTGTCTCCA ACAAAGCCCTCCAGCCCCCTCAGACAACCATCTCCAAA GCCAAAGGGCAGCCCGAGAACCCACAGGTGTACACCCCTGCC CCCATCCCGGGAGGAGATGACCAAGAACCAAGGTCAAGCTG ACCTGCCTGGTCAAGGGCTTCTATCCAGCGACATCGCCGT GGAGTGGGAGAGCAATGGGCAAGCCGGAACAACACTACAAG
			(SEQ ID NO: 130)	GAAATAGTGATGACGCAGTCT CCAGCCACCTGTCTGTGTCT CCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAAGAG TGTTGATGTCAACTTAGCCTG GTACCAGCAGAAACCTGGCC AGGC'TCCAGGCTCCTCATCT ACGAAGCAGCCACCAGGGCC ACTGGTATCCCAAGCAAGTTT AGTGGCAGTGGTCTGGGAC AGAGTTCAC'TCACCATCAG CAGCCTGCAGTCTGAAGATT TGCAGTTTATTACTGTGAGCA GTATAACAGTGGCTCTCAC TTTCGGCGGAGGACCAAGGT GGAGATCAAAACGAACGGTGG CTGCACCATCTGTCTTCACTTT CCCGCCATCTGATGAGCAGTT GAAATCTGGAACCTGCCTCTGT TGTTGCTCTGCTGAATAACTT CTATCCCAAGAGAGGCCAAAG TACAGTGGAAAGGTGGATAAC GCCCTCCAATCGGGTAACTCC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCCTCAGCAGCACCTGA CGCTGAGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCAACCCATCAGGG
		[hu anti- <huGIPR> 2G10.337 VK3 (1-236) VLJ::huKLC -CL + [Unknown anti- <huGIPR> 2G10.610 VH3 (1-472) VHJ::huIgG1 zSEFL2-2 (mAb); LMR ID: SS- 26214	NA	

2G10.337

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2G10.341	[hu anti- <huGIPR> 2G10.341 VK3 (1-236) VL]:huKLC -CL + [Unknown anti- <huGIPR> 2G10.610 VH3 (1-472) VH]:huIgG1 zSEFL2-2 (mAb): LMR ID: SS- 26218	NA	CCTGAGCTCGCCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT	ACCACGCCTCCCGTGGACTCCGACGGCTCCTTCTTCCTC TATAGCAAGCTACCGTGGACAAAGCAGGAGGTGGCAGCAGG GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC AACCACTACACGCAGAAAGAGCCTCCTCCGTCTCCGGGTAA A
			(SEQ ID NO: 132)	(SEQ ID NO: 133)
			AA	QVQLVESGGGVVQGRSLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAIWFDASDKYYADA VKGRFTISRDNKNTLYLQ MNSLRAEDTAVYYCARDLAIFGVVPDYWGQGLVTVSSASTK GPSVFLAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHNKPSN TKVDKKVEPKSCDKTHTCPCPAPELGGPSVFLPPKPKDNL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSYRCVSVLTVLHODWLNKEYCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPVPLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHREALHNHYTQKSLSLSPGK
2G10.341	[hu anti- <huGIPR> 2G10.341 VK3 (1-236) VL]:huKLC -CL + [Unknown anti- <huGIPR> 2G10.610 VH3 (1-472) VH]:huIgG1 zSEFL2-2 (mAb): LMR ID: SS- 26218	NA	EIVMTQSPATLSVSPGERATLS CRASQSDVNLAWYQQKPGQ APRLIYEAAATRAATGIPARFSGS GSGTEFTLTISLSQSEDFAVYYC QQYNQWPLTFGGGKVEIKRT VAAPSVFIAPPDEQLKSGTASV VCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSYLS LSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC	(SEQ ID NO: 135)
			(SEQ ID NO: 134)	(SEQ ID NO: 135)
			CCAGCCACCCCTGTCTGTGTCT CCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAG TGTTGATGTCCACTTAGCCTG GTACCAGCAGAAACCTGGCC AGGTCCCAAGGCTCCTCATCT ACGAAGCAGCCACCAGGGCC ACTGGTATCCAGCCAGGTTC AGTGGCAGTGGGTCTGGGAC AGAGTTCACTCTCACCATCAG CAGCCTGCAGTCTGAAGATT TGCAGTTTATTACTGTACGCA GTATAACCAAGTGCCCTCTCAC TTTCGGCGGAGGGACCAAGGT GGAGATCAAAACGAACGGTGT CTGCACCATCTGTCTTCATCTT CCCGCCATCTGATGAGCAGTT	CAGGTGCAGTGGTGGAGTCTGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCAGTAACTATGGCATGCATGGTCCGCCAGGTCCA GGCAGGGGCTGGAGTGGTGGCAGCTATATGTTTGTATGC AAGTGATAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAACCTCAAGAACACGCTGTATCTGCAA ATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTG TGCAGAGATTGGCGATTTTGGAGTGGTCCCCGACTACT GGGGCCAGGAAACCTGGTCAACCGTGTCTAGTCCCTCCACC AAGGCCCATCGGTCTTCCCCCTGGCACCTCTCTCAAGAG CACCCTGGGGGACACGGGCCCTGGCTGCCCTGGTCAAGG ACTACTCCCCGAACCGGTGACGGTGTCTGTGAACCTCAGGC GCCCTGACACAGCGGTGCACACCTCCCGGTGTCTCTACA GTCTCAGAGCTCTACTCCCTCAGCAGCGTGGTGAACCGTGC CCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTG AATCAACAAGCCAGCAACCAAGGTGGACAAAGAAAGTTG AGCCCAAATCTTGTGACAAACTCACACATGCCACCGCTGC CCAGCACCTGAACCTCCTGGGGGACCGGTCAAGTCTTCTCTTC

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		<div>GAAATCTGGAACTGCCTCTGT TGTGTGCTGTGAATAACTT CTATCCAGAGAGGCCAAAG TACAGTGGAAAGGTGGATAAC GCCCTCCAAATCGGTTAACTCC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGACCT ACAGCTCAGCAGCACCCCTGA CGCTGAGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT</div>	<div>CCCCAAAACCCAGGACACCCCTCATGATCTCCCGGACCCC TGAGGTACATCGTGGTGGACGTGAGCCACGAAGACC CTGAGGTCAAGTTCAACTGGTACGTGGACGGCTGGAGGTG CATAATGCCAAGACAAGCCGTGCGAGGAGCAGTACGGCA GCACGTACCGTTGCTCAGCGTCTCAACGCTCTGCACCAAG GACTGGTGAATGGCAAGGATCAAGTGC AAGGTGTCCA ACAAAGCCCTCCCAGCCCCATCGAGAAAACCATGTCCAAA GCCAAAGGGCAGCCCCGAGAACACAGGTGTACACCTGCC CCCATCCGGGAGGAGATGACCAAGAACAGGTACAGCTG ACCTGCTGTCAAAGGCTTCTATCCAGCGACATCGCCGT GGAGTGGGAGAGCAATGGGCGCCGGAGAACAACTACAAG ACCACGCTCCCGTCTGGACTCCGACGGCTCCTTCTTCCTC TATAGCAAGCTCACCGTGGAC AAGAGCAGGTGGCAGCAGG GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC AACCACTACAGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAA A</div>
	AA	<div>(SEQ ID NO: 136) EIVMTQSPATLSVSPGERATLS CRASQSDVHLAWYQKPGQ APRLIYEAAATRAITGIPARFSGS GSGTEFTLTISLQSEDFAVYYC QQYNQWPLTFGGGKVEIKRT VAAPSFIFFPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDYSTYS LSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC</div>	<div>(SEQ ID NO: 137) QVQLVESGGGVVQPGRLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAIWFDASDKYYADAVKGRFTISRDN SKNTLYLQ MNSLRAEDTAVYYCARDLAIFGVVPDYWGQGLTVTVSSASTK GPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSN TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPKPKDTLT MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQKSLSPGK</div>
2G10.302	[hu anti- <huGIPR> 2G10.302 VK3 (1-236) VL]:huKLC -CL + [hu anti-	NA	<div>(SEQ ID NO: 138) GAAATAGTGATGACGCAGTCT CCAGCCACCCTGTCTGTGTCT CCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAG TGTTTTGAACACTTAGCCTG GTACCAGCAGAAACCTGGCC AGGCTCCCAAGGCTCCTCATCT</div> <div>(SEQ ID NO: 139) CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCAGTAACCTATGGCATGCACTGGGTCCGCCAGGCTCCA GGCAGGGGTGGAGTGGGTGGCAGCTATATGGTTTGTATGC AAGTGATAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAACCTCCAGAACAACGCTGTATCTGCAA ATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTG</div>

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<p><huGIPR> 2G10.302 VH3 (1-472) VHJ::huIgG1 zSEFL2-2 (mAb); LMIR ID: SS- 26179</p>	<p>ACGAAGCAGCCACAGGGCC ACTGGTATCCAGCCAGGTTTC AGTGGCAGTGGGTCTGGGAC AGAGTTCACTCTACCATCAG CAGCCTGCAGTCTGAAGATT TGCAAGTTTATTACTGTACGA GTATAACAACTGGCTCTCAC TTTCGGCGGAGGACCAAGGT GGAGATCAACGAACGGTGG CTGCACCATCTGTCTTCATCTT CCCGCCATCTGATGAGCAGTT GAAATCTGAACTGCCCTCTGT TGTGTGCTGCTGAATAACTT CTATCCAGAGAGGCCAAAG TACAGTGGAAAGTGGATAAC GCCCTCCAATCGGGTAACCTC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCTCAGCAGCACCTGA CGCTGAGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCACAA GAGCTTCAACAGGGGAGAGT GT</p>	<p>TGCGAGAGATATTGCGATTTTGGAGTGTTCCTCCGACTACTG GGCCAGGGAACCTGTGTCACCGTGTCTAGTGCCTCCACCA AGGGCCCATCGGTCTTCCCTGGCACCCCTCCTCCAAAGAGC ACCTCTGGGGGCACAGCGCCCTGGGTGCTGCTCAAGGA CTACTTCCCGAACCGGTGACGGTGTGTTGAACTCAGGCG CCCTGACAGCGGCTGCACACCTTCCCGGCTGTCTCTACAG TCCTCAGGACTACTCCTCAGCAGCGTGGTACCGTGCCTC TCCAGCAGCTTGGCACCCAGACCTACATCTGCAACGTGAA TCACAAGCCAGCAACACCAAGGTGGACAAAGAAAGTTGAG CCCAATCTTGTGACAAAACCTCACACATGCCACCGTGCC AGCACCTGAACCTCTGGGGGACCGTCACTTCTTCTTCCC CCCAAAACCAAGACACCTCATGATCTCCCGGACCCCTG AGGTCACATGCTGTGTGGTGGACGTGAGCCACGAAGACCT GAGGTCAAGTTCAACTGTTACGTGAGCGGTGGAGGTGCA TAATGCCAAGACAAAGCGTGGAGGAGCAGTACGGCAGC ACGTACCGTTCGCTCAGCGTCTCACCGTCTGCACCCAGGA CTGGCTGAATGCCAAGGAGTACAAAGTGAAGGTGTCCAACA AAGCCCTCCAGCCCCATCGAGAAACCATCTCCAAAGCC AAAGGCGAGCCCCGAGAACACAGGTGTACACCTGCCCCC ATCCCGGAGGAGATGACCAAGAACAGGTGACCGTACCT GCCTGGTCAAAGGCTTCTATCCAGCGACATCGCGTGGAG TGGGAGAGCAATGGCAGCCGAGAACAACTACAAGACCA CGCTCCCGTGTGGACTCCGACGGTCTCTTCTCTCTATA GCAAGCTCACCGTGGACAAAGCAGGTGGCAGCAGGGGAA CGCTTCTCATGCTCCGTGATGATGAGGCTCTGCACAACCA CTACACGCGAGAAGAGCCCTCTCCCTGTCTCCGGGTAAA</p>
<p>AA</p>	<p>(SEQ ID NO: 140) EIVMTQSPATLSVSPGERATLS CRASQSVFEHLAWYQQKPGQA PRLIYEAAATRAATGIPARFSGS SGTEFTLTISLQSEDFAVYYCQ QYNNWPLTFGGGTVEIKRTV AAPSVFIFPPSDEQLKSGTASVV CLLNFFYPREAKVQVWKVDNAL QSGNSQESVTEQDSKDSYSL STLTLSKADYEEKHKVYACEVT</p>	<p>(SEQ ID NO: 141) QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAIWFDASDKYYADA VKGRFTISRDN SKNTLYLQ MNSLRAEDTAVYYCARDIAIFGVFPDYWGQGLVTVSSASTK GPSVFPLAPSSKTSGGTAALGKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNPKPSN TKVDKKVEPKSCDKTHTCPCPAPELLGGPSVFLPPKPKDYL MISRTPETCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSYRCVSLTFLHODWLNKEYCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKFGFYPDSIAV</p>

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			EWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQKSLSLSPGK	HOGLSSPVTKSFNRGEC	(SEQ ID NO: 142) GAAATAGTGATGACGCAGTCT CCAGCCACCCTGTCTGTGTCT CCAGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAG TGTTTTTGAACACTTAGCCTG GTACCAGCAGAAACCTGGCC AGGCTCCAGGCTCCTCATCT ACGAAGCAGCCACCAGGGCC ACTGGTATCCCAGCCAGGGTC AGTGGCAGTGGGTCTGGGAC AGAGTTCACTCTCACCATCAG CAGCCTGCAGTCTGAAGATTT TGCAGTTTATTACTGTACAGA GTATAACAACCTGGCTCTCAC TTTCGGCGGAGGACCAAGGT GGAGATCAACAGAACGGTGG CTGCACCATCTGTCTTCATCTT CCCGCCATCTGATGACAGTT GAAATCTGGAACCTGCCTCTGT TGTGTGCTGTGTAATAACTT CTATCCCAGAGAGGCCAAAG TACAGTGGAAGGTGGATAAC GCCCTCCAATCGGGTAACCTC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCCTCAGCAGCACCCCTGA CGCTGAGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCAACCATCAGGG CCTGAGCTGCCCCGTACAAA GAGCTTCAACAGGGGAGT GT	(SEQ ID NO: 143) CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGTCAGCATCTGGATTCA CCTTCAGTAACATAGCATGCACTGGGTCCGCCAGGCTCCA GGCGAGGGCTGGAGTGGGTGGCAGCTATATGGTTTGTATGC AAGTGATAAATACTATGCAGAGCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAACCTCCAAGAACAACGCTGTATCTGCAA ATGAACAGCTGAGAGCCGAGGACACGGCTGTGTATTACTG TGCAGAGATAATTGCGATTTTGGAGTGTTCCTCCGACTACTG GGCCAGGGAACCTGGTACCCGTGTCTAGTGCCTCCACCA AGGGCCCATCGGTCTTCCCTTGGCACCTCTCTCCAAAGAGC ACCTCTGGGGCACAGCGGCCCTGGGCTGCCGTGGTCAAGGA CTACTTCCCGAAACCGGTGACGGTGTCTGGAACCTCAGGGC CCCTGACCAGCGGTGCACACCTTCCCGGCTGTCTCTACAG TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAACCTGCCC TCCAGCAGCTTGGCACCCAGACCTACATCTGCAACGTGAA TCACAAGCCAGCAACACCAAGGTGGACAAAGAAAGTTGAG CCCAATCTTGTGACAAAACCTCACACATGCCACCGTGCCC AGCACCTGAACCTCTGGGGGACCGTCACTCTCTCTCTCCC CCCAAAACCCAAAGGACACCTCATGATCTCCCGAACCCCTG AGGTACATGCTGTGGTGGTGGACGTGAGCCACGAAGACCCCT GAGTCAAGTTCAACTTGTACGTACGTGGAGCGGTGGAGGTGCA TAATGCCAAGACAAAGCCGTGCGAGGAGCAGTACGGCAGC ACGTACCGTTGCGTCAAGCTCTCAACCGTCTGCACCCAGGA CTGGCTGAATGGCAAGGAGTACAAGTGAAGGTGTCCAACA AAGCCCTCCAGCCCCATCGAGAAAACCACTCTCCAAGCC AAAGGGCAGCCCCGAGAACCAACAGGTGTACACCTGCCCC ATCCCGGAGGAGATGACCAAGAACAGGTCAAGCTGACCT GCCGTGCTAAAGGCTTCTATCCAGCGACATCGCCGTGGAG TGGGAGAGCAATGGGACGCCGAGAACCACTACAAGACCA CGCTCCCGTGTGGACTCCGACGGCTCTCTTCTCTCTATA GCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAA CGTCTTCTCATGCTCCGTGATGATGAGGCTCTGCACAACCA CTACAGCAGAAAGAGCCCTCTCCCTGTCTCCGGGTAAA
		2G10.602	[hu anti- <huGIPR> 2G10.602 VK3 (1-236) VL]:huKLC -CL + [hu anti- <huGIPR> 2G10.302 VH3 (1-472) VH]:huIgG1 zSEFL2-2 (mAb); LMR ID: SS- 26227	NA		

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2G10.325	[hu anti- <huGIPR> 2G10.325 VK3 (1-236) VL]::huKLC -CL + [hu anti- <huGIPR> 2G10.325 VH3 (1-472) VH]::huIgG1 zSEFL2-2 (mAb); LMR ID: SS- 26202	AA	(SEQ ID NO: 144) EIVMTQSPATLSVSPGERATLS CRASQSVFEHLAWYQQKPGQA PRLIYEAAATRAATGIPARVSGSG SGTEFTLTISLQSEDFAVYYCQ QYNNWPLTFGGGKVEIKRTV AAPSVEFPPSDEQLKSGTASVV CLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSYSL STLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC	(SEQ ID NO: 145) QVQLVESGGVVQPGRLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAIWFDASDKYYADA VKGRFTISRDN SKNTLYLQ MNSLRAEDTAVYYCARDIAIFGVFPDYWGQGLTVTVSSASTK GPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTPVSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTPCPAPPELLGGPSVFLFPPKPKDRL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHREALHNHYTQKSLSLSPGK
			(SEQ ID NO: 146) GAAATAGTGATGACGCAGTCT CCAGCCACCCTGTCTGTGTCT CCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAG TGTTTTCGAACACTTAGCCTG GTACCAGCAGAAACCTGGCC AGGCTCCCAGGCTCCTCATCT ACGAAGCAGCCACCAGGGCC ACTGGTATCCCAGCCAGGTTC AGTGCGAGTGGGTCTGGGAC AGAGTTCACCTCACCCATCAG CAGCCTGCAGTCTGAAGATT TGCAGTTTATTACTGTACGA GTATAACCAAGTGGCTCTCAC TTTCGGCGGAGGGAACCAAGGT GGAGATCAAAACGAACGGTGG CTGCACCATCTGTCTTCATCT CCCGCATCTGATGAGCAGTT GAAATCTGGAACCTGCTCTGT TGTGTGCTGCTGAATAACTT CTATCCCAGAGAGGCCAAAG TACAGTGGAAGGTGGATAAC GCCCTCCAAATCGGGTAACCTC	(SEQ ID NO: 147) CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCAGTA ACTATGGCATGCACCTGGTCCGCCAGGTCCA GGCGAGGGCTGGAGTGGTGGCAGCTATATGGTTTGATGC AAGTGATAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAACCTCAAGAACACGCTGTATCTGCAA ATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTG TGGAGAGATATTGCGATTTTGGAGTGGTCCCCGACTACT GGGGCCAGGGAACCTGGTCAACCGTGTCTAGTGCCTCCACC AAGGCCCATCGGTCTTCCCCCTGGCACCCCTCTCTCAAGAG CAGCTCTGGGGGCAACGCGCCCTGGGCTGGCTGGTCAAGG ACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGC GCCCTGACCAGCGCGTGCACACCTTCCCCGCTGTCTTACA GTCTCTAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGC CCTCCAGCAGCTTGGGCAACCAAGACCTACATCTGCAACGTG AATCACAAGCCCAACCAACCAAGGTGGACAAGAAAGTTG AGCCCAATCTTGTGACAAACTCACATGCCACCCGTGC CCAGCACCTGAACCTCTGGGGGACCGTCACTCTCTCTTC CCCCCAAAACCAAGGACACCTTCAATCTCTCCGACCC TGAGGTACATGCTGGTGGAGCTGAGCCACGAAGACC CTGAGGTCAAGTTCAACTGTTACGTGGACGCGCTGGAGGTG CATAATGCCAAGCAAAAGCCGTGCGAGGAGCAGTACGGCA GCACGTACCGTTGCGTCAAGCTCTCAACCGTCTGCAACCAAG

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		CAGGAGAGTGTCACAGAGCA GGACAGCAAGGACAGCACCT ACAGCCTCAGCAGCACCCCTGA CGCTGAGCAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCAACCCATCAGGG CCTGAGCTCGCCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT	(SEQ ID NO: 148) EIVMTQSPATLSVSPGERATLS CRASQSVFEHLAWYQQKPGQA PRLIYEAAATRAATGIPARFSGS SGTEFTLTISLQSEDFAVYYCQ QYNQWPLTFGGGKVEIKRTV AAPSFIFFPPSDEQLKSGTASVV CLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSYSL STLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC	(SEQ ID NO: 149) QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAAIWFDASDKYYADAVKGRFTISRDNKNTLYLQ MNSLRAEDTAVYYCARDIAIFGVVPDYWGQGLVTVSSASTK GPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKHTHTCPCPAPELGGPSVFLPFPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHREALHNYTQKSLSPGK
	AA			
2G10.343	[hu anti- <huGIPR> 2G10.343 VK3 (1-236) VL]:huKLC -CL + [hu anti- <huGIPR> 2G10.325 VH3 (1-472) VH]:huIgG1 zSEFL2-2	NA	(SEQ ID NO: 150) GAAATAGTGATGACGCAGTCT CCAGCCACCCGTGTCTGTGTCT CCAGGGGAAAGAGCCACCCT CTCTGCAAGGCCAGTCAAGAG TGTTCTGGAACACTTAGCCTG GTACCAGCAGAAACCTGGCC AGGCCTCCAGGCTCCTCATCT ACGAAACAGCCACAGGGCC ACTGGTATCCCAAGCCAGGTTT AGTGCAAGTGGGCTGGGAC AGAGTTCACCTCACCATCAG CAGCCTGCAGTCTGAAAGATT	(SEQ ID NO: 151) CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCAGTAACTATGGCATGCACCTGGGTCCCGCAGGCTCCA GGCAGGGGCTGGAGTGGGTGGCAGCTATATGGTTTGATGC AAGTGATAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAACCTCAAGAACACGCTGTATCTGCAA ATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTG TGGAGAGATATTGCGATTCTTTGGAGTGGTCCCCGACTACT GGGGCCAGGGAACCCCTGGTACCGTGTCTAGTGCCTCCACC AAGGGCCCATCGGTCTTCCCCCTGGCACCTCTCTCCCAAGAG CACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGG ACTACTTCCCCGAAACCGGTGACGGTGTCTGTGGAACCTCAGGC

(mAb); LMR ID: SS- 26220		TGCAGTTTATTACTGTACGCA GTATAACAACTGGCCTCTCAC TTTCGGCGGAGGACCAAGGT GGAGATCAACGAACGGTGG CTGCACCATCTGTCTTCACTT CCCGCATCTGATGACAGTT GAAATCTGGAACCTGCCTCTGT TGTGTGCTGCTGAATAACTT CTATCCACAGAGAGGCCAAAG TACAGTGAAGGTGGATAAC GCCCTCCAATCGGGTAACTCC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCTCAGCAGACCCCTGA CGTGTGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCAACCATCAGGG CCTGAGCTCGCCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT	GGCCTGACAGCGGCGTGCACACCTTCCC GTCTCAGGACTACTCCCTCAGCAGCGTGGT CTCCAGCAGCTTGGGACCCAGACCTACATC AATCAACGCCAGCAACCAAGGTGGACAAG AGCCAAATCTGTGACAAACTCACATGCC CCAGCACTGAACTCTGGGGGACCGTCACT CCCCAAACCCAAAGACACCTCATGATCTC TGAGGTACATCGTGGTGGAGCTGAGCCAC CTGAGGTCAAGTCACTGTAACGTGACGGC CATAATGCCAAGACAAGCCGTGAGGAGCA GCAGTACCGTTGCTCAGCTCCTCACCCTG GACTGGTGAATGCCAAGGAGTACAAGTCA ACAAAGCCCTCCAGCCCCATCGAGAAACC GCCAAAGGCGCCCGAGAACCAAGGTGTAC CCCATCCGGGAGGAGTACCAAGAACAGGT ACCTGCCTGGTCAAGGCTTCTATCCAGGAC GGAGTGGGAGACAATGGCAGCCGAGAAC ACCACGCTCCCGTGTGACTCCGACGGCTC TATAGCAAGTCAACCTGGACAAAGAGGTG GGAAAGTCTTCTCATGCTCCGTGATGCAT AACCACACAGCAGAAAGACCTCTCCCTGT A
	AA	EIVMTQSPATLSVSPGERATLS CRASQSVLEHLAWYQQKPGQA PRLLIYEATRATGIPARFSGS SGTEFTLTISLSQSEDFAVYYCQ QYNWNPFTFGGGTKVEIKRTV AAPSVFIPPSDEQLKSGTASV CLLNIFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSYSL STLTLSKADYEKHKVYACEV HQGLSSPVTKSFNRGEC	(SEQ ID NO: 152) QVQLVESGGGVVQPGSRSLRSLSCAASGFTFSNYGMHWVVRQAP GEGLEWVAIWFDASDKYYADA VKGRFTISRDN SKNTLYLQ MNSLR AEDTAVYYCARDIAIFGVVPDYWGQGLTVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHRTCPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCPSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTI SKAKGQPRCPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMH EALHNHYTQKSLSLSPGK (SEQ ID NO: 155)
	NA	GAAATAGTGATGACGCAGTCT	(SEQ ID NO: 154) GAAATAGTGATGACGCAGTCTGGGGGAGGCGTGGTGTCCAGCC

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<p><huGIPR> 2G10.307 VK3 (1-236) VLJ::huKLC -CL + [hu anti- <huGIPR> 2G10.302 VH3 (1-472) VHJ::huIgG1 zSEFL2-2 (mAb); LMR ID: SS- 26190</p>	<p>CCAGCCACCCTGTCTGTGTCT CCAGGGAAAGAGCCACCCT CTCTGCAGGGCCAGTCAGAG TGTGATAGACACTTAGCCTG GTACCAGAGAAACCTGGCC AGCTCCACAGGCTCCTCATCT ACGAAGCAGCCACCAGGGCC ACTGGTATCCAGCCAGGTT AGTGGCAGTGGTCTGGGAC AGAGTTCACTCTCACCATCAG CAGCCTGCAGTCTGAAGATT TGCAGTTTATTACTGTACGA GTATAACCAAGTGGCTCTCAC TTTCGGCGGAGGGAACCAAGT GGAGATCAACCGAACGGTGG CTGACCATCTGTCTTCATCTT CCCGCCATCTGATGAGCAGTT GAAATCTGGAACCTGCCCTGT TGTGTGCTGCTGAATAACTT CTATCCAGAGAGGCCAAAG TACAGTGGAAGGTGGATAAC GCCCTCCAATCGGGTAACCTC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCTCAGCAGCACCCCTGA CGCTGAGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT</p>	<p>TGGAGGTCCTGAGACTCTCTCTGTGTCAGCATCTGGATTCA CCTTCAGTAACTATGGCATGCATGGTCCGCCAGGCTCCA GGCAGGGGCTGGAGTGGTGGCAGCTATATGGTTTATGC AAGTGATAAATACTATGCAGACGCCGTGAAGGCCGATTCA CCATCTCCAGAGACAACCTCAAGAACACGCTGTATCTGCAA ATGAACAGCTGAGAGCCGACACGGCTGTGTATTACTG TGGAGAGATATTGCGATTTTGGAGTGTTCGCCGACTACTG GGCCAGGGAACCTGGTACCGGTCTAGTGCCTCCACCA AGGGCCATCGGTCTTCCCTCGCACCTTCTCCCAAGAGC ACCTCTGGGGGCACAGCGGCCCTGGGCTGCCCTGGTCAAGGA CTACTTCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGGC CCCTGACACGGCGGTGCACACCTTCCCGGCTGTCTCTACAG TCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCC TCCAGCAGCTTGGCACCCAGACCTTACATCTGCAACGTGAA TCACAAGCCAGCAACCAAGGTGGACAAAGAAAGTTGAG CCCAATCTGTGACAAAACCTCACACATGCCACCGTGCCC AGCACCTGAACCTCTGGGGGACCGTCAAGTCTTCTCTCCC CCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTG AGTCACTGCTGGTGGTGGACGTGAGCCACGAAGACCTT GAGGTCAAGTTCAACTGTAAGTGGACGGCGTGGAGGTGCA TAATGCCAAGACAAGCCGTGCGAGGAGCAGTACGGCAGC ACGTACCGTTGCTCAGCTCCTCACCCTCTGCACCAGGA CTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTGTCCAACA AAGCCCTCCAGCCCCCATCGAGAAACCATCTCCAAAGCC AAAGGCGAGCCCCGAGAACCAACAGGTGTACACCTTGCCCC ATCCCGGAGGAGATGACCAAGAACCAAGGTACGCTGACCT GCTTGGTCAAGGGCTTCTATCCACGACATCGCCGTGGAG TGGGAGAGCAATGGGACGCCGGAGAACAACTACAAGACCA CGCTCCCGTGTGGACTCCGACGGCTCTTCTTCTCTCTATA GCAAGCTCACCGTGGACAAAGAGCAGGTGGCAGCAGGGGA CGTCTTCTCATGTCTCCGTGATGATGAGGCTCTGCACAACCA CTACAGCAGAGAAGCCCTCTCCCTGTCTCCGGGTAAA</p>
	<p>(SEQ ID NO: 156) EIVMTQSPATLSVSPGERATLS CRASQSVDRHLAWYQQKPGQ APRLIYEAAATRAITGIPARFSGS</p>	<p>(SEQ ID NO: 157) QVQLVESGGGVVQPRSLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAIIWFDASDKYYADA VKGRFTISRDN SKNTLYLQ MNSLRAEDTAVVYCARDIAIFGVFPDYWGQGTLVTVSSASTK</p>

[illegible]

A-2164-WO-PCT

2G10.311	[hu anti- <huGIPR> 2G10.311 VK3 (1-236) VLJ::huKLC -CL + [hu anti- <huGIPR> 2G10.302 VH3 (1-472) VHJ::huIgG1 zSEFL2-2 (mAb); LMR ID: SS- 26188	AA	GAGAAACACAAAGTCTACGC CTGCGAAGTCAACCCATCAGGG CCTGAGCTCGCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT	GCGTGTCAAGGGCTTCTATCCAGCAGCATCGCCGTGGAG TGGGAGAGCAATGGCAGCCGGAGAACAACTACAAGACCA CGCTCCGCTGGACTCCGACGGCTCTTCTTCTCTCTATA GCAAGCTCACCGTGGACAAGACAGGTGGCAGCAGGGGAA CGTCTCTCATCGCTCCGTGATGATGAGGCTCTGCACACCA CTACAGCAGAAGAGCCCTCTCCCTGTCTCCGGGTAAA
			(SEQ ID NO: 160) EIVMTQSPATLSVSPGERATLS CRASQSVNRHLAWYQQKPGQ APRLIYEAAATRAATGIPARFSGS GSGTEFTLTISLQSEDFAVYYC QQYQQWPLTFGGGKVEIKRT VAAPSVFIPPSDEQLKSGTASV VCLLNFFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSYIS LSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC	(SEQ ID NO: 161) QVQLVESGGGVQPGRSLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAIWFDASDKYYADA VKGRFTISRDN SKNTLYLQ MNSLRAEDTAVYYCARDIALIFGVPDYWGQGLVTVSSASTK GPSVFP LAPSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN HKPSN TKVDKKVEPKSCDKTHTCPCPAPEL LGGPSVFLFPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSYRCVSVLT VLVHQDWLNKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHREALHNYHTQKSLSLSPGK
2G10.311	[hu anti- <huGIPR> 2G10.311 VK3 (1-236) VLJ::huKLC -CL + [hu anti- <huGIPR> 2G10.302 VH3 (1-472) VHJ::huIgG1 zSEFL2-2 (mAb); LMR ID: SS- 26188	NA	GAAATAGTGATGACGCAGTCT CCAGCCACCCTGTCTGTGTCT CCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAG TGTTAACGTACACTTAGCCTG GTACCAGCAGAAACCTGGCC AGGCTCCAGGCTCCTCATCT ACCAAGCAGCCACCAGGGCC ACTGGTATCCAGCCAGGTTTC AGTGGCAGTGGTCTGGGAC AGAGTTCACTCTCACCATCAG CAGCCTGCAGTCTGAAGATT TGCAAGTTTATTACTGTCAGCA GTATAACCAAGTGGCTCTCAC TTTCGGCGGAGGACCAAGGT GGAGATCAAAACGAACGGTGG CTGCACCATCTGTCTTCATCTT	(SEQ ID NO: 162) GAAATAGTGATGACGCAGTCT CCAGCCACCCTGTCTGTGTCT CCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAG TGTTAACGTACACTTAGCCTG GTACCAGCAGAAACCTGGCC AGGCTCCAGGCTCCTCATCT ACCAAGCAGCCACCAGGGCC ACTGGTATCCAGCCAGGTTTC AGTGGCAGTGGTCTGGGAC AGAGTTCACTCTCACCATCAG CAGCCTGCAGTCTGAAGATT TGCAAGTTTATTACTGTCAGCA GTATAACCAAGTGGCTCTCAC TTTCGGCGGAGGACCAAGGT GGAGATCAAAACGAACGGTGG CTGCACCATCTGTCTTCATCTT
			(SEQ ID NO: 163) CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCAGTAACTATGGCATGCACCTGGTCCGCCAGGCTCCA GGCGAGGGCTGGAGTGGTGGCAGCTATATGGTTTGATGC AAGTGATAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAACCTCAAGAACACGCTGTATCTGCAA ATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTG TGGAGAGATATTGCGATTTTGGAGTGTTCGCCGACTACTG GGCCAGGGAACCTGTGTCACCGTGTCTAGTGCCTCCACCA AGGGCCCATCGGTCTTCCCTGGCACCCCTCTCCAAAGGC ACCTCTGGGGGCACAGCGGCCCTGGGTGCCTGGTCAAGGA CTACTTCCCGAACCGGTGACGGTGTGCTGGAACCTCAGGCG CCCTGACAGCGCGTGCACACCTTCCCGGTGTCTCTACAG TCCTCAGGACTACTCTCTCAGCAGCGGTGGTGACCGTGCCC TCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTGAA TCACAAGCCCCAGCAACACCAAGGTGGACAAAGAAAGTTGAG CCCCAAATCTTGTGACAAAACCTCACACATGCCCCACCGTGCCC	(SEQ ID NO: 163) CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCAGTAACTATGGCATGCACCTGGTCCGCCAGGCTCCA GGCGAGGGCTGGAGTGGTGGCAGCTATATGGTTTGATGC AAGTGATAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAACCTCAAGAACACGCTGTATCTGCAA ATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTG TGGAGAGATATTGCGATTTTGGAGTGTTCGCCGACTACTG GGCCAGGGAACCTGTGTCACCGTGTCTAGTGCCTCCACCA AGGGCCCATCGGTCTTCCCTGGCACCCCTCTCCAAAGGC ACCTCTGGGGGCACAGCGGCCCTGGGTGCCTGGTCAAGGA CTACTTCCCGAACCGGTGACGGTGTGCTGGAACCTCAGGCG CCCTGACAGCGCGTGCACACCTTCCCGGTGTCTCTACAG TCCTCAGGACTACTCTCTCAGCAGCGGTGGTGACCGTGCCC TCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTGAA TCACAAGCCCCAGCAACACCAAGGTGGACAAAGAAAGTTGAG CCCCAAATCTTGTGACAAAACCTCACACATGCCCCACCGTGCCC

A-2164-WO-PCT

2G10.306	[hu anti- <huGIPR> 2G10.306 VK3 (1-236) VL]:huKLC -CL + [hu anti-		<p>CCCGCCATCTGATGAGCAGTT GAAATCTGGAAGTGGCTCTGT TGTGTGCTGCTGAATAACTT CTATCCAGAGAGGCCAAAG TACAGTGGAAGGTGGATAAC GCCCTCAAATCGGGTAACCTC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCTCAGCAGCACCTGA CGCTGAGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCAACCATCAGGG CCTGAGCTCGCCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT</p> <p>(SEQ ID NO: 164)</p>	<p>AGCACCTGAACCTCTGGGGGACCGTCAAGTCTTCTCTTCCC CCCAAAACCAAGACACCTCATGATCTCCCGGACCCCTG AGTACATGCTGGTGGTGGAGCGAGCCACGAAGACCTT GAGGTCAAGTTCAACTGTTACGTGACGGCGTGGAGGTGCA TAATGCCAAGCAAAAGCGTGGAGGAGCAGTACGGCAGC AGTACCGTTGCTGAGCTCTCACTCCCTGTCACCCAGGA CTGGCTGAATGGCAAGGAGTAAAGTCAAGGTGTCCAACA AAGCCCTCCAGCCCCATCGAGAAACCATCTCCAAGCC AAAGGCGAGCCCCGAGAACACAGGTGTACACCTGCCCCC ATCCCGGAGGAGATGACCAAGAACAGGTCAAGCTGACCT GCCTGCTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAG TGGGAGAGCAATGGGACGCCGAGAACAACTACAAGACCA CGCTCCCGTGTGAGTCCGACCGGCTCTCTCTCTCTATA GCAAGCTCACCGTGGACAAAGACAGGTGGCAGCAGGGAA CGTCTTCTCATGCTCCGTGATGATGAGGCTCTGCACAACCA CTACAGCAGAAGACCTCTCCCTGTCTCCGGGTAAA</p> <p>(SEQ ID NO: 165)</p>
		AA	<p>EIVMTQSPATLSVSPGERATLS CRASQSNVHLAWYQQKPGQ APRLIYQAAATRAATGIPARFSGS GSGTEFTLTISLQSEDFAVYYC QQYNQWPLTFGGGKVEIKRT VAAPSVFIAPPDEQLKSGTASV VCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSYIS LSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC</p> <p>(SEQ ID NO: 166)</p>	<p>QVQLVESGGGVQVQGRSLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAIWFDASDKYYADA VKGRFTISRDN SKNTLYLQ MNSLRAEDTAVYYCARDIAIFGVFPDYWGQGLTVTVSSASTK GPSVFLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPPCPAPELLGSPSVFLPPPKDITL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSIVTLVHQQDWLNGKEYCKVSNKALPAPIEKTI SKAKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHAEALHNHYTQKSLSLSPGK</p> <p>(SEQ ID NO: 167)</p>
		NA	<p>GAAATAGTGATGACGCAGTCT CCAGCCACCTGTCTGTGTCT CCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTACAGAG TGTTCTGACGCACCTAGCCTG GTACCAGCAGAAACCTGGCC AGGCTCCCAAGGCTCCTCATCT</p> <p>(SEQ ID NO: 168)</p>	<p>CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCAGTAACCTATGGCATGCACTGGGTCCGCCAGGCTCCA GGCAGAGGGCTGAGTGGTGGCAGCTATATGGTTTGTATGC AAGTGATAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAACCTCCAGAACAACGCTGTATCTGCAA ATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTG</p> <p>(SEQ ID NO: 169)</p>

A-2164-WO-PCT

<huGIPR> 2G10.306 VH3 (1-472) VHJ::huIgG1 zSEFL2-2 (mAb); LMIR ID: SS- 26183	ACGAAGCAGCCACGAGGGCC ACTGGTATCCAGCCAGGTTC AGTGGCAGTGGTCTGGGAC AGAGTTCAC'TCACCATCAG CAGCCTGCAGTCTGAAGATT TGCA GTTTATTACTGTAGCA GTATCAGAACTGGCTCTCAC TTTTCGGCGGAGGACCAAGGT GGAGATCAAAAGAACGGTGG CTGCACCATCTGTCTTCATCTT CCCGCCATCTGATGAGCAGTT GAAATCTGAACTGCCCTGT TGTGTGCTGTGAATAACTT CTATCCAGAGAGGCCAAAG TACAGTGGAAAGTGGATAAC GCCCTCCAATCGGGTAACCTC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCCTCAGCAGCACCTGA CGCTGAGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT	TCGAGAGATATTGCGATTTTGGAGTGATCCCCGACTACT GGGCCAGGAACCTGGTCAACGTGTCTAGTGCCTCCACC AAGGCCCATCGGTCTTCCCCCTGGACCCCTCCTCCAAGAG CACCTCTGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGG ACTACTCCCCGAACCGGTGACGGTGTCTGTGAACCTCAGGC GCCCTGACAGCGGTGCACACCTTCCCCGGCTGTCTCTACA GTCTCAGAGCTCTACTCCCTCAGCAGCGGTGGTGAACCTGC CCTCAGCAGCTTGGCACCCAGACCTACATCTGCAACGTG AATCACAGCCAGCAACACCAAGGTGGACAAAGAAAGTTG AGCCAAATCTTGTGACAAAACCTACACATGCCACCGTGC CCAGCACCTGAACCTCTGGGGGAGCGTCACTCTTCTCTTC CCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCC TGAGGTACATCGGTGGTGGACGTGAGCCACGAAGACC CTGAGGTCAAGTTCAACTGTAACGTGACGGCTGGAGGTG CATATGCCAAGCAAAAGCGTGGGAGGAGCAGTACGGCA GCACGTACCGTTCGTGCTCAGCGTCTCACCGTCTGCACAG GACTGGCTGAATGGCAAGGAGTACAAGTCAAGGTGTCCA ACAAAGCCCTCCAGCCCCATCGAGAAACCATCTCCAAA GCCAAAGGCAAGCCCGAGAACACAGGTGTACACCTGCC CCCATCCCGGAGGAGATGACCAAGAACAGGTACGCTG ACCTGCCGTGTCAAAGGCTTCTATCCAGCGACATCGCCGT GGAGTGGGAGAGCAATGGGCAAGCCGAGAAACACTACAAG ACCAGCCTCCCTGCTGCTGGACTCCGACGGCTCTTCTCTC TATAGCAAGCTCACCGTGGACAAAGCAGGTGGCAGCAGG GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC AACCCTACACGCAAGAGAGCCTCTCCCTGTCTCCGGGTAA A
	(SEQ ID NO: 168) EIVMTQSPATLSVSPGERATLS CRASQSVLTHLAWYQQKPGQA PRLLIYEAATRAITGIPARFSGS SGTEFTLTISLQSEDFAVYYCQ QYQNWPFLTGGGKVEIKRTV AAPSVFIFPPSDEQLKSGTASVV CLLNNFYPREAKVQWVKVDNAL QSGNSQESVTEQDSKDSYSLS	(SEQ ID NO: 169) QVQLVESGGGVQPGRLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAIIWFDASDKYYADAVKGRFTISRDNKNTLYLQ MNSLRAEDTAVYYCARDIAIFGVPDYWGQGLVTVSSASTKG PSVFPLAPSKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNT KVDKKVEPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTRYCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK

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		STLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC	(SEQ ID NO: 170) GAAATAGTGATGACGCAAGTCT CCAGCCACCCTGTCTGTGTCT CCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAG TGTTCTGACGCACCTTAGCCTG GTACCAGCAGAAACCTGGCC AGGCTCCCAGGCTCCTCATCT ACGAAGCAGCCACCAGGGCC ACTGGTATCCAGCCAGGGTC AGTGGCAGTGGGTCTGGGAC AGAGTTCACTCTACCATCAG CAGCTGCAGTCTGAAGATT TGCAGTTTATTACTGTACAGA GTATCAGAACTGGCTCTCAC TTTCGGCGGAGGGAACCAAGGT GGAGATCAACGAAACGGTGG CTGCACCATCTGTCTTCATCTT CCCGCCATCTGATGAGCAGTT GAAATCTGGAACCTGCCTCTGT TGTGTGCTGCTGAATAACTT CTATCCCAGAGGCCCAAAG TACAGTGGAAGGTGGATAAC GCCCTCCAATCGGGTAACTCC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCTCAGCAGCACCCCTGA CGCTGAGCAAAAGCAGACTAC GAGAAACACAAGTCTACGC CTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCACAA GAGCTTCAACAGGGGAGAGT GT	(SEQ ID NO: 171) CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCAGTAACATGGCATGCATGGGTCCGCCAGGTCCA GGCGAGGGGTGGATGGGTGGCAGCTATATGGTTTGTATGC AAGTGATAAATACTATGCAGACGCCGTGAAGGCCGATTCA CCATCTCCAGAGACAACCTCAAGAACACGCTGTATCTGCAA ATGAACAGCTGAGAGCCGAGGACACGGCTGTGTATTACTG TGGAGAGATATTGCGATTTTGGAGTGTATCCCCGACTACT GGGGCCAGGAAACCTGGTCAACCGTGTCTAGTGCCTCCACC AAGGGCCATCGGTCTTCCCCCTGGCACCTCTCCAAGAG CACTCTGGGGGCACAGCGGCCCTGGGCTGCCGTGTCAAAG ACTACTTCCCCGAACCGGTGACGGTGTGCTGGAACACTCAGGC GCCCTGACCAGCGGTGCACACCTTCCCGGTGTCTCTACA GTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGC CCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTG AATCAACAAGCCAGCAACACCAAGGTGGACAAGAAAGTTG AGCCCAAATCTGTGACAAAACTCACATGCCACCCGTGC CCAGCACCTGAACCTCTGGGGGACCGTCAGTCTTCTCTTC CCCCAAACCCAAAGACACCTCATGATCTCCCGGACCCC TGAGGTACATGCTGGTGGTGGACGTGAGCCACGAAGACC CTGAGGTCAAGTTCAACTGGTACGTGGAGCGGCTGGAGGTG CATAATGCCAAGACAAGCCGTGCGAGGAGCAGTACGGCA GCACGTACCGTTGCTCAGCTCTCAACCGTCTGCACCCAG GACTGGTGAATGGCAAGGAGTACAAGTGAAGGTGTCCA ACAAAGCCCTCCAGCCCCATCGAGAAACCATCTCCAAA GCCAAAGGCAACCCGAGAACCAAGGTGTACACCTGCC CCCATCCCGGAGGAGATGACCAAGAACCCAGGTCAAGCCTG ACCTGCTGTCAAAGGCTTCTATCCCAAGCAGCATCGCCGT GGAGTGGGAGCAATGGGCGACCCGAGAACAACTACAAG ACCACGCTCCCGTGTGAGCTCCGACGGCTCCTTCTTCTC TATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGG GGAACGTCTTCTCATGTCTCCGTGATGCATGAGGCTCTGCAC
	[hu anti- <huGIPR> 2G10.606 VK3 (1-236) VL]:huKLC -CL + [hu anti- <huGIPR> 2G10.306 VH3 (1-472) VH]:huIgG1 zSEFL2-2 (mAb); LMR ID: SS- 26231	NA		

2610.606

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			AA	(SEQ ID NO: 172) EIVMTQSPATLSVSPGERATLS CRASQSVLTHLAWYQQKPGQA PRLLIYEAAATRAITGIPARVSGG SGTEFTLTISSLQSEDFAVYYCQ QYQNWPLTFGGGTKVEIKRTV AAPSVFIPTPSDEQLKSGTASVV CLLNIFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSITYSL STLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC	(SEQ ID NO: 173) QVQLVESGGGVQPRSLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAIWFDASDKYYADAVKGRFTISRDNKNTLYLQ MNSLRAEDAVYYCARDIAIFGVIDYWGQGLTVTVSSASTKG PSVFLAPSKTSGGTAAALGCLVKDYFPEPTVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNT KVDKKVEPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMI SRTEPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK	AACCACTACACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAA A
				(SEQ ID NO: 174) GAAATAGTGATGACGCAGTCT CCAGCCACCCTGTCTGTGTCT CCAGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAG TGTTAGCAGCAACTTAGCCTG GTACCAGCAGAAACCTGGCC AGGCTCCAGGCTCCTCATCT ATGGTGCAGCCACCAAGGCC ACTGGTATCCAGCCAGGTTTC AGTGGCAGTGGGTCTGGGAC AGAGTTCAC'TCTCACCATCAG CAGCCTGCAGTCTGAAGATT TGCAGTTTATTACTGTACGA GTATAATAACTGGCCTCTCAC TTTCGGCGGAGGGACCAAGGT GGAGATCAAAACGAACGGTGG CTGCACCATCTGTCTTCATCTT CCCCCATCTGATGAGCAGTT GAAATCTGGAACCTGCCCTGT TGTGTGCTGCTGAATAACTT CTATCCACAGAGAGGCCAAAG	(SEQ ID NO: 175) CAGGTGCAGTGGTGGAGTCTGGGGAGGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCAGTAACTATGGCATGCACCTGGGTCCGCCAGGCTCCA GGCGAGGGCTGGAGTGGGTGGCAGCTATATGTTTGTATGC AAGTGATAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAACCTCAAGAACACGCTGTATCTGCAA ATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTG TGCAGAGATTGGCGATTTTGGAGTGGTCCCAGCTACT GGGGCCAGGGAACCTGGTCAACCTGTCTAGTGCCTCCACC AAGGGCCCATCGGTCTTCCCTCCCTGGCACCTCTCCCAAGAG CACCTCTGGGGCACAGCGGCCCTGGGTGCCCTGGTCAAGG ACTACTTCCCGAACCGGTGACGGTGTGTGGAACCTCAGGC GCCCTGACCAGCGGTGTCACACCTTCCCGGTGTCTACAC GTCTTCAGGACTCTACTCCCTCAGCAGCGGTGGTGACCGTGC CCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTG AATCACAAAGCCAGCAACACCAAGGTGGACAAAGAAAGTTG AGCCAAATCTTGTGACAAAACCTACACATGCCACCGTGC CCAGCACCTGAACCTCTGGGGGACCGTCACTCTTCCCTTTC CCCCAAAACCCAAAGGACACCTCATGATCTCCCGGACCCC TGAGGTACATGCGTGGTGGACGTGAGCCACGAAGACC CTGAGGTCAAGTTCAACTGTTACGTGGACGGCGGTGGAGGTG	
2G10.347	anti- <huGIPR> 21- 143_2G10_L C1.005 (1- 237)(S73(85) A) VL + [Unknown anti- <huGIPR> 2G10.610 VH3 (1-472) VHJ::huIgG1 zSEFL2-2 (mAb); LMR ID: SS- 26224	NA				

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2G10.348	anti- <huGIPR> 21- 143_2G10_L C1.005 (1- 237)(S73(85) A) VL + [hu anti- <huGIPR> 2G10.348	NA	TACAGTGGAAGGTGGATAAC GCCCTCCAAATCGGGTAACTCC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCTCAGCAGCACCTGA CGTGAGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCAACCATCAGGG CCTGAGCTCGCCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT	CATAATGCCAAGACAAAGCCGTGCGAGGAGCAGTACGGCA GCACGTACCGTTGCTCAGCGTCTCACCCTCTGCACCAG GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTGTCCA ACAAAGCCCTCCAGCCCCATCGAGAAACCATCTCCAAA GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCTGCC CCCATCCCGGGAGAGATGACCAAGAACCCAGGTACGCCTG ACCTGCCCTGGTCAAGGCTTCTATCCCAGCGACATCGCCGT GGAGTGGGAGCAATGGGCGCCGAGAACAACTACAAG ACCAAGCTCCCGTCTGGACTCCGACGGCTCTTCTTCTC TATAGCAAGCTACCGTGGACAAAGCAGGTGGCAGCAGG GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC AACCACTACACGCAGAAAGACCTCTCCCTGTCTCCGGGTAA A
			(SEQ ID NO: 176) EIVMTQSPATLSVSPGERATLS CRASQSVSSNLAWYQQKPGQA PRLIYGAATRAATGIPARFSGSG SGTEFTLTISLSQSEDFAVYYCQ QYNNWPLTFGGGKVEIKRTV AAPSVFIPTPSDEQLKSGTASVV CLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSYLSLS STLTLSKADYEEKHKVYACEVT HQGLSSPVTKSFNRGEC	(SEQ ID NO: 177) QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAIWFDASDKYYADA VKGRFTISRDNKNTLYLQ MNSLR AEDTAVYYCARDLAIFGVVPDYWGQGLVTVSSASTK GPSVFLAPSSKTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHREALHNYTQKSLSPGK
			(SEQ ID NO: 178) GAAATAGTGATGACGCAGTCT CCAGCCACCCTGTCTGTGTCT CCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAG TGTTAGCAGCAACTTAGCCTG GTACACAGCAAAACCTGGCC AGGCTCCAGGGTCTCTCATCT ATGGTGCAGCCACCAAGGCC ACTGGTATCCAGCCAGGTC AGTGCGAGTGGGTCTGGGAC	(SEQ ID NO: 179) CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCAGTAACTATGGCATGCACCTGGTCCGCCAGGTCCA GGCGAGGGCTGGAGTGGTGGCAGCTATATGGTTTGTATGC AAGTGATAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAACCTCAAGAACACGCTGTATCTGCAA ATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTG TGCGAGAGATCAGCGGATTTTGGAGTGGTCCCCGATTACT GGGGCCAGGAAACCTGGTCAACCGTGTCTAGTGCCTCCACC AAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCTCTCCAAGAG

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<p>VH3 (1-472) VHJ::hulgG1 zSEFL2-2 (mAb); LMR ID: SS- 26225</p>	<p>AGAGTTACCTCTCACCATCAG CAGCCTGCAGTCTGAAGATTT TGCAGTTTATTACTGTGACGA GTATAATAACTGGCCTCTCAC TTTCGGCGGAGGACCAAGGT GGAGATCAAAACGAACGGTGG CTGCACCATCTGTCTTCATCTT CCCGCCATCTGATGAGCAGTT GAAATCTGGAACCTGCCCTGT TGTGTGCTGTCTGAATAACTT CTATCCCAGAGAGGCCAAAG TACAGTGGAAGGTGGATAAC GCCCTCCAAATCGGTAACCTC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCCTCAGCAGCACCCCTGA CGCTGAGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT</p>	<p>CACTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGG ACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGC GCCCCTGACCAGCGCGGTGCACACCTTCCCGGCTGTCTCTACA GTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGC CCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAACCGTG AATCAAAAGCCCAAGCAACCAAGGTGGACAAAGAAAGTTG AGCCCAATCTTGTGACAAACACTACACATGCCACCCAGTGC CCAGCACCTGAACCTCTGGGGGACCGTCACTCTTCTCTTC CCCCAAAACCCAGGACACCTCATGATCTCCCGGACCCC TGAGTACATGCTGGTGGTGGACGTGAGCCACGAAGACC CTGAGGTCAAGTTCAACTGCTACGTGGACGGCGTGGAGGTG CATAATGCCAAGACAAAGCCGTGCGAGGAGCAGTACGGCA GCACGTACCGTTCGTCAGCGTCTCACCCTTGCACCAAG GACTGGCTGAATGGCAAGGAGTACAAAGTCAAGGTGTCCA ACAAAGCCCTCCAGCCCCCTCAGAGAAACCATCTCCAAA GCCAAAGGCGACCCCGAGAACCCACAGGTGTACACCTGCC CCCATCCCGGAGGAGATGACCAAGAACAGGTACAGCTG ACCTGCTGCTCAAGGCTTCTATCCAGCGACATCGCGT GGAGTGGAGAGCAATGGGCAAGCGGAGAGCAACACTACAAG ACCACGCTCCCGTCTGTGAGTCCGACGGCTCTCTCTCTC TATAGCAAGCTCACCCTGGACAAAGCAGGTGGCAGCAGG GGAACGTCTTCTCATGCTCCGTGATGATGAGGCTCTGCAC AACCACTACAGCAGAAAGAGCCCTCTCCCTGTCTCCGGGTAA A</p>
	<p>(SEQ ID NO: 180) EIVMTQSPATLSVSPGERATLS CRASQSVSSNLAWYQKPGQA PRLIYGAAATRAATGIPARFSGS SGTEFTLTSSLSQSEDFAVYYCQ QYNNWPLTFGGGKVEIKRTV AAPSVFIFPPSDEQLKSGTASVV CLLNNFYPREAKVQWVKVDNAL QSGNSQESVTEQDSKDSYSL STLTLSKADYKEHKVYACEVT HQGLSSPVTKSFNRGEC</p>	<p>(SEQ ID NO: 181) QVQLVESGGGVQPGRLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAAIWFDASDKYYADA VKGRFTISRDN SKNTLYLQ MNSLRAEDTAVYYCARDQAIFGVVPDYWGQGLTVTVSSASTK GPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTL MISRTEPVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTPPVLDSGDSFFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQKSLSPGK</p>

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	(SEQ ID NO: 182)	(SEQ ID NO: 183)
anti- <huGIPR> 21- 143_2G10_L C1.005 (1- 237)(S73(85) A) VL + [hu anti- <huGIPR> 2G10.325 VH3 (1-472) VHJ::hulgG1 zSEFL2-2 (mAb); LMR ID: SS- 26223	GAAATAGTGATGACGCAGTCT CCAGCCACCCTGTCTGTGTCT CCAGGGAAAGAGCCACCCT CTCTGCAGGGCCAGTCAGAG TGTTAGCAGCAACTTAGCCTG GTACCAGCAAAACCTGGCC AGGCTCCAGGCTCCTCATCT ATGCTGAGCCACCAAGGCC ACTGATATCCAGCCAGGTTC AGTGGCAGTGGGTCTGGGAC AGAGTTCACTCTACCATCAG CAGCCTGCAGTCTGAAGATT TGCAGTTTATTACTGTCAGCA GTATAATAAAGTGGCTCTCAC TTTCGGCGGAGGACCAAGGT GGAGATCAACGAACGGTGG CTGCACCATCTGTCTTCATCT CCCGCATCTGATGACAGTT GAAATCTGGAACCTGCCTCTGT TGTGTGCTGCTGAATAACTT CTATCCAGAGAGGCCAAAG TACAGTGGAAGGTGGATAAC GCCCTCCAATCGGGTAACCTC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCTCAGCAGCACCTGA CGCTGAGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCAACCATCAGGG CCTGAGCTCGCCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCAGTAACTATGGCATGCACCTGGTCCGCCAGGCTCCA GGCGAGGGCTGGAGTGGTGGCAGCTATATGGTTTGATGC AAGTGATAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCATCTCCAGAGCAACTCCAGAACACGCTGTATCTGCAA ATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTG TGCGAGAGATATTGCGATTTTGGAGTGGTCCCGGACTACT GGGCCAGGGAACCTGTGTACCGTGTCTAGTGCCTCCACC AAGGCCCATCGGTCTTCCCTTGGCACCTCTCTCCAAAGAG CACCTCTGGGGCACAGGGGCCCTGGGTGCCCTGGTCAAGG ACTACTTCCCGGAACCGGTGACGGTGTCTGTGAACCTCAGGC GCCCTGACCAGCGGTGCACACCTTCCCGGTGTCTCTACA GTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAACGTGC CTCCAGCAGCTTGGGACCCAGACCTCATATCTGCCAACGTG AATCACAAAGCCAGCAACACCAAGGTGGACAAGAAGTTG AGCCAAATCTGTGACAAACACACATGCCACCGGTGC CCAGCCTGAACCTCTCTGGGGGACCGTCACTTCTCTCTTC CCCCAAACCCCAAGGACACCTCATATCTCCCGGACCCC TGAGGTACATGCTGTGGTGGTGGACGTGAGCCACGAAGACC CTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTG CATATGCCAAGACAAAGCCGTGCGAGGAGCAGTACGGCA GCACGTACCGTTGCGTCAAGCTCTCACCCTCTGCACCCAG GACTGGTGAATGGCAAGGAGTACAAGTGAAGTGTCCA ACAAAGCCCTCCAGCCCCATCGAGAAACCATCTCCAAA GCCAAAGGGCAGCCCCGAGAACCAAGGTGTACACCTGCC CCCATCCCGGGAGGAGATGACCAAGAACCCAGGTCAAGCTG ACCTGCCCTGGTCAAAAGCTTCTATCCAGCGACATCGCCGT GGAGTGGGAGAGCAATGGGCAAGCGGAGAACAACTACAAG ACCACGCCCTCCGTGTGGACTCCGACGGCTCTCTCTCTC TATAGCAAGCTCACCTGGGACAAAGCAGGTGGCAGCAGG GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC AACCCTACACGCAAGAGGCTCTCCCTGTCTCCGGGTAA A
	(SEQ ID NO: 184)	(SEQ ID NO: 185)

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	AA	EIVMTQSPATLSVSPGERATLS CRASQSVSSNLAWYQQKPGQA PRLIYGAAATRAATGIPARFSGS SGTEFTLTISLSQSEDFAVYYCQ QYNNWPLTFGGGKVEIKRTV AAPSVFIFPPSDEQLKSGTASVV CLLNFFYPREAKVQWQVDNAL QSGNSQESVTEQDSKDSYSL STLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC	QVQLVESGGGVQVGRSLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAIWFDASDKYYADA VKGRFTISRDN SKNTLYLQ MNSLRAEDTAVYYCARDIAIFGVVVDYWGQGLTVTVSSASTK GPSV/FPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHSTCPPEPAPELLGGPSVFLPPKPKDNL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTPCE EQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHREALHNHYTQKSLSLSPGK
		(SEQ ID NO: 186) GAAATAGTGATGACGCAGTCT CCAGCCACCCTGTCTGTGTCT CCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAG TGTTAGCAGCAACTTAGCCTG GTACCAGCAGAAACCTGGCC AGGCTCCCAGGCTCCTCATCT ATGGTGCAGCCACCAGGGCC ACTGGTATCCAGCCAGGGTC AGTGGCAGTGGGTCTGGGAC AGAGTTCACTCTCACCATCAG CAGCCTGCAGTCTGAAGATT TGCAGTTTATTACTGTACGA GTATAATAACTGGCTCTCAC TTTCGGCGGAGGGAACCAAGGT GGAGATCAAAACGAACGGTGG CTGCACCATCTGTCTTCATCT CCCGCCATCTGATGAGCAGTT GAAATCTGGAACCTGCCCTGT TGTGTGCTGTGAATAACTT CTATCCCAGAGGGCCAAAG TACAGTGGAAGGTGGATAAC GCCCTCCAAATCGGGTAACTCC CAGGAGAGTGTACAGAGCA	(SEQ ID NO: 187) CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCAGTA ACTATGGCATGCACTGGGTCCGCCAGGCTCCA GGCGAGGGCTGGAGTGGGTGGCAGCTATATGGTTTGTATGC AAGTGATAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAACCTCCAGAACACGCTGTATCTGCAA ATGAACAGCTGAGAGCCGAGACACGGCTGTGTATTACTG TGGGAGAGATTTGGCGATTTTGGAGTGGTCCCGGACTACT GGGGCCAGGAACCTGGTCAACCGTGTCTAGTGCCTCCACC AAGGGCCATCGGTCTTCCCTTGGCACCCTCCCTCCAGAG CACTCTGGGGGCACAGCGCCCTGGGCTGCCGTGTCAGG ACTACTTCCCGAACCGGTGACGGTGTCTGTGGA ACTCAGGC GCCCTGACCAGCGCGTGCACACTTCCCGGCTGTCTTACA GTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCCGTGC CCTCCAGCAGCTTGGGCAACCCAGACCTACATCTGCAACGTG AATCAACAGCCAGCAACCAAGGTGGACAAAGAAAGTTG AGCCCAATCTGTGACAAACTCACATGCCACCCGTGC CCAGCACCTGAACCTCTGGGGGACCGTCACTCTTCCCTTC CCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCC TGAGGTACATGCTGGTGGTGGACGTGAGCCACGAAGACC CTGAGGTCAAGTTCAACTGGTACGTGGACGGCTGGAGGTG CATAATGCCAAGACAAGCCGTGCGGAGGAGCAGTACGGCA GCACGTACCGTTGCGTACGCTCTCACCCTGCTGACCCAG GACTGGCTGAATGGCAAGGAGTACAAAGTGCAAGGTGTCCA

2G10.647

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2G10.649	[hu anti- <huGIPR> 2G10.649 VK3 (1-236) VL]:huKLC -CL + [hu anti- <huGIPR> 2G10.348 VH3 (1-472) VH]:huIgG1 zSEFL2-2 (mAb); LMIR	NA	GGACAGCAAGGACAGCACCT ACAGCCTCAGCAGCACCTGA CGCTGAGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT	ACAAAGCCCTCCAGCCCCCATCGAGAAACCAACCATCTCCAAA GCCAAAGGCGCCCCGAGAACACACAGGTGTACACCTGCCC CCCATCCCGGAGGATGACCAAGAACAGGTACAGCTG ACCTGCTGGTCAAAGGCTTCTATCCAGCGACATCGCGGT GGAGTGGGAGAGCAATGGGACGCCGAGAACTACAAG ACCACGCTCCCTGCTGGAGTCCGACGGCTCTCTTCTCTC TATAGCAAGCTACCCGTGGACAAAGCAGGTGGCAGCAGG GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC AACCCTACACGACAGAGAGCCTCTCCCTGTCTCCGGGTAA A
			(SEQ ID NO: 188) EIVMTQSPATLSVSPGERATLS CRASQSVSSNLAWYQQKPGQA PRLIYGAATRATGIPARVSGS GSGTEFTLTISSLSQSEDFAVYYC QQYNNWPLTFGGGKVEIKRT VAAPSVFIFFPSDEQLKSGTASV VCLLNFFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSSTYS LSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC	(SEQ ID NO: 189) QVQLVESGGGVQPGRSRLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAIWFDASDKYYADA VKGRFTISRDN SKNTLYLQ MNSLRAEDTAVYYCARDLAIFGVVPDYWGQGLVTVSSASTK GPSVFPLAPSSKTSGGTAALGLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHPKPSN TKVDKKVEPKSCDKTHTCPCPAPELLGGPSVFLPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHREALHNHYTQKSLSPGK
2G10.649	[hu anti- <huGIPR> 2G10.649 VK3 (1-236) VL]:huKLC -CL + [hu anti- <huGIPR> 2G10.348 VH3 (1-472) VH]:huIgG1 zSEFL2-2 (mAb); LMIR	NA	(SEQ ID NO: 190) GAAATAGTGATGACGCAGTCT CCAGCCACCCTGTCTGTGTCT CCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAG TGTTAGCAGCAACTTAGCCTG GTACCAGCAGAAACCTGGCC AGGCTCCAGGCTCCTCATCT ATGAAGCAGCCACCAGGGCC ACTGGTATCCAGCCAGGGTIC AGTGGCAGTGGGTCTGGGAC AGAGTTCACTCTCACCATCAG CAGCCTGCAGTCTGAAGATT TGCAGTTTATTACTGTACGCA	(SEQ ID NO: 191) CAGGTGCAGTGGTGGAGTCTGGGGAGGCGGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCAGTAACTATGGCATGCACCTGGTCCGCCAGGCTCCA GGCGAGGGCTGGAGTGGTGGCAGCTATATGGTTTGATGC AAGTGATAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAACCTCAAGAACACGCTGTATCTGCAA ATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTCTG TGGAGAGATCAGCGATTTTGGAGTGGTCCCGGATTACT GGGGCCAGGAACCCCTGGTCACTAGTGTCTAGTGCCTCCACC AAGGGCCCATCGGTCTTCCCTCCCTGGCACCCCTCTCCCAAGAG CACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGG ACTACTTCCCGCAACCGGTGACGGTGTGTGGAACATCAGGC GCCGTGACACGCGGCTGCACACCTTCCCGGCTGTCTCTACA

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ID: SS-26237		GTATAATAACTGGCCTCTCAC TTTCGGCGGAGGGAACCAAGGT GGAGATCAAAACGAACGGTGG CTGCACCATCTGTCTTCATCTT CCCGCCATCTGATGAGCAGTT GAAATCTGGAACCTGCTCTGT TGTGTGCTGCTGAATAACTT CTATCCCAGAGAGGCCAAAG TACAGTGGAAGGTGGATAAC GCCCTCCAAATCGGGTAACCTC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCTCAGCAGCACCTGA CGCTGAGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCAACCATCAGGG CCTGAGCTCGCCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT	GTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGC CCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTG AATCACAAGCCAGCAACCAAGGTGGACAAAGAAAGTTG AGCCCAATCTTGTGACAAACTCACACATGCCACCGTGC CCAGCACCTGAACCTCTGGGGGACCGCTAGTCTTCTCTTC CCCCAAACCCAGGACACCTCATATCTCCCGGACCCC TGAGGTACATGCTGGTGGTGGAGTGGAGCCAGCAAGACC CTGAGGTCAAGTTCAACTGTAAGTGGAGCGCGTGGAGGTG CATAATGCCAAGACAAAGCGTGGGAGGAGCAGTACGGCA GCACGTACCGTTGCTCAGCTCCTCACCCTCTGCACCCAG GACTGGCTGAATGGCAAGGATCAAGTCAAGTCAAGGTGTCCA ACAAAGCCCTCCAGCCCCATCGAGAAACCATCTCCAAA GCCAAAGGCGAGCCCGAGAACACAGGTGTACACCTGCC CCCATCCCGGAGGAGATGACCAAGAACCCAGGTACGCTG ACCTGCTGGTCAAGGCTTCTATCCAGCGACATCGCGGT GGAGTGGGAGCAATGGGCGCCGAGCAACAACTACAAG ACCACGCTCCCGTCTGGACTCCGACGCTCTCTTCTCTC TATAGCAAGCTACCGTGGACAAAGCAGGTGGCAGCAGG GGAACGTCTTCTCATGCTCCGTGATGATGAGGTCTGAC AACCACTACACGCAGAAAGACCTCTCCCTGTCTCCGGGTAA A
	AA	EIVMTQSPATLSVSPGERATLS CRASQSVSSNLAWYQQKPGQA PRLLIYEAATRAATGIPARVSGSG SGTEFTLTISLQSEDFAVYVCQ QYNNWPLTFGGGKVEIKRTV AAPSFIFFPPSDEQLKSGTASVV CLLNNFYPREAKVQWVDNAL QSGNSQESVTEQDSKDSYSL STLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC	(SEQ ID NO: 192) QVQLVESGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAIWFDASDKYYADA VKGRFTISRDNKNTLYLQ MNSLRAEDTAVYYCARDQAIFGVVDPYWGQGLVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKHTHTCPCPAPELLGGPSVFLPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTI SKAKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHREALHNYTQKSLSLSPGK
[hu anti- <huGIPR>	NA	GAAATAGTGATGACGCAGTCT CCAGCCACCCTGTCTGTGTCT	(SEQ ID NO: 194) (SEQ ID NO: 195) CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGTCAGCATCTGGATTCA

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2G10.305 VK3 (1-236) VLJ::huKLC -CL + [Unknown anti- <huGIPR> 2G10.610 VH3 (1-472) VHJ::huIgG1 zSEFL2-2 (mAb); LMR ID: SS- 26182	CCAGGGGAAAGAGCCACCCT CTCTGCAGGGCCAGTCAGAG TGTTGATGTTAACTTAGCCTG GTACCAGCAGAAACCTGGCC AGGCTCCAGGCTCCTCATCT ACAACGACGCCACCAGGGCC ACTGGTATCCCAAGCCAGGTTT AGTGCACTGGGCTCTGGGAC AGAGTTCACTCTCACCATCAG CAGCCTGCAGTCTGAAGATTT TGCAGTTTATTACTGTCAGCA GTATCAGAACTGGCCTCTCAC TTTCGGCGGAGGACCAAGGT GGAGATCAAAAGAACGGTGG CTGCACCATCTGTCTTCATCTT CCCGCCATCTGATGAGCAGTT GAAATCTGGAAGTGCCTCTGT TGTGTGCTGCTGAATAACTT CTATCCCAGAGAGGCCAAAG TACAGTGGAAGGTGGATAAC GCCCTCCAAATCGGGTAACTCC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCCTCAGCAGCACCTTGA CGCTGAGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCAACCATCAGGG CCTGAGCTCGCCCGTCACAA GAGCTTCAACAGGGGAGAGT GT	CCAGGGGAAAGAGCCACCCT CTCTGCAGGGCCAGTCAGAG TGTTGATGTTAACTTAGCCTG GTACCAGCAGAAACCTGGCC AGGCTCCAGGCTCCTCATCT ACAACGACGCCACCAGGGCC ACTGGTATCCCAAGCCAGGTTT AGTGCACTGGGCTCTGGGAC AGAGTTCACTCTCACCATCAG CAGCCTGCAGTCTGAAGATTT TGCAGTTTATTACTGTCAGCA GTATCAGAACTGGCCTCTCAC TTTCGGCGGAGGACCAAGGT GGAGATCAAAAGAACGGTGG CTGCACCATCTGTCTTCATCTT CCCGCCATCTGATGAGCAGTT GAAATCTGGAAGTGCCTCTGT TGTGTGCTGCTGAATAACTT CTATCCCAGAGAGGCCAAAG TACAGTGGAAGGTGGATAAC GCCCTCCAAATCGGGTAACTCC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCCTCAGCAGCACCTTGA CGCTGAGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCAACCATCAGGG CCTGAGCTCGCCCGTCACAA GAGCTTCAACAGGGGAGAGT GT	CCTTCAGTAACTATGGCATGCACTGGGTCCGCCAGGCTCCA GGCGAGGGCTGGAGTGGGTGGCAGCTATATGGTTTGATGC AAGTGATAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAACCTCAAGAACACGCTGTATCTGCAA ATGAACAGCTGAGAGCCGAGGACACGGCTGTGTATTACTG TGGAGAGATTGGCGAATTTTGGAGTGGTCCCCGACTACT GGGGCCAGGAAACCTTGGTACCGGTGCTAGTGCCTCCACC AAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCCAAGAG CACCTCTGGGGCACAGCGGCCCTGGGCTGCCGTGTCAAGG ACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGC GGCTTGACACGCGGCTGCACACTTCCCCGGCTGTCTCTACA GTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGC CCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTG AATCAAGCCCAAGCAACCAAGGTGGACAAAGAAAGTTG AGCCAAATCTTGTGACAAAACCTCACACATGCCACCGTGC CCAGCACCTGAACCTCTGGGGGACCGTCACTCTTCTCTTC CCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCC TGAGGTACATCGTGTGGTGGACGTGAGCCACGAAGACC CTGAGGTCAAGTTCAACTGTTAGTACGTGGACGGCGTGGAGGTG CATAATGCCAAGACAAGCCGTGCGAGGAGCAGTACGGCA GCACGTACCGTTGCGTCAGCTGCTCACCCTGCTGCACCA GACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTGTCCA ACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCCAA GCCAAAGGCAGCCCGGAGAACCAACAGGTGTACACCCCTGCC CCCATCCCGGGAGGAGATGACCAAGAACAGGTCAAGCTG ACCTGCCTGGTCAAGGCTTCTATCCAGCGACATCGCCGT GGAGTGGGAGAGCAATGGGCAAGCCGAGAAACAACATAAAG ACCAGCCTCCCGTCTGGACTCCGACGGCTCTTCTTCTCTC TATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGG GGAACGTCTTCTCATGCTCCGTGATGATAGGCTCTGCAC AACCACTACACGCAAGAGACCTCTCTCCCTGTCTCCGGGTAA A
	(SEQ ID NO: 196) EIVMTQSPATLSVSPGERATLS CRASQSDVNLAWYQQKPGQ APRLIYNAAATRAITGIPARFSGS	(SEQ ID NO: 197) QVQLVESGGGVQPRSLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAIWFDASDKYYADA VKGRFTISRDN SKNTLYLQ MNSLRAEDTAVYYCARDLAIIFGVVDPYWGQGTLVTVSSASTK	

AA

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		<p>GSGETFTLTISLSQSEDAFVYYC QQYQNWPLTFGGGKVEIKRT VAAPSVFIPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKSDSYS LSSTLTLSKADYEEKHKVYACE VTHQGLSSPVTKSFNRGEC</p>	<p>GPSVFPLAPSSKTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHSTCPCEPAPPELLGGPSVFLFPPKPKDNL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYSGTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHAEALHNHYTQKSLSLSPGK</p>
		<p>(SEQ ID NO: 198)</p> <p>GAAATAGTGATGACGCAGTCT CCAGCCACCTGTCTGTGTCT CCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAG TGTGATGTTAACTTAGCCTG GTACCAGCAGAAACCTGGCC AGGCTCCAGGCTCCTCATCT ACAACGACGCCACCAAGGCC ACTGGTATCCAGCCAGGGTC AGTGCAAGTGGGTCTGGGAC AGAGTTCAC'TCTCACCATCAG CAGCCTGCAGTCTGAAGATT TGCAGTTTATTACTGTGAGCA GTATCAGAACTGGCCTCTCAC TTTCGGCGGAGGGACCAAGGT GGAGATCAAAACGAACGGTGG CTGCACCATCTGTCTTCATCTT CCCGCCATCTGATGAGCAGTT GAAATCTGGAAC'TGGCTCTGT TGTGTGCTGCTGAATACTT CTATCCCAGAGAGGCCAAAG TACAGTGGAAGTGGATAAC GCCCTCCAA'TCGGGTAACTCC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCCTCAGCAGCACCTGA CGCTGAGCAAAAGCAGACTAC</p>	<p>(SEQ ID NO: 199)</p> <p>CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGGTCCAGCC TGGGAGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCAGTAAC'TATGGCATGCAC'TGGTCCGCCAGGTCCA GCGAGGGGCTGGAGTGGTGGCAGCTATATGTTTGTATGC AAGTGATAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCA'TCTCCAGAGACAAC'TCCAAGAACACGCTGTATCTGCAA ATGAACAGCCTGAGAGCCGACGACACGGCTGTGTATTACTG TGCAGAGATT'TGGCGATTTTGGAGTGGTCCCCGACTACT GGGGCCAGGAAACCTGGTCAACGCTGTCTAGTGCCTCCACC AAGGGCCATCGGTCTTCCCCCTGGCACCCCTCTCCAAGAG CACTCTGGGGGCACAGCGCCCTGGCTGGCTGGTCAAGG ACTACTCCCCGAACCGGTGACGGTGTCTGTGGAAC'TCAGGC GCCCTGACCAGCGGCTGCACACCTTCCCCGGCTGTCTACA GTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAACCGTGC CCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTG AATCACAAGCCCAAGCAACACCAAGGTGGACAAAGAAAGTTG AGCCCAAATCTTGTGACAAAC'TCACACATGCCACCCGTCG CCAGCACCTGAAC'TCTGGGGGACCGTCAAGTCTTCTCTTC CCCCCAAACCCAAAGGACACCTCATGATCTCCCGGACCCC TGAGGTCACTGCTGGTGGTGGACGTCGAGCCACGAAGACC CTGAGGTCAAGTCAACTGTAACGTGACGCGCTGGAGGTG CATAATGCCAAGACAAACCGCTGCGAGGAGCAGTACCGCA GCACGTACCGTGGTCAAGCTCTCACCCTCTGCAACAG GACTGGCTGAATGGCAAGGAGTACAAGTGAAGTCAAGGTGTC ACAAGGCCCTCCAGCCCCATCGAGAAACCACTCTCCAAA GCGCAAAGGGCAGCCCCGAGAACCAAGGTGTACACCTGCC CCCATCCCCGGGAGGAGATGACCAAGAACCAAGGTCAAGCTG</p>

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			<p>GAGAAACACAAAGTCTACGC CTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT</p> <p>(SEQ ID NO: 200)</p>	<p>ACCTGCCTGGTCAAGGCTTCTATCCAGCGACATCGCCGT GGAGTGGGAGAGCAATGGGCAAGCCGAGAAACAACACTACAAG ACCACGCTCCCTGCTGGACTCCGACGGCTCTTCTTCTCTC TATAGCAAGCTCACCGTGGACAAAGACAGGTGGCAGCAGG GGAACGTCTTCTCATGCTCCGTGATGATGAGGCTCTGCAC AACCACTACACGAGAAAGAGCCTCTCCCTGTCTCCGGGTAA A</p> <p>(SEQ ID NO: 201)</p>
		AA	<p>EIVMTQSPATLSVSPGERATLS CRASQSDVNLAIFYQQKPGQ APRLIYNAAATRAIGIPARVSG SGSGTEFTLTISLQSEDFAVYY COQYQNWPLTFGGGKVEIKR TVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVD NALQSGNSQESVTEQDSKDS YLSSTLTLSKADYEKHKVYA CEVTHQGLSPVTKSFNRGEC</p> <p>(SEQ ID NO: 202)</p>	<p>QVQLVESGGGVQPRSLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAAIWFDASDKYYADAVKGRFTISRDNKNTLYLQ MNSLRAEDTAVYYCARDLAIFGVVDPYWGQGTLVTVSSASTK GPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHCTCPPELGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTPPVLDSGFFLYSKLTVDKSRWQQGN VFSCSVMHREALHNYTQKSLSPGK</p> <p>(SEQ ID NO: 203)</p>
2G10.340	<p>[hu anti- <huGIPR> 2G10.340 VK3 (1-236) VL]:huKLC -CL + [hu anti- <huGIPR> 2G10.325 VH3 (1-472) VHJ]:huIgG1 zSEFL2-2 (mAb); LMR ID: SS- 26217</p>	NA	<p>GAAATAGTGATGACGCAGTCT CCAGCCACCTGTCTGTGTCT CCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAG TGTTTCATACGAACCTTAGCCTG GTACCAGCAGAAACCTGGCC AGGCTCCAGGCTCCTCATCT ACAACGCAGCCACCAGGGCC ACTGGTATCCAGCCAGGTTC AGTGCGAGTGGTCTGGGAC AGAGTTCACCTCACCATCAG CAGCCTGCAGTCTGAAGATT TGCAGTTTATTACTGTCAGCA GTATCAGAACTGGCTCTCAC TTTCGGCGGAGGACCAAGGT GGAGATCAAAACGAAACGGTGG</p> <p>(SEQ ID NO: 204)</p>	<p>CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCAGTAACTATGGCATGCATGGGTCCGCCAGGCTCCA GGCAGGGGCTGGAGTGGTGGCAGCTATATGGTTTGATGC AAGTGATAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAACCTCAAGAACACGCTGTATCTGCAA ATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTG TGGAGAGATATTGCGATTTTGGAGTGGTCCCGACTACT GGGGCCAGGAAACCTGGTACCGTGTCTAGTGCCTCCACC AAGGGCCCATCGTCTTCCCTCCCTGGCACCTCTCCCAAGAG CACCTCTGGGGCACAGCGGCTTGGGCTGCCTGGTCAAGG ACTACTTCCCGAACCGGTGACGGTGTGCGTGGAACTCAGGC GGCCTGACCCAGCGGTGCACACCTTCCCGGTGTCTTACA GTCTCAGGACTCTACTCCCTCAGCAGCGGTGGTGAACCGTGC CCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGCTG AATCAACAAGCCCAAGCAACCAAGGTGGACAAAGAAAGTTG</p> <p>(SEQ ID NO: 205)</p>

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2G10.334	hu anti- <huGIPR> 2G10.334 VK3 (1-236) VL ::huKLC	NA	CTGCACCATCTGTCTTCATCTT CCCGCCATCTGATGAGAGTT GAAATCTGGAACCTGCTCTGT TGTGTGCTGCTGAATACTT CTATCCAGAGAGGCCAAG TACAGTGAAGGTGGATAAC GCCCTCCAATCGGGTAACCTC CAGGAGAGTGCACAGAGCA GGACAGCAAGGACAGCACCT ACAGCTCAGCAGCACCTGA CGCTGAGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCAACCATCAGGG CCTGAGCTCGCCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT	AGCCAAATCTTGTGACAAAACTCACACATGCCACCGTGC CCAGCACCTGAACCTCTGGGGGACCGTCAGTCTTCTCTTC CCCCAAACCCAAAGACACCTCATGATCTCCCGGACCCC TGAGGTACATGCTGTGTGGACGTGAGCCACGAAGACC CTGAGGTCAAGTCAACTGTTACGTGACGCGGTGGAGGTG CATATGCCAAAGAAAAGCCGTGGAGGAGCAGTACGGCA GCACGTACCGTTCGCTCAGCGTCTCACCCGTCTGCACAG GACTGGCTGAATGGCAAGGAGTACAAGTCAAGGTGTCCA ACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAA GCCAAAGGCGACCCCGAGAACACAGGTGTACACCCCTGCC CCCATCCCGGGAGGAGATGACCAAGAACAGGTACAGCTG ACCTGCTGTGTCAAAGGCTTCTATCCAGCGACATCGCCGT GGAGTGGGAGAGCAATGGCGAGCCGGAGAACAACTACAAG ACCAAGCTCCCTGCTGCTGACTCCGACGGCTCTCTTCTCTC TATAGCAAGTCAACCTGGACAAAGCAGAGGTGGCAGCAGG GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC AACCACCTACCGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAA A
			(SEQ ID NO: 204)	(SEQ ID NO: 205)
			EIVMTQSPATLSVSPGERATLS CRASQSVHTNLAWYQQKPGQ APRLIYNAAATRAATGIPARFSGS GSGTEFTLTISLSQSEDFAVYYC QQYQNWPLTFGGGKVEIKRT VAAPSVFIPPPSDEQLKSGTASV VCLLNIFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSSTYS LSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC	QVQLVESGGGVVQGRSLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAIWFDASDKYYADA VKGRFTISRDN SKNTLYLQ MNSLRAEDTAVYYCARDIAIFGVVVDYWGQGLVTVSSASTK GPSVFLAPSSKTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVFPSSSLGTQTYICNVNHPKPSN TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPETCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSYRCVSVLTVLHQDWLNKKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHREALHNHYTQKSLSLSPGK
2G10.334	hu anti- <huGIPR> 2G10.334 VK3 (1-236) VL ::huKLC	NA	(SEQ ID NO: 206)	(SEQ ID NO: 207)
			GAAATAGTGATGACGCGAGTCT CCAGCCACCTGTCTGTGTCT CCAGGGGAAAGAGCCACCT CTCCTGCAGGGCCAGTCAGAG TGTTAACCTGAACCTTAGCCCTG	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCAGTAACCTATGGCATGCATGGGTCCGCCAGGCTCCA GGCGAGGGGCTGGAGTGGGTGGCAGCTATATGGTTTGATGC AAGTGATAAATACTATATGCAGACGCCGTGAAGGGGCCGATTCA

A-2164-WO-PCT

-CL + [Unknown anti- <huGIPR> 2G10.610 VH3 (1-472) VHJ::huIgG1 zSEFL2-2 (mAb); LMR ID: SS- 26211	GTACCAGCAGAAACCTGGCC AGGCTCCAGGCTCTCATCT ACCAGGCAGCCACCAGGGCC ACTGGTATCCAGCCAGGTT AGTGGCAGTGGTCTGGGAC AGAGTTCACTCTACCATCAG CAGCTGCAGTCTGAAGATT TGCAGTTTATTACTGTCAGCA GTATAACCAAGTGGCTCTCAC TTTCGGCGGAGGGAACCAAGT GGAGATCAACGAACGGTGG CTGCACCATCTGTCTTCATCTT CCCGCCATCTGATGAGCAGTT GAAATCTGGAACCTGCCTCTGT TGTGTCCGTCTGAATAACTT CTATGCCAGAGAGGCCAAAG TACAGTGGAAGGTGGATAAC GCCCTCCAATCGGGTAACCTC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCCTCAGCAGCACCTTGA CGCTGAGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT	CCATCTCCAGAGACAACCTCCAAGAACACGCTGTATCTGCAA ATGAACAGCTGAGAGCCGAGGACACGGCTGTGTATTACTG TGGAGAGATTTGGCGATTTTGGAGTGGTCCCCGACTACT GGGGCCAGGAACCTGGTCAACCGTGTCTAGTGCCTCCACC AAGGGCCCATCGGTCTTCCCCCTGGCACCTCTCTCCAAGAG CACTCTGGGGGCACAGCGGCCCTGGCTGCTTGGTCAAGG ACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGC GCCCTGACCAGCGGTGCACACCTTCCCCGGTGTCTCTACA GTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGC CCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTG AATCAAGGCCAGCAACACCAAGGTGGACAAGAAAGTTG AGCCCAATCTTGTGACAAAACTCACACATGCCACCGGTGC CCAGCACCTGAACCTCTGGGGGACCGTCACTTCTCTCTTC CCCCAAACCCAAAGGACACCTCATGATCTCCGGACCCC TGAGGTACATGCTGTGTGGTGGACGTGAGCCACGAAGACC CTGAGGTCAAGTTCAACTGTTAGTGGAGCGGCTGGAGGTG CATAATGCCAAGACAAGCCCTGCGAGGAGCAGTACGGCA GCACGTACCGTTGCGTCAAGCTCTCAACCGCTCTGCACCA GACTGGTGAATGGCAAGGATACAAAGTGAAGGTGTCCA ACAAAGCCCTCCAGCCCCATCGAGAAACCATCTCCAAA GCCAAAGGCGACCCGAGAACCAACAGGTGTACACCTGCC CCCATCCCGGAGGAGATGACCAAGAACAGGTCAAGCCTG ACCTGCTGGTCAAAGGCTTCTATCCAGCGACATCGCGCT GGAGTGGGAGACAATGGGCGACCCGAGAACCAACTACAAG ACCACGCTCCCGTCTGGACTCCGACGGCTCTCTTCTCTC TATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGG GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC AACCACTACACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAA A
	(SEQ ID NO: 208) EIVMTQSPATLSVSPGERATLS CRASQSVNLSAWYQQKPGQ APRLIYQAATRAITGIPARFSGS GSGTEFTLTISLQSEDFAVYYC QQYNQWPLTFGGGKVEIKRT VAAPSVEFPSPDEOLKSGTASV	(SEQ ID NO: 209) QVQLVESGGGVQPRSLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAIWFDASDKYYADA VKGRFTISRDN SKNTLYLQ MNSLRAEDTAVYYCARDLAIFGVVPDYWGQGTLVTVSSASTK GPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCTPCPAPEL LGGPSVFLFPPKPKDTI
AA		

[illegible]

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			GAGCTTCAACAGGGGAGAGT GT	(SEQ ID NO: 212) EIVMTQSPATLSVSPGERATLS CRASQSFQNLAWYQQKPGQ APRLIYQAAATRAATGIPARFSGS GSGTEFTLTISLQSEDFAVVYC QQYNQWPLTFGGGKVEIKRT VAAPSVFIPIPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSYSL LSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC	(SEQ ID NO: 213) QVQLVESGGVVQPGSRSLRSLCAASGFTFSNYGMHWVVRQAP GEGLEWVAIWFDASDKYYADA VKGRFTISRDN SKNTLYLQ MNSLRAEDTAVYYCARDIAIFGVVPDYWGQGLTVTVSSASTK GPSVFP LAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLPPKPKDITL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHREALHNYTQKSLSLSPGK	TATAGCAAGCTCACCGTGGACAAAGACAGGTGGCAGCAGG GGAACGTCTTCTCATGCTCGTGATGCATGAGGCTCTGCAC AACCACTACACGCAGAAAGAGCCCTCCTCCCTGTCTCCGGGTAA A
	AA			(SEQ ID NO: 214) GAAATAGTGATGACGCAGTCT CCAGCCACCCTGTCTGTGTCT CCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAG TGTTGATAGACACTTAGCCTG GTACCAGCAGAAACCTGGCC AGGCTCCAGGCTCCTCATCT ACGAAGCAGCCACCAGGGCC ACTGGTATCCAGCCAGGTTT AGTGGCAGTGGGTCTGGGAC AGAGTTCACTCTCACCATCAG CAGCCTGCAGTCTGAAGATT TGCAGTTTATTACTGTGAGCA GTATAACCAAGTGGCTCTCAC TTTCGGCGGAGGGACCAAGGT GGAGATCAAAACGAACGGTGG CTGCACCATCTGTCTCATCTT CCCGCCATCTGATGAGCAGT GAAATCTGGAACTGCCCTCTGT	(SEQ ID NO: 215) CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCCAGAACTATGGCATGCATGGGTCCGCCAGGCTCCA GGCAGGGGCTGGAGTGGGTGGCAGCTATATGGTTTGATGC GTACGGTAAATACTATGCAGACCCCTGGAAGGGCCGATTCA CCATCTCCAGAGACAACCTCCAGAACACGCTGTATCTGCAA ATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTG TGGAGAGATCAGACGATTTTGGAGTGGTCCCGACTACT GGGGCCAGGAACCTGGTACCGTGTCTAGTGCCTCCACC AAGGGCCATCGGTCTTCCCTGGCACCTCCCTCCAAAGAG CACTCTGGGGGCACAGCGCCCTGGGCTGCCGTGCTCAAGG ACTACTTCCCGAACCGGTGACGGTGTGCTGGAACCTCAGGC GCCCTGACCAGCGGTGCACACTTCCCGGTGTCTCTACA GTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAACCGTGC CCTCCAGAGCTTGGGACCCAGACCTACATCTGCAACGTG AATCAACAAGCCAGCAACCAAGGTGGACAAAGAAAGTTG AGCCCAAATCTGTGACAAACTCACATGCCCCACCGTGC CCAGCACCTGAACCTGGGGGACCGTCACTCTCCCTTC CCCCAAAACCCAAAGGACACCCCTCATGATCTCCCGGACCCC	
2G10.307	[hu anti- <huGIPR> 2G10.307 VK3 (1-236) VL]::huKLC -CL + [hu anti- <huGIPR> 2G10.307 VH3 (1-472) VH]::huIgG1 VH]::huIgG1 zSEFL2-2 (mAb); LMR ID: SS- 26184	NA				

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		<p>TGTGTGCTGCTGAATAACTT CTATCCAGAGAGGCCAAAG TACAGTGGAAAGGTGGATAAC GCCCTCAAATCGGTAACCTC CAGGAGAGTGTACAGAGCA GGACAGCAAAGGACAGCACCT ACAGCTCAGCAGCACCTTGA CGCTGAGCAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT</p>	<p>TGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACC CTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTG CATAATGCCAAGACAAAGCCGTGGAGGAGCAGTACGGCA GCACGTACCGTTCGTGCGTACGTCTCACCCTCTGCACAG GACTGGCTGAATGGCAAGAGTACAAGTGAAGGTGTCCA ACAAAGCTCTCCAGCCGCCATCGAGAAACCACTCTCCAAA GCCAAAGGCCAGCCCGAGAACCAACAGGTGTACACCTGCC CCCATCCGGGAGGATGACCAAGAACCAAGGTACAGCTG ACCTGCTGGTCAAGGCTTCTATCCAGCGACATCGCGT GGAGTGGAGAGCAATGGGAGCCGAGAAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCTTCTTCTC TATAGCAAGCTCACCGTGGACAAAGCAGGTGGCAGCAGG GGAACGTCTTCTCATGCTCCGTGATGATGAGGCTCTGCAC AACCACTACACGACAGAGAGCTCTCCCTGCTCCTCCGGTAA A</p>
	AA	<p>(SEQ ID NO: 216) EIVMTQSPATLSVSPGERATLS CRASQSDRHLAWYQQKPGQ APRLIYEAAATRAATGIPARFSGS GSGTEFTLTSSLSQSEDAFVYYC QQYNQWPLTFGGGKVEIKRT VAAPSVFIPPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSSTYS LSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC</p>	<p>(SEQ ID NO: 217) QVQLVESGGGVVQPGRSLRLSCAASGFTFQNYGMHWVRQAP GEGLEWVAIAIWFDAYGKYADAVKGRFTISRDNKNTLYLQ MNSLRAEDTAVYYCARDQTFIVGVPDYWQQGTLVTVSSASTK GPSVFLAPSSKTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHPN TKVDKKVEPKSCDKTHCTCPPELPGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHREALHNNHYTQKSLSPGK</p>
2G10.607	[hu anti- <huGIPR> 2G10.607 VK3 (1-236) VL]:huKLC -CL + [hu anti- <huGIPR>	<p>(SEQ ID NO: 218) GAAATAGTGATGACGCAGTCT CCAGCCACCTGTCTGTGTCT CCAGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAAGAG TGTTGATAGACACTTAGCCTG GTACCAGCAGAAACCTGGCC AGGCTCCAGGCTCCTCATCT ACGAAAGCAGCCACCAAGGCC</p>	<p>(SEQ ID NO: 219) CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCCAGAACTATGGCATGCACTGGTCCGCCAGGCTCCA GGCAGGGGCTGGAGTGGTGGCAGCTATATGGTTTGTATGC GTACGGTAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAACCTCAAGACACAGCTGTATCTGCAA ATGAACAGCTGAGAGCCGAGGACACGGCTGTGTATTACTG TGCAGAGATCAGACGATTTTGGAGTGGTCCCCGACTACT</p>

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2G10.307 VH3 (1-472) VHJ::hulgG1 zSEFL2-2 (mAb); LMR ID: SS- 26232	<p>ACTGGTATCCAGCCAGGGTC AGTGGCAGTGGGTCTGGGAC AGAGTTCACTCTACCATCAG CAGCCTGCAGTCTGAAGATT TGCAGTTTATTACTGTCAGCA GTATAACCAAGTGGCTCTCAC TTTCGGCGGAGGACCAAGGT GGAGATCAACGAAACGGTGG CTGCACCATCTGTCTTCATCTT CCCGCCATCTGATGAGCAGTT GAAATCTGGAACCTGCTCTGT TGTGTGCTGCTGAATACTT CTATCCAGAGAGGCCAAAG TACAGTGAAGGTGGATAAC GCCCTCCAATCGGGTAAGTCC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCCTCAGCAGCACCCCTGA CGCTGAGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCAACCATCAGGG CCTGAGCTCGCCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT</p>	<p>GGGGCCAGGAAACCCCTGGTCAACCGTGTCTAGTGCCTCCACC AAGGCCCATCGGTCTTCCCTTGGCACCCCTCCTCCTCAAGAG CACCTCTGGGGGCACAGCGGCCCTGGCTGCCCTGGTCAAGG ACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGC GCCCTGACCAGCGGTGACACCTTCCCGCTGTCTCTACA GTCTCAGAGCTCTACTCCCTCAGCAGCGTGGTGAACCGTGC CCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTG AATCAACAAGCCAGCAACCAAGGTGGACAAAGAAAGTTG AGCCCAATCTGTGACAAACTCACACATGCCACCCACCGTGC CCAGCACCTGAACCTCTGGGGGACCGTCAAGTCTTCTCTTC CCCCAAACCCAAAGACACCTCATGATCTCCCGGACCCC TGAGGTACATGCTGGTGGTGGACGTGAGCCACGAAGACC CTGAGGTCAAGTTCAACTGTAAGTGGACGCGGTGGAGGTG CATATGCCAAGACAAACCGCTGCGAGGAGCAGTACGGCA GCACGTACCGTTGGTCAAGCTCTCAGCTCTGCTGCAACAG GACTGGCTGAATGGCAAGGATGACAAAGTCAAGTCAAGGTGTCCA ACAAAGCCCTCCAGCCCCATCGAGAAACCACTCTCCAAA GCCAAAGGGCAGCCCCGAGAACACAGGTGTACACCCCTGCC CCCATCCCGGGAGGAGATGACCAAGAACAGGTCAAGCTG ACCTGCTGGTCAAGGCTTCTATCCAGCGACATCGCCGT GGAGTGGGAGACAATGGGACGCCGAGAACAACTACAAG ACCAAGCCTCCGCTGTGACTCCGACGGCTCTCTTCTCTC TATAGCAAGTCAACCGTGGACAAAGCAGGTGGCAGCAGG GGAACGTCTTCTCATGCTCCGTGATGATGAGGTCTGAC AACCCTACACGCAAGAGACCTCTCCCTGTCTCCGGGTAA A</p>
AA	<p>(SEQ ID NO: 220) EIVMTQSPATLSVSPGERATLS CRASQSVDRHLAWYQQKPGQ APRLIYEAAATRAATGIPARVSGS GSGTEFTLTISLSQSEDFAVVYC QQYNQWPLTFGGGTGKVEIKRT VAAPSVFIAPPDEQLKSGTASV VCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSYS LSSTLTLSKADYEKHKVYACE</p>	<p>(SEQ ID NO: 221) QVQLVESGGGVVQGRSLRLSCAASGFTFQNYGMHWVRQAP GEGLEWVAIWFDAYGKYADAVKGRFTISRDNKNTLYLQ MNSLRAEDTAVYYCARDQTFGVVDPYWGQGLVTVSSASTK GPSVFPLAPSSKTSGGTAALGLVKDYFPEPTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPCPAPELLGGPSVFLPPKPKDITL MISRTPETCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSYRCVSLTVLHODWLNKEYCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKFGFYPDSIAV</p>

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			VTHQGLSSPVTKSFNRGEC	EWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHREALHNHYTQKSLSLSPGK
			(SEQ ID NO: 222)	(SEQ ID NO: 223)
			GAAATAGTGATGACGCAGTCT CCAGCCACCCTGTCTGTGTCT CCAGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAG TGTTAACCGGCACCTTAGCCTG GTACCAGCAGAAACCTGGCC AGGCTCCAGGCTCCTCATCT ACGAAGCAGCCACCAGGGCC ACTGGTATCCAGCCAGGTTC AGTGGCAGTGGTCTGGGAC AGAGTTCAC'TCACCATCAG CAGCCTGCAGTCTGAAGATT TGCAGTTTATTACTGTCAGCA GTATAACCAAGTGGCTCTCAC TTTCGGCGGAGGACCAAGGT GGAGATCAAAACGAACGGTGG CTGCACCATCTGTCTTCATCTT CCCGCCATCTGATGAGCAGTT GAAATCTGGAACCTGCCCTGT TGTGTGCTGTGTAATAACTT CTATCCAGAGAGGCCAAAG TACAGTGGAAGGTGGATAAC GCCCTCCAATCGGGTAACTCC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCCTCAGCAGCACCCCTGA CGCTGAGCAAAAGCAGACTAC GAGAAACACAAAAGTCTACGC CTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGTCAGCATCTGGATTCA CCTTCCAGAACTATGGCATGCACTGGTCCGCCAGGCTCCA GGGAGGGGTGAGTGGTGGCAGCTATATGGTTTGTATGC GTACGGTAAATATATGACAGACCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAATCCAGAACACGCTGTATCTGCAA ATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTG TGGAGAGATAAGACGATTTTGGAGTGGTCCCGACTACT GGGGCCAGGGAACCTGGTCACTGTGTCTAGTGCCTCCACC AAGGGCCCATCGGTCTTCCCCCTGGCACCTTCTCCAGAG CACCTCTGGGGGCACAGCGGCCCTGGGCTGCCGTGTCGAAGG ACTACTTCCCCGAACCGGTGACGGTGTGTCGTGGAACCTCAGGC GCCCTGACCAAGCGGTGTCACACCTTCCCGGTGTCTTACA GTCTCAGGACTCTACTCCCTCAGCAGCGTGTGAGCCGTGC CCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTG AATCAAGCCCAAGCAACCAAGGTGGACAAAGAAAGTTG AGCCCAATCTTGTGACAAAACCTACACATGGCCACCCTGC CCAGACCTGAACCTCTGGGGGACCGTCACTTCTCTTTC CCCCAAAACCCAAAGGACACCTCATGATCTCCCGGACCCC TGAGTCACTGCTGGTGGTGGACGTGAGCCACGAAGACC CTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTG CATAATGCCAAGACAAGCCGTGCGAGGAGCAGTACGGCA GCACGTACCGTTCGTCAGCTCCTCACCCTGTCACCAAG GACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTGTCCA ACAAAGCCCTCCAGCCCCCTCAGAAACCAATCTCCAAA GCCAAAGGGCAGCCCCGAGAACCAAGGTGACACCTGCC CCCATCCCGGGAGGAGATGACCAAGAACAGGTCAAGCTG ACCTGCTGTGTCAGGCTTCTATCCAGCGACATCGCGGT GGAGTGGGAGAGCAATGGGCAAGCGGAGACAACACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCTTCTTCTC TATAGCAAGCTCACCCTGGACAAAGCAGGTGGCAGCAG GGAACGTCTTCTCATGTCTCCGTGATGATGAGGCTCTGCAC AACCACTACAGCAGAAAGAGCCCTCTCCCTGTCTCCGGGTAA
2G10.321	[hu anti- <huGIPR> 2G10.321 VK3 (1-236) VL]:huKLC -CL + [hu anti- <huGIPR> 2G10.321 VH3 (1-472) VH]:huIgG1 zSEFL2-2 (mAb); LMR ID: SS- 26198	NA		

		(SEQ ID NO: 224)	(SEQ ID NO: 225)	A
[hu anti- <huGIPR> 2G10.342 VK3 (1-236) VLJ]:huKLC -CL + [hu anti- <huGIPR> 2G10.321 VH3 (1-472) VHJ]:huIgG1 zSEFL2-2 (mAb); LMR ID: SS- 26219	AA	EIVMTQSPATLSVSPGERATLS CRASQSVNRHLAWYQQKPGQ APRLIYEAAATRAATGIPARFSGS GSGTEFLTJISLSQSEDAVYYC QQSNQWPLTFGGGKTKVEIKRT VAAPSVFIIPSPDEQLKSGTASV VCLLNIFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSYIS LSSTLTLKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC	QVQLVESGGGVVQPGRSRLRSCAASGFTFQNYGMHWVRQAP GEGLEWVAIWFDAYGKYADAVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCARDKTIFGVVPDYWGQGLTVTVSSASTK GPSVFPLAPSSKSTSGGTAALGLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSDKTHSTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVGVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMEALHNHYTQKSLSLSPGK	(SEQ ID NO: 227)
		[hu anti- <huGIPR> 2G10.342 VK3 (1-236) VLJ]:huKLC -CL + [hu anti- <huGIPR> 2G10.321 VH3 (1-472) VHJ]:huIgG1 zSEFL2-2 (mAb); LMR ID: SS- 26219	GAAATAGTATGATGACGCAGTCT CCAGCCACCCTGTCTGTCT CCAGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAG TGTTGAAAGACACTTAGCCTG GTACCAGCAGAAACCTGGCC AGGCTCCAGGCTCCTCATCT ACGAAGCAGCCACCAAGGCC ACTGGTATCCAGCCAGGTTC AGTGCGATGGGTCTGGGAC AGAGTTCACCTCACCATCAG CAGCTGCAGTCTGAAGATT TGCAGTTTACTGTCTCAGCA GTATACGAGTGGCCTCTCAC TTTCGGCGGAGGGACCAAGT GGAGATCAACGAACGGTGG CTGCACCATCTGTCTTCATCT CCCGCATCTGATGAGCAGTT GAAATCTGGAACCTGCCTGT TGTGTGCTGTGAATCACTT CTATCCCAAGAGAGGCCAAAG TACAGTGGAAAGGTGGATAAC	(SEQ ID NO: 226)

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2G10.319	[hu anti- <huGIPR> 2G10.316 VK3 (1-236) VL]:huKLC -CL + [hu anti- <huGIPR> 2G10.319 VH3 (1-472) VH]:huIgG1		<p>GCCCTCCAAATCGGGTAACTCC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCTCAGCAGCACCCCTGA CGTGAGCAAAAGCAGACTAC GAGAAACACAAAAGTCTACGC CTGCGAAGTCAACCCATCAGGG CCTGAGCTCGCCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT</p> <p>(SEQ ID NO: 228)</p>	<p>GCACGTACCGTTGCGTCAGCGTCTCCTCACCCTGCTGCAACAG GACTGGCTGAATGGCAAGGAGTACAAAGTCAAGGTGTCCCA ACAAAGCCCTCCAGCCCCATCGAGAAACCATCTCCAAA GCCAAAGGCGAGCCCCGAGAACACAGGTGTACACCTGCC CCCATCCCGGAGGAGATGACCAAGAACAGGTCAGCCTG ACTGCTGCTGTCAAAGGCTTCTATCCACGCGACATCGCCGT GGAGTGGGAGAGCAATGGGCGACCCGAGAACAACTACAAG ACCACGCTCCCGTCTGGACTCCGACGGCTCTTCTTCTCCTC TATAGCAAGCTACCGTGGACAAAGCAGGTGGCAGCAGG GGAACGTCTTCTCATGCTCCGTGATGATGAGGCTCTGCAC AACCACTACACGCAGAAAGCCCTCTCCCTGTCTCCGGGTAA A</p> <p>(SEQ ID NO: 229)</p>
		AA	<p>EIVMTQSPATLSVSPGERATLS CRASQSVVERHLAWYQKPGQ APRLIYEAAATRAIGIPARFSGS GSGTEFTLTISLQSEDFAVYYC QQYQQWPLTFGGGKVEIKRT VAAPSFIFFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDYSTYS LSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC</p> <p>(SEQ ID NO: 230)</p>	<p>QVQLVESGGGVQPGRLSLRSCAASGFTFQNYGMHWVRQAP GEGLEWVAAIWFDAYGKYADAVKGRFTISRDNKNTLYLQ MNSLRAEDTAVYYCARDKTIQVVDYWGQGTLVTVSSASTK GPSVFP LAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPCPAPELLGGPSVFLPPKPKDITL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTI SKAKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHREALHNYTQKSLSLSPGK</p> <p>(SEQ ID NO: 231)</p>
2G10.319	[hu anti- <huGIPR> 2G10.316 VK3 (1-236) VL]:huKLC -CL + [hu anti- <huGIPR> 2G10.319 VH3 (1-472) VH]:huIgG1	NA	<p>GAAATAGTGATGACGCAGTCT CCAGCCACCTGTCTGTGTCT CCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAG TGTTTTCAGACACTTAGCCTG GTACCAGCAGAAACCTGGCC AGGCTCCACAGGCTCCTCATCT ACGAAGCAGCCACCAAGGCC ACTGGTATCCACGCCAGGTTC AGTGCAAGTGGGTCTGGGAC AGAGTTCACTCTCACCATCAG</p> <p>(SEQ ID NO: 230)</p>	<p>CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCCTGTGCAGCATCTGGATTCA CCTTCAGTAACTATGGCATGCATGGGTCCGCCAGGCTCCA GGCGAGGGGTGGAGTGGGTGGCAGCTATATGGTTTGATGC GTACGGTAAATCTATGCAGACGCCCTGGAAGGGCCGATTCA CCATCTCCAGAGACAACCTCAAGAACACGCTGTATCTGCAA ATGAACAGCTGAGAGCCGAGACACGGCTGTGTATTACTG TGGGAGAGATAAGACGATTTTGGAGTGGTCCCGACTACT GGGGCCAGGAACCTGGTACCGCTGTCTAGTGCCTCCACC AAGGGCCCATCGGTCTTCCCTTGGCACCCCTCCTCCAAAGAG CACCTCTGGGGGCACAGCGGCCCTGGGCTGCCCTGGTCAAGG</p> <p>(SEQ ID NO: 231)</p>

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zSEFL2-2 (mAb); LMR ID: SS- 26196	CAGCCTGCAGTCTGAAGATT TGCAGTTTATTACTGTACGA GTATCAGAACTGGCCTCTAC TTTCGGCGGAGGACCAAGGT GGAGATCAAAACGAACGGTGG CTGACCATCTGTCTTCATCTT CCCGCCATCTGATGAGCAGTT GAAATCTGAACTGCCCTCTGT TGTGTGCTGCTGAATAACTT CTATCCAGAGAGGCCAAAG TACAGTGGAAAGGTGGATAAC GCCCTCCAATCGGGTAACTCC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCCTCAGCAGCACCTGA CGCTGAGCAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCACCCATCAGGG CCTGAGCTGCCCCGTACAAA GAGCTTCAACAGGGGAGAGT GT	ACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGC GCCCTGACGACGGGTGACACACCTTCCCGGTGTCTCTACA GTCTCAGGACTCTACTCCTCAGCAGCGTGGTGACCGTGC CCTCCAGCAGCTTGGCACCCAGACCTACATCTGCAACGTG AATCAACAGCCAGCAACACCAAGGTGGACAAAGAAAGTTG AGCCAAATCTTGTGACAAAACCTACACATGCCACCGTGC CCAGCACCTGAACTCTGGGGGACCGTACGTCTTCTCTCTC CCCCAAAACCCAGACACCTCATGATCTCCCGGACCCC TGAGGTACATGCTGTGTGGTGGACGTGAGCCACGAAGACC CTGAGGTCAAGTTCAACTGTTACGTGACGGCTGGAGGTG CATAATGCCAAGACAAGCCGTGCGAGGAGCAGTACGGCA GCACGTACCGTTGCTCAGCTCCTCACCCTCTCTGCACCA GACTGGCTGAATGCCAAGGAGTACAAGTGCAAGGTGTCCA ACAAAGCCTCCCAGCCCCATCGAGAAAACCATCTCCAAA GCCAAAGGGCAGCCCCGAGAACACAGGTGTACACCTGCC CCCATCCCGGAGGAGTACCAAGAACACGAGTACAGCTG ACCTGCCTGGTCAAAGGCTTCTATCCAGCGACATCGCGT GGAGTGGGAGAGCAATGGGACGCCGAGAACAACTACAAG ACCACGCTCCCGTGTGAGTCCGACGGCTCCTCTTCTCTC TATAGCAAGCTCACCCTGGACAAAGACAGGTGGCAGCAGG GGAACGCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC AACCACTACACGCAAGAGACCTCTCCCTGTCTCCGGGTAA A
	(SEQ ID NO: 232) EIVMTQSPATLSVSPGERATLS CRASQSVFRHLAWYQQKPGQA PRLIYEAAATRAATGIPARFSGS SGTEFTLTISLQSEDFAVYYCQ QYQNWPLTFGGGTKEIKRTV AAPSVFIFPPSDEQLKSGTASV CLLNFFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSYSL STLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC	(SEQ ID NO: 233) QVQLVESGGGVVQPGRLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAAIWFDAYGKYYADAVKGRFTISRDNKNTLYLQ MNSLRAEDTAVYCARDKTIQVVPDYWGQGLVTVSSASTK GPSVFPPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHPKPSN TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKTPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQKSLSLSPGK

AA	(SEQ ID NO: 234)	(SEQ ID NO: 235)
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2G10.332	[hu anti- <huGIPR> 2G10.318 VK3 (1-236) VLJ]:huKLC -CL + [hu anti- <huGIPR> 2G10.332 VH3 (1-472) VHJ]:huIgG1 zSEFL2-2 (mAb); LMR ID: SS- 26209	NA	GAAATAGTGATGACGCAGTCT CCAGCCACCCTGTCTGTGTCT CCAGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAG TGTTCTGAGTCACCTTAGCCTG GTACCAGCAGAAACCTGGCC AGGCTCCAGGCTCCTCATCT ACGAAGCAGCCACCAGGGCC ACTGGTATCCAGCCAGGTTTC AGTGGCAGTGGGTCTGGGAC AGAGTTCACTCTCAACCATCAG CAGCCTGCAGTCTGAAGATT TGCAGTTTATTACTGTCAGCA GTATAACAACCTGGCCTCTCAC TTTCGGCGGAGGACCAAGGT GGAGATCAAAACGAACGGTGG CTGCACCATCTGTCTTCATCTT CCCGCCATCTGATGAGCAGTT GAAATCTGGAACCTGCCTCTGT TGTGTGCTGTCTGAATAACTT CTATCCCAGAGAGGCCAAAG TACAGTGGAAAGGTGGATAAC GCCCTCCAATCGGGTAACCTC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCTCAGCAGCACCCCTGA CGCTGAGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCAACAA GAGCTTCAACAGGGGAGAGT GT	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCCAGAACTATGGCATGCATGGTCCGCCAGGCTCCA GGCGAGGGCTGGAGTGGTGGCAGCTATATGTTTGTATGC GTACGACAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAACCTCAAGAACAACGCTGTATCTGCAA ATGAACAGCTGAGAGCCGAGGACACAGGCTGTGTATTACTG TGCAGAGATAAGTCGATTTTGGAGTGGTCCCCGACTACT GGGGCCAGGAAACCTGGTCAACGCTGTCTAGTGCCTCCACC AAGGGCCCATCGGTCTTCCCTTGGCACCCCTCCTCCAAGAG CACCTCTGGGGCACAGCGGCCCTGGGCTGCCCTGGTCAAGG ACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGC GCCCTGACCAGCGGCTGCACACCTTCCCGGCTGTCTCTACA GTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAACCGTGC CCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTTG AATCAACAAGCCAGCAACACCAAGGTGGACAAAGAAAGTTG AGCCCAAATCTTGTGACAAAACTCACACATGCCACCCTGC CCAGCACCTGAACTCTTGGGGGACCGTCACTTCTCTCTTTC CCCCAAACCCAAAGGACACCTCATGATCTCCCGGACCCC TGAGGTACATGCTGGTGGTGGACGTGAGCCACGAAGACCC CTGAGGTCAAGTTCAACTGGTACGTGGACGGCTGGAGGGTG CATAATGCCAAAGACAAGCCGTGCGAGGAGCAGTACGGCA GCACGTACCGTTGCTCAGCTCTCACCCTCCTGCAACCCAG GACTGGCTGAATGGCAAGGAGTACAAAGTGAAGGTGTCCA ACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAA GCCAAAGGGCAGCCCCGAGAACCCACAGGTGTACACCTGGCC CCCATCCCGGGAGGAGATGACCAAGAACCCAGGTCAAGCTG ACCTGCCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGT GGAGTGGGAGAGCAATGGGACGCCGAGAACCAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCTTCTTCTCCTC TATAGCAAGCTCACCTGGGACAAAGCAGAGTGGGACGACAGG GGAAAGCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC AACCCTACACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAA A
		AA	(SEQ ID NO: 236) EIVMTQSPATLVSVPGERATLS (SEQ ID NO: 237) QVQLVESGGGVVQPRSLRLSCAASGFTFQNYGMHWVVRQAP	

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		CRASQSVLSHLAWYQOKPGOA PRLIYEAAATRATGIPARFSGS SGTEFTLTSSLSQSEDFAVYYCQ QYNNWPLTFGGGKVEIKRTV AAPSFIFFPSDEQLKSGTASVV CLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSITYSL STLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC	GEGLWVAIWFDAIDKYADAVKGRFTISRDNKNTLYLQ MNSLRAEDTAVYCARDKSIQVVPDYWQGTLVTVSSASTK GPSVFLPAPSSKSTGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHNKPSN TKVDKKVEPKSCDKTHSTCPPELGGPSVFLFPPKPKDTL MISRTPEVTVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHREALHNYTQKSLSPGK
		(SEQ ID NO: 238)	(SEQ ID NO: 239)
		GAAATAGTGATGACGCAGTCT CCAGCCACCTGTCTGTGTCT CCAGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAG TGTTAACAGACACTTAGCCTG GTACCAGACAGAACCTGGCC AGGCTCCAGGCTCCTCATCT ACGAAAGCAGCCACCAGGGCC ACTGGTATCCAGCCAGGTTT AGTGGCAGTGGTCTGGGAC AGAGTTCACCTCACCATCAG CAGCCTGCAGTCTGAAGATT TGCAGTTTATTACTGTACGA GTATAACAACCTGGCTCTCAC TTTCGGCGGAGGACCAAGGT GGAGATCAAAACGAACGGTGG CTGCACCATCTGTCTTCATCTT CCCGCCATCTGATGAGCAGTT GAAATCTGGAACTGCCTCTGT TGTGTGCTGTGTAATAACTT CTATCCAGAGAGGCAAAAG TACAGTGGAAAGGTGGATAAC GCCCTCCAAATCGGGTAACCTC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCCAGAACTATGGCATGCACTGGTCCGCCAGGCTCCA GGCAGGGGCTGGAGTGGTGGCAGCTATATGGTTTGATGC GTACGACAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAATCCAGAACACCGTGTATCTGCAA ATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTG TGCAGAGATAAGTCGATTTTGGAGTGTCTCCCGACTACT GGGGCCAGGGAACCTGGTCAACCGTGTCTAGTGCCTCCACC AAGGGCCCATCGTCTTCCCGCTGGCACCTCTCTCCAGAG CACCTCTGGGGGCACAGCGGCTTGGGCTGCCTGGTCAAGG ACTACTTCCCGCAACCGGTGACGGTGTCTGTGGAACCTCAGGC GCCCTGACCAAGCGGCTGCACACCTTCCCGGCTGTCTTACA GTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGGACCGTGC CCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTG AATCAACAGCCCAACCAACCAAGGTGGACAAAGAAAGTTG AGCCCAATCTGTGACAAACTCACAATGCCCACCGTGC CCAGCACCTGAACCTCTGGGGGACCGTCACTCTCTCTTC CCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCC TGAGGTACATCGTGGTGGACGTGAGCCACGAAGACC CTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTG CATAATGCCAAGACAAGCCGTGCGAGGAGCAGTACGGCA GCACGTACCGTTCGTCAGCTCCTCACCCTCTGACCAAG GACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTGTCCA ACAAAGCCCTCCCAAGCCCCCATCGAGAAACCACTCTCCAAA
2G10.345	[hu anti- <huGIPR> 2G10.345 VK3 (1-236) VL]:huKLC -CL + [hu anti- <huGIPR> 2G10.332 VH3 (1-472) VH]:huIgG1 zSEFL2-2 (mAb); LMR ID: SS- 26222	NA	

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2G10.335	[hu anti- <huGIPR> 2G10.335 VK3 (1-236) VL]::huKLC -CL + [hu anti- <huGIPR> 2G10.335 VH3 (1-472) VH]::huIgG1 zSEFL2-2 (mAb); LMR ID: SS-		ACAGCCTCAGCAGCACCCCTGA CGCTGAGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT	GCCAAAGGGCAGCCCCGAGAACCAACACAGGTGTACACCCCTGCC CCCATCCCGGGAGAGATGACCAAGAACCAAGGTACAGCCTG ACCTGCCCTGGTCAAAAGGCTTCTATCCACGACATCGCCGT GGAGTGGGAGAGCAATGGGACGCCGAGAACAACTACAAG ACACGCTCCCGTCTGGACTCCGACGGCTCTCTTCTCCTC TATAGCAAGCTACCCGTGGACAAAGCAGGTGGCAGCAGG GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC AACCCTACACGACAGAGCCCTCTCCCTGTCTCCGGGTAA A
		AA	(SEQ ID NO: 240) EIVMTQSPATLSVSPGERATLS CRASQSVNRHLAWYQQKPGQ APRLIYEAAATRAATGIPARFSGS GSGTEFTLTISLSQSEDFAVVYC QQYNNWPLTFGGGKVEIKRT VAAPSVFIPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSYS LSSTLTLSKADYEEKHKVYACE VTHQGLSSPVTKSFNRGEC	(SEQ ID NO: 241) QVQLVESGGGVVQGRSLRLSCAASGFTFQNYGMHWVRQAP GEGLEWVAIWFDAYDKYYADAVKGRFTISRDNKNTLYLQ MNSLRAEDTAVYYCARDKSFIFGVDPDYWGQGLVTVSSASTK GPSVFPLAPSSKTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPCPAPELLGGPSVFLPPKPKDNL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTI SKAKGQPREPVVTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGOPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHREALHNHYTQKSLSLSPGK
		NA	(SEQ ID NO: 242) GAAATAGTGATGACGCAGTCT CCAGCCACCCTGTCTGTGTCT CCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAG TGTTACCAGCCACTTAGCCTG GTACCAGCAGAAACCTGGCC AGGTCCCAAGGCTCCTCATCT ACGAAGCAGCCACCAGGGCC ACTGGTATCCAGCCAGGTTC AGTGGCAGTGGGTCTGGGAC AGAGTTCACCTCACCATCAG CAGCCTGCAGTCTGAAGATT TGCAGTTTATTACTGTCAGCA GTATAACCAAGTGGGCTCTCAC	(SEQ ID NO: 243) CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCTGTGCAGCATCTGGATTCA CCTTCCAGAACTATGGCATGCATGGTGGCCAGGCTCCA GGCGAGGGCTGGAGTGGTGGCAGCTATATGGTTTGATGC GTACGACAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAACCTCAAGAACACGCTGTATCTGCAA ATGAACAGCCTGAGAGCCAGGACACGGCTGTGTATTACTG TGCAGAGATCTCGCGATTTTGGAGTGGTCCCCGACTACT GGGGCCAGGAACCTGGTCAACCGTGTCTAGTGCCTCCACC AAGGGCCCACTGGTCTTCCCCCTGGCACCTCTCTCAAGAG CACTCTGGGGGCACAGGGCCCTGGGCTGGCTGGTCAAGG ACTACTCCCCGAACCGGTGACGGTGTGCTGGAACCTCAGGC GCCCTGACAGCGGCGTGCACACCTTCCCGGCTGTCTCTACA GTCTCTCAGGACTCTACTCCCTCAGCAGCGGTGGTGGACCGTGC

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26212		TTTCGGCGGAGGGAACAAAGGT GGAGATCAAAACGAACGGTGG CTGCACCATCTGTCTTCATCTT CCCGCCATCTGATGAGCAGTT GAAATCTGGAACCTGCCCTCTGT TGTGTGCTGCTGAATAACTT CTATCCCAGAGAGGCCAAAG TACAGTGGAAGGTGGATAAC GCCCTCAAATCGGTAACCTC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCTCAGCAGCACCCCTGA CGCTGAGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT	CCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTG AATCAAGCCCAAGCAACCAAGGTGGACAAAGAAAGTTG AGCCCAATCTTGTGACAAACTCACACATGCCACCCGTGC CCAGCACCTGAACCTCTGGGGGACCGTCAGTCTTCTCTTC CCCCAAACCAAGGACACCTCATGATCTCCCGAACCC TGAGTACATCGTGTGTGGACGTGAGCCACGAAGACC CTGAGGTCAAGTTCAACTGATACGTGGACGGCTGGAGGTG CATAATGCCAAGACAAGCCGTGCGAGGAGCAGTACGGCA GCACGTACCGTGTGCTAGCTCACCCTACCGTCTGCACCAG GACTGGTGAATGGCAAGGAGTACAAAGTCAAGGTGTCCA ACAAAGCCCTCCAGCCCCATCGAGAAACCATCTCCAAA GCCAAAGGCGACCCCGAGAACCAACAGGTGTACACCTGCC CCCATCCGGGAGGAGATGACCAAGAACAGGTACAGCTG ACCTGCTGGTCAAGGGCTTCTATCCAGCGACATCGCCGT GGAGTGGGAGAGCAATGGGACCGCGGAGAACAACTACAA ACCACGCTCCCGTCTGGACTCCGACGGCTCCTTCTTCCTC TATAGCAAGCTCACCTGCGGACAAAGAGCAGGTGGCAGCAG GGAACGTCTTCTCATGCTCCGTGATGATGAGGCTCTGCAC AACCACTACAGCAGAGAAGCCTCTCCTGTCTCCGGGTAA A	(SEQ ID NO: 244) EIVMTQSPATLSVSPGERATLS CRASQSVTSHLAWYQOKPGQA PRLIYEAAATRAATGIPARFSGS SGTEFTLTISLQSEDFAVYYCQ QYNQWPLTFGGGKVEIKRTV AAPSVFIFPPSDEQLKSGTASV CLLNNFYPREAKVQWVKVDNAL QSGNSQESVTEQDSKDSYSL STLTLSKADYEKHKVYACEVT HQLSSPVTKSFNRGEC	(SEQ ID NO: 245) QVQLVESGGGVQPGRSLRLSCAASGFTFQNYGMHWVRQAP GEGLEWVAAIWFDAYDKYYADAVKGRFTISRDNKNTLYLQ MNSLRAEDTAVYYCARDLAIFGVVPDYWGQGTLVTVSSASTK GPSVFP LAPSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPCPAPELLGGPSVFLPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTTPVLDSGDFLYSKLTVDKSRWQQGN VFSCSVMHAEALHNHYTQKSLSLSPGK
26213	hu anti- <huGIPR> 2G10.330	NA	(SEQ ID NO: 246) GAAATAGTGATGACGCAGTCT CCAGCCACCTGTCTGTGTCT CCAGGGGAAAGAGCCACCCT	(SEQ ID NO: 247) CAGGTGCAGTGTGGAGTCTGGGGGAGGCGTGGTCCAGCC TGGGAGGTCCCTGAGACTCTCCTGTGACAGCATCTGGATTCA CCTTCCAGAACTATGGCATGCACTGGGTCCGCCAGGCTCCA	

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VK3 (1-236) VLJ::huKLC -CL + [hu anti- <huGIPR> 2G10.330 VH3 (1-472) VHJ::huIgG1 zSEFL2-2 (mAb); LMR ID: SS- 26207	CTCCTGCAGGGCCAGTCAGAG TGTTGATCAGCACTTAGCCTG GTACCAGCAGAAACCTGGCC AGGCTCCAGGCTCCTCATCT ACCAGGCAGCCACCAGGGCC ACTGGTATCCAGCCAGGTTTC AGTGGCAGTGGGTCTGGGAC AGAGTTCACTCTCACCATCAG CAGCCTGCAGTCTGAAGATT TGCAGTTTATTACTGTACGCA GTATCAGAACTGGCTCTCAC TTTCGGCGGAGGACCAAGGT GGAGATCAAAACGAACGGTGG CTGCACCATCTGTCTTCATCTT CCCGCCATCTGATGAGCAGTT GAAATCTGGAATCGCTCTGT TGTGTGCTGCTGAATAACTT CTATCCAGAGAGGCCAAAG TACAGTGGAAGGTGGATAAC GCCCTCCAATCGGGTAACTCC CAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCT ACAGCCTCAGCAGCACCTGA CGCTGAGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGC CTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCACAAA GAGCTTCAACAGGGGAGAGT GT	GGCGAGGGGCTGGAGTGGGTGGCAGCTATATGGTTTGATGC GGCTTTCAAATACTATGCAGACGCCGTGAAGGGCCGATTCA CCATCTCCAGAGACAACCTCCAAGAACACGGCTGTATCTGCAA ATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTG TGGAGAGATCTCGGATTTTGGAGTGGTCCCGACTACT GGGGCCAGGAAACCTTGGTACCGTGTCTAGTGCCTCCACC AAGGGCCCATCGGTCTTCCCTCCGACCCCTCCTCCAAGAG CACCTTGGGGGCACAGCGGCCCTGGGTGCCTGGTCAAGG ACTACTCCCCGAACCGGTGACGGTGTGCTGGAACCTCAGGC GGCCTGACACGCGGTGCACACCTTCCCGGTGTCTACAA GTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGC CCTCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTG AATCACAAAGCCAGCAACACCAAGGTGGACAAGAAAGTTG AGCCAAATCTTGTGACAAAACCTCACACATGCCACCGTGC CCAGCACCTGAATCTCTGGGGGAGCGTCAAGTCTTCTCTTC CCCCAAAACCCAAAGACACCCCTCATGATCTCCCGGACCCC TGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACC CTGAGGTCAAGTTCAACTGTACGTGACGGCGGTGGAGGTG CATAATGCCAAGACAAAAGCGGTGGAGGAGCAGTACGGCA GCACGTACCGTTGCGTCAGCGTCTCACCCTCTGCACCCAG GACTGGCTGAATGGCAAGGAGTACAAGTGCAGGTGTCCA ACAAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAA GCCAAAGGCGAGCCCCGAGAACCAAGGTGTACACCTGCC CCCATCCCGGGAGGAGATGACCAAGAACAGGTGACGCTG ACCTGCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGT GGAGTGGGAGAGCAATGGGACGCCGAGAAACAACTACAAG ACCAGCCTCCCGTGTGCTGGACTCCGACGGCTCCTTCTCTC TATAGCAAGCTCACCGTGGACAAAGCAGGTGGCAGCAGG GGAACGCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC AACCACCTACACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAA A
	(SEQ ID NO: 248) EIVMTQSPATLSVSPGERATLS CRASQSVDDQHLAWYQQKPGQ APRLIYQAAATRAATGIPARFSGS GSGTEFTLTISLSQSEDFAVYYC	(SEQ ID NO: 249) QVQLVESGGGVQPGSRSLRLSCAASGFTFQNYGMHWVRQAP GEGLEWVAIWFDAAFKYYADAVKGRFTISRDNSKNTLYLQ MNSLRAREDYVYCARDLAIFGVVDPYWGQGLTVTVSSASTK GPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT

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		<p>QQYQNWPLTFGGGKVEIKRT V/AAPSVFIPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKSDSTYS LSSTLTLSKADYKHKVYACE VTHQGLSSPVTKSFNRGEC</p>	<p>SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSN TKVDKKVEPKSCDKTHTCPCPAPELLGGPSVFLPPKPKDITL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHLEALHNHYTQKSLSLSPGK</p>
		<p>(SEQ ID NO: 250) ATGGACATGAGGGTGCCCGCT CAGCTCCTGGGGCTCCTGCTG CTGTGGCTGAGAGGTGGCGC TGTGAAATCGTGATGACGCAG TCTCCAGCCACCTGTCTGTG TCTCCAGGGAAAGAGCCAC CCTCTCTGCGAGGGCCAGTCA GAGTGTTAGCGAACACTTAGC CTGGTACCAGCAGAAACCTG GCCAGGCTCCAGGCTCCTCA TCTACGAAGCAGCCACAGG GCCACTGGTATCCAGCCAGG TTCAGTGGCAGTGGGTCTGGG ACAGAGTTCACCTCACCATC AGCAGCCTGCAGTCTGAAGAT TTTGCAAGTTTATTACTGTGAG CAGTATCAGAACTGGCCTCTC ACTTTCGGCGGAGGACCA GGTGGAGATCAACGAACGG TGGGTGCACCATCTGTCTTCA TCTTCCCGCCATCTGATGAGC AGTTGAAATCTGGAACCTGCCT CTGTTGTGTGCTGTGAATA ACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAAGGTGGAT AACGCCCTCCAATCGGGTAAC TCCCAGGAGAGTGTACAGA GCAGGACAGCAAGGACAGCA</p>	<p>(SEQ ID NO: 251) ATGGACATGAGGGTGCCCGCTCAGCTCCTGGGGCTCCTGCT GCTGTGGCTGAGAGGTGCGCTGTCAAGTGCAGCTGGTGG AGTCTGGGGGAGCGTGGTCCAGCTGGGAGGTCCCTGAGA CTCTCCTGTGACGACTGTGGATTCACTTCAAGTAACATATGGC ATGCACCTGGTCCGCCAGGTCCAGGCGAGGGGCTGGAGTG GGTGGCAGCTATCTGTTTGTATGCAAGTGATAAATACTATG CAGACGCGTGAAGGGCCGATTCAACATCTCCAGAGACAAC TCCAGAAACACGCTGTATCTGCAAAATGAACGCTGAGAGC CGAGGACACGGCTGTATATTCTGTGCGAGAGATCTGGCGA TTTTGGAGTATCCCGACTACTGGGGCCAGGGAACCCGTG GTCAACGCTGTAGTGCCTCCACCAAGGGCCCATCGGTCTTC CCCCCTGGCACCCTCTCCAGAGACCTCTGGGGGACAGC GGCCCTGGGCTGCTGGTCAAGGACTACTTCCCCGAACCGG TGACGGTGTCTGGAACTCAGGCGCCTGACCAGCGGCGTG CACACCTTCCCGGCTGCTACAGTCTCAGGACTCTACTCC CTCAGCAGCGTGGTACCGTGGCTCCAGCAGCTTGGGCAC CCAGACCTACATCTGCAACGTGAATCAAGCCCAAGCAACA CCAGGTGGACAAGAAAGTTGAGCCCAATCTTGTGACAAA ACTCACACATGCCACCGTGGCCAGCACCTGAACTCCTGGG GGGACCGTCAAGTCTTCTCTTCCCCCAAAACCAAGGACA CCCTCTACATCAACCGGGAGCCTGAGGTCAATGCGTGGTG GTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTG GTACGTGGAGCGGTGGAGTGCATAATGCCAAGACAAAG CCGTGGGAGGACGAGTACGGCAGCAGTACCGTTGCGTCAG CGTCTCACCGTCTGCACCAAGGACTGGCTGAATGGCAAGG AGTACAAGTGAAGGTGTCCAAACAAGCCCTCCCAGCCCC ATCGAGAAAACCATCTCCAAAGCAAAAGGGCAGCCCCGAG AACACAGGTGTACACCTGCCCCCATCCCCGGGAGGAGATG</p>

IPS:529381

NA

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		CCTACAGCCTCAGCAGCACCC TGACGCTGAGCAAAAGCAGAC TACGAGAAACACAAAGTCTA CGCTGCGAAGTCACCCATCA GGCCTGAGCTCGCCCGTCAC AAAGAGCTTCAACAGGGGAG AGTGT (SEQ ID NO: 1361)	ACCAGAACCAGGTACGCTGACCTGACCTGCCTGGTCAAAAGGCTT CTATCCACGATATCGCCGTGGAGTGGGAGAGCAATGGGC AGCCGAGAACTACAAAGACCACGCTCCCGTGGTGGAC TCCGACGGCTCTCTCTCTATAGCAAGCTCACCGTGGAC AAGAGTAGGTGGCAGAGGGGACGCTCTCTCATGCTCCGT GATGCATGAGGCTCTGCACAAACCACTACAGCAGAGAGCC TCTCCCTGCTCCGGGTAA (SEQ ID NO: 1362)
	AA	EIVMTQSPATLSVSPGERATLS CRASQSVSEHLAWYQQKPGQA PRLIYEAAATRAITGIPARFSGS SGTEFTLTISLQSEDFAVYYCQ QYQNWPLTFGGGTKVEIKRTV AAPSVFIFPPSDEQLKSGTASVV CLLNNFYPREAKVQWVKVDNAL QSGNSQESVTEQDSKDSYSL STLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC (SEQ ID NO: 1288)	QVQLVESGGGVQVQPSRLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAIWFDAADSKYYADAVKGRFTISRDNKNTLYLQ MNSLRAEDTAVYYCARDLAIFGVIPDYWGQGLTVTVSSASTK GPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHPKPSN TKVDKKVEPKSCDKTHCTCPPELPGPSVFLFPPKPKDTLY ITREPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGSYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSRREMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHREALHNYHTQKSLSPGK (SEQ ID NO: 1289)
IPS:529382	NA	ATGGACATGAGGGTGCCCGCT CAGCTCCTGGGGTCTCTGTG CTGTGGCTGAGAGGTGCGCGC TGTGAAATCGTGATGACGCAG TCTCCAGCCACCCTGTCTGTG TCTCCAGGGGAAAGAGCCAC CCTCTCCTGCAGGCCAGTCA GAGTGTTAGCAGCAACTTAGC CTGGTACCAAGCAAAACCTG GCCAGGCTCCAGGCTCCTCA TCTATGGTGACGCCACAGGG CCACTGGTATCCAGCCAGGT TCAGTGGCAGTGGGTCTGGGA CAGAGTTCACTCTCACCATCA GCAGCCTGCAGTCTGAAGATT TTGCAGTTTATTACTGTACGC (SEQ ID NO: 1288)	ATGGACATGAGGGTGCCCGCTCAGCTCCTGGGGCTCCTGCT GCTGTGGCTGAGAGGTGCGCGCTGTCAAGTGCACTGGTGG AGTCTGGGGAGGCGTGTCTCAGCCTGGGAGGTCCCTGAGA CTCTCCTGTGCAAGCATCTGGATTACCTTCACTAATATGGC ATGCACTGGGTCCCGCAGGCTCCAGGAGGGGCTGGAGTG GGTGGCAGCTATCTGTTTGTATGCAAGTGATAAATACTATG CAGACGCCGTGAGGGCGGATTCAACCATCTCCAGAGACAAC TCCAAGAACACGCTGTATCTGCAAAATGAACAGCCTGAGAGC CGAGGACACGGCTGTATTAATGTGCGAGAGATATTGCGA TTTTTGGAGTGTCCCGACTACTGGGGCCAGGAAACCTG GTCAACCGTGTCTAGTGCCTCCACCAAGGCCCATCGGTCTTC CCCTGGCACCTCCTCCAAAGCAGCCTCTGGGGGACAGC GGCCCTGGGTGCTGCTGGTCAAGGACTACTTCCCCGAACCGG TGACGGTGTGCGTGAACCTCAGGCGCCCTGACCAAGCGGCTG CACACCTTCCCGGCTGTCTCTACAGTCTCAGGACTCTACTCC CTCAGCAGCGTGGTGACCGTGCCCCCTCCAGCAGCTTGGGCAC

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		AGTATAATAACTGGCCTCTCA CITTCGGCGGAGGGACCAAG GTGGAGATCAACGAACGGT GGCTGCACCATCTGTCTTCAT CTTCCCGCCATCTGATGAGCA GTTGAAATCTGGAAC TGCC TC TGTTGTGTGCCTGCTGAATAA CTTCTATCCAGAGAGGCCAA AGTACAGTGGAAGGTGGATA ACGCCCTCCAATCGGGTAACT CCCAGGAGAGTGTACAGAG CAGGACAGCAAGGACAGCAC CTACAGCCTCAGCAGCACCT GACGCTGAGCAAAAGCAGACT ACGAGAAACACAAAAGTCTAC GCCTGCGAAGTCAACCATCAG GGCCTGAGCTCGCCCGTCACA AAGAGCTTCAACAGGGGAGA GTGT	CCAGACCTACATCTGCACGTGAATCACAAGCCCCAGCAACA CCAAAGTGGACAAGAAAGTTGAGCCCCAAATCTTGTGACAAA ACTCACATGCCCCACCGTGCACGACCTGAACCTCTGGG GGGACCGTCAGTCTCTCTTCCCCCAAAACCCAAAGGACA CCCTCTACATCACCGGGAGCCTGAGGTACATGCGTGGTG GTGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTG GTAGTGGAGCGGTGGAGGTGCATAATGCCAAGACAAAAG CCGTGCGAGGAGCAGTACGGCAGCACGTACCGTTGCGTCAG CGTCTCACCGTCTGCACCAAGGACTGGCTGAATGGCAAGG AGTACAAAGTCAAGGTGTCCAAACAAGCCCTCCAGCCCC ATCGAGAAAACCATCTCCAAAGCAAGGGCAGCCCCGAG AACCACAGGTGTACACCTGCCCTCCCGGAGGAGATG ACCAAGAACCAGGTACGCTGACCTGCCTGGTCAAAAGCTT CTATCCAGCGATATCGCCGTGGAGTGGAGAGCAATGGGC AGCCGGAGAACTACAAGACCACGCTCCCGTGGTGGAC TCCGACGGTCTCTCTCTCTATAGCAAGCTCACCGTGGAC AAGAGTAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGT GATGCATGAGGCTCTGCACAAACCACTACACGACAGAGAGCC TCTCCCTGTCTCCGGTAAA
		(SEQ ID NO: 1363) EIVMTQSPATLSVSPGERATLS CRASQSVSSNLA WYQKPGQA PRLIYGAATRA TGIPARFSGS SGTEFTLTISLQSEDFAVYYCQ QYNNWPLTFGGGTVKVEIKRTV AAPSVFIFPPSDEQLKSGTASVV CLLNIFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSYSL STLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC	(SEQ ID NO: 1364) QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVA AIWFDASDKYYADAVKGRFTISRDN SKNTLYLQ MNSLRAEDTAVYYCARDIAIFGVVPDYWGQGTLVTVSSASTK GPSVFLAPSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN HKPSN TKVDKKVEPKSCDKTHTCPPCPAPELLGPPSVFLFPPKPKDTLY ITREPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHREALHNHYTQKSLSLSPGK
IPS:529	NA	(SEQ ID NO: 1299) ATGGACATGAGGTGCCCCGCT CAGCTCCTGGGGCTCCTGCTG CTGTGGCTGAGAGGTGCGCGC TGTGAAATCGTGTGACGCAG	(SEQ ID NO: 1300) ATGGACATGAGGTGCCCCGCTCAGCTCTGGGGCTCCTGCT GCTGTGGCTGAGAGGTGCGCGCTGTCAAGTGCGAGCTGGTGG AGTCTGGGGGAGCGGTGCTCCAGCCTGGGAGGTCCCTGAGA CTCTCCTGTGTCAGCATCTGGGATTACCTTTCAGTAAGTATGGC

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	<p>TCTCCAGCCACCCTGTCTCTG TCTCCAGGGGAAAGAGCCAC CCTCTCTGCAGGGCCAGTCA GAGTGTAGCAGCAACTTAGC CTGGTACCAGCAGAAACCTG GCCAGGCTCCAGAGCTCCTCA TCTATGGTGCAGCCACCAGGG CCACTGGTATCCCAGACAGGT TCAGTGGCAGTGGGTCTGGGA CAGAGTTCACCTCACCATCA GCAGGCTGGAGCCTGAAGATT TTGCAGTTTATTACTGTCAGC AGTATAATAACTGGCCTCTCA CTTCGGCGGAGGGACCAAG GTGGAGATCAAACGAACGGT GGCTGCACCATCTGTCTTCAT CTTCCCGCCATCTGATGAGCA GTTGAAATCTGGAACCTGCCCTC TGTGTGTGCTGCTGAATAA CTTCTATCCCAGAGAGGCCAA AGTACAGTGGAAGGTGGATA ACGCCCTCCAAATCGGTAACT CCCAGGAGAGTGTACACAGAG CAGGACAGCAAGGACAGCAC CTACAGCCTCAGCAGCACCTT GACGCTGAGCAAAAGCAGACT ACGAGAAACACAAAGTCTAC GCCTGCCAAGTACCCATCAG GGCCTGAGCTCGCCCGTCACA AAGAGCTTCAACAGGGGAGA GTGT</p>	<p>ATGCACTGGGTCCGCCAGGCTCCAGGCGAGGGGCTGGAGTG GGTGGCAGCTATCTGGTTTGATGCAAGTGATAAATACTATG CAGACGCCGTGAAGGCCGATTCAACCATCTCCAGAGACAAC TCCAAAGAACACGCTGTATCTGCAATGAACAGCCTGAGAGC CGAGGACACGGCTGTATTACTGTGCGAGAGATCAGGCGA TTTTTGGAGTGTCCCGGATTACTGGGGCCAGGGAACCCCTG GTCACCGTGTCTAGTGCCTCCACCAAGGGCCCATCGGTCTTC CCCCTGGCACCTCTCCAAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGTGCTGTGTAAGGACTACTTCCCCGAACCCGG TGACGGTGTCTGGAACCTCAGGCGCCCTGACAGCGGCGTG CACACCTTCCCGGCTGTCTACAGTCTCAGGACTCTACTCC CTCAGCAGCGTGTGACCGTGCCCTCCAGCAGCTTGGGCAC CCAGACCTACATCTGCAACGTGAATCAAGCCCCAGCAACA CCAAAGTGGACAAGAAAGTTGAGCCCAATCTTGTGACAAA ACTCAGCATGCCACCCGTGCCAGCACCTGAACCTCTGGG GGGACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAGGACA CCCTCTACATCACCCGGGAGCTGAGGTACATCGCTGGTG GTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTG GTAGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAAG CCGTGCGAGGAGCAGTACGGCAGCACGTACCGTTGCGTCAG CGTCTCACCGTCTGCACCAAGGACTGGTGAATGGCAAGG AGTACAAGTGAAGGTGTCCAAACAAGCCCTCCAGCCCCC ATCGAGAAAACCATCTCCAAAAGCCAAAGGGCAGCCCCGAG AACCCACAGGTGTACACCTGCCCTGCCCTCCGGGAGGAGATG ACCAAGAACCAGGTACGCTGACCTGCCCTGGTCAAAAGCTT CTATCCCAGCGATATCGCCGTGGAGTGGAGAGCAATGGGC AGCCGGAGAACAACATAAGAACACGCTCCCTGGTGGAC TCCGACGGCTCTTCTTCTCTATAGCAAGCTCACCGTGGAC AAGAGTAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGT GATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCC TCTCCCTGTCTCCGGTAAA</p>
	<p>(SEQ ID NO: 1365)</p>	<p>(SEQ ID NO: 1366)</p>
AA	<p>EIVLTQSPATLSLSPGERATLSC RASQSVSSNLAWYQQKPGQAP RLLIYGAATRAITGIPDRFSGSGS GTEFTLTISRLEPEDFAVYYCQ</p>	<p>QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAIWFDASDKYYADAVKGRFTISRDNKNTLYLQ MNSLRAREDYAVYYCARDQAIQFVVDYWGQGTLVTVSSASTK GPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT</p>

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	QYNNWPLTFGGGKVEIKRTV AAPSFIFFPPSDEQLKSGTASVV CLLNNFYPREAKVQW'KVDNAL QSGNSQESVTEQDSKSDSTYSL STLTLKADYKHKVYACEVT HQGLSSPVTKSFNRGEC	SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSN TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDITLY ITREPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGSTYRCVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRWQQGNV FSCVMHEALHNYTQKSLSPGK
	(SEQ ID NO: 1309)	(SEQ ID NO: 1310)
	ATGGACATGAGGGTGCCCGT CAGCTCCTGGGGCTCCTGCTG CTGTGGCTGAGAGGTGGCGC TGTGAAATCGTGTGACGCGAG TCTCCAGCCACCCTGTCTCTG TCTCCAGGGAAAGAGCCAC CCTCTCTGAGGGCCAGTCA GAGTGTTAGCGAACAATTAGC CTGGTACCAGCAGAAACCTG GCCAGGCTCCAGGCTCCTCA TCTACGAAGCAGCCACCAGG GCCACTGGTATCCAGACAGG TTCAGTGGCAGTGGGTCTGGG ACAGAGTTCACTCTCACCATC AGCAGGCTGGAGCCTGAAGA TTTTGCAAGTTATTACTGTGAG CAGTATCAGAACTGGCCTCTC ACTTTCGGCGGAGGGACCAA GGTGGAGATCAAAACGAACGG TGGGTGCACCATCTGTCTTCA TCTTCCCGCCATCTGATGAGC AGTTGAAATCTGGAACTGCCT CTGTTGTGTGCTGTGAATA ACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAAGGTGGAT AACGCCCTCCAATCGGGTAAC TCCAGGAGAGTGTACACAGA GCAGGACAGCAAGGACAGCA	ATGGACATGAGGGTGCCCGTCAAGCTCCTGGGGCTCCTGCT GCTGTGGCTGAGAGGTGCGCGCTGTCAAGTGCAAGCTGGTGG AGTCTGGGGGAGGCGTGTGCTCCAGCCTGGGAGGTCCCTGAGA CTCTCCTGTGCAAGCATCTGGATTCACTTCAAGTAACTATGGC ATGCACCTGGTCCGCCAGGCTCCAGGCGAGGGGCTGGAGTG GGTGGCAGCTATCTGTTTGTATGCAAGTGATAAATACTATG CAGACGCCGTGAAGGGCCGATTCAACCATCTCCAGAGACAAC TCCAGAAACACGCTGTATCTGCAAAATGAACGCCCTGAGAGC CGAGGACACGGCTGTGATTACTGTGCGAGAGATCTGGCGA TTTTTGAGTGATCCCGACTACTGGGGCCAGGAAACCCCTG GTCAACCGTGTCTAGTGCCTCCACCAAGGGCCCATCGGTCTTC CCCCCTGGCACCCCTCTCCAGAGCACCTCTGGGGGACAGC GGCCCTGGGCTGCTGTGTCAGGACTACTTCCCCGAACCGG TGACGGTGTCTGTGAACCTCAGGCGCCCTGACCAGCGGCGTG CACACCTTCCCGGCTGCTCTACAGTCTCAGGACTCTACTCC CTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGGCAC CCAGACCTACATCTGCAACGTGAATCAAGCCCAAGCAACA CCAAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAA ACTCAACATGCCACCGTGGCCAGCACCTGAACCTCCTGGG GGGACCGTCAAGTCTTCTCTTCCCCCAAAACCCCAAGGACA CCCTCTACATCAACCCGGGAGCCTGAGGTCAATGCGTGGTG GTGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTG GTACGTGGACGGCGTGGAGGTGCAATAATGCCAAGACAAAAG CCGTGGAGGAGCAGTACGGCAGCAGTACCGTTGCGTCTAG CGTCTCAACCGTCTGACACGAGGACTGGCTGAATGGCAAGG AGTACAAGTGAAGGTGTCCAAACAAGCCCTCCCCAGCCCC ATCGAGAAAACCATCTCCAAAGCAAAAGGGCAGCCCCGAG AACACAGGTGTACACCTGCCCCCATCCCCGGGAGGAGATG
IPS:529399	NA	

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		CCTACAGCCTCAGCAGCACCC TGACGCTGAGCAAAAGCAGAC TACGAGAAACACAAAGTCTA CGCCTGCGAAGTCACCCATCA GGGCTGAGCTCGCCCGTCAC AAAGAGCTTCAACAGGGGAG AGTGT (SEQ ID NO: 1367)	ACCAAGAACCAGGTACGCTGACCTGCCTGGTCAAAAGGCTT CTATCCCAAGCATATCGCCGTGGAGTGGGAGAGCAATGGGC AGCCGGAGAACTACAAAGACCACGCCTCCCGTGTGGAC TCCGACGGCTCTTCTCTCTATAGCAAGCTCACCGTGGAC AAGAGTAGGTGGCAGAGGGGACGCTCTCTCATGCTCCGT GATGCATGAGGCTCTGCACAAACCACTACACGCAGAGAGGCC TCTCCCTGTCTCCGGGTAA (SEQ ID NO: 1368)
	AA	EIVLTQSPATLSLSPGERATLSC RASQSVSEHLAWYQQKPGQAP RLIYEAAATRAIGIPDRFSGSGS GTEFTLTISRLEPEDFAVYYCQ QYQNWPLTFGGGTKVEIKRTV AAPSVFIFPPSDEQLKSGTASVV CLLNNFYPREAKVQWVKVDNAL QSGNSQESVTEQDSKDSYSL STLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC (SEQ ID NO: 1319)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAAIWFDASDKYYADAVKGRFTISRDNKNTLYLQ MNSLRAEDTAVYYCARDLAIFGVIPDYWGQGTLLVTVSSASTK GPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCPCPAPELGGPSVFLFPPKPKDTLY ITREPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHREALHNHYTQKSLSLSPGK (SEQ ID NO: 1320)
		(SEQ ID NO: 1367)	(SEQ ID NO: 1368)

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IP:529400		<div>ATGGACATGAGGGTGCCCCGCT CAGCTCCTGGGGCTCCTGCTG CTGTGGCTGAGAGGTGCGCGC TGTGAAATCGTGTGACGCAG TCTCCAGCCACCTGTCTCTG TCTCCAGGGGAAAGAGCCAC CCTCTCCTGCAGGGCCAGTCA GAGTGTAGCAGCAACTTAGC CTGGTACCAGCAGAAACCTG GCCAGGCTCCCAGGCTCCTCA TCTATGGTGCAGCCACCAAGG CCACTGGTATCCAGACAGGT TCAGTGGCAGTGGGTCTGGGA CAGAGTTCACTCTACCATCA GCAGGCTGGAGCTGAAGATT TTGCAGTTTATTACTGTCAGC AGTATAATAACTGGCCTCTCA CTTTCGGCGGAGGGACCAAG GTGGAGATCAAACGAACGGT GGCTGCACCATCTGTCTTCAT CTTCCCGCCATCTGATGAGCA GTTGAAATCTGGAACCTGCCCTC TGTGTGTGCTGCTGAATAA CTTCTATCCCAAGAGGCCAA AGTACAGTGGAAAGGTGGATA ACGCCCTCCAATCGGGTAAC CCCAGGAGAGTGTACAGAG CAGGACAGCAAGGACAGCAC CTACAGCCTCAGCAGCACCT GACGCTGAGCAAAAGCAGACT ACGAGAAACACAAAGTCTAC GCCTGCGAAGTCACCCATCAG GGCCTGAGCTCGCCCGTCACA AAGAGCTTCAACAGGGGAGA GTGT</div>	<div>ATGGACATGAGGGTGCCCCGCTCAGCTCCTGGGGCTCCTCTGCT GCTGTGGCTGAGAGGTGCGCGCTGTCAAGTGTGAGTGCAGCTGCTGTTGG AGTCTGGGGAGGCGTGTGTCAGCCTGGGAGGTCCCTGAGAGTCCCTGAGA CTCTCCTGTGCAGCATCTGGATTCACTTCACTTAAGTAACATATGGC ATGCACCTGGGTCCGCCAGGCTCCAGGCGAGGGGTGGAGTG GGTGGCAGCTATCTGTTTGATGCAAGTGATAAATACTATG CAGACGCCGTGAAGGCCGATTCAACCATCTCCAGAGACAAC TCCAAAGAACACGCTGTATCTGCAAAATGAACAGCCTGAGAGC CGAGGACACGGCTGTGTATTACTGTGCGAGAGATATTGCGA TTTTTGGAGTGTCCCGGACTACTGGGGCCAGGGAACCCCTG GTCACCGTGTCTAGTGCCTCCACCAAGGGCCCATCGGTCTTC CCCCTGGCACCCCTCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGG TGACGGTGTGCTGGAACCTCAGGCGCCCTGACCAGCGGCGTG CACACCTTCCCGGCTGTCTACAAGTCTCAGGACTCTACTCTCC CTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCAC CCAGACCTACATCTGCAACGTGAATCAAGCCCCAGCAACA CCAAAGTGGACAAGAAAGTTGAGCCCCAAATCTTGTGACAAA ACTCACATGCCACCGTGGCCAGCACCTGAACTCCTCTGGG GGGACCGTCACTTCTCTTCCCCCACAACCCCAAGGACA CCCTCTACATCACCCGGGAGCCTGAGGTACATGCGTGGTG GTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTG GTACGTGGACGGCGTGGAGGTGCAATAATGCCAAGACAAAAG CCGTGCGAGGAGCAGTACGGCAGCACGTACCGTTGCGTCAG CGTCTCACCGCTCTGCACCAAGGACTGGCTGAATGGCAAG AGTACAAGTGAAGGTGTCCAACAAGCCCTCCCAGCCCCC ATCGAGAAAACCATCTCCAAGGCCAAAGGCGACGCCCGAG AACCACAGGTGTACACCTGCCCTCCCATCCCGGAGGAGATG ACCAAGAACCAGGTCAAGCTGACCTGCCTGGTCAAAAGCTT CTATCCCAGCGATATCGCCGTGGAGTGGGAGAGCAATGGGC AGCCGGAGAAACAACTACAAGACACGCTCCCTGCTGGAC TCCGAGGGCTCTTCTTCTCTATAGCAAGTCAACGTTGGAC AAGAGTAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGT GATGCATGAGGCTCTGCACAACCACTACACGCAAGAGGCC TCTCCCTGTCTCCGGGTAAA</div>	(SEQ ID NO: 1369)	(SEQ ID NO: 1370)
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	<p>AA</p> <p>EIVLTQSPATLSLSPGERATLSC RASQSVSSNLAWYQQKPGQAP RLLIYGAATRAIGIPDRFSGSGS GTEFTLTISRLEPEDFAVYYCQ QYNNWPLTFGGGTKVEIKRTV AAPSVFIFPPSDEQLKSGTASVV CLLNNFYPREAKVQWVKVDNAL QSGNSQESVTEQDSKDSSTYSLS STLTLSKADYKEHKVYACEVT HQGLSSPVTKSFNRGEC</p>	<p>QVQLVESGGGVQVQGRSLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAIWFADSKYYADA VKGRFTISRDN SKNTLYLQ MNSLRAEDTAVYYCARDIAIFGVVPDYWGQGLTVTVSSASTK GPSVFP LAPSSKSTSGGTAA LGLVKDYFPEPVTVSWNSGALT SGVHTFP AVLQSSGLYSLSSVTVPSSSLGTQTYICNVN HKPSN TKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPKPKDITLY ITREPEVTCVVVDVSHEDPEVKFNWYVDGVVEVHN AKTKPCEE QYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMH EALHNHYTQKSLSLSPGK</p>
<p>IPS:5293403</p>	<p>NA</p> <p>(SEQ ID NO: 1329) ATGGACATGAGGGTGCCCGCT CAGCTCCTGGGGCTCCTGCTG CTGTGGCTGAGAGGTGCGCGC TGTGAAATCGTGTGACGCGAG TCTCCAGCCACCTGTCTCTG TCTCCAGGGAAAGAGCCAC CCTCTCTGCGAGGGCCAGTCA GAGTGTGATCTGCACTTAGC CTGTACCAAGCAGAAACCTG GCCAGGCTCCAGGCTCCTCA TCTACGAAGCAGCCACCAAG GCCACTGGTATCCAGACAGG TTCAGTGGCAGTGGGTCTGGG ACAGAGTCACTCTCACCATC AGCAGGCTGGAGCCTGAAGA TTTTGCA GTTTATTACTGTCAG CAGTATCAGAACTGGCCTCTC ACTTTCGGCGGAGGGACCAA GGTGAGATCAAAACGAACGG TGGGTGCACCATCTGTCTTCA TCTTCCCGCCATCTGATGAGC AGTTGAAATCTGGAACCTGCT CTGTGTGTGCTGCTGAATA ACTTCTATCCCAAGAGAGGCCA</p>	<p>(SEQ ID NO: 1230) ATGGACATGAGGGTGCCCGCTCAGCTCTGGGGCTCCTGCT GCTGTGGCTGAGAGGTGCGCGCTGTCAAGTGCAAGCTGGTGG AGTCTGGGGGAGGCGTGTCCAGCCTGGGAGGTCCCTGAGA CTCTCCTGTGACGCACTCTGGATTACCTTCAGTAACATATGGC ATGCACCTGGGTCCGCCAGGCTCCAGGCGAGGGGCTGGAGTG GGTGGCAGCTATCTGTTTGTATGCAAGTGATAAATACTATG CAGACGCGGTGAAGGGCGGATTCAACATCTCCAGAGACAAC TCCAAGAACACGCTGTATCTGCAAAATGAACAGCCTGAGAGC CGAGGACACGGCTGTGATTA CTGTGCGAGAGATTGTGGCGA TTTTTGAGTGTGCCCCGACTACTGGGGCCAGGAAACCCCTG GTCAACGTGTCTAGTCCCTCCACCAAGGGCCCATCGGTCTTC CCCCGTGGCACCTCTCC AAGAGCACCTCTTGGGGGCACAGC GGCCCTGGGCTGCTGTGTC AAGGACTACTTCCCCGAACCGG TGACGGTGTGCTGGAAC TCAAGCGCCCTGACCAGCGCGTG CACACCTTCCCGGCTGCTCCTACAGTCTCAGGACTCTACTCC CTCAGCAGCTGGTGACCGTGCCCTCCAGCAGCTTGGGCAC CCAGACCTACATCTGCAACGTGAATCAACAGCCCAAGCAACA CCAAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAA ACTCAACATGCCACCGTGGCCAGCACCTGAACTCCTCTGGG GGGACCGTCACTCTCTCTTCCCCCAAAAACCAAGGACA CCCTCTACATCAACCGGGAGCCTGAGGTCAATGCGGTGGTG GTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTG GTACGTGGACGGCTGGAGGTGCAATATGCCAAGACAAAG CCGTGCGAGGAGCAGTACGGCAGCACGTACCGTTGCGTCAAG</p>

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		AAGTACAGTGGAAAGGTGGAT AACGCCCTCCAATCGGTAAC TCCAGGAGAGTGTACAGA GCAGGACAGCAAGGACAGCA CCTACAGCCTCAGCAGCACCC TGACGCTGAGCAAAAGCAGAC TACGAGAAACACAAAGTCTA CGCTGCGAAGTCAACCATCA GGGCTGAGCTCGCCCGTCAC AAAGAGCTTCAACAGGGGAG AGTG	AAGTACAGTGGTCCGCAAGG AGTACAAAGTCAAGGTGTCCA ATCGAGAAAACCATCTCCAAAG AACACAGGTGTACACCTGCCCA ACCAGAACCAGGTACGCTGACCT CTATCCCAAGATATCGCCGTGG AGCCGAGAACTACAAAGACCCCT TCCGAGGCTCTTCTCTCTATAG AAGAGTAGGTGGCAGAGGGGAA GATGCATGAGGCTCTGCACAACT TCTCCCTGTCTCCGGTAA
	AA	EIVLTQSPATLSLSPGERATLSC RASQSVDLHLAWYQQKPGQAP RLIYEAAATRAATGIPDRFSGSGS GTEFTLTISRLEPEDFAVYYCQ QYQNWPLTFGGGKVEIKRTV AAPSVFIFPPSDEQLKSGTASVV CLLNFFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSYSL STLTLSKADYEKHKVYACEVT HQLSSPVTKSFNRGEC	(SEQ ID NO: 1371) QVQLVESGGGVQPGRSLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAIWFDASDKYYADAVKGRFTISRDNKNTLYLQ MNSLRAEDTAVYYCARDLAIFGVVPDYWQQGLVTVSSASTK GPSVFLAPSSKSTSGGTAAALGCLVKDYFPEPTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHPKPSN TKVDKKVEPKSCDKHTHTCPCPAPELLGGPSVFLPFPKPKDTLY ITREPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGSTYRCVSVLTVLHQQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHREALHNYHTQKSLSPGK
!PS:529404	NA	ATGGACATGAGGGTGCCCGCT CAGCTCCTGGGCTCCTGCTG CTGTGGCTGAGAGGTGCGCGC TGTGAAATCGTGTGACGCGAG TCTCCAGCCACCCTGTCTCTG TCTCCAGGGGAAAGAGCCAC CCTCTCCTGCAGGCCAGTCA GAGTGTTAACCTGAACCTTAGC CTGGTACCAAGCAAACTCTG GCCAGGCTCCAGGCTCCTCA TCTACAGGCAGCCACCAAGG GCCACTGGTATCCACAGACAGG	(SEQ ID NO: 1339) ATGGACATGAGGGTGCCCGCTCAGCTCCTGGGGCTCCTGCT GCTGTGGCTGAGAGGTGCGCGCTGTCAAGTGCACTGGTGG AGTCTGGGGAGGCGTGTCCAGCCTGGGAGGTCCTTGAGA CTCTCCTGTGCAAGCATCTGGATTACCTTCACTAATATGGC ATGCACCTGGTCCCGCAGGCTCCAGGCGAGGGGCTGGAGTG GGTGGCAGCTATCTGTTTGTATGCAAGTGATAAATACTATG CAGACGCCGTGAAGGCCGATTCAACCATCTCCAGAGACAAC TCCAAAGAACACGCTGTATCTGCAAAATGAACAGCCTGAGAGC CGAGGACAGGCTGTGTATTACTGTGCGAGAGATTGGCGGA TTTTTGGAGTGTCCCGGACTACTGGGGCCAGGAAACCTCTG GTACACCGTGTCTAGTGCCTCCACCAAGGGCCCATCGGTCTC CCCCTGCGACCCCTCCTCCAAGAGCACCTCTCTGGGGGCAACAGC

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	<p>TTCAGTGGCAGTGGGTCTGGG ACAGAGTTCACTCTACCATC AGCAGGTGGAAGCCTGAAGA TTTTGCAGTTTATTACTGTCAG CAGTATAACCAAGTGGCCTCTC ACTTTCGGCGGAGGGACCAA GGTGAGATCAACGAACGG TGGCTGCACCATCTGTCTCA TCTTCCCGCCATCTGATGAGC AGTTGAAATCTGGAAC TGCCCT CTGTTGTGTGCTGCTGAATA ACTTCTATCCAGAGAGGCCA AAGTACAGTGAAGGTGGAT AACGCCCTCCAATCGGGTAAC TCCCAGGAGAGTGTACAGA GCAGGACAGCAAGGACAGCA CCTACAGCCTCAGCAGCACCC TGACGCTGAGCAAAAGCAGAC TACGAGAAACACAAAGTCTA CGCCTGCGAAGTCAACCATCA GGCCTGAGCTCGCCCGTCAC AAAGAGCTTCAACAGGGGAG AGTGT</p>	<p>GGCCCTGGGTGCCTGGTCAAGGACTACTTCCCGGAACCGG TGACGGTGTCTGGAACCTAGGCGCCCTGACCAAGCGCGTG CACACCTTCCCGGTGTCTACAGTCTCAGGACTCTACTCC CTCAGCAGCGTGGTACCGTGCCCTCCAGCAGCTTGGGCAC CCAGACCTACATCTGCAACGTGAATCAAGCCCCAGCAACA CCAAAGTGGACAAAGAAAGTTGAGCCCAATCTTGTGACAAA ACTCACATGCCACCCGTCGCCAGCACCTGA ACTCTCTGGG GGGACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAGGACA CCCTCTACATCACCCGGGAGCCTGAGGTACATGCGTGGTG GTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTG GTAGTGGACGGCGTGGAGGTGCATATGCCCAGACAAAAG CCGTGCGAGGAGCAGTACGGCAGCACGTACCGTTGCGTCAG CGTCTCACCGTCTGCAACAGGACTGGTGAATGGCAAGG AGTACAAGTGAAGGTGTCCAACAAGCCCTCCAGCCCCC ATCGAGAAACCATCTCCAAGCAAGGGCAGCCCCGAG AACCACAGGTACACCTGCCCTCCCTCCCGGAGGAGATG ACCAAGAACCAGGTACGCTGACCTGCGCTGGTCAAAAGCTT CTATCCACGATATCGCCGTGGAGTGGAGAGCAATGGGC AGCCGGAGAAACATAAGACACCGCTCCCTGCTGGAC TCCGACGGCTCTTCTTCTCTATAGCAAGCTCACCGTGGAC AAGAGTAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGT GATGCATGAGGCTCTGCACAACCACTACACGCAGAAAGAGCC TCTCCCTGTCTCCGGGTAAA</p>
	<p>(SEQ ID NO: 1373)</p>	<p>(SEQ ID NO: 1374)</p>
AA	<p>EIVLTQSPATLSLSPGERATLSC RASQSVNLSLAWYQQKPGQAP RLIYQAATRAATGIPDRFSGSGS GTEFTLTISRLEPEDFAVYYCQ QYNQWPLTFGGGTKVEIKRTV AAPSVFIFPPSDEQLKSGTASVV CLLNFFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSYSL STLTLSKADYEKHKVYACEV HQGLSSPVTKSFNRGEC</p>	<p>QVQLVESGGGVQPGRSLRLSCAASGFTFSNYGMHWVRQAP GEGLEWVAIWFDASDKYYADAVKGRFTISRDNKNTLYLQ MNSLRAEDTAVYCARDLAIFGVDPDYWGQGLVTVSSASTK GPSVFLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHPKPSN TKVDKKVEPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLY ITREPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGSTYRCVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSYMHEALHNHYTQKSLSLSPGK</p>
	<p>(SEQ ID NO: 1349)</p>	<p>(SEQ ID NO: 1350)</p>

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IP:529405	NA	ATGGACATGAGGGTGCCCCGCTCAGCTCCTGGGGCTCCTGCT CAGCTCCTGGGGCTCCTGCTG CTGTGGCTGAGAGGTGGCGC TGTGAAATCGTGTGACGCAG TCTCCAGCCACCTGTCTCTG TCTCCAGGGGAAAGAGCCAC CCTCTCCTGCAGGGCCAGTCA GAGTGTTCAGCCACTTAGC CTGGTACCAAGCAAAACCTG GCCAGGC'TCCCAGCTCCTCA TCTACGAAGCAGCCACAGG GCCACTGGTATCCAGACAGG TTCAGTGGCAGTGGGTCTGG ACAGAGTTCACCTCACCATC AGCAGGCTGGAGCCTGAAGA TTTTGCAAGTTTATTACTGTGAG CAGTATCAGAACTGGCCTCTC ACTTCGGCGGAGGGACCAA GGTGGAGATCAAACGAACGG TGGCTGCACCATCTGTCTCA TCTTCCCGCCATCTGATGAGC AGTTGAAATCTGGAACCTGCCT CTGTTGTGTGCTGCTGAATA ACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAAGGTGGAT AACGCCCTCCAATCGGGTAAC TCCAGGAGAGTGTACAGA GCAGGACAGCAAGGACAGCA CCTACAGCCTCAGCAGCACCC TGACGCTGAGCAAAGCAGAC TACGAGAAACACAAAGTCTA CGCTGCGAAGTCAACCATCA GGGCTGAGCTCGCCCGTCAC AAAGAGCTTCAACAGGGGAG AGTGT	ATGGACATGAGGGTGCCCCGCTCAGCTCCTGGGGCTCCTGCT GCTGTGGCTGAGAGGTGCGCGTGTCAAGTGTGAGTGGTGG AGTCTGGGGAGGCGTGTCTCAGCTTGGGAGGTCCCTGAGA CTCTCCTGTGACGACTGTGATTCACTTCCAGAACTATGGC ATGCACCTGGGTCCGCCAGGTCCAGGCAGGGGTGGAGTG GGTGGCAGCTATCTGTTGTGATCGCTTGACAAATACTATG CAGACGCCGTGAAGGCCGATTCAACCATCTCCAGAGACAAC TCCAAAGAACACGCTGTATCTGCAAAATGAACGCCCTGAGGC CGAGGACACGGCTGTGTATTACTGTGCGAGAGATCTTGCGA TTTTTGGAGTGTCCCGGACTACTTGGGGCCAGGGAACCCCTG GTCAACGTGTCTAGTGCCTCCACCAAGGGCCCATCGGTCTTC CCCCTGGCACCCCTCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGG TGACGGTGTGCGTGAACCTCAGGCGCCCTGACCCAGCGGCGTG CACACCTTCCCGGCTGTCTACAGTCTCAGGACTCTACTCC CTCAGCAGCGTGTGACCGTGCCCTCCAGAGCTTGGGCAC CCAGACCTACATCTGCAACGTGAATCAAGCCCCAGCAACA CCAAAGTGGACAAGAAAGTTGAGCCCCAAATCTTGTGACAAA ACTCACATGCCACCCGTGCCAGCACCTGAACTCCTGGG GGGACCGTCACTTCTCTCTTCCCCCCTCAACCCCAAGGACA CCCTCTACATCAACCCGGGAGCCTGAGGTACATGCGTGGTG GTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTG GTAGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAAG CCGTGGAGGAGCAGTACGGCAGCACGTACCGTTGCGTCAG CGTCTCACCGCTCTGCACCAAGGACTGGTGAATGGCAAGG AGTACAAGTGCAGGTGTCCAAACAAGCCCTCCCAGCCCCC ATCGAGAAAACCATCTCCAAGGCCAAAGGGCAGCCCCGAG AACCACAGGTGTACACCTGCCCTGCCCTCCCGGAGGAGATG ACCAAGAACCAGGTACGCTGACCTGCCCTGGTCAAAAGCTT CTATCCAGCGATATCGCCGTGGAGTGGAGAGCAATGGGC AGCCGGAGAAACATAACAAGACCACGCTCCCTGGTGGAC TCCGAGGGCTCTTCTTCTCTATAGCAAGCTCACCGTGGAC AAGAGTAGGTGGCAGCGGGGAACGTCTTCTCATGCTCCGT GATGCATGAGGCTCTGCACAAACCATACACGCAAGAGAGCC TCTCCCTGTCTCCGGGTAAA
		(SEQ ID NO: 1375) AGTGT	(SEQ ID NO: 1376) TCTCCCTGTCTCCGGGTAAA

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	AA	EIVLTQSPATLSLSPGERATLSC RASQSFVSHLAWYQQKPGQAP RLLIYEAAATRAIGIPDRFSGSGS GTEFTLTISRLEPEDFAVYYCQ QYQNWPFLTGGGKVEIKRTV AAPSVFIFPPSDEQLKSGTASVV CLLNNFYPREAKVQWVKVDNAL QSGNSQESVTEQDSKDSSTYSLS STLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC	QVQLVESGGGVQPGRSRLRSCAASGFTFQNYGMHWVRQAP GEGLEWVAAIWFDASDKYYADA VKGRFTISRDN SKNTLYLQ MNSLRAEDTAVYYCARDLAIFGVVPDYWGQGTLVTVSSASTK GPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSCDKTHTCTPCPAPELLGGPSVFLFPPKPKDTLY ITREPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHAEALHNHYTQKSLSLSPGK
		(SEQ ID NO: 1359)	(SEQ ID NO: 1360)

[0203] In one embodiment the antibody or fragment thereof comprises a light chain variable region comprising a sequence selected from the group consisting of SEQ ID NOs: 723, 727, 731, 735, 739, 743, 747, 751, 755, 759, 763, 767, 771, 775, 779, 783, 787, 791, 795, 799, 803, 807, 811, 815, 819, 823, 827, 831, 835, 839, 843, 847, 851, 855, 859, 863, 867, 871, 875, 879, 883, 887, 891, 895, 899, 903, 907, 911, 915, 919, 923, 927, 931, 935, 939, 943, 947, 951, 955, 959, 1286, 1296, 1306, 1316, 1326, 1336, 1346, and 1356. In one embodiment the antibody or fragment thereof comprises a heavy chain variable region comprising a sequence selected from the group consisting of SEQ ID NOs: 724, 728, 732, 736, 740, 744, 748, 752, 756, 760, 764, 768, 772, 776, 780, 784, 788, 792, 796, 800, 804, 808, 812, 816, 820, 824, 828, 832, 836, 840, 844, 848, 852, 856, 860, 864, 868, 872, 876, 880, 884, 888, 892, 896, 900, 904, 908, 912, 916, 920, 924, 928, 932, 936, 940, 944, 948, 952, 956, 960, 1287, 1297, 1307, 1317, 1327, 1337, 1347, and 1357. In one embodiment the antibody or fragment thereof comprises a light chain variable region comprising a sequence selected from the group consisting of SEQ ID NOs: 723, 727, 731, 735, 739, 743, 747, 751, 755, 759, 763, 767, 771, 775, 779, 783, 787, 791, 795, 799, 803, 807, 811, 815, 819, 823, 827, 831, 835, 839, 843, 847, 851, 855, 859, 863, 867, 871, 875, 879, 883, 887, 891, 895, 899, 903, 907, 911, 915, 919, 923, 927, 931, 935, 939, 943, 947, 951, 955, 959, 1286, 1296, 1306, 1316, 1326, 1336, 1346, and 1356 and a heavy chain variable region comprising a sequence selected from the group consisting of SEQ ID NOs: 724, 728, 732, 736, 740, 744, 748, 752, 756, 760, 764, 768, 772, 776, 780, 784, 788, 792, 796, 800, 804, 808, 812, 816, 820, 824, 828, 832, 836, 840, 844, 848, 852, 856, 860, 864, 868, 872, 876, 880, 884, 888, 892, 896, 900, 904, 908, 912, 916, 920, 924, 928, 932, 936, 940, 944, 948, 952, 956, 960, 1287, 1297, 1307, 1317, 1327, 1337, 1347, and 1357.

[0204] In one embodiment the antibody or fragment thereof 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: 723 and a heavy chain variable region comprising SEQ ID NO: 724; a light chain variable region comprising SEQ ID NO: 727 and a heavy chain variable region comprising SEQ ID NO: 728; a light chain variable region comprising SEQ ID NO: 731 and a heavy chain variable region comprising SEQ ID NO: 732; a light chain variable region comprising SEQ ID NO: 735 and a heavy chain variable region comprising SEQ ID NO: 736; a light chain variable region comprising SEQ ID NO: 739 and a heavy chain variable region comprising SEQ ID NO: 740; a light chain variable region comprising SEQ ID NO: 743 and a heavy chain variable region comprising SEQ ID NO: 744; a light chain variable region comprising SEQ ID NO: 747 and a heavy chain variable region

[illegible]

[illegible]

comprising SEQ ID NO: 952; a light chain variable region comprising SEQ ID NO: 955 and a heavy chain variable region comprising SEQ ID NO: 956; a light chain variable region comprising SEQ ID NO: 959 and a heavy chain variable region comprising SEQ ID NO: 960; a light chain variable region comprising SEQ ID NO: 1286 and a heavy chain variable region comprising SEQ ID NO: 1287; a light chain variable region comprising SEQ ID NO: 1296 and a heavy chain variable region comprising SEQ ID NO: 1297; a light chain variable region comprising SEQ ID NO: 1306 and a heavy chain variable region comprising SEQ ID NO: 1307; a light chain variable region comprising SEQ ID NO: 1316 and a heavy chain variable region comprising SEQ ID NO: 1317; a light chain variable region comprising SEQ ID NO: 1326 and a heavy chain variable region comprising SEQ ID NO: 1327; a light chain variable region comprising SEQ ID NO: 1336 and a heavy chain variable region comprising SEQ ID NO: 1337; a light chain variable region comprising SEQ ID NO: 1346 and a heavy chain variable region comprising SEQ ID NO: 1347; and a light chain variable region comprising SEQ ID NO: 1356 and a heavy chain variable region comprising SEQ ID NO: 1357.

[0205] In one embodiment the antibody or fragment thereof comprises a light chain variable region encoded by a polynucleotide sequence selected from the group consisting of SEQ ID NOs: 721, 725, 729, 733, 737, 741, 745, 749, 753, 757, 761, 765, 769, 773, 777, 781, 785, 789, 793, 797, 801, 805, 809, 813, 817, 821, 825, 829, 833, 837, 841, 845, 849, 853, 857, 861, 865, 869, 873, 877, 881, 885, 889, 893, 897, 901, 905, 909, 913, 917, 921, 925, 929, 933, 937, 941, 945, 949, 953, 955, 1377, 1379, 1381, 1383, 1385, 1387, 1389, and 1391. In one embodiment the antibody or fragment thereof comprises a heavy chain variable region encoded by a polynucleotide selected from the group consisting of SEQ ID NOs: 722, 726, 730, 734, 738, 742, 746, 750, 754, 758, 762, 766, 770, 774, 778, 782, 786, 790, 794, 798, 802, 806, 810, 814, 818, 822, 826, 830, 834, 838, 842, 846, 850, 854, 858, 862, 866, 870, 874, 878, 882, 886, 890, 894, 898, 902, 906, 910, 914, 918, 922, 926, 930, 934, 938, 942, 946, 950, 954, 958, 1378, 1380, 1382, 1384, 1386, 1388, 1390, and 1392. In one embodiment the antibody or fragment thereof comprises a light chain variable region encoded by a polynucleotide sequence selected from the group consisting of SEQ ID NOs: 721, 725, 729, 733, 737, 741, 745, 749, 753, 757, 761, 765, 769, 773, 777, 781, 785, 789, 793, 797, 801, 805, 809, 813, 817, 821, 825, 829, 833, 837, 841, 845, 849, 853, 857, 861, 865, 869, 873, 877, 881, 885, 889, 893, 897, 901, 905, 909, 913, 917, 921, 925, 929, 933, 937, 941, 945, 949, 953, 955, 1377, 1379, 1381, 1383, 1385, 1387, 1389, and 1391 and a heavy chain variable region encoded by a polynucleotide sequence selected from the group consisting of

SEQ ID NOs: 722, 726, 730, 734, 738, 742, 746, 750, 754, 758, 762, 766, 770, 774, 778, 782, 786, 790, 794, 798, 802, 806, 810, 814, 818, 822, 826, 830, 834, 838, 842, 846, 850, 854, 858, 862, 866, 870, 874, 878, 882, 886, 890, 894, 898, 902, 906, 910, 914, 918, 922, 926, 930, 934, 938, 942, 946, 950, 954, 958, 1378, 1380, 1382, 1384, 1386, 1388, 1390, and 1392.

In one embodiment the antibody or fragment thereof 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 encoded by a polynucleotide sequence comprising SEQ ID NO: 721 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 722; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 725 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 726; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 729 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 730; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 733 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 734; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 737 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 738; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 741 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 742; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 745 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 746; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 749 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 750; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 753 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 754; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 757 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 758; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 761 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 762; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 765 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 766; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 769

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comprising SEQ ID NO: 954; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 957 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 958; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1377 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1378; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1379 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1380; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1381 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1382; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1383 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1384; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1385 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1386; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1387 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1388; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1389 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1390; and a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1391 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1392.

[0206] Some antigen binding proteins comprise a variable light domain and a variable heavy domain as listed in one of the rows for one of the antibodies listed in TABLE 3. In some instances, the antigen binding protein comprises two identical variable light domains and two identical variable heavy domains from one of the antibodies listed in TABLE 3. Some antigen binding proteins that are provided comprise a variable light domain and a variable heavy domain as listed in one of the rows for one of the antibodies listed in TABLE 3, except that one or both of the domains differs from the sequence specified in the table at only 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15 amino acid residues, wherein each such sequence difference is independently either a 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, 10, 11, 12, 13, 14 or 15 amino acid changes relative to the variable domain sequences specified in TABLE 3. In one embodiment, the antigen binding protein comprises a variable region sequence from Table 3, but with the N-terminal methionine deleted. Other antigen

binding proteins also comprise a variable light domain and a variable heavy domain as listed in one of the rows for one of the antibodies listed in TABLE 3, except that one or both of the domains differs from the sequence specified in the table in that the heavy chain variable domain and/or light chain variable domain comprises or consists of a sequence of amino acids that has at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequences of the heavy chain variable domain or light chain variable domain sequences as specified in TABLE 3.

[0207] In another aspect, the antigen binding protein consists just of a variable light or variable heavy domain from an antibody listed in TABLE 3. In still another aspect, the antigen binding protein comprises two or more of the same variable heavy domains or two or more of the same variable light domains from those listed in TABLE 3. Such domain antibodies can be fused together or joined via a linker as described in greater detail below. The domain antibodies can also be fused or linked to one or more molecules to extend the half-life (e.g., PEG or albumin).

[0208] In certain embodiments it is desired that the antigen binding protein is an antibody with reduced viscosity. Such of antigen binding proteins can be produced by modifying sequences in framework regions and/or the Fc domain that are shown to be associated with high viscosity.

[0209] Such reduced-viscosity antigen binding proteins included antibodies wherein:

[0210] the VH1|1-18 germline subfamily sequence comprises one or more substitutions selected from 82R, 94S, and 95R;

[0211] the VH3|3-33 germline subfamily sequence comprises one or more of substitutions 1E, 17G, and 85A;

[0212] the VK3|L16 germline subfamily sequence comprises one or more substitutions selected from 4L, 13L, 76D, 95R, 97E, and 98P;

[0213] the VK3|L6 germline subfamily sequence comprises one or more substitutions selected from 76D and 95R;

[0214] the Fc domain sequence comprises one or more substitutions selected from 253A, 440K, and 439E; and

[0215] the Fc domain C-terminus comprises a sequence selected from KP, KKP, KKKP, and E. .

[0216] All of the foregoing preferred viscosity-reducing amino acid substitutions in variable regions are identified by the Aho numbering system. All viscosity-reducing residues in conserved regions including Fc are identified by the EU numbering system.

[0217]

[0218] Other antigen binding proteins that are provided are variants of antibodies formed by combination of the heavy and light chains shown in TABLE 3 and comprise light and/or heavy chains that each have at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequences of these chains. In some instances, such antibodies include at least one heavy chain and one light chain, whereas in other instances the variant forms contain two identical light chains and two identical heavy chains.

[0219] The various combinations of heavy chain variable regions may be combined with any of the various combinations of light chain variable regions.

[0220] In a further embodiment, the isolated antigen binding protein provided herein is a human antibody comprising a sequence as set forth in TABLE 3 and is of the IgG₁-, IgG₂-, IgG₃- or IgG₄-type.

[0221] The antigen binding proteins disclosed herein are polypeptides into which one or more CDRs are grafted, inserted and/or joined. An antigen binding protein can have 1, 2, 3, 4, 5 or 6 CDRs. An antigen binding protein thus can have, for example, one heavy chain CDR1 ("CDRH1"), and/or one heavy chain CDR2 ("CDRH2"), and/or one heavy chain CDR3 ("CDRH3"), and/or one light chain CDR1 ("CDRL1"), and/or one light chain CDR2 ("CDRL2"), and/or one light chain CDR3 ("CDRL3"). Some antigen binding proteins include both a CDRH3 and a CDRL3. Specific light and heavy chain CDRs are identified in TABLES 4A and 4B, respectively.

[0222] Complementarity determining regions (CDRs) and framework regions (FR) of a given antibody may be identified using the system described by Kabat et al. in *Sequences of Proteins of Immunological Interest*, 5th Ed., US Dept. of Health and Human Services, PHS, NIH, NIH Publication no. 91-3242, 1991. Certain antibodies that are disclosed herein comprise one or more amino acid sequences that are identical or have substantial sequence identity to the amino acid sequences of one or more of the CDRs presented in TABLES 4A and 4B. These CDRs use the system described by Kabat et al. as noted above.

[0223] The structure and properties of CDRs within a naturally occurring antibody has been described, *supra*. Briefly, in a traditional antibody, the CDRs are embedded within a framework in the heavy and light chain variable region where they constitute the regions responsible for antigen binding and recognition. A variable region comprises at least three heavy or light chain CDRs, *see, supra* (Kabat et al., 1991, *Sequences of Proteins of Immunological Interest*, Public Health Service N.I.H., Bethesda, MD; *see also* Chothia and Lesk, 1987, *J. Mol. Biol.* 196:901-917; Chothia et al., 1989, *Nature* 342: 877-883), within a

framework region (designated framework regions 1-4, FR1, FR2, FR3, and FR4, by Kabat *et al.*, 1991, *supra*; see also Chothia and Lesk, 1987, *supra*). The CDRs provided herein, however, may not only be used to define the antigen binding domain of a traditional antibody structure, but may be embedded in a variety of other polypeptide structures, as described herein.

[0224] In one embodiment the antibody or fragment thereof comprises a CDRL1, a CDRL2, a CDRL3, a CDRH1, a CDRH2, and a CDRH3. In one embodiment the antibody or fragment thereof comprises a CDRL1 comprising a sequence selected from the group consisting of SEQ ID NOs: 4, 10, 16, 22, 28, 34, 40, 46, 52, 58, 64, 70, 76, 82, 88, 94, 100, 106, 112, 118, 124, 130, 136, 142, 148, 154, 160, 166, 172, 178, 184, 190, 196, 202, 208, 214, 220, 226, 232, 238, 244, 250, 256, 262, 268, 274, 280, 286, 292, 298, 304, 310, 316, 322, 328, 334, 340, 346, 352, 358, 1290, 1300, 1310, 1320, 1330, 1340, and 1350. In one embodiment the antibody or fragment thereof comprises a CDRL2 comprising a sequence selected from the group consisting of SEQ ID NOs: 5, 11, 17, 23, 29, 35, 41, 47, 53, 59, 65, 71, 77, 83, 89, 95, 101, 107, 113, 119, 125, 131, 137, 143, 149, 155, 161, 167, 173, 179, 185, 191, 197, 203, 209, 215, 221, 227, 233, 239, 245, 251, 257, 263, 269, 275, 281, 287, 293, 299, 305, 311, 317, 323, 329, 335, 341, 347, 353, 359, 1291, 1301, 1311, 1321, 1331, 1341, and 1351. In one embodiment the antibody or fragment thereof comprises a CDRL3 comprising a sequence selected from the group consisting of SEQ ID NOs: 6, 12, 18, 24, 30, 36, 42, 48, 54, 60, 66, 72, 78, 84, 90, 96, 102, 108, 114, 120, 126, 132, 138, 144, 150, 156, 162, 168, 174, 180, 186, 192, 198, 204, 210, 216, 222, 228, 234, 240, 246, 252, 258, 264, 270, 276, 282, 288, 294, 300, 306, 312, 318, 324, 330, 336, 342, 348, 354, 360, 1292, 1302, 1312, 1322, 1332, 1342, and 1352. In one embodiment the antibody or fragment thereof comprises a CDRH1 comprising a sequence selected from the group consisting of SEQ ID NOs: 364, 370, 376, 382, 388, 394, 400, 406, 412, 418, 424, 430, 436, 442, 448, 454, 460, 466, 472, 478, 484, 490, 496, 502, 508, 514, 520, 526, 532, 538, 544, 550, 556, 562, 568, 574, 580, 586, 592, 598, 604, 610, 616, 622, 628, 634, 640, 646, 652, 658, 664, 670, 676, 682, 688, 694, 700, 706, 712, 718, 1293, 1303, 1313, 1323, 1333, 1343, and 1353. In one embodiment the antibody or fragment thereof comprises a CDRH2 comprising a sequence selected from the group consisting of SEQ ID NOs: 365, 371, 377, 383, 389, 395, 401, 407, 413, 419, 425, 431, 437, 443, 449, 455, 461, 467, 473, 479, 485, 491, 497, 503, 509, 515, 521, 527, 533, 539, 545, 551, 557, 563, 569, 575, 581, 587, 593, 599, 605, 611, 617, 623, 629, 635, 641, 647, 653, 659, 665, 671, 677, 683, 689, 695, 701, 707, 713, 719, 1294, 1304, 1314, 1324, 1334, 1344, and 1354. In one embodiment the antibody or fragment thereof comprises a CDRH3

comprising a sequence selected from the group consisting of SEQ ID NOs: 366, 372, 378, 384, 390, 396, 402, 408, 414, 420, 426, 432, 438, 444, 450, 456, 462, 468, 474, 480, 486, 492, 498, 504, 510, 516, 522, 528, 534, 540, 546, 552, 558, 564, 570, 576, 582, 588, 594, 600, 606, 612, 618, 624, 630, 636, 642, 648, 654, 660, 666, 672, 678, 684, 690, 696, 702, 708, 714, 720, 1295, 1305, 1315, 1325, 1335, 1345, and 1355. In one embodiment the antibody or fragment thereof comprises a CDRL1, a CDRL2, a CDRL3, a CDRH1, a CDRH2, and a CDRH3, wherein each CDRL1, CDRL2, CDRL3, CDRH1, CDRH2, and CDRH3, respectively, comprises a sequence selected from the group consisting of SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 364, SEQ ID NO: 365, and SEQ ID NO: 366; SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 370, SEQ ID NO: 371, and SEQ ID NO: 372; SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 376, SEQ ID NO: 377, and SEQ ID NO: 378; SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 382, SEQ ID NO: 383, and SEQ ID NO: 384; SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 388, SEQ ID NO: 389, and SEQ ID NO: 390; SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 394, SEQ ID NO: 395, and SEQ ID NO: 396; SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 400, SEQ ID NO: 401, and SEQ ID NO: 402; SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 406, SEQ ID NO: 407, and SEQ ID NO: 408; SEQ ID NO: 52, SEQ ID NO: 53, SEQ ID NO: 54, SEQ ID NO: 412, SEQ ID NO: 413, and SEQ ID NO: 414; SEQ ID NO: 58, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 418, SEQ ID NO: 419, and SEQ ID NO: 420; SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 424, SEQ ID NO: 425, and SEQ ID NO: 426; SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 72, SEQ ID NO: 430, SEQ ID NO: 431, and SEQ ID NO: 432; SEQ ID NO: 76, SEQ ID NO: 77, SEQ ID NO: 78, SEQ ID NO: 436, SEQ ID NO: 437, and SEQ ID NO: 438; SEQ ID NO: 82, SEQ ID NO: 83, SEQ ID NO: 84, SEQ ID NO: 442, SEQ ID NO: 443, and SEQ ID NO: 444; SEQ ID NO: 88, SEQ ID NO: 89, SEQ ID NO: 90, SEQ ID NO: 448, SEQ ID NO: 449, and SEQ ID NO: 450; SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 454, SEQ ID NO: 455, and SEQ ID NO: 456; SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 460, SEQ ID NO: 461, and SEQ ID NO: 462; SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 466, SEQ ID NO: 467, and SEQ ID NO: 468; SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 472, SEQ ID NO: 473, and SEQ ID NO: 474; SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 478, SEQ ID NO: 479, and SEQ ID NO: 480; SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 484, SEQ ID NO: 485, and SEQ ID NO: 486; SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 132, SEQ ID NO: 490, SEQ

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ID NO: 654; SEQ ID NO: 298, SEQ ID NO: 299, SEQ ID NO: 300, SEQ ID NO: 658, SEQ ID NO: 659, and SEQ ID NO: 660; SEQ ID NO: 304, SEQ ID NO: 305, SEQ ID NO: 306, SEQ ID NO: 664, SEQ ID NO: 665, and SEQ ID NO: 666; SEQ ID NO: 310, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 670, SEQ ID NO: 671, and SEQ ID NO: 672; SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 318, SEQ ID NO: 676, SEQ ID NO: 677, and SEQ ID NO: 678; SEQ ID NO: 322, SEQ ID NO: 323, SEQ ID NO: 324, SEQ ID NO: 682, SEQ ID NO: 683, and SEQ ID NO: 684; SEQ ID NO: 328, SEQ ID NO: 329, SEQ ID NO: 330, SEQ ID NO: 688, SEQ ID NO: 689, and SEQ ID NO: 690; SEQ ID NO: 334, SEQ ID NO: 335, SEQ ID NO: 336, SEQ ID NO: 694, SEQ ID NO: 695, and SEQ ID NO: 696; SEQ ID NO: 340, SEQ ID NO: 341, SEQ ID NO: 342, SEQ ID NO: 700, SEQ ID NO: 701, and SEQ ID NO: 702; SEQ ID NO: 346, SEQ ID NO: 347, SEQ ID NO: 348, SEQ ID NO: 706, SEQ ID NO: 707, and SEQ ID NO: 708; SEQ ID NO: 352, SEQ ID NO: 353, SEQ ID NO: 354, SEQ ID NO: 712, SEQ ID NO: 713, and SEQ ID NO: 714; SEQ ID NO: 358, SEQ ID NO: 359, SEQ ID NO: 360, SEQ ID NO: 718, SEQ ID NO: 719, and SEQ ID NO: 720; SEQ ID NO: 1290, SEQ ID NO: 1291, SEQ ID NO: 1292, SEQ ID NO: 1293, SEQ ID NO: 1294, and SEQ ID NO: 1295; SEQ ID NO: 1300, SEQ ID NO: 1301, SEQ ID NO: 1302, SEQ ID NO: 1303, SEQ ID NO: 1304, and SEQ ID NO: 1305; SEQ ID NO: 1310, SEQ ID NO: 1311, SEQ ID NO: 1312, SEQ ID NO: 1313, SEQ ID NO: 1314, and SEQ ID NO: 1315; SEQ ID NO: 1320, SEQ ID NO: 1321, SEQ ID NO: 1322, SEQ ID NO: 1323, SEQ ID NO: 1324, and SEQ ID NO: 1325; SEQ ID NO: 1330, SEQ ID NO: 1331, SEQ ID NO: 1332, SEQ ID NO: 1333, SEQ ID NO: 1334, and SEQ ID NO: 1335; SEQ ID NO: 1340, SEQ ID NO: 1341, SEQ ID NO: 1342, SEQ ID NO: 1343, SEQ ID NO: 1344, and SEQ ID NO: 1345; SEQ ID NO: 1350, SEQ ID NO: 1351, SEQ ID NO: 1352, SEQ ID NO: 1353, SEQ ID NO: 1354, and SEQ ID NO: 1355; and SEQ ID NO: 1360, SEQ ID NO: 1361, SEQ ID NO: 1362, SEQ ID NO: 1363, SEQ ID NO: 1364, and SEQ ID NO: 1365.

[0225] In another aspect, an antigen binding protein includes 1, 2, 3, 4, 5, or 6 variant forms of the CDRs listed in TABLES 4A and 4B, each having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% sequence identity to a CDR sequence listed in TABLES 4A and 4B. Some antigen binding proteins include 1, 2, 3, 4, 5, or 6 of the CDRs listed in TABLES 4A and 4B, each or collectively differing by no more than 1, 2, 3, 4 or 5 amino acids from the CDRs listed in this table.

[0226] In various other embodiments, the antigen binding protein is derived from such antibodies. For instance, in one aspect, the antigen binding protein comprises 1, 2, 3, 4, 5 or all 6 of the CDRs listed in one of the rows for any particular antibody listed in TABLES 4A

and 4B. In another aspect, an antigen binding protein includes 1, 2, 3, 4, 5, or 6 variant forms of the CDRs listed in one of the rows for an antibody in TABLES 4A and 4B, each CDR having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% sequence identity to a CDR sequence listed in TABLES 4A and 4B. Some antigen binding proteins include 1, 2, 3, 4, 5, or 6 of the CDRs listed in one of the rows of TABLES 4A and 4B, each differing by no more than 1, 2, 3, 4 or 5 amino acids from the CDRs listed in these tables. In another aspect, the antigen binding protein comprises all 6 of the CDRS listed in a row of TABLES 4A and 4B and the total number of amino acid changes to the CDRs collectively is no more than 1, 2, 3, 4, or 5 amino acids.

[0227] In one embodiment the antibody or fragment thereof comprises a light chain comprising a sequence selected from the group consisting of SEQ ID NOs: 963, 967, 971, 975, 979, 983, 987, 991, 995, 999, 1003, 1007, 1011, 1015, 1019, 1023, 1027, 1031, 1035, 1039, 1043, 1047, 1051, 1055, 1059, 1063, 1067, 1071, 1075, 1079, 1083, 1087, 1091, 1095, 1099, 1103, 1107, 1111, 1115, 1119, 1123, 1127, 1131, 1135, 1139, 1143, 1147, 1151, 1155, 1159, 1163, 1167, 1171, 1175, 1179, 1183, 1187, 1191, 1195, 1199, 1288, 1298, 1308, 1318, 1328, 1338, 1348, and 1358. In one embodiment the antibody or fragment thereof comprises a heavy chain comprising a sequence selected from the group consisting of SEQ ID NOs: 964, 968, 972, 976, 980, 984, 988, 992, 996, 1000, 1004, 1008, 1012, 1016, 1020, 1024, 1028, 1032, 1036, 1040, 1044, 1048, 1052, 1056, 1060, 1064, 1068, 1072, 1076, 1080, 1084, 1088, 1092, 1096, 1100, 1104, 1108, 1112, 1116, 1120, 1124, 1128, 1132, 1136, 1140, 1144, 1148, 1152, 1156, 1160, 1164, 1168, 1172, 1176, 1180, 1184, 1188, 1192, 1196, 1200, 1289, 1299, 1309, 1319, 1329, 1339, 1349, and 1359. In one embodiment the antibody or fragment thereof comprises a light chain comprising a sequence selected from the group consisting of SEQ ID NOs: 963, 967, 971, 975, 979, 983, 987, 991, 995, 999, 1003, 1007, 1011, 1015, 1019, 1023, 1027, 1031, 1035, 1039, 1043, 1047, 1051, 1055, 1059, 1063, 1067, 1071, 1075, 1079, 1083, 1087, 1091, 1095, 1099, 1103, 1107, 1111, 1115, 1119, 1123, 1127, 1131, 1135, 1139, 1143, 1147, 1151, 1155, 1159, 1163, 1167, 1171, 1175, 1179, 1183, 1187, 1191, 1195, 1199, 1288, 1298, 1308, 1318, 1328, 1338, 1348, and 1358 and a heavy chain comprising a sequence selected from the group consisting of SEQ ID NOs: 964, 968, 972, 976, 980, 984, 988, 992, 996, 1000, 1004, 1008, 1012, 1016, 1020, 1024, 1028, 1032, 1036, 1040, 1044, 1048, 1052, 1056, 1060, 1064, 1068, 1072, 1076, 1080, 1084, 1088, 1092, 1096, 1100, 1104, 1108, 1112, 1116, 1120, 1124, 1128, 1132, 1136, 1140, 1144, 1148, 1152, 1156, 1160, 1164, 1168, 1172, 1176, 1180, 1184, 1188, 1192, 1196, 1200, 1289, 1299, 1309, 1319, 1329, 1339, 1349, and 1359. In one embodiment the antibody or fragment thereof comprises a

combination of a light chain and a heavy chain selected from the group consisting of a light chain comprising SEQ ID NO: 963 and a heavy chain comprising SEQ ID NO: 964; a light chain comprising SEQ ID NO: 967 and a heavy chain comprising SEQ ID NO: 968; a light chain comprising SEQ ID NO: 971 and a heavy chain comprising SEQ ID NO: 972; a light chain comprising SEQ ID NO: 975 and a heavy chain comprising SEQ ID NO: 976; a light chain comprising SEQ ID NO: 979 and a heavy chain comprising SEQ ID NO: 980; a light chain comprising SEQ ID NO: 983 and a heavy chain comprising SEQ ID NO: 984; a light chain comprising SEQ ID NO: 987 and a heavy chain comprising SEQ ID NO: 988; a light chain comprising SEQ ID NO: 991 and a heavy chain comprising SEQ ID NO: 992; a light chain comprising SEQ ID NO: 995 and a heavy chain comprising SEQ ID NO: 996; a light chain comprising SEQ ID NO: 999 and a heavy chain comprising SEQ ID NO: 1000; a light chain comprising SEQ ID NO: 1003 and a heavy chain comprising SEQ ID NO: 1004; a light chain comprising SEQ ID NO: 1007 and a heavy chain comprising SEQ ID NO: 1008; a light chain comprising SEQ ID NO: 1011 and a heavy chain comprising SEQ ID NO: 1012; a light chain comprising SEQ ID NO: 1015 and a heavy chain comprising SEQ ID NO: 1016; a light chain comprising SEQ ID NO: 1019 and a heavy chain comprising SEQ ID NO: 1020; a light chain comprising SEQ ID NO: 1023 and a heavy chain comprising SEQ ID NO: 1024; a light chain comprising SEQ ID NO: 1027 and a heavy chain comprising SEQ ID NO: 1028; a light chain comprising SEQ ID NO: 1031 and a heavy chain comprising SEQ ID NO: 1032; a light chain comprising SEQ ID NO: 1035 and a heavy chain comprising SEQ ID NO: 1036; a light chain comprising SEQ ID NO: 1039 and a heavy chain comprising SEQ ID NO: 1040; a light chain comprising SEQ ID NO: 1043 and a heavy chain comprising SEQ ID NO: 1044; a light chain comprising SEQ ID NO: 1047 and a heavy chain comprising SEQ ID NO: 1048; a light chain comprising SEQ ID NO: 1051 and a heavy chain comprising SEQ ID NO: 1052; a light chain comprising SEQ ID NO: 1055 and a heavy chain comprising SEQ ID NO: 1056; a light chain comprising SEQ ID NO: 1059 and a heavy chain comprising SEQ ID NO: 1060; a light chain comprising SEQ ID NO: 1063 and a heavy chain comprising SEQ ID NO: 1064; a light chain comprising SEQ ID NO: 1067 and a heavy chain comprising SEQ ID NO: 1068; a light chain comprising SEQ ID NO: 1071 and a heavy chain comprising SEQ ID NO: 1072; a light chain comprising SEQ ID NO: 1075 and a heavy chain comprising SEQ ID NO: 1076; a light chain comprising SEQ ID NO: 1079 and a heavy chain comprising SEQ ID NO: 1080; a light chain comprising SEQ ID NO: 1083 and a heavy chain comprising SEQ ID NO: 1084; a light chain comprising SEQ ID NO: 1087 and a heavy chain comprising SEQ ID NO: 1088; a light chain comprising SEQ ID NO: 1091 and a heavy chain comprising SEQ ID NO: 1092; a light

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chain comprising SEQ ID NO: 1348 and a heavy chain comprising SEQ ID NO: 1349; and a light chain comprising SEQ ID NO: 1358 and a heavy chain comprising SEQ ID NO: 1359.

[0228] In one embodiment the antibody or fragment thereof comprises a light chain encoded by a polynucleotide sequence selected from the group consisting of SEQ ID NOs: 961, 965, 969, 973, 977, 981, 985, 989, 993, 997, 1001, 1005, 1009, 1013, 1017, 1021, 1025, 1029, 1033, 1037, 1041, 1045, 1049, 1053, 1057, 1061, 1065, 1069, 1073, 1077, 1081, 1085, 1089, 1093, 1097, 1101, 1105, 1109, 1113, 1117, 1121, 1125, 1129, 1133, 1137, 1141, 1145, 1149, 1153, 1157, 1161, 1165, 1169, 1173, 1177, 1181, 1185, 1189, 1193, 1197, 1361, 1363, 1365, 1367, 1369, 1371, 1373, and 1375. In one embodiment the antibody or fragment thereof comprises a heavy chain encoded by a polynucleotide sequence selected from the group consisting of SEQ ID NOs: 962, 966, 970, 974, 978, 982, 986, 990, 994, 998, 1002, 1006, 1010, 1014, 1018, 1022, 1026, 1030, 1034, 1038, 1042, 1046, 1050, 1054, 1058, 1062, 1066, 1070, 1074, 1078, 1082, 1086, 1090, 1094, 1098, 1102, 1106, 1110, 1114, 1118, 1122, 1126, 1130, 1134, 1138, 1142, 1146, 1150, 1154, 1158, 1162, 1166, 1170, 1174, 1178, 1182, 1186, 1190, 1194, 1198, 1362, 1364, 1366, 1368, 1370, 1372, 1374, and 1376. In one embodiment the antibody or fragment thereof comprises a light chain encoded by a polynucleotide sequence selected from the group consisting of SEQ ID NOs: 961, 965, 969, 973, 977, 981, 985, 989, 993, 997, 1001, 1005, 1009, 1013, 1017, 1021, 1025, 1029, 1033, 1037, 1041, 1045, 1049, 1053, 1057, 1061, 1065, 1069, 1073, 1077, 1081, 1085, 1089, 1093, 1097, 1101, 1105, 1109, 1113, 1117, 1121, 1125, 1129, 1133, 1137, 1141, 1145, 1149, 1153, 1157, 1161, 1165, 1169, 1173, 1177, 1181, 1185, 1189, 1193, 1197, 1361, 1363, 1365, 1367, 1369, 1371, 1373, and 1375 and a heavy chain comprising a sequence selected from the group consisting of SEQ ID NOs: 962, 966, 970, 974, 978, 982, 986, 990, 994, 998, 1002, 1006, 1010, 1014, 1018, 1022, 1026, 1030, 1034, 1038, 1042, 1046, 1050, 1054, 1058, 1062, 1066, 1070, 1074, 1078, 1082, 1086, 1090, 1094, 1098, 1102, 1106, 1110, 1114, 1118, 1122, 1126, 1130, 1134, 1138, 1142, 1146, 1150, 1154, 1158, 1162, 1166, 1170, 1174, 1178, 1182, 1186, 1190, 1194, 1198, 1362, 1364, 1366, 1368, 1370, 1372, 1374, and 1376. In one embodiment the antibody or fragment thereof comprises a combination of light chain variable region and a heavy chain variable region selected from the group consisting of a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 961 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 962; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 965 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 966; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 969 and a heavy chain encoded by a

polynucleotide sequence comprising SEQ ID NO: 970; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 973 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 974; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 977 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 978; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 981 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 982; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 985 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 986; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 989 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 990; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 993 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 994; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 997 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 998; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1001 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1002; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1005 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1006; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1009 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1010; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1013 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1014; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1017 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1018; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1021 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1022; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1025 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1026; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1029 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1030; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1033 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1034; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1037 and a heavy chain encoded by a

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polynucleotide sequence comprising SEQ ID NO: 1174; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1177 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1178; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1181 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1182; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1185 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1186; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1189 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1190; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1193 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1194; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1197 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1198; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1361 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1362; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1363 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1364; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1365 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1366; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1367 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1368; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1369 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1370; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1371 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1372; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1373 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1374; and a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1375 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1376.

[0229] In some aspects, the invention comprises an antibody that binds to GIPR, wherein the antibody binds to GIPR and reduces the likelihood that GIPR binds to GIP.

[0230] In another aspect, the antigen binding protein comprises 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 5. Some antigen binding proteins 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 5, 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, 10, 11, 12, 13, 14 or 15 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, 10, 11, 12, 13, 14 or 15 amino acid changes relative to the full length sequences specified in TABLE 5. In one embodiment the antigen binding protein comprises a full length light chain and/or a full length heavy chain from Table 5 with the N-terminal methionine deleted. In one embodiment the antigen binding protein comprises a full length light chain and/or a full length heavy chain from Table 5 with the C-terminal lysine deleted. Other antigen binding proteins 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 5, 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 70%, 75%, 80%, 85%, 90%, 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 5.

[0231] In another embodiment, the antigen binding protein consists of a just a light or a heavy chain polypeptide as set forth in TABLE 5.

[0232] In still another aspect, antigen-binding proteins containing the CDRs, variable domains and/or full length sequences listed in TABLES 3, 4A, 4B, and 5 is a monoclonal antibody, a chimeric antibody, a humanized antibody, a human antibody, a multispecific antibody, or an antibody fragment of the foregoing. In another embodiment, the antibody fragment of the isolated antigen-binding proteins provided herein is a Fab fragment, a Fab' fragment, an F(ab')₂ fragment, an Fv fragment, a diabody, or a scFv based upon an antibody with the sequences as listed in TABLE 5.

[0233] In yet another aspect, the isolated antigen-binding protein provided in TABLE 5 can be coupled to a labeling group and can compete for binding to GIPR with an antigen binding protein of one of the isolated antigen-binding proteins provided herein.

[0234] In another embodiment, antigen binding proteins are provided that compete with one of the exemplified antibodies or functional fragments described above for specific binding to a human GIPR (e.g., SEQ ID NO: 1201). Such antigen binding proteins may bind to the same epitope as one of the antigen binding proteins described herein, or to an overlapping epitope. Antigen binding proteins and fragments that compete with the exemplified antigen binding proteins are expected to show similar functional properties. The exemplified antigen binding

proteins and fragments include those described above, including those with heavy and light chains, variable region domains and CDRs included in TABLES 3, 4A, 4B, and 5. Thus, as a specific example, the antigen binding proteins that are provided include those that compete with an antibody having:

[0235] all 6 of the CDRs listed for any antibody listed in TABLES 4A and 4B;

[0236] a VH and a VL listed for any antibody listed in TABLE 3; or

[0237] two light chains and two heavy chains as specified for any antibody listed in TABLE 5.

[0238] The antigen binding proteins that are provided include 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 the transgenic animal after completion of the immunization schedule. The spleen cells can be immortalized using any technique known in the art, e.g., by fusing them with myeloma cells to produce hybridomas. Myeloma cells for use in hybridoma-producing fusion procedures preferably are non-antibody-producing, have high fusion efficiency, and enzyme deficiencies that render them incapable of growing in certain selective media which support the growth of only the desired fused cells (hybridomas). Examples of suitable cell lines for use in mouse fusions include Sp-20, P3-X63/Ag8, P3-X63-Ag8.653, NS1/1.Ag 4 1, Sp210-Ag14, FO, NSO/U, MPC-11, MPC11-X45-GTG 1.7 and S194/5XXO Bul; examples of cell lines used in rat fusions include R210.RCY3, Y3-Ag 1.2.3, IR983F and 4B210. Other cell lines useful for cell fusions are U-266, GM1500-GRG2, LICR-LON-HMy2 and UC729-6.

[0239] In some instances, a hybridoma cell line is produced by immunizing an animal (e.g., a transgenic animal having 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. Such hybridoma cell lines, and anti-GIPR monoclonal antibodies produced by them, are aspects of the present application.

[0240] 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 increase GIPR activity.

[0241] Chimeric and humanized antibodies based upon the foregoing sequences are also provided. Monoclonal antibodies for use as therapeutic agents 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.

[0242] Generally, the goal of making a chimeric antibody is to create a chimera in which the number of amino acids from the intended patient 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.

[0243] One useful type of chimeric antibody is a “humanized” antibody. Generally, a humanized antibody is produced from a monoclonal antibody raised initially in a non-human animal. Certain amino acid residues in this monoclonal antibody, typically from non-antigen recognizing portions of the antibody, are modified to be homologous to corresponding residues in a human antibody of corresponding isotype. Humanization can be performed, for example, using various methods by substituting at least a portion of a rodent variable region for the corresponding regions of a human antibody (*see, e.g.*, United States Patent No. 5,585,089, and No. 5,693,762; Jones *et al.*, 1986, *Nature* 321:522-525; Riechmann *et al.*, 1988, *Nature* 332:323-27; Verhoeven *et al.*, 1988, *Science* 239:1534-1536).

[0244] 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. In other embodiments, the grafted variable regions are part of a single chain Fv antibody.

[0245] In certain embodiments, constant regions from species other than human can be used along with the human variable region(s) to produce hybrid antibodies.

[0246] Fully human GIPR antibodies are also provided. Methods are available for making fully human antibodies specific for a given antigen without exposing human beings to the antigen ("fully human antibodies"). One specific means provided for implementing the production of fully human antibodies is the "humanization" of the mouse humoral immune system. Introduction of human immunoglobulin (Ig) loci into mice in which the endogenous Ig genes have been inactivated is one means of producing fully human monoclonal antibodies (mAbs) in mouse, an animal that can be immunized with any desirable antigen. Using fully human antibodies can minimize the immunogenic and allergic responses that can sometimes be caused by administering mouse or mouse-derived mAbs to humans as therapeutic agents.

[0247] Fully human antibodies can be produced by immunizing transgenic animals (usually mice) that are capable of producing a repertoire of human antibodies in the absence of endogenous immunoglobulin production. Antigens for this purpose typically have six or more contiguous amino acids, and optionally are conjugated to a carrier, such as a hapten. *See, e.g., Jakobovits et al., 1993, Proc. Natl. Acad. Sci. USA 90:2551-2555; Jakobovits et al., 1993, Nature 362:255-258; and Bruggermann et al., 1993, Year in Immunol. 7:33.* In one example of such a method, transgenic animals are produced by incapacitating the endogenous mouse immunoglobulin loci encoding the mouse heavy and light immunoglobulin chains therein, and inserting into the mouse genome large fragments of human genome DNA containing loci that encode human heavy and light chain proteins. Partially modified animals, which have less than the full complement of human immunoglobulin loci, are then cross-bred to obtain an animal having all of the desired immune system modifications. When administered an immunogen, these transgenic animals produce antibodies that are immunospecific for the

immunogen but have human rather than murine amino acid sequences, including the variable regions. For further details of such methods, *see*, for example, WO96/33735 and WO94/02602. Additional methods relating to transgenic mice for making human antibodies are described in United States Patent No. 5,545,807; No. 6,713,610; No. 6,673,986; No. 6,162,963; No. 5,545,807; 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.

[0248] The transgenic mice described above, referred to herein as "HuMab" mice, contain a human immunoglobulin gene minilocus that encodes unrearranged human heavy ([mu] and [gamma]) and [kappa] light chain immunoglobulin sequences, together with targeted mutations that inactivate the endogenous [mu] and [kappa] chain loci (Lonberg *et al.*, 1994, *Nature* 368:856-859). Accordingly, the mice exhibit reduced expression of mouse IgM or [kappa] and in response to immunization, and the introduced human heavy and light chain transgenes undergo class switching and somatic mutation to generate high affinity human IgG [kappa] monoclonal antibodies (Lonberg *et al.*, *supra.*; Lonberg and Huszar, 1995, *Intern. Rev. Immunol.* 13: 65-93; Harding and Lonberg, 1995, *Ann. N.Y Acad. Sci.* 764:536-546). The preparation of HuMab mice is described in detail in Taylor *et al.*, 1992, *Nucleic Acids Research* 20:6287-6295; Chen *et al.*, 1993, *International Immunology* 5:647-656; Tuaillon *et al.*, 1994, *J. Immunol.* 152:2912-2920; Lonberg *et al.*, 1994, *Nature* 368:856-859; Lonberg, 1994, *Handbook of Exp. Pharmacology* 113:49-101; Taylor *et al.*, 1994, *International Immunology* 6:579-591; Lonberg and Huszar, 1995, *Intern. Rev. Immunol.* 13:65-93; Harding and Lonberg, 1995, *Ann. N.Y Acad. Sci.* 764:536-546; Fishwild *et al.*, 1996, *Nature Biotechnology* 14:845-851; the foregoing references are hereby incorporated by reference in their entirety for all purposes. *See*, further United States Patent No. 5,545,806; No. 5,569,825; No. 5,625,126; No. 5,633,425; No. 5,789,650; No. 5,877,397; No. 5,661,016; No. 5,814,318; No. 5,874,299; and No. 5,770,429; as well as United States Patent No. 5,545,807; International Publication Nos. WO 93/1227; WO 92/22646; and WO 92/03918, the disclosures of all of which are hereby incorporated by reference in their entirety for all purposes. Technologies utilized for producing human antibodies in these transgenic mice are disclosed also in WO 98/24893, and Mendez *et al.*, 1997, *Nature Genetics* 15:146-156, which are hereby incorporated by reference. For example, the HCo7 and HCo12 transgenic mice strains can be used to generate human monoclonal antibodies against GIPR. Further details regarding the production of human antibodies using transgenic mice are provided below.

[0249] Using hybridoma technology, antigen-specific human mAbs with the desired specificity can be produced and selected from the transgenic mice such as those described above. Such antibodies may be cloned and expressed using a suitable vector and host cell, or the antibodies can be harvested from cultured hybridoma cells.

[0250] Fully human antibodies can also 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).

[0251] The GIPR binding protein can also be a variant, mimetic, derivative or oligomer based upon the structure of GIPR antigen binding proteins have the CDRs, variable regions and/or full length chains as described above.

[0252] In one embodiment, for instance, an antigen binding protein is a variant form of the antigen binding proteins disclosed above. For instance, some of the antigen binding proteins have one or more conservative amino acid substitutions in one or more of the heavy or light chains, variable regions or CDRs.

[0253] Naturally-occurring amino acids may be divided into classes based on common side chain properties:

[0254] 1) hydrophobic: norleucine, Met, Ala, Val, Leu, Ile;

[0255] 2) neutral hydrophilic: Cys, Ser, Thr, Asn, Gln;

[0256] 3) acidic: Asp, Glu;

[0257] 4) basic: His, Lys, Arg;

[0258] 5) residues that influence chain orientation: Gly, Pro; and

[0259] 6) aromatic: Trp, Tyr, Phe.

[0260] Conservative amino acid substitutions may involve exchange of a member of one of these classes with another member of the same class. Conservative amino acid substitutions may encompass non-naturally occurring amino acid residues, which are typically incorporated by chemical peptide synthesis rather than by synthesis in biological systems. These include peptidomimetics and other reversed or inverted forms of amino acid moieties.

[0261] Non-conservative substitutions may involve the exchange of a member of one of the above classes for a member from another class. Such substituted residues may be introduced into regions of the antibody that are homologous with human antibodies, or into the non-homologous regions of the molecule.

[0262] In making such changes, according to certain embodiments, the hydropathic index of amino acids may be considered. The hydropathic profile of a protein is calculated by assigning each amino acid a numerical value ("hydropathy index") and then repetitively averaging these values along the peptide chain. Each amino acid has been assigned a hydropathic index on the basis of its hydrophobicity and charge characteristics. They are: isoleucine (+4.5); valine (+4.2); leucine (+3.8); phenylalanine (+2.8); cysteine/cystine (+2.5); methionine (+1.9); alanine (+1.8); glycine (-0.4); threonine (-0.7); serine (-0.8); tryptophan (-0.9); tyrosine (-1.3); proline (-1.6); histidine (-3.2); glutamate (-3.5); glutamine (-3.5); aspartate (-3.5); asparagine (-3.5); lysine (-3.9); and arginine (-4.5).

[0263] The importance of the hydropathic profile in conferring interactive biological function on a protein is understood in the art (*see, e.g., Kyte et al., 1982, J. Mol. Biol.* 157:105-131). It is known that certain amino acids may be substituted for other amino acids having a similar hydropathic index or score and still retain a similar biological activity. In making changes based upon the hydropathic index, in certain embodiments, the substitution of amino acids whose hydropathic indices are within ± 2 is included. In some aspects, those which are within ± 1 are included, and in other aspects, those within ± 0.5 are included.

[0264] It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity, particularly where the biologically functional protein or peptide thereby created is intended for use in immunological embodiments, as in the present case. In certain embodiments, the greatest local average hydrophilicity of a protein, as governed by the hydrophilicity of its adjacent amino acids, correlates with its immunogenicity and antigen-binding or immunogenicity, that is, with a biological property of the protein.

[0265] The following hydrophilicity values have been assigned to these amino acid residues: arginine (+3.0); lysine (+3.0); aspartate (+3.0 $\pm$ 1); glutamate (+3.0 $\pm$ 1); serine (+0.3); asparagine (+0.2); glutamine (+0.2); glycine (0); threonine (-0.4); proline (-0.5 $\pm$ 1); alanine (-0.5); histidine (-0.5); cysteine (-1.0); methionine (-1.3); valine (-1.5); leucine (-1.8); isoleucine (-1.8); tyrosine (-2.3); phenylalanine (-2.5) and tryptophan (-3.4). In making changes based upon similar hydrophilicity values, in certain embodiments, the substitution of amino acids whose hydrophilicity values are within ± 2 is included, in other embodiments, those which are within ± 1 are included, and in still other embodiments, those within ± 0.5 are included. In some instances, one may also identify epitopes from primary amino acid sequences on the basis of hydrophilicity. These regions are also referred to as "epitopic core regions."

[0266] Exemplary conservative amino acid substitutions are set forth in Table 6.

Table 8: Conservative Amino Acid Substitutions

Original Residue	Exemplary Substitutions
Ala	Ser
Arg	Lys
Asn	Gln, His
Asp	Glu
Cys	Ser
Gln	Asn
Glu	Asp
Gly	Pro
His	Asn, Gln
Ile	Leu, Val
Leu	Ile, Val
Lys	Arg, Gln, Glu
Met	Leu, Ile
Phe	Met, Leu, Tyr
Ser	Thr
Thr	Ser
Trp	Tyr
Tyr	Trp, Phe
Val	Ile, Leu

[0267] A skilled artisan will be able to determine suitable variants of polypeptides as set forth herein using well-known techniques. One skilled in the art may identify suitable areas of the molecule that may be changed without destroying activity by targeting regions not believed to be important for activity. The skilled artisan also will be able to identify residues and portions of the molecules that are conserved among similar polypeptides. In further embodiments, even areas that may be important for biological activity or for structure may be subject to conservative amino acid substitutions without destroying the biological activity or without adversely affecting the polypeptide structure.

[0268] Additionally, one skilled in the art can review structure-function studies identifying residues in similar polypeptides that are important for activity or structure. In view of such a

comparison, one can predict the importance of amino acid residues in a protein that correspond to amino acid residues important for activity or structure in similar proteins. One skilled in the art may opt for chemically similar amino acid substitutions for such predicted important amino acid residues.

[0269] One skilled in the art can also analyze the 3-dimensional structure and amino acid sequence in relation to that structure in similar polypeptides. In view of such information, one skilled in the art may predict the alignment of amino acid residues of an antibody with respect to its three dimensional structure. One skilled in the art may choose not to make radical changes to amino acid residues predicted to be on the surface of the protein, since such residues may be involved in important interactions with other molecules. Moreover, one skilled in the art may generate test variants containing a single amino acid substitution at each desired amino acid residue. These variants can then be screened using assays for GIPR activity, thus yielding information regarding which amino acids can be changed and which must not be changed. In other words, based on information gathered from such routine experiments, one skilled in the art can readily determine the amino acid positions where further substitutions should be avoided either alone or in combination with other mutations.

[0270] A number of scientific publications have been devoted to the prediction of secondary structure. See, Moulton, 1996, *Curr. Op. in Biotech.* 7:422-427; Chou *et al.*, 1974, *Biochem.* 13:222-245; Chou *et al.*, 1974, *Biochemistry* 113:211-222; Chou *et al.*, 1978, *Adv. Enzymol. Relat. Areas Mol. Biol.* 47:45-148; Chou *et al.*, 1979, *Ann. Rev. Biochem.* 47:251-276; and Chou *et al.*, 1979, *Biophys. J.* 26:367-384. Moreover, computer programs are currently available to assist with predicting secondary structure. One method of predicting secondary structure is based upon homology modeling. For example, two polypeptides or proteins that have a sequence identity of greater than 30%, or similarity greater than 40% can have similar structural topologies. The recent growth of the protein structural database (PDB) has provided enhanced predictability of secondary structure, including the potential number of folds within a polypeptide's or protein's structure. See, Holm *et al.*, 1999, *Nucl. Acid. Res.* 27:244-247. It has been suggested (Brenner *et al.*, 1997, *Curr. Op. Struct. Biol.* 7:369-376) that there are a limited number of folds in a given polypeptide or protein and that once a critical number of structures have been resolved, structural prediction will become dramatically more accurate.

[0271] Additional methods of predicting secondary structure include "threading" (Jones, 1997, *Curr. Opin. Struct. Biol.* 7:377-387; Sippl *et al.*, 1996, *Structure* 4:15-19), "profile analysis" (Bowie *et al.*, 1991, *Science* 253:164-170; Gribskov *et al.*, 1990, *Meth.*

Enzym. 183:146-159; Gribskov *et al.*, 1987, *Proc. Nat. Acad. Sci.* 84:4355-4358), and “evolutionary linkage” (See, Holm, 1999, *supra*; and Brenner, 1997, *supra*).

[0272] In some embodiments, amino acid substitutions are made that: (1) reduce susceptibility to proteolysis, (2) reduce susceptibility to oxidation, (3) alter binding affinity for forming protein complexes, (4) alter ligand or antigen binding affinities, and/or (4) confer or modify other physicochemical or functional properties on such polypeptides. For example, single or multiple amino acid substitutions (in certain embodiments, conservative amino acid substitutions) may be made in the naturally-occurring sequence. Substitutions can be made in that portion of the antibody that lies outside the domain(s) forming intermolecular contacts). In such embodiments, conservative amino acid substitutions can be used that do not substantially change the structural characteristics of the parent sequence (e.g., one or more replacement amino acids that do not disrupt the secondary structure that characterizes the parent or native antigen binding protein). Examples of art-recognized polypeptide secondary and tertiary structures are described in *Proteins, Structures and Molecular Principles* (Creighton, Ed.), 1984, W. H. New York: Freeman and Company; *Introduction to Protein Structure* (Branden and Tooze, eds.), 1991, New York: Garland Publishing; and Thornton *et al.*, 1991, *Nature* 354:105, which are each incorporated herein by reference.

[0273] Additional preferred antibody variants include cysteine variants wherein one or more cysteine residues in the parent or native amino acid sequence are deleted from or substituted with another amino acid (e.g., serine). Cysteine variants are useful, *inter alia* when antibodies must be refolded into a biologically active conformation. Cysteine variants may have fewer cysteine residues than the native antibody, and typically have an even number to minimize interactions resulting from unpaired cysteines.

[0274] The heavy and light chains, variable regions domains and CDRs that are disclosed can be used to prepare polypeptides that contain an antigen binding region that can specifically bind to GIPR. For example, one or more of the CDRs can be incorporated into a molecule (e.g., a polypeptide) covalently or noncovalently to make an immunoadhesion. An immunoadhesion may incorporate the CDR(s) as part of a larger polypeptide chain, may covalently link the CDR(s) to another polypeptide chain, or may incorporate the CDR(s) noncovalently. The CDR(s) enable the immunoadhesion to bind specifically to a particular antigen of interest (e.g., an GIPR polypeptide or epitope thereof).

[0275] Mimetics (e.g., “peptide mimetics” or “peptidomimetics”) based upon the variable region domains and CDRs that are described herein are also provided. These analogs can be peptides, non-peptides or combinations of peptide and non-peptide regions. Fauchere, 1986,

Adv. Drug Res. 15:29; Veber and Freidinger, 1985, *TINS* p. 392; and Evans *et al.*, 1987, *J. Med. Chem.* 30:1229, which are incorporated herein by reference for any purpose. Peptide mimetics that are structurally similar to therapeutically useful peptides may be used to produce a similar therapeutic or prophylactic effect. Such compounds are often developed with the aid of computerized molecular modeling. Generally, peptidomimetics are proteins that are structurally similar to an antibody displaying a desired biological activity, such as here the ability to specifically bind GIPR, but have one or more peptide linkages optionally replaced by a linkage selected from: -CH₂NH-, -CH₂S-, -CH₂-CH₂-, -CH-CH-(cis and trans), -COCH₂-, -CH(OH)CH₂-, and -CH₂SO-, by methods well known in the art. Systematic substitution of one or more amino acids of a consensus sequence with a D-amino acid of the same type (*e.g.*, D-lysine in place of L-lysine) may be used in certain embodiments to generate more stable proteins. In addition, constrained peptides comprising a consensus sequence or a substantially identical consensus sequence variation may be generated by methods known in the art (Rizo and Gierasch, 1992, *Ann. Rev. Biochem.* 61:387), incorporated herein by reference), for example, by adding internal cysteine residues capable of forming intramolecular disulfide bridges which cyclize the peptide.

[0276] Derivatives of the antigen binding proteins that are described herein are also provided. The derivatized antigen binding proteins can comprise any molecule or substance that imparts a desired property to the antibody or fragment, such as increased half-life in a particular use. The derivatized antigen binding protein can comprise, for example, a detectable (or labeling) moiety (*e.g.*, a radioactive, colorimetric, antigenic or enzymatic molecule, a detectable bead (such as a magnetic or electrodense (*e.g.*, gold) bead), or a molecule that binds to another molecule (*e.g.*, biotin or streptavidin)), a therapeutic or diagnostic moiety (*e.g.*, a radioactive, cytotoxic, or pharmaceutically active moiety), or a molecule that increases the suitability of the antigen binding protein for a particular use (*e.g.*, administration to a subject, such as a human subject, or other *in vivo* or *in vitro* uses). Examples of molecules that can be used to derivatize an antigen binding protein include albumin (*e.g.*, human serum albumin) and polyethylene glycol (PEG). Albumin-linked and PEGylated derivatives of antigen binding proteins can be prepared using techniques well known in the art. Certain antigen binding proteins include a pegylated single chain polypeptide as described herein. In one embodiment, the antigen binding protein is conjugated or otherwise linked to transthyretin (TTR) or a TTR variant. The TTR or TTR variant can be chemically modified with, for example, a chemical selected from the group consisting of dextran, poly(n-vinyl pyrrolidone),

polyethylene glycols, propylene glycol homopolymers, polypropylene oxide/ethylene oxide co-polymers, polyoxyethylated polyols and polyvinyl alcohols.

[0277] Other derivatives include covalent or aggregative conjugates of GIPR antigen binding proteins with other proteins or polypeptides, such as by expression of recombinant fusion proteins comprising heterologous polypeptides fused to the N-terminus or C-terminus of an GIPR antigen binding protein. For example, the conjugated peptide may be a heterologous signal (or leader) polypeptide, *e.g.*, the yeast alpha-factor leader, or a peptide such as an epitope tag. GIPR antigen binding protein-containing fusion proteins can comprise peptides added to facilitate purification or identification of the GIPR antigen binding protein (*e.g.*, poly-His). A GIPR antigen binding protein also can be linked to the FLAG peptide as described in Hopp *et al.*, 1988, *Bio/Technology* 6:1204; and United States Patent No. 5,011,912. The FLAG peptide is highly antigenic and provides an epitope reversibly bound by a specific monoclonal antibody (mAb), enabling rapid assay and facile purification of expressed recombinant protein. Reagents useful for preparing fusion proteins in which the FLAG peptide is fused to a given polypeptide are commercially available (Sigma, St. Louis, MO).

[0278] In some embodiments, the antigen binding protein comprises one or more labels. The term “labeling group” or “label” means any detectable label. Examples of suitable labeling groups include, but are not limited to, the following: radioisotopes or radionuclides (*e.g.*, ^3H , ^{14}C , ^{15}N , ^{35}S , ^{90}Y , ^{99}Tc , ^{111}In , ^{125}I , ^{131}I), fluorescent groups (*e.g.*, FITC, rhodamine, lanthanide phosphors), enzymatic groups (*e.g.*, horseradish peroxidase, β -galactosidase, luciferase, alkaline phosphatase), chemiluminescent groups, biotinyl groups, or predetermined polypeptide epitopes recognized by a secondary reporter (*e.g.*, leucine zipper pair sequences, binding sites for secondary antibodies, metal binding domains, epitope tags). In some embodiments, the labeling group is coupled to the antigen binding protein *via* spacer arms of various lengths to reduce potential steric hindrance. Various methods for labeling proteins are known in the art and may be used as is seen fit.

[0279] The term “effector group” means any group coupled to an antigen binding protein that acts as a cytotoxic agent. Examples for suitable effector groups are radioisotopes or radionuclides (*e.g.*, ^3H , ^{14}C , ^{15}N , ^{35}S , ^{90}Y , ^{99}Tc , ^{111}In , ^{125}I , ^{131}I). Other suitable groups include toxins, therapeutic groups, or chemotherapeutic groups. Examples of suitable groups include calicheamicin, auristatins, geldanamycin and maytansine. In some embodiments, the effector group is coupled to the antigen binding protein *via* spacer arms of various lengths to reduce potential steric hindrance.

[0280] In general, labels fall into a variety of classes, depending on the assay in which they are to be detected: a) isotopic labels, which may be radioactive or heavy isotopes; b) magnetic labels (*e.g.*, magnetic particles); c) redox active moieties; d) optical dyes; enzymatic groups (*e.g.* horseradish peroxidase, β -galactosidase, luciferase, alkaline phosphatase); e) biotinylated groups; and f) predetermined polypeptide epitopes recognized by a secondary reporter (*e.g.*, leucine zipper pair sequences, binding sites for secondary antibodies, metal binding domains, epitope tags, etc.). In some embodiments, the labeling group is coupled to the antigen binding protein *via* spacer arms of various lengths to reduce potential steric hindrance. Various methods for labeling proteins are known in the art.

[0281] Specific labels include optical dyes, including, but not limited to, chromophores, phosphors and fluorophores, with the latter being specific in many instances. Fluorophores can be either “small molecule” fluors, or proteinaceous fluors.

[0282] By “fluorescent label” is meant any molecule that may be detected *via* its inherent fluorescent properties. Suitable fluorescent labels include, but are not limited to, fluorescein, rhodamine, tetramethylrhodamine, eosin, erythrosin, coumarin, methyl-coumarins, pyrene, Malachite green, stilbene, Lucifer Yellow, Cascade BlueJ, Texas Red, IAEDANS, EDANS, BODIPY FL, LC Red 640, Cy 5, Cy 5.5, LC Red 705, Oregon green, the Alexa-Fluor dyes (Alexa Fluor 350, Alexa Fluor 430, Alexa Fluor 488, Alexa Fluor 546, Alexa Fluor 568, Alexa Fluor 594, Alexa Fluor 633, Alexa Fluor 660, Alexa Fluor 680), Cascade Blue, Cascade Yellow and R-phycoerythrin (PE) (Molecular Probes, Eugene, OR), FITC, Rhodamine, and Texas Red (Pierce, Rockford, IL), Cy5, Cy5.5, Cy7 (Amersham Life Science, Pittsburgh, PA). Suitable optical dyes, including fluorophores, are described in Molecular Probes Handbook by Richard P. Haugland, hereby expressly incorporated by reference.

[0283] Suitable proteinaceous fluorescent labels also include, but are not limited to, green fluorescent protein, including a Renilla, Ptilosarcus, or Aequorea species of GFP (Chalfie *et al.*, 1994, *Science* 263:802-805), EGFP (Clontech Labs., Inc., Genbank Accession Number U55762), blue fluorescent protein (BFP, Quantum Biotechnologies, Inc., Quebec, Canada; Stauber, 1998, *Biotechniques* 24:462-471; Heim *et al.*, 1996, *Curr. Biol.* 6:178-182), enhanced yellow fluorescent protein (EYFP, Clontech Labs., Inc.), luciferase (Ichiki *et al.*, 1993, *J. Immunol.* 150:5408-5417), β galactosidase (Nolan *et al.*, 1988, *Proc. Natl. Acad. Sci. U.S.A.* 85:2603-2607) and Renilla (WO92/15673, WO95/07463, WO98/14605, WO98/26277, WO99/49019, United States Patents No. 5292658, No. 5418155, No. 5683888, No. 5741668, No. 5777079, No. 5804387, No. 5874304, No. 5876995, No. 5925558).

[0284] Nucleic acids that encode for the antigen binding proteins described herein, or portions thereof, are also provided, including nucleic acids encoding one or both chains of an antibody, or a fragment, derivative, mutein, or variant thereof, polynucleotides encoding heavy chain variable regions or only CDRs, polynucleotides sufficient for use as hybridization probes, PCR primers or sequencing primers for identifying, analyzing, mutating or amplifying a polynucleotide encoding a polypeptide, anti-sense nucleic acids for inhibiting expression of a polynucleotide, and complementary sequences of the foregoing. The nucleic acids can be any length. They can be, for example, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 75, 100, 125, 150, 175, 200, 250, 300, 350, 400, 450, 500, 750, 1,000, 1,500, 3,000, 5,000 or more nucleotides in length, and/or can comprise one or more additional sequences, for example, regulatory sequences, and/or be part of a larger nucleic acid, for example, a vector. The nucleic acids can be single-stranded or double-stranded and can comprise RNA and/or DNA nucleotides, and artificial variants thereof (e.g., peptide nucleic acids). Any variable region provided herein may be attached to these constant regions to form complete heavy and light chain sequences. However, it should be understood that these constant regions sequences are provided as specific examples only. In some embodiments, the variable region sequences are joined to other constant region sequences that are known in the art.

[0285] Nucleic acids encoding certain antigen binding proteins, or portions thereof (*e.g.*, full length antibody, heavy or light chain, variable domain, or CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, or CDRL3) may be isolated from B-cells of mice that have been immunized with GIPR or an immunogenic fragment thereof. The nucleic acid may be isolated by conventional procedures such as polymerase chain reaction (PCR). Phage display is another example of a known technique whereby derivatives of antibodies and other antigen binding proteins may be prepared. In one approach, polypeptides that are components of an antigen binding protein of interest are expressed in any suitable recombinant expression system, and the expressed polypeptides are allowed to assemble to form antigen binding proteins.

[0286] An aspect further provides nucleic acids that hybridize to other nucleic acids under particular hybridization conditions. Methods for hybridizing nucleic acids are well-known in the art. *See, e.g.*, Current Protocols in Molecular Biology, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. As defined herein, a moderately stringent hybridization condition uses a prewashing solution containing 5x sodium chloride/sodium citrate (SSC), 0.5% SDS, 1.0 mM EDTA (pH 8.0), hybridization buffer of about 50% formamide, 6x SSC, and a hybridization temperature of 55°C (or other similar hybridization solutions, such as one containing

about 50% formamide, with a hybridization temperature of 42°C), and washing conditions of 60°C, in 0.5x SSC, 0.1% SDS. A stringent hybridization condition hybridizes in 6x SSC at 45°C, followed by one or more washes in 0.1x SSC, 0.2% SDS at 68°C. Furthermore, one of skill in the art can manipulate the hybridization and/or washing conditions to increase or decrease the stringency of hybridization such that nucleic acids comprising nucleotide sequences that are at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% identical to each other typically remain hybridized to each other.

[0287] The basic parameters affecting the choice of hybridization conditions and guidance for devising suitable conditions are set forth by, for example, Sambrook, Fritsch, and Maniatis (2001, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., *supra*; and *Current Protocols in Molecular Biology*, 1995, Ausubel *et al.*, eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4), and can be readily determined by those having ordinary skill in the art based on, *e.g.*, the length and/or base composition of the nucleic acid.

[0288] Changes can be introduced by mutation into a nucleic acid, thereby leading to changes in the amino acid sequence of a polypeptide (*e.g.*, an antibody or antibody derivative) that it encodes. Mutations can be introduced using any technique known in the art. In one embodiment, one or more particular amino acid residues are changed using, for example, a site-directed mutagenesis protocol. In another embodiment, one or more randomly selected residues is changed using, for example, a random mutagenesis protocol. However it is made, a mutant polypeptide can be expressed and screened for a desired property.

[0289] Mutations can be introduced into a nucleic acid without significantly altering the biological activity of a polypeptide that it encodes. For example, one can make nucleotide substitutions leading to amino acid substitutions at non-essential amino acid residues. Alternatively, one or more mutations can be introduced into a nucleic acid that selectively changes the biological activity of a polypeptide that it encodes. For example, the mutation can quantitatively or qualitatively change the biological activity. Examples of quantitative changes include increasing, reducing or eliminating the activity. Examples of qualitative changes include changing the antigen specificity of an antibody. In one embodiment, a nucleic acid encoding any antigen binding protein described herein can be mutated to alter the amino acid sequence using molecular biology techniques that are well-established in the art.

[0290] Another aspect provides nucleic acid molecules that are suitable for use as primers or hybridization probes for the detection of nucleic acid sequences. A nucleic acid molecule can

comprise only a portion of a nucleic acid sequence encoding a full-length polypeptide, for example, a fragment that can be used as a probe or primer or a fragment encoding an active portion of a polypeptide.

[0291] Probes based on the sequence of a nucleic acid can be used to detect the nucleic acid or similar nucleic acids, for example, transcripts encoding a polypeptide. The probe can comprise a label group, *e.g.*, a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used to identify a cell that expresses the polypeptide.

[0292] Another aspect provides vectors comprising a nucleic acid encoding a polypeptide or a portion thereof (*e.g.*, a fragment containing one or more CDRs or one or more variable region domains). Examples of vectors include, but are not limited to, plasmids, viral vectors, non-episomal mammalian vectors and expression vectors, for example, recombinant expression vectors. The recombinant expression vectors can comprise a nucleic acid in a form suitable for expression of the nucleic acid in a host cell. The recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operably linked to the nucleic acid sequence to be expressed. Regulatory sequences include those that direct constitutive expression of a nucleotide sequence in many types of host cells (*e.g.*, SV40 early gene enhancer, Rous sarcoma virus promoter and cytomegalovirus promoter), those that direct expression of the nucleotide sequence only in certain host cells (*e.g.*, tissue-specific regulatory sequences, *see*, Voss *et al.*, 1986, *Trends Biochem. Sci.* **11**:287, Maniatis *et al.*, 1987, *Science* **236**:1237, incorporated by reference herein in their entireties), and those that direct inducible expression of a nucleotide sequence in response to particular treatment or condition (*e.g.*, the metallothionin promoter in mammalian cells and the tet-responsive and/or streptomycin responsive promoter in both prokaryotic and eukaryotic systems (*see, id.*). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein.

[0293] Another aspect provides host cells into which a recombinant expression vector has been introduced. A host cell can be any prokaryotic cell (for example, *E. coli*) or eukaryotic cell (for example, yeast, insect, or mammalian cells (*e.g.*, CHO cells)). Vector DNA can be introduced into prokaryotic or eukaryotic cells *via* conventional transformation or transfection techniques. For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction

of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, for resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die), among other methods.

[0294] Expression systems and constructs in the form of plasmids, expression vectors, transcription or expression cassettes that comprise at least one polynucleotide as described above are also provided herein, as well host cells comprising such expression systems or constructs.

[0295] The antigen binding proteins provided herein may be prepared by any of a number of conventional techniques. For example, GIPR antigen binding proteins may be produced by recombinant expression systems, using any technique known in the art. *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).

[0296] Antigen binding proteins can be expressed in hybridoma cell lines (*e.g.*, in particular antibodies may be expressed in hybridomas) or in cell lines other than hybridomas.

Expression constructs encoding the 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 optimal transformation procedure used will depend upon which type of host cell is being transformed. Methods for introduction of heterologous polynucleotides into mammalian cells are well 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.

[0297] Recombinant expression constructs typically comprise a nucleic acid molecule encoding a polypeptide comprising one or more of the following: one or more CDRs provided herein; 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/or another scaffold portion of a GIPR antigen binding protein. 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). In some embodiments, vectors are used that employ protein-fragment complementation assays using protein reporters, such as dihydrofolate reductase (*see*, for example, U.S. Pat. No. 6,270,964, which is hereby incorporated by reference). Suitable expression vectors can be purchased, for example, from Invitrogen Life Technologies or BD Biosciences (formerly "Clontech"). Other useful vectors for cloning and expressing the antibodies and fragments include those described in Bianchi and McGrew, 2003, *Biotech. Biotechnol. Bioeng.* 84:439-44, which is hereby incorporated by reference. Additional suitable expression vectors are discussed, for example, in *Methods Enzymol.*, vol. 185 (D. V. Goeddel, ed.), 1990, New York: Academic Press.

[0298] 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" in certain embodiments will typically 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. Each of these sequences is discussed below.

[0299] Optionally, the vector may contain a "tag"-encoding sequence, *i.e.*, an oligonucleotide molecule located at the 5' or 3' end of the GIPR antigen binding protein 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 GIPR antigen binding protein 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 GIPR antigen binding protein by various means such as using certain peptidases for cleavage.

[0300] 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.

[0301] Flanking sequences useful in the vectors may be obtained by any of several methods well known in the art. Typically, flanking sequences useful herein 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. Here, the flanking sequence may be synthesized using the methods described herein for nucleic acid synthesis or cloning.

[0302] Whether all or only a portion of the flanking sequence is known, it may be obtained using polymerase chain reaction (PCR) and/or by screening a genomic library with a suitable probe such as an oligonucleotide and/or flanking sequence fragment from the same or another species. Where the flanking sequence is not known, a fragment of DNA containing a flanking sequence may be isolated from a larger piece of DNA that may contain, for example, a coding sequence or even another gene or genes. Isolation may be accomplished by restriction endonuclease digestion to produce the proper DNA fragment followed by isolation using agarose gel purification, Qiagen[®] column chromatography (Chatsworth, CA), or other methods known to the skilled artisan. The selection of suitable enzymes to accomplish this purpose will be readily apparent to one of ordinary skill in the art.

[0303] An origin of replication is typically a part of those prokaryotic expression vectors purchased commercially, and the origin 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 stomatitis virus (VSV), or papillomaviruses such as HPV or BPV) are useful for cloning vectors in mammalian cells. 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).

[0304] 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 methods for nucleic acid synthesis such as those described herein.

[0305] 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.

[0306] 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 promoterless 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 antigen binding protein that binds GIPR polypeptide. As a result, increased quantities of a polypeptide such as an antigen binding protein are synthesized from the amplified DNA.

[0307] 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.

[0308] 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.

[0309] Expression and cloning will typically contain a promoter that is recognized by the host organism and operably linked to the molecule encoding the GIPR antigen binding protein. 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 well known. A suitable promoter is operably linked to the DNA encoding heavy chain or light chain comprising a GIPR antigen binding protein by removing the promoter from the source DNA by restriction enzyme digestion and inserting the desired promoter sequence into the vector.

[0310] Suitable promoters for use with yeast hosts are also well known in the art. Yeast enhancers are advantageously used with yeast promoters. Suitable promoters for use with mammalian host cells are well known and include, but are not limited to, those obtained from the genomes of viruses such as polyoma virus, fowlpox virus, adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, retroviruses, hepatitis-B virus, and Simian Virus 40 (SV40). Other suitable mammalian promoters include heterologous mammalian promoters, for example, heat-shock promoters and the actin promoter.

[0311] An enhancer sequence may be inserted into the vector to increase transcription of DNA encoding light chain or heavy chain comprising a GIPR antigen binding protein by

higher eukaryotes. Enhancers are cis-acting elements of DNA, usually about 10-300 bp in length, that 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). Typically, however, an enhancer from a virus is used. The SV40 enhancer, the cytomegalovirus early promoter enhancer, the polyoma enhancer, and adenovirus enhancers known in the art are exemplary 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, 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. 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.

[0312] In one embodiment the leader sequence comprises SEQ ID NO: 1217 (MDMRVPAQLL GLLLLWLRGA RC) which is encoded by SEQ ID NO: 1218 (atggacatga gagtgctgc acagctgctg ggctgctgc tgctgtggct gagaggcgcc agatgc). In another embodiment the leader sequence comprises SEQ ID NO: 1219 (MAWALLLLTL LTQGTGSWA) which is encoded by SEQ ID NO: 1220 (atggcctggg ctctgctgct cctcaccctc ctactcagg gcacagggtc ctgggccc).

[0313] The expression vectors that are provided 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 well known to one skilled in the art.

[0314] After the vector has been constructed and a nucleic acid molecule encoding light chain, a heavy chain, or a light chain and a heavy chain comprising a GIPR antigen binding sequence 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 for an antigen-binding protein into a selected host cell may be accomplished by well-known methods including 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. These methods and other suitable methods are well known to the skilled artisan, and are set forth, for example, in Sambrook *et al.*, 2001, *supra*.

[0315] A host cell, when cultured under appropriate conditions, synthesizes an antigen binding protein 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 desired expression levels, polypeptide modifications that are desirable or necessary for activity (such as glycosylation or phosphorylation) and ease of folding into a biologically active molecule.

[0316] Mammalian cell lines available as hosts for expression are well 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 certain embodiments, cell lines may be selected through determining which cell lines have high expression levels and constitutively produce antigen binding proteins with GIPR binding properties. In another 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.

[0317] In one embodiment, the present invention is directed to an antigen binding protein produced by a cell expressing one or more of the polynucleotides identified in Tables 2, 3, 4, and 5.

[0318] In one aspect, a GIPR binding protein is administered for chronic treatment. In another aspect, the binding proteins are administered for acute therapy.

[0319] Pharmaceutical compositions that comprise a GIPR antigen binding protein are also provided and can be utilized in any of the preventive and therapeutic methods disclosed herein. In an embodiment, a therapeutically effective amount of one or a plurality of the

antigen binding proteins and a pharmaceutically acceptable diluent, carrier, solubilizer, emulsifier, preservative, and/or adjuvant are also provided. Acceptable formulation materials are nontoxic to recipients at the dosages and concentrations employed.

[0320] In certain embodiments, the pharmaceutical composition may contain formulation materials for modifying, maintaining or preserving, for example, the pH, osmolarity, viscosity, clarity, color, isotonicity, odor, sterility, stability, rate of dissolution or release, adsorption or penetration of the composition. In such embodiments, suitable formulation materials include, but are not limited to, amino acids (such as glycine, glutamine, asparagine, arginine or lysine); antimicrobials; antioxidants (such as ascorbic acid, sodium sulfite or sodium hydrogen-sulfite); buffers (such as borate, bicarbonate, Tris-HCl, citrates, phosphates or other organic acids); bulking agents (such as mannitol or glycine); chelating agents (such as ethylenediamine tetraacetic acid (EDTA)); complexing agents (such as caffeine, polyvinylpyrrolidone, beta-cyclodextrin or hydroxypropyl-beta-cyclodextrin); fillers; monosaccharides; disaccharides; and other carbohydrates (such as glucose, mannose or dextrans); proteins (such as serum albumin, gelatin or immunoglobulins); coloring, flavoring and diluting agents; emulsifying agents; hydrophilic polymers (such as polyvinylpyrrolidone); low molecular weight polypeptides; salt-forming counterions (such as sodium); preservatives (such as benzalkonium chloride, benzoic acid, salicylic acid, thimerosal, phenethyl alcohol, methylparaben, propylparaben, chlorhexidine, sorbic acid or hydrogen peroxide); solvents (such as glycerin, propylene glycol or polyethylene glycol); sugar alcohols (such as mannitol or sorbitol); suspending agents; surfactants or wetting agents (such as pluronics, PEG, sorbitan esters, polysorbates such as polysorbate 20, polysorbate, triton, tromethamine, lecithin, cholesterol, tyloxapal); stability enhancing agents (such as sucrose or sorbitol); tonicity enhancing agents (such as alkali metal halides, preferably sodium or potassium chloride, mannitol sorbitol); delivery vehicles; diluents; excipients and/or pharmaceutical adjuvants. REMINGTON'S PHARMACEUTICAL SCIENCES, 18th Edition, (A.R. Genrmo, ed.), 1990, Mack Publishing Company provides additional details and options for suitable agents that can be incorporated into the pharmaceutical compositions.

[0321] In certain embodiments, the optimal pharmaceutical composition will be determined by one skilled in the art depending upon, for example, the intended route of administration, delivery format and desired dosage. *See*, for example, REMINGTON'S PHARMACEUTICAL SCIENCES, *supra*. In certain embodiments, such compositions may influence the physical state, stability, rate of *in vivo* release and rate of *in vivo* clearance of the antigen binding proteins disclosed. In certain embodiments, the primary vehicle or carrier

in a pharmaceutical composition may be either aqueous or non-aqueous in nature. For example, a suitable vehicle or carrier may be water for injection or physiological saline solution. In certain embodiments, GIPR antigen binding protein compositions may be prepared for storage by mixing the selected composition having the desired degree of purity with optional formulation agents (REMMINGTON'S PHARMACEUTICAL SCIENCES, *supra*) in the form of a lyophilized cake or an aqueous solution. Further, in certain embodiments, the GIPR antigen binding protein may be formulated as a lyophilizate using appropriate excipients such as sucrose.

[0322] The pharmaceutical compositions can be selected for parenteral delivery.

Alternatively, the compositions may be selected for inhalation or for delivery through the digestive tract, such as orally. Preparation of such pharmaceutically acceptable compositions is within the skill of the art.

[0323] The formulation components are present preferably in concentrations that are acceptable to the site of administration. In certain embodiments, buffers are used to maintain the composition at physiological pH or at a slightly lower pH, typically within a pH range of from about 5 to about 8.

[0324] When parenteral administration is contemplated, the therapeutic compositions may be provided in the form of a pyrogen-free, parenterally acceptable aqueous solution comprising the desired human GIPR antigen binding protein in a pharmaceutically acceptable vehicle. A particularly suitable vehicle for parenteral injection is sterile distilled water in which the GIPR antigen binding protein is formulated as a sterile, isotonic solution, properly preserved. In certain embodiments, the preparation can involve the formulation of the desired molecule with an agent, such as injectable microspheres, bio-erodible particles, polymeric compounds (such as polylactic acid or polyglycolic acid), beads or liposomes, that may provide controlled or sustained release of the product which can be delivered *via* depot injection. In certain embodiments, hyaluronic acid may also be used, having the effect of promoting sustained duration in the circulation. In certain embodiments, implantable drug delivery devices may be used to introduce the desired antigen binding protein.

[0325] Certain pharmaceutical compositions are formulated for inhalation. In some embodiments, GIPR antigen binding proteins are formulated as a dry, inhalable powder. In specific embodiments, GIPR antigen binding protein inhalation solutions may also be formulated with a propellant for aerosol delivery. In certain embodiments, solutions may be nebulized. Pulmonary administration and formulation methods therefore are further described in International Patent Application No. PCT/US94/001875, which is incorporated by

reference and describes pulmonary delivery of chemically modified proteins. Some formulations can be administered orally. GIPR antigen binding proteins that are administered in this fashion can be formulated with or without carriers customarily used in the compounding of solid dosage forms such as tablets and capsules. In certain embodiments, a capsule may be designed to release the active portion of the formulation at the point in the gastrointestinal tract when bioavailability is maximized and pre-systemic degradation is minimized. Additional agents can be included to facilitate absorption of the GIPR antigen binding protein. Diluents, flavorings, low melting point waxes, vegetable oils, lubricants, suspending agents, tablet disintegrating agents, and binders may also be employed.

[0326] Some pharmaceutical compositions comprise an effective quantity of one or a plurality of GIPR antigen binding proteins in a mixture with non-toxic excipients that are suitable for the manufacture of tablets. By dissolving the tablets in sterile water, or another appropriate vehicle, solutions may be prepared in unit-dose form. Suitable excipients include, but are not limited to, inert diluents, such as calcium carbonate, sodium carbonate or bicarbonate, lactose, or calcium phosphate; or binding agents, such as starch, gelatin, or acacia; or lubricating agents such as magnesium stearate, stearic acid, or talc.

[0327] Additional pharmaceutical compositions will be evident to those skilled in the art, including formulations involving GIPR binding proteins in sustained- or controlled-delivery formulations. Techniques for formulating a variety of other sustained- or controlled-delivery means, such as liposome carriers, bio-erodible microparticles or porous beads and depot injections, are also known to those skilled in the art. *See*, for example, International Patent Application No. PCT/US93/00829, which is incorporated by reference and describes controlled release of porous polymeric microparticles for delivery of pharmaceutical compositions. Sustained-release preparations may include semipermeable polymer matrices in the form of shaped articles, *e.g.*, films, or microcapsules. Sustained release matrices may include polyesters, hydrogels, polylactides (as disclosed in U.S. Patent No. 3,773,919 and European Patent Application Publication No. EP 058481, each of which is incorporated by reference), copolymers of L-glutamic acid and gamma ethyl-L-glutamate (Sidman *et al.*, 1983, *Biopolymers* 2:547-556), poly (2-hydroxyethyl-methacrylate) (Langer *et al.*, 1981, *J. Biomed. Mater. Res.* 15:167-277 and Langer, 1982, *Chem. Tech.* 12:98-105), ethylene vinyl acetate (Langer *et al.*, 1981, *supra*) or poly-D(-)-3-hydroxybutyric acid (European Patent Application Publication No. EP 133,988). Sustained release compositions may also include liposomes that can be prepared by any of several methods known in the art. *See, e.g.*, Epstein *et al.*, 1985, *Proc. Natl. Acad. Sci. U.S.A.* 82:3688-3692; European Patent

Application Publication Nos. EP 036,676; EP 088,046 and EP 143,949, incorporated by reference.

[0328] Pharmaceutical compositions used for *in vivo* administration are typically provided as sterile preparations. Sterilization can be accomplished by filtration through sterile filtration membranes. When the composition is lyophilized, sterilization using this method may be conducted either prior to or following lyophilization and reconstitution. Compositions for parenteral administration can be stored in lyophilized form or in a solution. Parenteral compositions generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

[0329] In certain formulations, an antigen binding protein has a concentration of at least 10 mg/mL, 20 mg/mL, 30 mg/mL, 40 mg/mL, 50 mg/mL, 60 mg/mL, 70 mg/mL, 80 mg/mL, 90 mg/mL, 100 mg/mL or 150 mg/mL. In one embodiment, a pharmaceutical composition comprises the antigen binding protein, a buffer and polysorbate. In other embodiments, the pharmaceutical composition comprises an antigen binding protein, a buffer, sucrose and polysorbate. An example of a pharmaceutical composition is one containing 50-100 mg/mL of antigen binding protein, 5-20 mM sodium acetate, 5-10% w/v sucrose, and 0.002-0.008% w/v polysorbate. Certain compositions, for instance, contain 65-75 mg/mL of an antigen binding protein in 9-11 mM sodium acetate buffer, 8-10% w/v sucrose, and 0.005-0.006% w/v polysorbate. The pH of certain such formulations is in the range of 4.5-6. Other formulations have a pH of 5.0-5.5 (e.g., pH of 5.0, 5.2 or 5.4).

[0330] Once the pharmaceutical composition has been formulated, it may be stored in sterile vials as a solution, suspension, gel, emulsion, solid, crystal, or as a dehydrated or lyophilized powder. Such formulations may be stored either in a ready-to-use form or in a form (e.g., lyophilized) that is reconstituted prior to administration. Kits for producing a single-dose administration unit are also provided. Certain kits contain a first container having a dried protein and a second container having an aqueous formulation. In certain embodiments, kits containing single and multi-chambered pre-filled syringes (e.g., liquid syringes and lyosyringes) are provided. The therapeutically effective amount of a GIPR antigen binding protein-containing pharmaceutical composition to be employed will depend, for example, upon the therapeutic context and objectives. One skilled in the art will appreciate that the appropriate dosage levels for treatment will vary depending, in part, upon the molecule delivered, the indication for which the GIPR antigen binding protein is being used, the route of administration, and the size (body weight, body surface or organ size) and/or condition

(the age and general health) of the patient. In certain embodiments, the clinician may titer the dosage and modify the route of administration to obtain the optimal therapeutic effect.

[0331] Dosing frequency will depend upon the pharmacokinetic parameters of the particular GIPR antigen binding protein in the formulation used. Typically, a clinician administers the composition until a dosage is reached that achieves the desired effect. The composition may therefore be administered as a single dose, or as two or more doses (which may or may not contain the same amount of the desired molecule) over time, or as a continuous infusion *via* an implantation device or catheter. Appropriate dosages may be ascertained through use of appropriate dose-response data. In certain embodiments, the antigen binding proteins can be administered to patients throughout an extended time period. In certain embodiments, the antigen binding protein is dosed every two weeks, every month, every two months, every three months, every four months, every five months, or every six months.

[0332] The route of administration of the pharmaceutical composition is in accord with known methods, *e.g.*, orally, through injection by intravenous, intraperitoneal, intracerebral (intra-parenchymal), intracerebroventricular, intramuscular, intra-ocular, intraarterial, intraportal, or intralesional routes; by sustained release systems or by implantation devices. In certain embodiments, the compositions may be administered by bolus injection or continuously by infusion, or by implantation device.

[0333] The composition also may be administered locally *via* implantation of a membrane, sponge or another appropriate material onto which the desired molecule has been absorbed or encapsulated. In certain embodiments, where an implantation device is used, the device may be implanted into any suitable tissue or organ, and delivery of the desired molecule may be *via* diffusion, timed-release bolus, or continuous administration.

[0334] It also may be desirable to use GIPR antigen binding protein pharmaceutical compositions according to the disclosed *ex vivo*. In such instances, cells, tissues or organs that have been removed from the patient are exposed to GIPR antigen binding protein pharmaceutical compositions after which the cells, tissues and/or organs are subsequently implanted back into the patient.

[0335] A physician will be able to select an appropriate treatment indication and target lipid levels depending on the individual profile of a particular patient. One well-accepted standard for guiding treatment of hyperlipidemia is the Third Report of the National Cholesterol Education Program (NCEP) Expert Panel on Detection, Evaluation, and Treatment of the High Blood Cholesterol in Adults (Adult Treatment Panel III) Final Report, National

Institutes of Health, NIH Publication No. 02-5215 (2002), the printed publication of which is hereby incorporated by reference in its entirety.

[0336] The efficacy of a particular dose can be assessed by reference to biomarkers or improvement in certain physiological parameters. Examples of suitable biomarkers include, the ratio of free cholesterol to plasma lipid, free cholesterol to membrane protein, phosphatidylcholine to sphingomyelin, or HDL-C levels.

[0337] Also provided herein are compositions comprising a GIPR antigen binding protein and one or more additional therapeutic agents, as well as methods in which such agents are administered concurrently or sequentially with a GIPR antigen binding protein for use in the preventive and therapeutic methods disclosed herein. The one or more additional agents can be co-formulated with a GIPR antigen binding protein or can be co-administered with a GIPR antigen binding protein. In general, the therapeutic methods, compositions and compounds may also be employed in combination with other therapeutics in the treatment of various disease states, with the additional agents being administered concurrently.

[0338] . In one aspect the present invention is directed to a method of treating a subject with a metabolic disorder, the method comprising administering to the subject a therapeutically effective amount of a GLP-1 receptor agonist and a therapeutically effective amount of a GIPR antagonist that specifically binds to a protein having an amino acid sequence having at least 90% amino acid sequence identity to an amino acid sequence of a GIPR.

[0339] A “GLP-1 receptor agonist” refers to compounds having GLP-1 receptor activity. Such exemplary compounds include exendins, exendin analogs, exendin agonists, GLP-1(7-37), GLP-1(7-37) analogs, GLP-1(7-37) agonists, and the like. The GLP-1 receptor agonist compounds may optionally be amidated. The terms “GLP-1 receptor agonist” and “GLP-1 receptor agonist compound” have the same meaning.

[0340] The term “exendin” includes naturally occurring (or synthetic versions of naturally occurring) exendin peptides that are found in the salivary secretions of the Gila monster. Exendins of particular interest include exendin-3 and exendin-4. The exendins, exendin analogs, and exendin agonists for use in the methods described herein may optionally be amidated, and may also be in an acid form, pharmaceutically acceptable salt form, or any other physiologically active form of the molecule.

[0341] In one embodiment, the molar ratio of a GLP-1 receptor agonist to a GIPR antagonist is from about 1:1 to 1:110, 1:1 to 1:100, 1:1 to 1:75, 1:1 to 1:50, 1:1 to 1:25, 1:1 to 1:10, 1:1 to 1:5, and 1:1. In one embodiment, the molar ratio of a GIPR antagonist to a GLP-1 receptor

agonist is from about 1:1 to 1:110, 1:1 to 1:100, 1:1 to 1:75, 1:1 to 1:50, 1:1 to 1:25, 1:1 to 1:10, and 1:1 to 1:5.

[0342] In one embodiment, the GLP-1 receptor agonist is used in combination with the GIPR antagonist at therapeutically effective molar ratios of between about 1:1.5 to 1:150, preferably 1:2 to 1:50.

[0343] In one embodiment, the GLP-1 receptor agonist and the GIPR antagonist are present in doses that are at least about 1.1 to 1.4, 1.5, 2, 3, 4, 5, 6, 7, 8, 9, or 10 fold lower than the doses of each compound alone required to treat a condition and/or disease.

[0344] In one embodiment, the GLP-1 receptor agonist is GLP-1(7-37) or a GLP-1(7-37) analog.

[0345] In one embodiment, the GLP-1 receptor agonist is selected from the group consisting of exenatide, liraglutide, lixisenatide, albiglutide, dulaglutide, semaglutide, and taspoglutide.

[0346] In one aspect the present invention is directed to a method of treatment comprising administering to a subject a therapeutically effective amount of at least one GLP-1 receptor agonist in combination with administration of at least one GIPR antagonist which upon administration to a subject with symptoms of a metabolic disorder provides sustained beneficial effects.

[0347] In one embodiment, administration of at least one GLP-1 receptor agonist in combination with administration of at least one GIPR antagonist provides sustained beneficial effects of at least one symptom of a metabolic disorder.

[0348] In one embodiment, the therapeutically effective amounts of the GLP-1 receptor agonist and the GIPR antagonist are combined prior to administration to the subject.

[0349] In one embodiment, the therapeutically effective amounts of the GLP-1 receptor agonist and the GIPR antagonist are administered to the subject sequentially.

[0350] In one embodiment, the therapeutically effective amounts of a GLP-1 receptor agonist and a GIPR antagonist are synergistically effective amounts.

[0351] Exendin-4 (HGEFTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGAPPPS-NH₂ (SEQ ID NO: 1223)) is a peptide found in the saliva of the Gila monster, *Heloderma suspectum*; and exendin-3 (HSDGTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGAPPPS-NH₂ (SEQ ID NO: 1224)) is a peptide found in the saliva of the beaded lizard, *Heloderma horridum*.

Exendins have some amino acid sequence similarity to some members of the glucagon-like peptide (GLP) family. For example, exendin-4 has about 53% sequence identity with glucagon-like peptide-1(GLP-1)(7-37) (HAEGTFTSDVSSYLEGQAAKEFIAWLKGRG (SEQ ID NO: 1244)). However, exendin-4 is transcribed from a distinct gene, not the Gila

monster homolog of the mammalian proglucagon gene from which GLP-1 is expressed. Additionally, exendin-4 is not an analog of GLP-1(7-37) because the structure of synthetic exendin-4 peptide was not created by sequential modification of the structure of GLP-1. Nielsen et al., *Current Opinion in Investigational Drugs*, 4(4):401-405 (2003).

[0352] Synthetic exendin-4, also known as exenatide, is commercially available as BYETTA® (Amylin Pharmaceuticals, Inc. and Eli Lilly and Company). A once weekly formulation of exenatide is described in WO 2005/102293, the disclosure of which is incorporated by reference herein.

[0353] “Exendin analog” refers to peptides which elicit a biological activity of an exendin reference peptide, preferably having a potency equal to or better than the exendin reference peptide (e.g., exendin-4), or within five orders of magnitude (plus or minus) of potency compared to the exendin reference peptide, when evaluated by art-known measures such as receptor binding and/or competition studies as described, e.g., by Hargrove et al., *Regulatory Peptides*, 141:113-119 (2007), the disclosure of which is incorporated by reference herein. Preferably, the exendin analogs will bind in such assays with an affinity of less than 1 μ M, and more preferably with an affinity of less than 3 nM, less than 1 nM, or less than 0.1 nM. The term “exendin analog” may also be referred to as “exendin agonist”. In a preferred embodiment, the exendin analog is an exendin-4 analog.

[0354] Exendin analogs also include the peptides described herein which have been chemically derivatized or altered, for example, peptides with non-natural amino acid residues (e.g., taurine, β -amino acid residues, γ -amino acid residues, and D-amino acid residues), C-terminal functional group modifications, such as amides, esters, and C-terminal ketone modifications and N-terminal functional group modifications, such as acylated amines, Schiff bases, or cyclization, as found, for example, in the amino acid pyroglutamic acid. Exendin analogs may also contain other chemical moieties, such as peptide mimetics.

[0355] Exemplary exendins and exendin analogs exendin-4 (SEQ ID NO: 1223); exendin-3 (SEQ ID NO: 1224); Leu¹⁴-exendin-4 (SEQ ID NO: 1225); Leu¹⁴,Phe²⁵-exendin-4 (SEQ ID NO: 1226); Leu¹⁴,Ala¹⁹,Phe²⁵-exendin-4 (SEQ ID NO: 1227); exendin-4(1-30) (SEQ ID NO: 1228); Leu¹⁴-exendin-4(1-30) (SEQ ID NO: 1229); Leu¹⁴,Phe²⁵-exendin-4(1-30) (SEQ ID NO: 1230); Leu¹⁴,Ala¹⁹,Phe²⁵-exendin-4(1-30) (SEQ ID NO: 1231); exendin-4(1-28) (SEQ ID NO: 1232); Leu¹⁴-exendin-4(1-28) (SEQ ID NO: 1233); Leu¹⁴,Phe²⁵-exendin-4(1-28) (SEQ ID NO: 1234); Leu¹⁴,Ala¹⁹,Phe²⁵-exendin-4 (1-28) (SEQ ID NO: 1235); Leu¹⁴,Lys^{17,20},Ala¹⁹,Glu²¹,Phe²⁵,Gln²⁸-exendin-4 (SEQ ID NO: 1236); Leu¹⁴,Lys^{17,20},Ala¹⁹,Glu²¹,Gln²⁸-exendin-4 (SEQ ID NO: 1237); octylGly¹⁴,Gln²⁸-exendin-4

(SEQ ID NO: 1238); Leu¹⁴, Gln²⁸, octylGly³⁴-exendin-4 (SEQ ID NO: 1239); Phe⁴, Leu¹⁴, Gln²⁸, Lys³³, Glu³⁴, Ile^{35,36}, Ser³⁷-exendin-4(1-37) (SEQ ID NO: 1240); Phe⁴, Leu¹⁴, Lys^{17,20}, Ala¹⁹, Glu²¹, Gln²⁸-exendin-4 (SEQ ID NO: 1241); Val¹¹, Ile¹³, Leu¹⁴, Ala¹⁶, Lys²¹, Phe²⁵-exendin-4 (SEQ ID NO: 1242); exendin-4-Lys⁴⁰ (SEQ ID NO: 1243); lixisenatide (Sanofi-Aventis/Zealand Pharma); CJC-1134 (ConjuChem, Inc.); [N^ε-(17-carboxyheptadecanoic acid)Lys²⁰]exendin-4-NH₂ (SEQ ID NO: 1268); [N^ε-(17-carboxyhepta-decanoyl)Lys³²]exendin-4-NH₂ (SEQ ID NO: 1269); [desamino-His¹, N^ε-(17-carboxyheptadecanoyl)Lys²⁰]exendin-4-NH₂ (SEQ ID NO: 1270); [Arg^{12,27}, NLe¹⁴, N^ε-(17-carboxy-heptadecanoyl)Lys³²]exendin-4-NH₂ (SEQ ID NO: 1271); [N^ε-(19-carboxy-nonadecanoylamino)Lys²⁰]exendin-4-NH₂ (SEQ ID NO: 1272); [N^ε-(15-carboxypentadecanoylamino)Lys²⁰]exendin-4-NH₂ (SEQ ID NO: 1273); [N^ε-(13-carboxytridecanoylamino)Lys²⁰]exendin-4-NH₂ (SEQ ID NO: 1274); [N^ε-(11-carboxy-undecanoyl-amino)Lys²⁰]exendin-4-NH₂ (SEQ ID NO: 1275); exendin-4-Lys⁴⁰(e-MPA)-NH₂ (SEQ ID NO: 1276); exendin-4-Lys⁴⁰(e-AEEA-AEEA-MPA)-NH₂ (SEQ ID NO: 1277); exendin-4-Lys⁴⁰(e-AEEA-MPA)-NH₂ (SEQ ID NO: 1278); exendin-4-Lys⁴⁰(e-MPA)-albumin (SEQ ID NO: 1279); exendin-4-Lys⁴⁰(e-AEEA-AEEA-MPA)-albumin (SEQ ID NO: 1280); exendin-4-Lys⁴⁰(e-AEEA-MPA)-albumin (SEQ ID NO: 1281); and the like. AEEA refers to [2-(2-amino)ethoxy]acetic acid. EDA refers to ethylenediamine. MPA refers to maleimidopropionic acid. The exendins and exendin analogs may optionally be amidated.

[0356] In one embodiment, the GLP-1 receptor agonist compound is an exendin-4 analog that has at least 80% sequence identity to exendin-4 (SEQ ID NO: 1223); at least 85% sequence identity to exendin-4 (SEQ ID NO: 1223); at least 90% sequence identity to exendin-4 (SEQ ID NO: 1223); or at least 95% sequence identity to exendin-4 (SEQ ID NO: 1223).

[0357] Other exendins and exendin analogs useful in the methods described herein include those described in WO 98/05351; WO 99/07404; WO 99/25727; WO 99/25728; WO 99/40788; WO 00/41546; WO 00/41548; WO 00/73331; WO 01/51078; WO 03/099314; U.S. Pat. No. 6,956,026; U.S. Pat. No. 6,506,724; U.S. Pat. No. 6,703,359; U.S. Pat. No. 6,858,576; U.S. Pat. No. 6,872,700; U.S. Pat. No. 6,902,744; U.S. Pat. No. 7,157,555; U.S. Pat. No. 7,223,725; U.S. Pat. No. 7,220,721; US Publication No. 2003/0036504; and US Publication No. 2006/0094652, the disclosures of which are incorporated by reference herein in their entirety.

[0358] "GLP-1(7-37) analogs" refers to peptides which elicit a biological activity similar to that of GLP-1(7-37), when evaluated by 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, the term “GLP-1(7-37) analog” refers to a peptide that has an amino acid sequence with 1, 2, 3, 4, 5, 6, 7 or 8 amino acid substitutions, insertions, deletions, or a combination of two or more thereof, when compared to the amino acid sequence of GLP-1(7-37). In one embodiment, the GLP-1(7-37) analog is GLP-1(7-36)-NH₂. GLP-1(7-37) analogs include the amidated forms, the acid form, the pharmaceutically acceptable salt form, and any other physiologically active form of the molecule.

[0359] Exemplary GLP-1(7-37) and GLP-1(7-37) analogs include GLP-1(7-37) (SEQ ID NO: 1244); GLP-1(7-36)-NH₂ (SEQ ID NO: 1245); liraglutide (VICTOZA® from Novo Nordisk); albiglutide (SYNCRIA® from GlaxoSmithKline); taspoglutide (Hoffman La-Roche); dulaglutide (also known LY2189265; Eli Lilly and Company); LY2428757 (Eli Lilly and Company); desamino-His⁷,Arg²⁶,Lys³⁴(N^ε-(γ-Glu(N-α-hexadecanoyl))) -GLP-1(7-37) (core peptide disclosed as SEQ ID NO: 1282); desamino-His⁷,Arg²⁶,Lys³⁴(N^ε-octanoyl)-GLP-1(7-37) (SEQ ID NO: 1283); Arg^{26,34},Lys³⁸(N^ε-(ω-carboxypentadecanoyl))-GLP-1(7-38) (SEQ ID NO: 1284); Arg^{26,34},Lys³⁶(N^ε-(γ-Glu(N-α-hexadecanoyl))) -GLP-1(7-36) (core peptide disclosed as SEQ ID NO: 1285); Aib^{8,35},Arg^{26,34},Phe³¹-GLP-1(7-36)) (SEQ ID NO: 1246); HXaa₈EGTFTSDVSSYLEXaa₂₂Xaa₂₃AAKEFIXaa₃₀WLXaa₃₃Xaa₃₄G Xaa₃₆Xaa₃₇; wherein Xaa₃ is A, V, or G; Xaa₂₂ is G, K, or E; Xaa₂₃ is Q or K; Xaa₃₀ is A or E; Xaa₃₃ is V or K; Xaa₃₄ is K, N, or R; Xaa₃₆ is R or G; and Xaa₃₇ is G, H, P, or absent (SEQ ID NO: 1247); Arg³⁴-GLP-1(7-37) (SEQ ID NO: 1248); Glu³⁰-GLP-1(7-37) (SEQ ID NO: 1249); Lys²²-GLP-1(7-37) (SEQ ID NO: 1250); Gly^{8,36},Glu²²-GLP-1(7-37) (SEQ ID NO: 1251); Val⁸,Glu²²,Gly³⁶-GLP-1(7-37) (SEQ ID NO: 1252); Gly^{8,36},Glu²²,Lys³³,Asn³⁴-GLP-1(7-37) (SEQ ID NO: 1253); Val⁸,Glu²²,Lys³³,Asn³⁴,Gly³⁶-GLP-1(7-37) (SEQ ID NO: 1254); Gly^{8,36},Glu²²,Pro³⁷-GLP-1(7-37) (SEQ ID NO: 1255); Val⁸,Glu²²,Gly³⁶Pro³⁷-GLP-1(7-37) (SEQ ID NO: 1256); Gly^{8,36},Glu²²,Lys³³,Asn³⁴,Pro³⁷-GLP-1(7-37) (SEQ ID NO: 1257); Val⁸,Glu²²,Lys³³,Asn³⁴,Gly³⁶,Pro³⁷-GLP-1(7-37) (SEQ ID NO: 1258); Gly^{8,36},Glu²²-GLP-1(7-36) (SEQ ID NO: 1259); Val⁸,Glu²²,Gly³⁶-GLP-1(7-36) (SEQ ID NO: 1260); Val⁸,Glu²²,Asn³⁴,Gly³⁶-GLP-1(7-36) (SEQ ID NO: 1261); Gly^{8,36},Glu²²,Asn³⁴-GLP-1(7-36) (SEQ ID NO: 1262). Each of the GLP-1(7-37) and GLP-1(7-37) analogs may optionally be amidated.

[0360] In one embodiment, the GLP-1(7-37) or GLP-1(7-37) analogs are covalently linked (directly or by a linking group) to an Fc portion of an immunoglobulin (e.g., IgG, IgE, IgG, and the like). For example, any one of SEQ ID NOs:25-40 may be covalently linked to the Fc

portion of an immunoglobulin comprising the sequence of:

AESKYGPPCPPCPAPX_{aa16}X_{aa17}X_{aa18}GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQ
EDPEVQFNWYVDGVEVHNAKTKPREEQFX_{aa80}STYRVVSVLTVLHQDWLNGKEYK
CKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTTPVLDSGDSFFLYSRLTVDKSRWQEGNVFSCSVMEALHN
HYTQKSLSLSLGX_{aa230}; wherein X_{aa16} is P or E; X_{aa17} is F, V or A; X_{aa18} is L, E or A;

X_{aa80} is N or A; and X_{aa230} is K or absent (SEQ ID NO: 1263). The linking group may be any chemical moiety (e.g., amino acids and/or chemical groups). In one embodiment, the linking group is (-GGGS-)_x (SEQ ID NO: 1264) where x is 1, 2, 3, 4, 5 or 6; preferably 2, 3 or 4; more preferably 3. In one embodiment, the GLP-1(7-37) analog covalently linked to the Fc portion of an immunoglobulin comprises the amino acid sequence:

HGEGTFTSDVSSYLEEQAAKEFIWLKGGGGGGSGGGGSAGGGSAESKYGPPCP
PCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEV
HNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKG
QPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVL
DSGDSFFLYSR LTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLSLG (SEQ ID
NO: 1265).

[0361] In another embodiment, the GLP-1(7-37) or GLP-1(7-37) analog may be covalently linked (directly or through a linking group) to one or two polyethylene glycol molecules. For example, a GLP-1(7-37) analog may comprise the amino acid sequence: HX_{aa8}EGTFTSDVS
SYLEX_{aa22}QAAKEFIWLX_{aa33}KGGPSSGAPPPC₄₅C₄₆-Z, wherein X_{aa8} is: D-Ala, G, V,
L, I, S or T; X_{aa22} is G, E, D or K; X_{aa33} is: V or I; and Z is OH or NH₂, (SEQ ID NO: 1266),
and, optionally, wherein (i) one polyethylene glycol moiety is covalently attached to C₄₅, (ii)
one polyethylene glycol moiety is covalently attached to C₄₆, or (iii) one polyethylene glycol
moiety is attached to C₄₅ and one polyethylene glycol moiety is attached to C₄₆. In one
embodiment, the GLP-1(7-37) analog is HVEGTFTSDVSSYLEEQAAKEFI
AWLIKGGPSSGAPPPC₄₅C₄₆-NH₂ (SEQ ID NO: 1267) and, optionally, wherein (i) one
polyethylene glycol moiety is covalently attached to C₄, (ii) one polyethylene glycol moiety is
covalently attached to C₄₆, or (iii) one polyethylene glycol moiety is attached to C₄₅ and one
polyethylene glycol moiety is attached to C₄₆.

[0362] In one embodiment, the GLP-1 receptor agonist compound is a peptide that has at
least 80% sequence identity to GLP-1(7-37) (SEQ ID NO: 1244); at least 85% sequence
identity to GLP-1(7-37) (SEQ ID NO: 1244); at least 90% sequence identity to GLP-1(7-37)
(SEQ ID NO: 1244); or at least 95% sequence identity to GLP-1(7-37) (SEQ ID NO: 1244).

[0363] GLP-1 receptor agonist compounds may be prepared by processes well known in the art, e.g., peptide purification as described in Eng et al., *J. Biol. Chem.*, 265:20259-62 (1990); standard solid-phase peptide synthesis techniques as described in Raufman et al., *J. Biol. Chem.*, 267:21432-37 (1992); recombinant DNA techniques as described in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2d Ed., Cold Spring Harbor (1989); and the like.

[0364] Table 7. Examples of GLP-1 Agonist Sequences

SEQ ID NO:	Sequence	Description
1223	HGEGTFTSDLSKQMEEEEAVRLFIEWLKN GGPSSGAPPPS	Exendin-4
1224	HSDGTFTSDLSKQMEEEEAVRLFIEWLKN GGPSSGAPPPS	Exendin-3
1225	HGEGTFTSDLSKQLEEEEAVRLFIEWLKN GGPSSGAPPPS	Leu ¹⁴ -exendin-4
1226	HGEGTFTSDLSKQLEEEEAVRLFIEFLKN GGPSSGAPPPS	Leu ¹⁴ ,Phe ²⁵ -exendin-4
1227	HGEGTFTSDLSKQLEEEAARLFIEFLKN GGPSSGAPPPS	Leu ¹⁴ ,Ala ¹⁹ ,Phe ²⁵ -exendin-4
1228	HGEGTFTSDLSKQMEEEEAVRLFIEWLKN GG	exendin-4(1-30)
1229	HGEGTFTSDLSKQLEEEEAVRLFIEWLKN GG	Leu ¹⁴ -exendin-4(1-30)
1230	HGEGTFTSDLSKQLEEEEAVRLFIEFLKN GG	Leu ¹⁴ ,Phe ²⁵ -exendin-4(1-30)
1231	HGEGTFTSDLSKQLEEEAARLFIEFLKN GG	Leu ¹⁴ ,Ala ¹⁹ ,Phe ²⁵ -exendin-4(1-30)
1232	HGEGTFTSDLSKQMEEEEAVRLFIEWLKN	exendin-4(1-28)
1233	HGEGTFTSDLSKQLEEEEAVRLFIEWLKN	Leu ¹⁴ -exendin-4(1-28)
1234	HGEGTFTSDLSKQLEEEEAVRLFIEFLKN	Leu ¹⁴ ,Phe ²⁵ -exendin-4(1-28)
1235	HGEGTFTSDLSKQLEEEAARLFIEFLKN	Leu ¹⁴ ,Ala ¹⁹ ,Phe ²⁵ -exendin-4 (1-28)
1236	HGEGTFTSDLSKQLEEKAAKEFIEFLKQ GGPSSGAPPPS	Leu ¹⁴ ,Lys ^{17,20} ,Ala ¹⁹ ,Glu ²¹ ,Phe ²⁵ ,Gln ²⁸ -exendin-4
1237	HGEGTFTSDLSKQLEEKAAKEFIEWLKQ GGPSSGAPPPS	Leu ¹⁴ ,Lys ^{17,20} ,Ala ¹⁹ ,Glu ²¹ ,Gln ²⁸ -exendin-4
1238	HGEGTFTSDLSKQ(octylG)EEEAVRLFIEWLKQGGPSSGAPPPS	octylGly ¹⁴ ,Gln ²⁸ -exendin-4
1239	HGEGTFTSDLSKQLEEEEAVRLFIEWLKQGGPSS(octylG)APPPS	Leu ¹⁴ ,Gln ²⁸ ,octylGly ³⁴ -exendin-4
1240	HGEFTFTSDLSKQLEEEEAVRLFIEWLKQGGPSKEIIS	Phe ⁴ ,Leu ¹⁴ ,Gln ²⁸ ,Lys ³³ ,Glu ³⁴ ,Ile ^{35,36} ,Ser ³⁷ -exendin-4(1-37)
1241	HGEFTFTSDLSKQLEEKAAKEFIEWLKQGGPSSGAPPPS	Phe ⁴ ,Leu ¹⁴ ,Lys ^{17,20} ,Ala ¹⁹ ,Glu ²¹ ,Gln ²⁸ -exendin-4
1242	HGEGTFTSDLVKILEAEAVRKFIEFLKNGGPSSGAPPPS	Val ¹¹ ,Ile ¹³ ,Leu ¹⁴ ,Ala ¹⁶ ,Lys ²¹ ,Phe ²⁵ -exendin-4

1243	HGEGTFTSDLKQMEEEAVRLFIEWLKN GGPSSGAPPPSK	exendin-4-Lys ⁴⁰
1244	HAEGTFTSDVSSYLEGQAAKEFIAWLK GRG	GLP-1(7-37)
1245	HAEGTFTSDVSSYLEGQAAKEFIAWLK GR	GLP-1(7-36)-NH ₂
1246	H(Aib)EGTFTSDVSSYLEGQAAREFIA FLVR(Aib)R	Aib ^{8,35} ,Arg ^{26,34} ,Phe ³¹ -GLP-1(7- 36))
1247	HXaa ₈ EGTFTSDVSSYLEXaa ₂₂ Xaa ₂₃ AA KEFI Xaa ₃₀ WLXaa ₃₃ Xaa ₃₄ GXaa ₃₆ Xaa ₃₇ wherein Xaa ₈ is A, V, or G Xaa ₂₂ is G, K, or E Xaa ₂₃ is Q or K Xaa ₃₀ is A or E Xaa ₃₃ is V or K Xaa ₃₄ is K, N, or R Xaa ₃₆ is R or G and Xaa ₃₇ is G, H, P, or absent	HXaa ₈ EGTFTSDVSSYLEXaa ₂₂ X aa ₂₃ AAKEFIXaa ₃₀ WLXaa ₃₃ Xaa ₃₄ G Xaa ₃₆ Xaa ₃₇ wherein Xaa ₈ is A, V, or G Xaa ₂₂ is G, K, or E Xaa ₂₃ is Q or K Xaa ₃₀ is A or E Xaa ₃₃ is V or K Xaa ₃₄ is K, N, or R Xaa ₃₆ is R or G and Xaa ₃₇ is G, H, P, or absent
1248	HAEGTFTSDVSSYLEGQAAKEFIAWLVR GRG	Arg ³⁴ -GLP-1(7-37)
1249	HAEGTFTSDVSSYLEGQAAKEFIEWLVR GRG	Glu ³⁰ -GLP-1(7-37)
1250	HAEGTFTSDVSSYLEKQAAKEFIAWLVR GRG	Lys ²² -GLP-1(7-37)
1251	HGEGTFTSDVSSYLEEQAAKEFIAWLVR GGG	Gly ^{8,36} ,Glu ²² -GLP-1(7-37)
1252	HVEGTFTSDVSSYLEEQAAKEFIAWLVR GGG	Val ⁸ ,Glu ²² ,Gly ³⁶ -GLP-1(7-37)
1253	HGEGTFTSDVSSYLEEQAAKEFIAWLKN GGG	Gly ^{8,36} ,Glu ²² ,Lys ³³ ,Asn ³⁴ -GLP- 1(7-37)
1254	HVEGTFTSDVSSYLEEQAAKEFIAWLKN GGG	Val ⁸ ,Glu ²² ,Lys ³³ ,Asn ³⁴ ,Gly ³⁶ - GLP-1(7-37)
1255	HGEGTFTSDVSSYLEEQAAKEFIAWLVR GGP	Gly ^{8,36} ,Glu ²² ,Pro ³⁷ -GLP-1(7-37)
1256	HVEGTFTSDVSSYLEEQAAKEFIAWLVR GGP	Val ⁸ ,Glu ²² ,Gly ³⁶ ,Pro ³⁷ -GLP-1(7- 37)
1257	HGEGTFTSDVSSYLEEQAAKEFIAWLKN GGP	Gly ^{8,36} ,Glu ²² ,Lys ³³ ,Asn ³⁴ ,Pro ³⁷ - GLP-1(7-37)
1258	HVEGTFTSDVSSYLEEQAAKEFIAWLKN GGP	Val ⁸ ,Glu ²² ,Lys ³³ ,Asn ³⁴ ,Gly ³⁶ ,Pro ³⁷ -GLP-1(7-37)
1259	HGEGTFTSDVSSYLEEQAAKEFIAWLVR GG	Gly ^{8,36} ,Glu ²² -GLP-1(7-36)
1260	HVEGTFTSDVSSYLEEQAAKEFIAWLVR GG	Val ⁸ ,Glu ²² ,Gly ³⁶ -GLP-1(7-36)
1261	HVEGTFTSDVSSYLEEQAAKEFIAWLVR GG	Val ⁸ ,Glu ²² ,Asn ³⁴ ,Gly ³⁶ -GLP-1(7- 36)
1262	HGEGTFTSDVSSYLEEQAAKEFIAWLVR GG	Gly ^{8,36} ,Glu ²² ,Asn ³⁴ -GLP-1(7-36)

1263	<p>AESKYGPPCPPCPAPXaa₁₆Xaa₁₇Xaa₁₈ GGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSQEDPEVQFNWYVDGVEVHNAKTKP REEQFXaa₈₀STYRVVSVLTVLHQDWLNG KEYKCKVSNKGLPSSIEKTISKAKGQPR EPQVYITLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSD DGSFFLYSRLTVDKSRWQEGNVFSCSVM HEALHNHYTQKSLSLGLXaa₂₃₀ wherein Xaa₁₆ is P or E Xaa₁₇ is F, V or A Xaa₁₈ is L, E or A Xaa₈₀ is N or A and Xaa₂₃₀ is K or absent</p>	Fc portion of an immunoglobulin
1264	(-GGGGS-) _x where x is 1, 2, 3, 4, 5 or 6	Linker
1265	<p>HGEGTFTSDVSSYLEEQAAKEFIAWLVK GGGGGGGSGGGGSGGGGSAESKYGPPCP PCPAPEAAGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSQEDPEVQFNWYVDGVE VHNAKTKPREEQFNSTYRVVSVLTVLHQ DWLNGKEYKCKVSNKGLPSSIEKTISKA KGQPREPQVYITLPPSQEEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKTTP PVLDS DGSFFLYSR LTVDKSRWQEGNVFSCSVMHEALHNHYT QKSLSLGLG</p>	Fc portion of an immunoglobulin
1266	<p>HXaa₈EGTFTSDVS SYLEXaa₂₂QAAKEFIAWLXaa₃₃KGGPSS GAPPPC₄₅C₄₆-Z, wherein Xaa₈ is: D-Ala, G, V, L, I, S or T Xaa₂₂ is G, E, D or K Xaa₃₃ is: V or I and Z is OH or NH₂ and, optionally, wherein (i) one polyethylene glycol moiety is covalently attached to C₄₅, (ii) one polyethylene glycol moiety is covalently attached to C₄₆, or (iii) one polyethylene glycol moiety is attached to C₄₅ and one polyethylene glycol moiety is attached to C₄₆.</p>	GLP analog
1267	<p>HVEGTFTSDVSSYLEEQAAKEFIAWLIK GGPSSGAPPPC₄₅C₄₆-NH₂ and, optionally, wherein (i) one polyethylene glycol moiety is covalently attached to C₄, (ii) one polyethylene</p>	GLP analog

	glycol moiety is covalently attached to C ₄₅ , or (iii) one polyethylene glycol moiety is attached to C ₄₅ and one polyethylene glycol moiety is attached to C ₄₆	
1268	HGEGTFTSDLSKQMEEEEAVKLFIEWLKN GGPSSGAPPPS	[N ^ε -(17-carboxyheptadecanoic acid)Lys ²⁰]exendin-4-NH ₂
1269	HGEGTFTSDLSKQMEEEEAVRLFIEWLKN GGPKSGAPPPS	[N ^ε -(17-carboxyheptadecanoyl)Lys ³²]exendin-4-NH ₂
1270	GEGTFTSDLSKQMEEEEAVKLFIEWLKNG GPSSGAPPPS	[desamino-His ¹ ,N ^ε -(17-carboxyheptadecanoyl)Lys ²⁰]exendin-4-NH ₂
1271	HGEGTFTSDLSRQNorLeEEEAVRLFIEWLKN WLRNGGPKSGAPPPS	[Arg ^{12,27} ,NLe ¹⁴ ,N ^ε -(17-carboxyheptadecanoyl)Lys ³²]exendin-4-NH ₂
1272	HGEGTFTSDLSKQMEEEEAVKLFIEWLKN GGPSSGAPPPS	[N ^ε -(19-carboxy-nonadecanoylamino)Lys ²⁰]-exendin-4-NH ₂
1273	HGEGTFTSDLSKQMEEEEAVKLFIEWLKN GGPSSGAPPPS	[N ^ε -(15-carboxypentadecanoylamino)Lys ²⁰]-exendin-4-NH ₂
1274	HGEGTFTSDLSKQMEEEEAVKLFIEWLKN GGPSSGAPPPS	[N ^ε -(13-carboxytridecanoylamino)Lys ²⁰]exendin-4-NH ₂
1275	HGEGTFTSDLSKQMEEEEAVKLFIEWLKN GGPSSGAPPPS	[N ^ε -(11-carboxy-undecanoylamino)Lys ²⁰]exendin-4-NH ₂
1276	HGEGTFTSDLSKQMEEEEAVRLFIEWLKN GGPSSGAPPPSK	exendin-4-Lys ⁴⁰ (e-MPA)-NH ₂
1277	HGEGTFTSDLSKQMEEEEAVRLFIEWLKN GGPSSGAPPPSK	exendin-4-Lys ⁴⁰ (e-AEEA-AEEA-MPA)-NH ₂
1278	HGEGTFTSDLSKQMEEEEAVRLFIEWLKN GGPSSGAPPPSK	exendin-4-Lys ⁴⁰ (e-AEEA-MPA)-NH ₂
1279	HGEGTFTSDLSKQMEEEEAVRLFIEWLKN GGPSSGAPPPSK	exendin-4-Lys ⁴⁰ (e-MPA)-albumin
1280	HGEGTFTSDLSKQMEEEEAVRLFIEWLKN GGPSSGAPPPSK	exendin-4-Lys ⁴⁰ (e-AEEA-AEEA-MPA)-albumin
1281	HGEGTFTSDLSKQMEEEEAVRLFIEWLKN GGPSSGAPPPSK	exendin-4-Lys ⁴⁰ (e-AEEA-MPA)-albumin
1282	AEGTFTSDVSSYLEGQAAREFIAWLKVRG	desamino-His ⁷ ,Arg ²⁶ ,Lys ³⁴ (N ^ε -(γ-Glu(N-α-hexadecanoyl)))-GLP-1(7-37) (core peptide disclosed as SEQ ID NO: 1282)
1283	AEGTFTSDVSSYLEGQAAREFIAWLKVRG	desamino-His ⁷ ,Arg ²⁶ ,Lys ³⁴ (N ^ε -octanoyl)-GLP-1(7-37)
1284	HAEGTFTSDVSSYLEGQAAREFIAWLVRGRGK	Arg ^{26,34} ,Lys ³⁸ (N ^ε -(ω-carboxypentadecanoyl)))-GLP-1(7-38)
1285	HAEGTFTSDVSSYLEGQAAREFIAWLVRGRGK	Arg ^{26,34} ,Lys ³⁶ (N ^ε -(γ-Glu(N-α-hexadecanoyl)))-GLP-1(7-36)

		(core peptide disclosed as SEQ ID NO: 1285)
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[0365] AEEA refers to [2-(2-amino)ethoxy]acetic acid

[0366] EDA refers to ethylenediamine.

[0367] MPA refers to maleimidopropionic acid.

[0368] The disclosure also provides pharmaceutical compositions comprising the GLP-1 receptor agonist compounds described herein and a pharmaceutically acceptable carrier. The GLP-1 receptor agonist compounds can be present in the pharmaceutical composition in a therapeutically effective amount and can be present in an amount to provide a minimum blood plasma level of the GLP-1 receptor agonist compound necessary for therapeutic efficacy. Such pharmaceutical compositions are known in the art and described, e.g., in U.S. Pat. No. 7,521,423; U.S. Pat. No. 7,456,254; WO 2000/037098; WO 2005/021022; WO 2005/102293; WO 2006/068910; WO 2006/125763; WO 2009/068910; US Publication No. 2004/0106547; and the like, the disclosures of which are incorporated herein by reference.

[0369] Pharmaceutical compositions containing the GLP-1 receptor agonist compounds described herein may be provided for peripheral administration, such as parenteral (e.g., subcutaneous, intravenous, intramuscular), a continuous infusion (e.g., intravenous drip, intravenous bolus, intravenous infusion), topical, nasal, or oral administration. Suitable pharmaceutically acceptable carriers and their formulation are described in standard formulation treatises, such as Remington's Pharmaceutical Sciences by Martin; and Wang et al., *Journal of Parenteral Science and Technology*, Technical Report No. 10, Supp. 42:2S (1988). The GLP-1 receptor agonist compounds described herein can be provided in parenteral compositions for injection or infusion. They can, for example, be suspended in water; an inert oil, such as a vegetable oil (e.g., sesame, peanut, olive oil, and the like); or other pharmaceutically acceptable carrier. In one embodiment, the compounds are suspended in an aqueous carrier, for example, in an isotonic buffer solution at a pH of about 3.0 to 8.0, or about 3.0 to 5.0. The compositions may be sterilized by conventional sterilization techniques or may be sterile filtered. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions, such as pH buffering agents.

[0370] Useful buffers include for example, acetic acid buffers. 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 agents such as dextrose, boric acid, sodium tartrate, propylene glycol, polyols (such as mannitol and sorbitol), or other inorganic or organic solutes. In one embodiment for intravenous infusion, the formulation may comprise (i) the GLP-1 receptor agonist compound, (2) sterile water, and, optionally (3) sodium chloride, dextrose, or a combination thereof.

[0371] Carriers or excipients can also be used to facilitate administration of the GLP-1 receptor agonist compounds. Examples of carriers and excipients include calcium carbonate, calcium phosphate, various sugars such as lactose, glucose, or sucrose, or types of starch, cellulose derivatives, gelatin, vegetable oils, polyethylene glycols and physiologically compatible solvents.

[0372] The GLP-1 receptor agonist compounds can also be formulated as pharmaceutically acceptable salts (e.g., acid addition salts) and/or complexes thereof. Pharmaceutically acceptable salts are non-toxic salts at the concentration at which they are administered. Pharmaceutically acceptable salts include acid addition salts such as those containing sulfate, hydrochloride, phosphate, sulfamate, acetate, citrate, lactate, tartrate, methanesulfonate, ethanesulfonate, benzenesulfonate, p-toluenesulfonate, cyclohexylsulfamate and quinate. Pharmaceutically acceptable salts can be obtained from acids such as hydrochloric acid, sulfuric acid, phosphoric acid, sulfamic acid, acetic acid, citric acid, lactic acid, tartaric acid, malonic acid, methanesulfonic acid, ethanesulfonic acid, benzenesulfonic acid, p-toluenesulfonic acid, cyclohexylsulfamic acid, and quinic acid. Such salts may be prepared by, for example, reacting the free acid or base forms of the product with one or more equivalents of the appropriate base or acid in a solvent or medium in which the salt is insoluble, or in a solvent such as water which is then removed in vacuo or by freeze-drying or by exchanging the ions of an existing salt for another ion on a suitable ion exchange resin.

[0373] Exemplary pharmaceutical formulations of GLP-1 receptor agonist compounds are described in U.S. Pat. No. 7,521,423, U.S. Pat. No. 7,456,254; US Publication No 2004/0106547, WO 2006/068910, WO 2006/125763, and the like, the disclosures of which are incorporated by reference herein.

[0374] The therapeutically effective amount of the GLP-1 receptor agonist compounds described herein for use in the methods described herein will typically be from about 0.01 µg to about 5 mg; about 0.1 µg to about 2.5 mg; about 1 µg to about 1 mg; about 1 µg to about

50 µg; or about 1 µg to about 25 µg. Alternatively, the therapeutically effective amount of the GLP-1 receptor agonist compounds may be from about 0.001 µg to about 100 µg based on the weight of a 70 kg patient; or from about 0.01 µg to about 50 µg based on the weight of a 70 kg patient. These therapeutically effective doses may be administered once/day, twice/day, thrice/day, once/week, biweekly, or once/month, depending on the formulation. The exact dose to be administered is determined, for example, by the formulation, such as an immediate release formulation or an extended release formulation. For transdermal, nasal or oral dosage forms, the dosage may be increased from about 5-fold to about 10-fold.

[0375] In certain embodiments the GLP-1 receptor agonist will be administered concurrently with the GIPR antigen binding protein. In one embodiment the GLP-1 receptor agonist will be administered after the GIPR antigen binding protein. In one embodiment the GLP-1 receptor agonist will be administered before the GIPR antigen binding protein. In certain embodiments the subject or patient will already be being treated with a GLP-1 receptor agonist before being subjected to further treatment with a GIPR antigen binding protein.

[0376] The GIPR antigen binding proteins that are provided herein are useful for detecting GIPR in biological samples. For instance, the GIPR antigen binding proteins can be used in diagnostic assays, *e.g.*, binding assays to detect and/or quantify GIPR expressed in serum.

[0377] The antigen binding proteins of the described can be used for diagnostic purposes to detect, diagnose, or monitor diseases and/or conditions associated with GIPR. The disclosed antigen binding proteins provide a means for the detection of the presence of GIPR in a sample using classical immunohistological methods known to those of skill in the art (*e.g.*, Tijssen, 1993, *Practice and Theory of Enzyme Immunoassays*, Vol 15 (Eds R.H. Burdon and P.H. van Knippenberg, Elsevier, Amsterdam); Zola, 1987, *Monoclonal Antibodies: A Manual of Techniques*, pp. 147-158 (CRC Press, Inc.); Jalkanen *et al.*, 1985, *J. Cell. Biol.* 101:976-985; Jalkanen *et al.*, 1987, *J. Cell Biol.* 105:3087-3096). The detection of GIPR can be performed *in vivo* or *in vitro*.

[0378] Diagnostic applications provided herein include use of the antigen binding proteins to detect expression of GIPR. Examples of methods useful in the detection of the presence of GIPR include immunoassays, such as the enzyme linked immunosorbent assay (ELISA) and the radioimmunoassay (RIA).

[0379] For diagnostic applications, the antigen binding protein typically will be labeled with a detectable labeling group. Suitable labeling groups include, but are not limited to, the following: radioisotopes or radionuclides (*e.g.*, ³H, ¹⁴C, ¹⁵N, ³⁵S, ⁹⁰Y, ⁹⁹Tc, ¹¹¹In, ¹²⁵I, ¹³¹I), fluorescent groups (*e.g.*, FITC, rhodamine, lanthanide phosphors), enzymatic groups (*e.g.*,

horseradish peroxidase, β -galactosidase, luciferase, alkaline phosphatase), chemiluminescent groups, biotinyl groups, or predetermined polypeptide epitopes recognized by a secondary reporter (*e.g.*, leucine zipper pair sequences, binding sites for secondary antibodies, metal binding domains, epitope tags). In some embodiments, the labeling group is coupled to the antigen binding protein *via* spacer arms of various lengths to reduce potential steric hindrance. Various methods for labeling proteins are known in the art and may be used.

[0380] In some embodiments, the GIPR antigen binding protein is isolated and measured using techniques known in the art. *See, for example, Harlow and Lane, 1988, Antibodies: A Laboratory Manual*, New York: Cold Spring Harbor (ed. 1991 and periodic supplements); *John E. Coligan, ed., 1993, Current Protocols In Immunology* New York: John Wiley & Sons.

[0381] Another aspect of the disclosed provides for detecting the presence of a test molecule that competes for binding to GIPR with the antigen binding proteins provided. An example of one such assay would involve detecting the amount of free antigen binding protein in a solution containing an amount of GIPR in the presence or absence of the test molecule. An increase in the amount of free antigen binding protein (*i.e.*, the antigen binding protein not bound to GIPR) would indicate that the test molecule is capable of competing for GIPR binding with the antigen binding protein. In one embodiment, the antigen binding protein is labeled with a labeling group. Alternatively, the test molecule is labeled and the amount of free test molecule is monitored in the presence and absence of an antigen binding protein.

[0382] GIPR binding proteins can be used to treat, diagnose or ameliorate, a metabolic condition or disorder. In one embodiment, the metabolic disorder to be treated is diabetes, *e.g.*, type 2 diabetes. In another embodiment, the metabolic condition or disorder is obesity. In other embodiments the metabolic condition or disorder is dyslipidemia, elevated glucose levels, elevated insulin levels or diabetic nephropathy. For example, a metabolic condition or disorder that can be treated or ameliorated using a GIPR binding peptide includes a state in which a human subject has a fasting blood glucose level of 125 mg/dL or greater, for example 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190, 195, 200 or greater than 200 mg/dL. Blood glucose levels can be determined in the fed or fasted state, or at random. The metabolic condition or disorder can also comprise a condition in which a subject is at increased risk of developing a metabolic condition. For a human subject, such conditions include a fasting blood glucose level of 100 mg/dL. Conditions that can be treated using a pharmaceutical composition comprising a GIPR binding protein can also be found in the American Diabetes Association Standards of Medical Care in Diabetes Care-2011, American

Diabetes Association, Diabetes Care Vol. 34, No. Supplement 1, S11-S61, 2010, incorporated herein by reference.

[0383] In application, a metabolic disorder or condition, such as Type 2 diabetes, elevated glucose levels, elevated insulin levels, dyslipidemia, obesity or diabetic nephropathy, can be treated by administering a therapeutically effective dose of a GIPR binding protein to a patient in need thereof. The administration can be performed as described herein, such as by IV injection, intraperitoneal (IP) injection, subcutaneous injection, intramuscular injection, or orally in the form of a tablet or liquid formation. In some situations, a therapeutically effective or preferred dose of a GIPR binding protein can be determined by a clinician. A therapeutically effective dose of GIPR binding protein will depend, *inter alia*, upon the administration schedule, the unit dose of agent administered, whether the GIPR binding protein is administered in combination with other therapeutic agents, the immune status and the health of the recipient. The term “therapeutically effective dose,” as used herein, means an amount of GIPR binding protein that elicits a biological or medicinal response in a tissue system, animal, or human being sought by a researcher, medical doctor, or other clinician, which includes alleviation or amelioration of the symptoms of the disease or disorder being treated, *i.e.*, an amount of a GIPR binding protein that supports an observable level of one or more desired biological or medicinal response, for example lowering blood glucose, insulin, triglyceride, or cholesterol levels; reducing body weight; or improving glucose tolerance, energy expenditure, or insulin sensitivity.

[0384] It is noted that a therapeutically effective dose of a GIPR binding protein can also vary with the desired result. Thus, for example, in situations in which a lower level of blood glucose is indicated a dose of GIPR binding protein will be correspondingly higher than a dose in which a comparatively lower level of blood glucose is desired. Conversely, in situations in which a higher level of blood glucose is indicated a dose of GIPR binding protein will be correspondingly lower than a dose in which a comparatively higher level of blood glucose is desired.

[0385] In various embodiments, a subject is a human having a blood glucose level of 100 mg/dL or greater can be treated with a GIPR binding protein.

[0386] In one embodiment, a method of the instant disclosure comprises first measuring a baseline level of one or more metabolically-relevant compounds such as glucose, insulin, cholesterol, lipid in a subject. A pharmaceutical composition comprising a GIPR binding protein is then administered to the subject. After a desired period of time, the level of the one or more metabolically-relevant compounds (*e.g.*, blood glucose, insulin, cholesterol, lipid) in

the subject is again measured. The two levels can then be compared in order to determine the relative change in the metabolically-relevant compound in the subject. Depending on the outcome of that comparison another dose of the pharmaceutical composition comprising a GIPR binding protein can be administered to achieve a desired level of one or more metabolically-relevant compound.

[0387] It is noted that a pharmaceutical composition comprising a GIPR binding protein can be co-administered with another compound. The identity and properties of compound co-administered with the GIPR binding protein will depend on the nature of the condition to be treated or ameliorated. A non-limiting list of examples of compounds that can be administered in combination with a pharmaceutical composition comprising a GIPR binding protein include rosiglitazone, pioglitazone, repaglinide, nateglinide, metformin, exenatide, stagliptin, pramlintide, glipizide, glimepirideacarbose, and miglitol.

[0388] Also provided are kits for practicing the disclosed methods. Such kits can comprise a pharmaceutical composition such as those described herein, including nucleic acids encoding the peptides or proteins provided herein, vectors and cells comprising such nucleic acids, and pharmaceutical compositions comprising such nucleic acid-containing compounds, which can be provided in a sterile container. Optionally, instructions on how to employ the provided pharmaceutical composition in the treatment of a metabolic disorder can also be included or be made available to a patient or a medical service provider.

[0389] In one aspect, a kit comprises (a) a pharmaceutical composition comprising a therapeutically effective amount of a GIPR binding protein; and (b) one or more containers for the pharmaceutical composition. Such a kit can also comprise instructions for the use thereof; the instructions can be tailored to the precise metabolic disorder being treated. The instructions can describe the use and nature of the materials provided in the kit. In certain embodiments, kits include instructions for a patient to carry out administration to treat a metabolic disorder, such as elevated glucose levels, elevated insulin levels, obesity, type 2 diabetes, dyslipidemia or diabetic nephropathy.

[0390] Instructions can be printed on a substrate, such as paper or plastic, etc., and can be present in the kits as a package insert, in the labeling of the container of the kit or components thereof (e.g., associated with the packaging), etc. In other embodiments, the instructions are present as an electronic storage data file present on a suitable computer readable storage medium, e.g. CD-ROM, diskette, etc. In yet other embodiments, the actual instructions are not present in the kit, but means for obtaining the instructions from a remote source, such as over the internet, are provided. An example of this embodiment is a kit that

includes a web address where the instructions can be viewed and/or from which the instructions can be downloaded.

[0391] Often it will be desirable that some or all components of a kit are packaged in suitable packaging to maintain sterility. The components of a kit can be packaged in a kit containment element to make a single, easily handled unit, where the kit containment element, e.g., box or analogous structure, may or may not be an airtight container, e.g., to further preserve the sterility of some or all of the components of the kit.

[0392] Example 1

[0393] Materials and Methods--Yeast Display

[0394] Construction of the yeast displayed molecules and libraries used gBlocks and degenerate codon primers (IDT DNA). Standard PCR and overlap assembly PCR was done using Q5 HotStart polymerase (NEB). Transformation by electroporation into yeast strain BJ5464 (ATCC) was done using homologous recombination of inserts and digested vector previously purified through PCR purification kits (Qiagen). Briefly, BJ5464 cells were picked from YPD agar plates and grown overnight at 30 °C in YPD media. Cells were then expanded to a starting OD of 0.2 and grown for 6 hrs at 30 °C. After pelleting and resuspension in room temperature 10 mM Tris, 100 mM LiOAc, 0.6 M sorbitol, 10mM DTT was added followed by a 30 min incubation at RT with gentle shaking at 220rpm. Cells were pelleted and washed in cold 1 M sorbitol, 1 mM CaCl₂ and resuspended at 2×10^{10} cells/mL. Electroporation of 0.5ug of DNA in 5uL volume/cuvette with 120uL of cells using the following settings: 540 V; 25 uF; ∞ ohms. Cells were quickly rescued with 2mL of YPD, 0.5 M sorbitol, 0.5 mM CaCl₂. Following a 1hr recovery at 30 °C, cells were transferred to SCDDextrose media without Leucine or Uracil and passaged for 2 days at 30 °C. Induction of displayed Fab molecules was done through media change into SCD Galactose media allowing the activation of the Gal10 promotor. Cells we induced for 48 hrs at 20 °C. Surface displayed molecules were evaluated using an Alexafluor 647 conjugated anti-huFab antibody to measure amount of displayed molecules. Antigen binding was measured with a biotin conjugated GIPR ECD fragment 21-129aa along with a streptavidin PE molecule. Fluorescence was measured using a BD Canto or sorted using an AriaII FACS. Yeast were sorted and then grown on SCD –leu –ura agar plates. Following 2-3 days growth at 30 °C, clones were picked and grown in SCD –leu –ura media. PCR was done from yeast cultures using Phire Plant Direct PCR (ThermoFisher). PCR samples were then sequenced by Genewiz.

[0395] Molecular Biology/Golden Gate Assembly

[0396] PCR samples used for sequencing were also used as template for molecular cloning. Golden Gate Assembly (GGA) strategy used PCR to add compatible cloning ends. Briefly, GGA relies upon TypeII restriction enzymes to cut and seamlessly ligate together multiple DNA fragments. In this example, the multiple DNA fragments consisted of a synthetic nucleic acid sequence (gBlock, Integrated DNA Technologies, Coralville, IA) encoding signal, another gBlock encoding anti-GIPR variable domains; an antibody constant domain fragment released from a Parts vector; and the expression vector backbone. Table 9 breaks out these representative fragments.

[0397] Table 9

[0398] Fragments Assembled to create GLP1-GIPR Fusion Constructs

Fragment	Expression units encoded by the Fragment
Part1	Signal Peptide
PCR product	Variable domain of anti-GIPR antibody
Part2	Constant domain corresponding to anti-GIPR variable domain
Vector	Desired Expression Vector

[0399] The GGA reactions were composed of 10ng of Part1, 10ng of PCR product, 10ng of the Part2, 10ng of the expression vector, 1µl 10x Fast Digest Reaction Buffer + 0.5 mM ATP (Thermo Fisher, Waltham, MA), 0.5 µl FastDigest Esp3I (Thermo Fisher, Waltham, MA), 1 µl T4 DNA Ligase (5U/ µl, Thermo Fisher, Waltham, MA) and water to 10 µl. The reactions were performed over 15 cycles consisting of a 2 minute digestion step at 37 °C and a 3 minute ligation step at 16 °C. The 15 cycles were followed by a final 5 minute 37 °C digestion step and a 5 minute enzyme inactivation step at 80 °C. DNA amplification was done using chemically competent Top10 cells (Invitrogen). Colonies were picked, grown in 2XYT media overnight at 37 °C, and then DNA was extracted and purified using Turbo kits a QiaRobot (Qiagen). DNA was sequence confirmed prior to mammalian expression.

[0400] Mammalian Expression

[0401] The monoclonal antibodies were stably expressed in suspension adapted CHO-K1 cells with the corresponding cDNAs. Transfections were performed using Lipofectamine LTX (Thermo Fisher) according to the manufacturer's protocol. Briefly, a total of 2 µg of the

mammalian expression plasmid DNA was used at a 1:1 heavy chain/light chain ratio. For each, the plasmid DNA was added to 0.5 ml OPTI-MEM (Thermo Fisher) and mixed. In a separate tubes, 10 µl Lipofectamine LTX was added to 0.5 ml OPTI-MEM. The solutions were incubated for 5 minutes at room temperature. To form the transfection complex, the DNA and Lipofectamine LTX mixtures for each were combined and incubated at room temperature for an additional 10 minutes.

[0402] Log phase CHO-K1 cells were pelleted by centrifugation (1200 - 1500 RPM for 5 minutes), washed one time with 1X PBS (Thermo Fisher) and resuspended to 1.5 - 2e6 viable cells/mL in OPTI-MEM. For each transfection, 1 mL of the washed cells were added to a transfection complex in a 24 deep well block. The plates were incubated at 36°C, 5% CO₂, shaking at 225 RPM for 6 hours. To stop the transfection, 2 ml growth media was added to each flask and incubated for 48 hours.

[0403] To begin selection, cells were pelleted by centrifugation (1200 - 1500 RPM for 5 minutes) 48 hours post-transfection and the media was replaced with 4 mL of growth media supplemented with antibiotics (puromycin 10mg/L/hygromycin 600mg/L). Selection media was changed 2-3 times per week, diluting cultures when needed to ensure cultures did not over-grow (<5 - 6 e6 vc/mL), until cell viability and density recovered.

[0404] Productions (100mL) were carried out in shake flasks at 36 °C. Productions were seeded at 2e6 vc/mL in production media. Conditioned media was harvested on day 7 by centrifugation followed by filtration (0.45 µm).

[0405]

[0406] Purification

[0407] The molecules were purified from cell culture media using an AKTA Purifier (GE Healthcare Life Sciences, Little Chalfont, Buckinghamshire, UK) tandem liquid chromatography system with a 1 mL MabSelect SuRe (MSS) HiTrap (GE Healthcare Life Sciences) as the first column, and a 5 mL Desalting HiTrap (GE Healthcare Life Sciences) as the second column. The media was loaded directly onto the MSS column, then washed with 8 column volumes (CV) of 25 mM Tris-HCl, 100 mM NaCl, pH 7.4 and eluted with 2 CV of 100 mM acetic acid. The MSS column eluate was automatically channeled to the Desalting column where the protein was eluted isocratically over 4 CV of 10 mM Na-acetate, 150 mM NaCl, pH 5.2. The samples were sterile filtered through a 3.0 µm glass fiber/0.2 µm Supor membrane (Pall Corporation, Port Washington, New York, USA).

[0408] Protein Concentration Determination

[0409] The protein concentration of each purified molecule was determined by UV absorbance at 280 nm using a Multiskan GO microplate spectrophotometer (Thermo Fisher Scientific, Rockford, Illinois, USA).

[0410] Size Exclusion Chromatography Analysis

[0411] Samples were analyzed by size exclusion chromatography using an ACQUITY UPLC Protein BEH SEC column, 200Å, 1.7 µm, 4.6 x 300 mm (Waters Corporation, Milford, Massachusetts, USA) running in 100 mM NaH₂PO₄, 50 mM NaCl, 7.5% ethanol, pH 6.9 at 0.4 mL/min observing the absorbance at 280 nm on a Waters ACQUITY UPLC system (Waters Corporation).

[0412] LCMS Methods

[0413] For reduced LCMS analysis, 20µg of material was denatured in 8M guanidine HCl/TRIS pH 8.0 (Teknova, Hollister, CA), and reduced with 10mM DTT (EMD Millipore, Darmstadt, Germany) at 50°C for 20 minutes. The sample was acidified with trifluoroacetic acid, and 3µg injected on a Waters BEH reverse phase C4 column using a Waters Acquity HPLC (Waters Corporation, Milford, MA). The column effluent was introduced to an electrospray source of a Xevo QTOF mass spectrometer (Waters Corporation, Milford, MA) and mass spectra were collected. Relevant spectra were deconvoluted using the MaxEnt algorithm within the Waters MassLynx software package. The resulting mass spectra for the LC and HC were compared to the theoretically calculated masses for each chain and denoted as pass/fail.

[0414] Tagg Methods:

[0415] Thermal aggregation onset temperatures were determined by running a Stepped Thermal Unfolding and Aggregation Study on the Avacta, Optim-1000. Data analysis and Tagg determination was performed using Optim Analysis software (Igor version 6.31). Samples with concentrations greater than 1mg/ml were normalized to 1.0 mg/ml in formulation buffer prior to Tagg analysis. Step thermal ramp was applied with start temperature 20 °C and stop temperature with 90 °C. Temperature step was 1 °C and temperature hold time was 30 seconds. Exposure time was 500ms with center wavelength 380 nm and slit with 250 µm.

[0416] cAMP Methods**[0417]** Methods

[0418] This method is intended for the quantitative determination of cAMP in HEK 293T cells expressing the human GIPR or cynomolgus monkey GIPR. GIP binding causes GIPR conformation change, stimulating the G protein to active adenylyl cyclase resulting in cAMP production from ATP. Antibody binding to GIPR prevents GIP binding to GIPR. This is measurable by a cAMP assay.

[0419] The cAMP assay is a HTRF immunoassay designed to measure cAMP produced upon modulation of adenylyl cyclase activity by GPCRs. The assay is based on the competition between native cAMP produced by the cells and the cAMP labeled with the dye d2 for binding sites on cAMP-specific monoclonal antibodies labeled with the Eu3+-Cryptate. When Eu3+-Cryptate conjugated antibodies are bound to the cAMP-d2 tracer, light pulse at 337 nm excites the Eu3+-Cryptate. The energy emitted by the excited Eu3+-Cryptate is transferred by FRET to d2 molecule on cAMP tracer, which in turn emits light at 665 nm. Residual energy from the Eu3+-Cryptate will produce light at 620 nm. In the absence of free cAMP, maximal HTRF signal is achieved. Free cAMP produced by stimulated cells competes with the cAMP-d2 tracer for the binding to the anti-cAMP Eu3+-Cryptate, causing a decrease in HTRF signal. The specific signal (i.e. energy transfer) is inversely proportional to the concentration of cAMP in the sample.

[0420] Experimental Design

[0421] Cells were maintained in DMEM, 10% FBS, 1× sodium pyruvate, 1× Penicillin-Streptomycin-Glutamine, 2 to 5 µg/mL puromycin. Prior to experiments, cells were washed with DBPS, and dissociated with 0.5 mM EDTA in DPBS.

[0422] To establish a GIP response, a solution of GIP (in H₂O) was prepared and 3-fold serially diluted (Ham's F-12 with 0.1% BSA) and added to 30,000 recombinant cells in a 96 well black round bottomed plate. Cells were incubated in the presence of 0.5 mM IBMX at 5% CO₂, 37°C for 30 minutes. After incubation, 25 µL of d2-cAMP, and 25 µL of Eu3+-Cryptate-cAMP antibody were added, followed by incubation at room temperature for 1 hour. Wavelengths at 665 nm and 620 nm were measured using the EnVision Multilabel Reader and the ratio 665/620 ratio was calculated.

[0423] To establish a test article response, a solution of antibody (10 mM sodium acetate, 9% sucrose, pH 5.2) was prepared and 3-fold serially diluted (Ham's F-12 with 0.1% BSA)

and added to 30,000 recombinant cells in a 96 well black round bottomed plate and the cells were incubated at 5% CO₂, 37 °C for 30 min. GIP was added to a final concentration of 50 pM. Cells were incubated in the presence of 0.5 mM IBMX at 5% CO₂, 37°C for 30 minutes. After incubation, 25 µL of d2-cAMP, and 25 µL of Eu³⁺-Cryptate-cAMP antibody were added, followed by incubation at room temperature for 1 hour. Wavelengths at 665 nm and 620 nm were measured using the EnVision Multilabel Reader and the ratio 665/620 ratio was calculated.

[0424] Graphs were generated by plotting the concentration of GIP and antibody on the abscissa, against the average of the two replicate values for cAMP levels (665/620 ratio). The data points were then fit with a log (agonist) versus response - variable slope GraphPad Prism to give fit values for top, bottom, hill slope and both EC₅₀ and IC₅₀ (Table 10).

[0425] Verify GIPR Binding to Variants of 2G10 Affinity Maturation Hits Using BIAcore

[0426] Equipment, reagents and preparation of sensor chip surfaces:

[0427] Biacore T200, Biacore series S-CM5 sensor chip, amine coupling kit, surfactant P-20, 10 mM sodium acetate, pH4.0, and 10 mM glycine pH1.5 were from GE (Pittsburgh, PA). Phosphate-buffered saline (PBS, 1X, no calcium chloride, no magnesium chloride) was from Thermo Fisher Scientific (Waltham, MA). Bovine serum albumin (BSA, fraction V, IgG free) was from Sigma-Aldrich Corp. (St. Louis, MO). Goat-anti-huFc antibody was from Jackson ImmunoResearch Inc. (West Grove, PA).

[0428] Preparation of sensor chip surfaces

[0429] Immobilization of Goat-anti-huFc antibody to a S-CM5 sensor chip surface was performed according to manufacturer's instructions. The Biacore instrument running buffer is 0.005% P20 / PBS 1X, pH7.4, no calcium chloride, no magnesium chloride. Briefly, carboxyl groups on the sensor chip surfaces were activated by injecting 60 µL of a mixture containing 0.2 M N-ethyl-N'-(dimethylaminopropyl) carbodiimide (EDC) and 0.05 M N-hydroxysuccinimide (NHS). Goat-anti-huFc antibody was diluted in 10 mM sodium acetate, pH 4.0 at 20 µg/ml and injected over the activated chip surface at 30 uL/min for 6 minutes. Excess reactive groups on the surfaces were deactivated by injecting 60 µL of 1 M ethanolamine. Final immobilized level was ~ 8000 resonance units (RU).

[0430] Binding assays were carried out on the immobilized goat anti-huFc antibody surface by Biacore T200. The experiment was performed at 25°C. The instrument running buffer was 0.005% P20/PBS. The goat anti-huFc capture antibody was covalently attached to the

sensor chip surface via standard amine coupling to flow cells channel 1-4. The anti-huGIPR antibodies were diluted in sample buffer (0.1 mg/ml BSA, 0.005% P20, PBS) to ~ 10 nM then captured to flow cells channel 2, 3, 4. Flow cell channel 1 was as a blank reference surface without injection of anti-huGIPR antibody. The captured antibody response range was ~ 250 RU. Then 200 nM huGIPR ECD was injected over the goat anti-huFc antibody captured anti-huGIPR antibody surfaces at flow rate 50 ul/min for 3 minutes. After a 10 minutes dissociation, each surface was regenerated by injecting 10 mM Glycine, pH 1.5 for 30 seconds twice. The sensorgrams was analyzed using Biacore T200 evaluation software (v. 2.0). k_s (1/s) for each antibody is shown in Table 10.

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[0431] Table 10. Properties of affinity-matured anti-GIPR antibodies

Antibody	PB CHOK1 titer mg/L	MSQC Score	Tagg °C	eAMP IC50 (nM)	lot amount (mg)	lot purity %	lot HMW %	k _s (1/s)	Normalized Binding Response (Binding/ Capture RL)
2G10.301	360	PASS	72.569 °C	17.64	4.68	94.18	5.66	7E-05	0.22
2G10.302	299.2	PASS	69.672 °C	19.92	3.89	94.37	7.2	<5E-5	0.22
2G10.303	313.2	PASS	72.657 °C	23.13	4.18	94.4	8.02	7E-05	0.23
2G10.304	283.5	PASS	72.796 °C	16.93	3.32	94.96	6.7	<5E-5	0.22
2G10.305	353.5	PASS	71.69 °C	27.22	4.74	94.24	8.23	<5E-5	0.24
2G10.306	358.1	PASS	70.206 °C	20.74	4.33	94.52	6.09	<5E-5	0.23
2G10.307	242.8	PASS	68.246 °C	17.43	2.89	95.54	13.63	6E-05	0.21
2G10.308	360	PASS	71.285 °C	18.27	4.32	94.56	7.52	<5E-5	0.22
2G10.309	352.4	PASS	71.321 °C	29.48	4.13	94.94	7.19	<5E-5	0.23
2G10.311	292.6	PASS	65.478 °C	14.86	3.87	83.6	5.14	6E-05	0.22
2G10.312	316.4	PASS	69.692 °C	23.23	4.24	95.4	7.55	<5E-5	0.23
2G10.313	302.5	PASS	71.541 °C	20.7	3.76	95.48	6.5	<5E-5	0.22
2G10.314	275.9	PASS	72.619 °C	17.53	3.55	95.12	10.77	6E-05	0.22
2G10.315	332.1	PASS	68.86 °C	22.02	4.05	94.47	6.66	<5E-5	0.23
2G10.316	357	PASS	68.325 °C	14.71	3.7	95.35	7.29	<5E-5	0.22
2G10.317	338.5	PASS	67.887 °C	13.66	3.6	95.81	4.77	<5E-5	0.21
2G10.318	327.4	PASS	68.83 °C	20.94	3.87	94.86	7.73	<5E-5	0.22

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2G10.319	123.2	PASS	66.392 °C	7.903	1.46	92.18	21.17	6E-05	0.14
2G10.320	294.2	PASS	68.03 °C	13.96	3.86	95.98	10.08	<5E-5	0.23
2G10.321	111	PASS	66.459 °C	7.461	1.05	90.06	22.53	<5E-5	0.15
2G10.322	343.8	PASS	68.427 °C	17.88	4.15	95.46	6.78	6E-05	0.22
2G10.323	271	PASS	70.608 °C	17.45	3.25	94.06	9.6	<5E-5	0.21
2G10.324	334.5	PASS	69.167 °C	14.11	3.97	95.3	6.98	<5E-5	0.24
2G10.325	360	PASS	67.573 °C	26.22	4.3	93.95	4.72	<5E-5	0.23
2G10.326	308.6	PASS	68.909 °C	26.61	3.76	94.92	5.03	6E-05	0.23
2G10.327	328.7	PASS	68.819 °C	19.26	4.06	93.28	10.64	<5E-5	0.22
2G10.328	280.9	PASS	69.58 °C	24.38	4.1	94.24	7.98	7E-05	0.24
2G10.329	306.2	PASS	68.346 °C	26.79	4.45	94.19	8.27	6E-05	0.24
2G10.330	138.5	PASS	65.007 °C	18.64	1.85	93.81	4.07	<5E-5	0.21
2G10.331	360	PASS	70.325 °C	19.68	5.17	93.93	7.95	5E-05	0.24
2G10.332	328	PASS	68.838 °C	12.86	4.57	90.68	13.16	6E-05	0.21
2G10.333	349.5	PASS	66.902 °C	12.07	4.04	94.97	7.48	<5E-5	0.22
2G10.334	316.8	PASS	66.137 °C	13.74	4.05	94.97	7.44	6E-05	0.23
2G10.335	243.2	PASS	66.531 °C	25.91	3.99	94.15	7.07	6E-05	0.21
2G10.336	341.8	PASS	71.808 °C	29.61	5.04	94.22	4.96	2E-04	0.24
2G10.337	238.2	PASS	69.706 °C	32.53	4.53	95.38	7.77	<5E-5	0.24
2G10.338	235.3	PASS	70.165 °C	23.36	4.38	93.9	11.06	8E-05	0.22
2G10.339	315.5	PASS	70.224 °C	22.61	4.27	95.39	4.9	7E-05	0.23
2G10.340	331.2	PASS	73.132 °C	25.92	3.79	96.19	4.39	6E-05	0.23
2G10.341	360	PASS	67.97 °C	24.74	5.23	95.03	8.5	7E-05	0.21

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2G10.342	252.6	PASS	70.554 °C	11.58	2.16	94.51	15.47	<5E-5	0.16
2G10.343	289.5	PASS	70.649 °C	37.61	4.99	94.75	5.07	6E-05	0.22
2G10.344	266.3	PASS	70.783 °C	21.9	4.84	95.43	5.63	6E-05	0.22
2G10.345	151.8	PASS	68.885 °C	18.85	2.75	94.93	14.09	8E-05	0.19
2G10.346	315.8	PASS	69.926 °C	22.25	5.11	95.25	5.13	1E-04	0.23
2G10.347	332.4	PASS	68.252 °C	28.41	4.56	95.73	7.47	1E-04	0.24
2G10.348	353.6	PASS	70.752 °C	42.8	5.55	96.06	8.17	6E-04	0.24
2G10.601	350.9	PASS	70.55 °C	21.45	4.75	94.78	5.76	6E-05	0.23
2G10.602	252.3	PASS	67.651 °C	16.81	4.06	95.53	6.63	<5E-5	0.23
2G10.603	232.7	PASS	71.14 °C	30.51	4.33	95.75	7.43	<5E-5	0.23
2G10.604	246.9	PASS	70.673 °C	27.07	4.18	95.9	7.2	<5E-5	0.23
2G10.605	250.7	PASS	67.318 °C	25.62	4.49	96.13	7.57	7E-05	0.24
2G10.606	224.6	PASS	70.046 °C	20.36	3.95	95.86	5.33	<5E-5	0.23
2G10.607	251.7	PASS	66.65 °C	19.38	3.08	96.45	15.36	6E-05	0.21
2G10.608	360	PASS	69.596 °C	21.67	4.55	95.01	7.79	<5E-5	0.22
2G10.609	353.7	PASS	70.855 °C	26.93	5.14	95.74	7.75	6E-05	0.23
2G10.610	307	PASS	69.433 °C	12.94	4.5	94.84	7.87	<5E-5	0.22

Antibody 2G10.248 was further affinity matured, resulting in antibodies iPS:529381, iPS:529382, iPS:529397, iPS:529399, iPS:529400, iPS:529403, iPS:529404, and iPS:529405. These antibodies all contain the half-life extending YTE mutations at positions M252 (M252Y), S254 (S254T), and T256 (T256E) of the heavy chain. In addition, antibodies iPS:529397, iPS:529399, iPS:529400, iPS:529403, iPS:529404, and iPS:529405 all also contain the viscosity reducing mutations M4L, V13L, A76D, S95S, Q97E, S98P in the light chain.

Identifier	Visc. Mut.	HLE - YTE	Tm1	Tagg	IC50 (nM)	human cAMP IC50 (nM)	murine cAMP (nM)
2G10.348	None	none	76.2	100	18.3	53	14600
iPS:529381	None	YTE	77.7	77.5	13.7	33.2	9.3
iPS:529382	None	YTE	77.8	78.8	12.1	26.2	49.7
iPS:529397	+VM	YTE	75.5	76	35.6	50	108
iPS:529399	+VM	YTE	77.7	76.8	20.2	39.3	12.9
iPS:529400	+VM	YTE	77.9	78	17.5	36.6	79.5
iPS:529403	+VM	YTE	77.4	76.2	22.5	33.9	12
iPS:529404	+VM	YTE	76.4	76.3	18.1	27.8	3.9
iPS:529405	+VM	YTE	69	73.5	15.1	22.7	6.1

CLAIMS

What is claimed is:

1. A method of treating a subject with a metabolic disorder, the method comprising administering to the subject a therapeutically effective amount of an antigen binding protein that specifically binds to a protein having an amino acid sequence having at least 90% amino acid sequence identity to an amino acid sequence of a GIPR.
2. The method of claim 1, wherein said metabolic disorder is a disorder of glucose metabolism.
3. The method of claim 2, wherein said glucose metabolism disorder comprises hyperglycemia and wherein said administering reduces plasma glucose in said subject.
4. The method of claim 2, wherein said glucose metabolism disorder comprises hyperinsulinemia and wherein said administering reduces plasma insulin in said subject.
5. The method of claim 2, wherein said glucose metabolism disorder comprises glucose intolerance and wherein said administering increases glucose tolerance in said subject.
6. The method of claim 2, wherein said glucose metabolism disorder comprises insulin resistance and wherein said administering decreases insulin resistance in said subject.
7. The method of claim 2, wherein said glucose metabolism disorder comprises diabetes mellitus.
8. The method of claim 2, wherein said subject is obese.
9. The method of claim 8, wherein said administering reduces body weight in said subject.
10. The method of claim 8, wherein said administering reduces body weight gain in said subject.
11. The method of claim 8, where said administering reduces fat mass in said subject.

12. The method of claim 8, wherein said glucose metabolism disorder comprises insulin resistance and wherein said administering reduces insulin resistance in said subject.
13. The method of claim 8, where said subject has increased liver steatosis, and wherein said administering reduces liver steatosis in said subject.
14. The method of claim 8, where said subject has increased liver fat content, and wherein said administering reduces liver fat content in said subject.
15. The method of claim 1, wherein said subject is a mammal.
16. The method of claim 1, wherein said subject is human.
17. The method of claim 1, wherein said administering is by parenteral injection.
18. The method of claim 1, wherein said administering is by subcutaneous injection.
19. An isolated antigen binding protein that specifically binds to a human gastric inhibitory peptide receptor (GIPR) polypeptide.
20. The isolated antigen binding protein of claim 19, wherein said human GIPR has a sequence comprising a sequence selected from the group consisting of SEQ ID NO: 1201, SEQ ID NO: 1203, and SEQ ID NO: 1205.
21. The isolated antigen binding protein of claim 20, wherein said antigen binding protein is a monoclonal antibody, a polyclonal antibody, a recombinant antibody, a human antibody, a humanized antibody, a chimeric antibody, a multispecific antibody, or an antibody fragment thereof.
22. The isolated antigen binding protein of claim 21, wherein said antibody fragment is a Fab fragment, a Fab' fragment, or a F(ab')₂ fragment.
23. The isolated antigen binding protein of claim 21, wherein said antigen binding protein is a human antibody.
24. The isolated antigen binding protein of claim 21, wherein said antigen binding protein is a monoclonal antibody.

25. The isolated antigen binding protein of claim 21, wherein said antigen binding protein is of the IgG1-, IgG2- IgG3- or IgG4-type.

26. The isolated antigen binding protein of claim 25, wherein said antigen binding protein is of the IgG1- or the IgG2-type.

27. The isolated antigen binding protein of any of claim 21, wherein said antigen binding protein is coupled to a labeling group.

28. The isolated antigen binding protein of one of claim 21, wherein said antigen binding protein inhibits binding of GIP to the extracellular portion of human GIPR.

29. The isolated antigen binding protein of claim 21, wherein said antigen binding protein is an antibody or a fragment thereof, and wherein said antibody comprises a CDRL1, a CDRL2, a CDRL3, a CDRH1, a CDRH2, and a CDRH3, wherein said CDRL1 comprises a sequence selected from the group consisting of SEQ ID NOs: 4, 10, 16, 22, 28, 34, 40, 46, 52, 58, 64, 70, 76, 82, 88, 94, 100, 106, 112, 118, 124, 130, 136, 142, 148, 154, 160, 166, 172, 178, 184, 190, 196, 202, 208, 214, 220, 226, 232, 238, 244, 250, 256, 262, 268, 274, 280, 286, 292, 298, 304, 310, 316, 322, 328, 334, 340, 346, 352, 358, 1290, 1300, 1310, 1320, 1330, 1340, and 1350; said CDRL2 comprises a sequence selected from the group consisting of SEQ ID NOs: 5, 11, 17, 23, 29, 35, 41, 47, 53, 59, 65, 71, 77, 83, 89, 95, 101, 107, 113, 119, 125, 131, 137, 143, 149, 155, 161, 167, 173, 179, 185, 191, 197, 203, 209, 215, 221, 227, 233, 239, 245, 251, 257, 263, 269, 275, 281, 287, 293, 299, 305, 311, 317, 323, 329, 335, 341, 347, 353, 359, 1291, 1301, 1311, 1321, 1331, 1341, and 1351; said CDRL3 comprises a sequence selected from the group consisting of SEQ ID NOs: 6, 12, 18, 24, 30, 36, 42, 48, 54, 60, 66, 72, 78, 84, 90, 96, 102, 108, 114, 120, 126, 132, 138, 144, 150, 156, 162, 168, 174, 180, 186, 192, 198, 204, 210, 216, 222, 228, 234, 240, 246, 252, 258, 264, 270, 276, 282, 288, 294, 300, 306, 312, 318, 324, 330, 336, 342, 348, 354, 360, 1292, 1302, 1312, 1322, 1332, 1342, and 1352; said CDRH1 comprises a sequence selected from the group consisting of SEQ ID NOs: 364, 370, 376, 382, 388, 394, 400, 406, 412, 418, 424, 430, 436, 442, 448, 454, 460, 466, 472, 478, 484, 490, 496, 502, 508, 514, 520, 526, 532, 538, 544, 550, 556, 562, 568, 574, 580, 586, 592, 598, 604, 610, 616, 622, 628, 634, 640, 646, 652, 658, 664, 670, 676, 682, 688, 694, 700, 706, 712, 718, 1293, 1303, 1313, 1323, 1333, 1343, and 1353; said CDRH2 comprises a sequence selected from the group consisting of SEQ ID NOs: 365, 371, 377, 383, 389, 395, 401, 407, 413, 419, 425, 431, 437, 443, 449, 455, 461, 467, 473, 479, 485, 491, 497, 503, 509, 515, 521, 527, 533, 539, 545, 551, 557, 563,

569, 575, 581, 587, 593, 599, 605, 611, 617, 623, 629, 635, 641, 647, 653, 659, 665, 671, 677, 683, 689, 695, 701, 707, 713, 719, 1294, 1304, 1314, 1324, 1334, 1344, and 1354; and said CDRH3 comprises a sequence selected from the group consisting of SEQ ID NOs: 366, 372, 378, 384, 390, 396, 402, 408, 414, 420, 426, 432, 438, 444, 450, 456, 462, 468, 474, 480, 486, 492, 498, 504, 510, 516, 522, 528, 534, 540, 546, 552, 558, 564, 570, 576, 582, 588, 594, 600, 606, 612, 618, 624, 630, 636, 642, 648, 654, 660, 666, 672, 678, 684, 690, 696, 702, 708, 714, 720, 1295, 1305, 1315, 1325, 1335, 1345, and 1355.

30. The isolated antigen binding protein of claim 21, wherein said antigen binding protein is an antibody or a fragment thereof, and wherein said antibody comprises a CDRL1, a CDRL2, a CDRL3, a CDRH1, a CDRH2, and a CDRH3, wherein each CDRL1, CDRL2, CDRL3, CDRH1, CDRH2, and CDRH3, respectively, comprises a sequence selected from the group consisting of SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 364, SEQ ID NO: 365, and SEQ ID NO: 366; SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 370, SEQ ID NO: 371, and SEQ ID NO: 372; SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 376, SEQ ID NO: 377, and SEQ ID NO: 378; SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 382, SEQ ID NO: 383, and SEQ ID NO: 384; SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 388, SEQ ID NO: 389, and SEQ ID NO: 390; SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 394, SEQ ID NO: 395, and SEQ ID NO: 396; SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 400, SEQ ID NO: 401, and SEQ ID NO: 402; SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 406, SEQ ID NO: 407, and SEQ ID NO: 408; SEQ ID NO: 52, SEQ ID NO: 53, SEQ ID NO: 54, SEQ ID NO: 412, SEQ ID NO: 413, and SEQ ID NO: 414; SEQ ID NO: 58, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 418, SEQ ID NO: 419, and SEQ ID NO: 420; SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 424, SEQ ID NO: 425, and SEQ ID NO: 426; SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 72, SEQ ID NO: 430, SEQ ID NO: 431, and SEQ ID NO: 432; SEQ ID NO: 76, SEQ ID NO: 77, SEQ ID NO: 78, SEQ ID NO: 436, SEQ ID NO: 437, and SEQ ID NO: 438; SEQ ID NO: 82, SEQ ID NO: 83, SEQ ID NO: 84, SEQ ID NO: 442, SEQ ID NO: 443, and SEQ ID NO: 444; SEQ ID NO: 88, SEQ ID NO: 89, SEQ ID NO: 90, SEQ ID NO: 448, SEQ ID NO: 449, and SEQ ID NO: 450; SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 454, SEQ ID NO: 455, and SEQ ID NO: 456; SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 460, SEQ ID NO: 461, and SEQ ID NO: 462; SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 466, SEQ ID NO: 467, and SEQ ID NO: 468; SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 472, SEQ ID NO: 473, and SEQ ID NO:

474; SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 478, SEQ ID NO: 479, and SEQ ID NO: 480; SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 484, SEQ ID NO: 485, and SEQ ID NO: 486; SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 132, SEQ ID NO: 490, SEQ ID NO: 491, and SEQ ID NO: 492; SEQ ID NO: 136, SEQ ID NO: 137, SEQ ID NO: 138, SEQ ID NO: 496, SEQ ID NO: 497, and SEQ ID NO: 498; SEQ ID NO: 142, SEQ ID NO: 143, SEQ ID NO: 144, SEQ ID NO: 502, SEQ ID NO: 503, and SEQ ID NO: 504; SEQ ID NO: 148, SEQ ID NO: 149, SEQ ID NO: 150, SEQ ID NO: 508, SEQ ID NO: 509, and SEQ ID NO: 510; SEQ ID NO: 154, SEQ ID NO: 155, SEQ ID NO: 156, SEQ ID NO: 514, SEQ ID NO: 515, and SEQ ID NO: 516; SEQ ID NO: 160, SEQ ID NO: 161, SEQ ID NO: 162, SEQ ID NO: 520, SEQ ID NO: 521, and SEQ ID NO: 522; SEQ ID NO: 166, SEQ ID NO: 167, SEQ ID NO: 168, SEQ ID NO: 526, SEQ ID NO: 527, and SEQ ID NO: 528; SEQ ID NO: 172, SEQ ID NO: 173, SEQ ID NO: 174, SEQ ID NO: 532, SEQ ID NO: 533, and SEQ ID NO: 534; SEQ ID NO: 178, SEQ ID NO: 179, SEQ ID NO: 180, SEQ ID NO: 538, SEQ ID NO: 539, and SEQ ID NO: 540; SEQ ID NO: 184, SEQ ID NO: 185, SEQ ID NO: 186, SEQ ID NO: 544, SEQ ID NO: 545, and SEQ ID NO: 546; SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 550, SEQ ID NO: 551, and SEQ ID NO: 552; SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 556, SEQ ID NO: 557, and SEQ ID NO: 558; SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 562, SEQ ID NO: 563, and SEQ ID NO: 564; SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 568, SEQ ID NO: 569, and SEQ ID NO: 570; SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 574, SEQ ID NO: 575, and SEQ ID NO: 576; SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 580, SEQ ID NO: 581, and SEQ ID NO: 582; SEQ ID NO: 226, SEQ ID NO: 227, SEQ ID NO: 228, SEQ ID NO: 586, SEQ ID NO: 587, and SEQ ID NO: 588; SEQ ID NO: 232, SEQ ID NO: 233, SEQ ID NO: 234, SEQ ID NO: 592, SEQ ID NO: 593, and SEQ ID NO: 594; SEQ ID NO: 238, SEQ ID NO: 239, SEQ ID NO: 240, SEQ ID NO: 598, SEQ ID NO: 599, and SEQ ID NO: 600; SEQ ID NO: 244, SEQ ID NO: 245, SEQ ID NO: 246, SEQ ID NO: 604, SEQ ID NO: 605, and SEQ ID NO: 606; SEQ ID NO: 250, SEQ ID NO: 251, SEQ ID NO: 252, SEQ ID NO: 610, SEQ ID NO: 611, and SEQ ID NO: 612; SEQ ID NO: 256, SEQ ID NO: 257, SEQ ID NO: 258, SEQ ID NO: 616, SEQ ID NO: 617, and SEQ ID NO: 618; SEQ ID NO: 262, SEQ ID NO: 263, SEQ ID NO: 264, SEQ ID NO: 622, SEQ ID NO: 623, and SEQ ID NO: 624; SEQ ID NO: 268, SEQ ID NO: 269, SEQ ID NO: 270, SEQ ID NO: 628, SEQ ID NO: 629, and SEQ ID NO: 630; SEQ ID NO: 274, SEQ ID NO: 275, SEQ ID NO: 276, SEQ ID NO: 634, SEQ ID NO: 635, and SEQ ID NO: 636; SEQ ID NO: 280,

SEQ ID NO: 281, SEQ ID NO: 282, SEQ ID NO: 640, SEQ ID NO: 641, and SEQ ID NO: 642; SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 646, SEQ ID NO: 647, and SEQ ID NO: 648; SEQ ID NO: 292, SEQ ID NO: 293, SEQ ID NO: 294, SEQ ID NO: 652, SEQ ID NO: 653, and SEQ ID NO: 654; SEQ ID NO: 298, SEQ ID NO: 299, SEQ ID NO: 300, SEQ ID NO: 658, SEQ ID NO: 659, and SEQ ID NO: 660; SEQ ID NO: 304, SEQ ID NO: 305, SEQ ID NO: 306, SEQ ID NO: 664, SEQ ID NO: 665, and SEQ ID NO: 666; SEQ ID NO: 310, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 670, SEQ ID NO: 671, and SEQ ID NO: 672; SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 318, SEQ ID NO: 676, SEQ ID NO: 677, and SEQ ID NO: 678; SEQ ID NO: 322, SEQ ID NO: 323, SEQ ID NO: 324, SEQ ID NO: 682, SEQ ID NO: 683, and SEQ ID NO: 684; SEQ ID NO: 328, SEQ ID NO: 329, SEQ ID NO: 330, SEQ ID NO: 688, SEQ ID NO: 689, and SEQ ID NO: 690; SEQ ID NO: 334, SEQ ID NO: 335, SEQ ID NO: 336, SEQ ID NO: 694, SEQ ID NO: 695, and SEQ ID NO: 696; SEQ ID NO: 340, SEQ ID NO: 341, SEQ ID NO: 342, SEQ ID NO: 700, SEQ ID NO: 701, and SEQ ID NO: 702; SEQ ID NO: 346, SEQ ID NO: 347, SEQ ID NO: 348, SEQ ID NO: 706, SEQ ID NO: 707, and SEQ ID NO: 708; SEQ ID NO: 352, SEQ ID NO: 353, SEQ ID NO: 354, SEQ ID NO: 712, SEQ ID NO: 713, and SEQ ID NO: 714; SEQ ID NO: 358, SEQ ID NO: 359, SEQ ID NO: 360, SEQ ID NO: 718, SEQ ID NO: 719, and SEQ ID NO: 720; SEQ ID NO: 1290, SEQ ID NO: 1291, SEQ ID NO: 1292, SEQ ID NO: 1293, SEQ ID NO: 1294, and SEQ ID NO: 1295; SEQ ID NO: 1300, SEQ ID NO: 1301, SEQ ID NO: 1302, SEQ ID NO: 1303, SEQ ID NO: 1304, and SEQ ID NO: 1305; SEQ ID NO: 1310, SEQ ID NO: 1311, SEQ ID NO: 1312, SEQ ID NO: 1313, SEQ ID NO: 1314, and SEQ ID NO: 1315; SEQ ID NO: 1320, SEQ ID NO: 1321, SEQ ID NO: 1322, SEQ ID NO: 1323, SEQ ID NO: 1324, and SEQ ID NO: 1325; SEQ ID NO: 1330, SEQ ID NO: 1331, SEQ ID NO: 1332, SEQ ID NO: 1333, SEQ ID NO: 1334, and SEQ ID NO: 1335; SEQ ID NO: 1340, SEQ ID NO: 1341, SEQ ID NO: 1342, SEQ ID NO: 1343, SEQ ID NO: 1344, and SEQ ID NO: 1345; SEQ ID NO: 1350, SEQ ID NO: 1351, SEQ ID NO: 1352, SEQ ID NO: 1353, SEQ ID NO: 1354, and SEQ ID NO: 1355; and SEQ ID NO: 1360, SEQ ID NO: 1361, SEQ ID NO: 1362, SEQ ID NO: 1363, SEQ ID NO: 1364, and SEQ ID NO: 1365.

31. The isolated antigen binding protein of claim 21, wherein said antigen binding protein is an antibody or a fragment thereof, and wherein said antibody or fragment thereof comprises a light chain variable region comprising a sequence selected from the group consisting of SEQ ID NOs: 723, 727, 731, 735, 739, 743, 747, 751, 755, 759, 763, 767, 771, 775, 779, 783, 787, 791, 795, 799, 803, 807, 811, 815, 819, 823, 827, 831, 835, 839, 843,

847, 851, 855, 859, 863, 867, 871, 875, 879, 883, 887, 891, 895, 899, 903, 907, 911, 915, 919, 923, 927, 931, 935, 939, 943, 947, 951, 955, 959, 1286, 1296, 1306, 1316, 1326, 1336, 1346, and 1356 and a heavy chain variable region comprising a sequence selected from the group consisting of SEQ ID NOs: 724, 728, 732, 736, 740, 744, 748, 752, 756, 760, 764, 768, 772, 776, 780, 784, 788, 792, 796, 800, 804, 808, 812, 816, 820, 824, 828, 832, 836, 840, 844, 848, 852, 856, 860, 864, 868, 872, 876, 880, 884, 888, 892, 896, 900, 904, 908, 912, 916, 920, 924, 928, 932, 936, 940, 944, 948, 952, 956, 960, 1287, 1297, 1307, 1317, 1327, 1337, 1347, and 1357.

32. The isolated antigen binding protein of claim 21, wherein said antigen binding protein is an antibody or a fragment thereof, and wherein said antibody or fragment thereof comprises a combination of a 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: 723 and a heavy chain variable region comprising SEQ ID NO: 724; a light chain variable region comprising SEQ ID NO: 727 and a heavy chain variable region comprising SEQ ID NO: 728; a light chain variable region comprising SEQ ID NO: 731 and a heavy chain variable region comprising SEQ ID NO: 732; a light chain variable region comprising SEQ ID NO: 735 and a heavy chain variable region comprising SEQ ID NO: 736; a light chain variable region comprising SEQ ID NO: 739 and a heavy chain variable region comprising SEQ ID NO: 740; a light chain variable region comprising SEQ ID NO: 743 and a heavy chain variable region comprising SEQ ID NO: 744; a light chain variable region comprising SEQ ID NO: 747 and a heavy chain variable region comprising SEQ ID NO: 748; a light chain variable region comprising SEQ ID NO: 751 and a heavy chain variable region comprising SEQ ID NO: 752; a light chain variable region comprising SEQ ID NO: 755 and a heavy chain variable region comprising SEQ ID NO: 756; a light chain variable region comprising SEQ ID NO: 759 and a heavy chain variable region comprising SEQ ID NO: 760; a light chain variable region comprising SEQ ID NO: 763 and a heavy chain variable region comprising SEQ ID NO: 764; a light chain variable region comprising SEQ ID NO: 767 and a heavy chain variable region comprising SEQ ID NO: 768; a light chain variable region comprising SEQ ID NO: 771 and a heavy chain variable region comprising SEQ ID NO: 772; a light chain variable region comprising SEQ ID NO: 775 and a heavy chain variable region comprising SEQ ID NO: 776; a light chain variable region comprising SEQ ID NO: 779 and a heavy chain variable region comprising SEQ ID NO: 780; a light chain variable region comprising SEQ ID NO: 783 and a heavy chain variable region comprising SEQ ID NO: 784; a light chain variable region comprising SEQ ID NO: 787 and a heavy chain variable region

[illegible]

[illegible]

SEQ ID NO: 1347; and a light chain variable region comprising SEQ ID NO: 1356 and a heavy chain variable region comprising SEQ ID NO: 1357.

33. The isolated antigen binding protein of claim 21, wherein said antigen binding protein is an antibody, and wherein said antibody comprises a light chain comprising a sequence selected from the group consisting of SEQ ID NOs: 963, 967, 971, 975, 979, 983, 987, 991, 995, 999, 1003, 1007, 1011, 1015, 1019, 1023, 1027, 1031, 1035, 1039, 1043, 1047, 1051, 1055, 1059, 1063, 1067, 1071, 1075, 1079, 1083, 1087, 1091, 1095, 1099, 1103, 1107, 111 and a heavy chain comprising a sequence selected from the group consisting of SEQ ID NOs: 964, 968, 972, 976, 980, 984, 988, 992, 996, 1000, 1004, 1008, 1012, 1016, 1020, 1024, 1028, 1032, 1036, 1040, 1044, 1048, 1052, 1056, 1060, 1064, 1068, 1072, 1076, 1080, 1084, 1088, 1092, 1096, 1100, 1104, 1108, 1112, 1116, 1120, 1124, 1128, 1132, 1136, 1140, 1144, 1148, 1152, 1156, 1160, 1164, 1168, 1172, 1176, 1180, 1184, 1188, 1192, 1196, 1200, 1289, 1299, 1309, 1319, 1329, 1339, 1349, and 1359.

34. The isolated antigen binding protein of claim 21, wherein said antigen binding protein is an antibody, and wherein said antibody comprises a combination of a light chain and a heavy chain selected from the group consisting of a light chain comprising SEQ ID NO: 963 and a heavy chain comprising SEQ ID NO: 964; a light chain comprising SEQ ID NO: 967 and a heavy chain comprising SEQ ID NO: 968; a light chain comprising SEQ ID NO: 971 and a heavy chain comprising SEQ ID NO: 972; a light chain comprising SEQ ID NO: 975 and a heavy chain comprising SEQ ID NO: 976; a light chain comprising SEQ ID NO: 979 and a heavy chain comprising SEQ ID NO: 980; a light chain comprising SEQ ID NO: 983 and a heavy chain comprising SEQ ID NO: 984; a light chain comprising SEQ ID NO: 987 and a heavy chain comprising SEQ ID NO: 988; a light chain comprising SEQ ID NO: 991 and a heavy chain comprising SEQ ID NO: 992; a light chain comprising SEQ ID NO: 995 and a heavy chain comprising SEQ ID NO: 996; a light chain comprising SEQ ID NO: 999 and a heavy chain comprising SEQ ID NO: 1000; a light chain comprising SEQ ID NO: 1003 and a heavy chain comprising SEQ ID NO: 1004; a light chain comprising SEQ ID NO: 1007 and a heavy chain comprising SEQ ID NO: 1008; a light chain comprising SEQ ID NO: 1011 and a heavy chain comprising SEQ ID NO: 1012; a light chain comprising SEQ ID NO: 1015 and a heavy chain comprising SEQ ID NO: 1016; a light chain comprising SEQ ID NO: 1019 and a heavy chain comprising SEQ ID NO: 1020; a light chain comprising SEQ ID NO: 1023 and a heavy chain comprising SEQ ID NO: 1024; a light chain comprising SEQ ID NO: 1027 and a heavy chain comprising SEQ ID NO: 1028; a light chain comprising SEQ ID NO: 1031

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and a heavy chain comprising SEQ ID NO: 1168; a light chain comprising SEQ ID NO: 1171 and a heavy chain comprising SEQ ID NO: 1172; a light chain comprising SEQ ID NO: 1175 and a heavy chain comprising SEQ ID NO: 1176; a light chain comprising SEQ ID NO: 1179 and a heavy chain comprising SEQ ID NO: 1180; a light chain comprising SEQ ID NO: 1183 and a heavy chain comprising SEQ ID NO: 1184; a light chain comprising SEQ ID NO: 1187 and a heavy chain comprising SEQ ID NO: 1188; a light chain comprising SEQ ID NO: 1191 and a heavy chain comprising SEQ ID NO: 1192; a light chain comprising SEQ ID NO: 1195 and a heavy chain comprising SEQ ID NO: 1196; a light chain comprising SEQ ID NO: 1199 and a heavy chain comprising SEQ ID NO: 1200; a light chain comprising SEQ ID NO: 1288 and a heavy chain comprising SEQ ID NO: 1289; a light chain comprising SEQ ID NO: 1298 and a heavy chain comprising SEQ ID NO: 1299; a light chain comprising SEQ ID NO: 1308 and a heavy chain comprising SEQ ID NO: 1309; a light chain comprising SEQ ID NO: 1318 and a heavy chain comprising SEQ ID NO: 1319; a light chain comprising SEQ ID NO: 1328 and a heavy chain comprising SEQ ID NO: 1329; a light chain comprising SEQ ID NO: 1338 and a heavy chain comprising SEQ ID NO: 1339; a light chain comprising SEQ ID NO: 1348 and a heavy chain comprising SEQ ID NO: 1349; and a light chain comprising SEQ ID NO: 1358 and a heavy chain comprising SEQ ID NO: 1359.

35. A nucleic acid molecule encoding the antibody or fragment thereof according to any one of claims 29-34.

36. The nucleic acid molecule according to claim 35, wherein said nucleic acid molecule is operably linked to a control sequence.

37. A vector comprising a nucleic acid molecule according to claim 36.

38. A host cell comprising the nucleic acid molecule according to claim 37.

39. An antibody or fragment thereof produced by the host cell of claim 38.

40. A method of making the antibody or fragment thereof according to any one of claims 29-34, comprising the step of preparing said antibody or fragment thereof from a host cell that secretes said antibody.

41. A pharmaceutical composition comprising at least one antibody or fragment thereof according to any one of claims 29-34, and pharmaceutically acceptable excipient.

42. An isolated antigen binding protein that competes for binding to the extracellular portion of human GIPR with an antibody or fragment thereof of one of claims 29-34.

43. A composition comprising a therapeutically effective amount of a GLP-1 receptor agonist and a therapeutically effective amount of a GIPR antagonist that specifically binds to a protein having an amino acid sequence having at least 90% amino acid sequence identity to an amino acid sequence of a GIPR.

44. The composition of claim 43, wherein the molar ratio of a GLP-1 receptor agonist to a GIPR antagonist is from about 1:1 to 1:110, 1:1 to 1:100, 1:1 to 1:75, 1:1 to 1:50, 1:1 to 1:25, 1:1 to 1:10, 1:1 to 1:5, and 1:1.

45. The composition of claim 43, wherein the molar ratio of a GIPR antagonist to a GLP-1 receptor agonist is from about 1:1 to 1:110, 1:1 to 1:100, 1:1 to 1:75, 1:1 to 1:50, 1:1 to 1:25, 1:1 to 1:10, and 1:1 to 1:5.

46. The composition of claim 43, wherein the GLP-1 receptor agonist is used in combination with the GIPR antagonist at therapeutically effective molar ratios of between about 1:1.5 to 1:150, preferably 1:2 to 1:50.

47. The composition of claim 43, wherein the GLP-1 receptor agonist and the GIPR antagonist are present in doses that are at least about 1.1 to 1.4, 1.5, 2, 3, 4, 5, 6, 7, 8, 9, or 10 fold lower than the doses of each compound alone required to treat a condition and/or disease.

48. The composition of claim 43, wherein the GLP-1 receptor agonist is GLP-1(7-37) or a GLP-1(7-37) analog.

49. The composition of claim 48, wherein the GLP-1 receptor agonist is selected from the group consisting of exenatide, liraglutide, lixisenatide, albiglutide, dulaglutide, semaglutide, and taspoglutide.

50. The composition of claim 43, wherein the GLP-1 receptor agonist is selected from the group consisting of GLP-1(7-37) (SEQ ID NO: 1244); GLP-1(7-36)-NH₂ (SEQ ID NO: 1245); liraglutide; albiglutide; taspoglutide; dulaglutide; semaglutide; LY2428757; desamino-His⁷,Arg²⁶,Lys³⁴(N^ε-(γ-Glu(N-α-hexadecanoyl)))-GLP-1(7-37) (core peptide disclosed as SEQ ID NO: 1282); desamino-His⁷,Arg²⁶,Lys³⁴(N^ε-octanoyl)-GLP-1(7-37) (SEQ

ID NO: 1283); Arg^{26,34},Lys³⁸(N⁶-(ω-carboxypentadecanoyl))-GLP-1(7-38) (SEQ ID NO: 1284); Arg^{26,34},Lys³⁶(N⁶-(γ-Glu(N-α-hexadecanoyl)))-GLP-1(7-36) (core peptide disclosed as SEQ ID NO: 1285); Aib^{8,35},Arg^{26,34},Phe³¹-GLP-1(7-36)) (SEQ ID NO: 1246); HXaa₈EGTFTSDVSSYLEXaa₂₂Xaa₂₃AAKEFIXaa₃₀WLXaa₃₃Xaa₃₄G Xaa₃₆Xaa₃₇; wherein Xaa₈ is A, V, or G; Xaa₂₂ is G, K, or E; Xaa₂₃ is Q or K; Xaa₃₀ is A or E; Xaa₃₃ is V or K; Xaa₃₄ is K, N, or R; Xaa₃₆ is R or G; and Xaa₃₇ is G, H, P, or absent (SEQ ID NO: 1247); Arg³⁴-GLP-1(7-37) (SEQ ID NO: 1248); Glu³⁰-GLP-1(7-37) (SEQ ID NO: 1249); Lys²²-GLP-1(7-37) (SEQ ID NO: 1250); Gly^{8,36},Glu²²-GLP-1(7-37) (SEQ ID NO: 1251); Val⁸,Glu²²,Gly³⁶-GLP-1(7-37) (SEQ ID NO: 1252); Gly^{8,36},Glu²²,Lys³³,Asn³⁴-GLP-1(7-37) (SEQ ID NO: 1253); Val⁸,Glu²²,Lys³³,Asn³⁴,Gly³⁶-GLP-1(7-37) (SEQ ID NO: 1254); Gly^{8,36},Glu²²,Pro³⁷-GLP-1(7-37) (SEQ ID NO: 1255); Val⁸,Glu²²,Gly³⁶Pro³⁷-GLP-1(7-37) (SEQ ID NO: 1256); Gly^{8,36},Glu²²,Lys³³, Asn³⁴,Pro³⁷-GLP-1(7-37) (SEQ ID NO: 1257); Val⁸,Glu²²,Lys³³,Asn³⁴,Gly³⁶,Pro³⁷-GLP-1(7-37) (SEQ ID NO: 1258); Gly^{8,36},Glu²²-GLP-1(7-36) (SEQ ID NO: 1259); Val⁸,Glu²²,Gly³⁶-GLP-1(7-36) (SEQ ID NO: 1260); Val⁸,Glu²²,Asn³⁴,Gly³⁶-GLP-1(7-36) (SEQ ID NO: 1261); and Gly^{8,36},Glu²²,Asn³⁴-GLP-1(7-36) (SEQ ID NO: 1262).

51. The composition of claim 43, wherein human GIPR has a sequence comprising a sequence selected from the group consisting of SEQ ID NO: 1201, SEQ ID NO: 1203, and SEQ ID NO: 1205.

52. The composition of claim 43, wherein the GIPR antagonist is an antigen binding protein.

53. The composition of claim 52, wherein the antigen binding protein is a monoclonal antibody, a polyclonal antibody, a recombinant antibody, a human antibody, a humanized antibody, a chimeric antibody, a multispecific antibody, or an antibody fragment thereof.

54. The composition of claim 53, wherein the antibody fragment is a Fab fragment, a Fab' fragment, or a F(ab')₂ fragment.

55. The composition of claim 53, wherein the antigen binding protein is a human antibody.

56. The composition of claim 53, wherein the antigen binding protein is a monoclonal antibody.

57. The composition of claim 53, wherein the antigen binding protein is of the IgG1-, IgG2-, IgG3- or IgG4-type.

58. The composition of claim 57, wherein the antigen binding protein is of the IgG1- or the IgG2-type.

59. The composition of claim 53, wherein the antigen binding protein is coupled to a labeling group.

60. The composition of claim 53, wherein the antigen binding protein inhibits binding of GIP to the extracellular portion of human GIPR.

61. The composition of claim 53, wherein the antigen binding protein is an antibody or a fragment thereof, and wherein the antibody comprises a CDRL1, a CDRL2, a CDRL3, a CDRH1, a CDRH2, and a CDRH3, wherein the CDRL1 comprises a sequence selected from the group consisting of SEQ ID NOs: 4, 10, 16, 22, 28, 34, 40, 46, 52, 58, 64, 70, 76, 82, 88, 94, 100, 106, 112, 118, 124, 130, 136, 142, 148, 154, 160, 166, 172, 178, 184, 190, 196, 202, 208, 214, 220, 226, 232, 238, 244, 250, 256, 262, 268, 274, 280, 286, 292, 298, 304, 310, 316, 322, 328, 334, 340, 346, 352, 358, 1290, 1300, 1310, 1320, 1330, 1340, and 1350; the CDRL2 comprises a sequence selected from the group consisting of SEQ ID NOs: 5, 11, 17, 23, 29, 35, 41, 47, 53, 59, 65, 71, 77, 83, 89, 95, 101, 107, 113, 119, 125, 131, 137, 143, 149, 155, 161, 167, 173, 179, 185, 191, 197, 203, 209, 215, 221, 227, 233, 239, 245, 251, 257, 263, 269, 275, 281, 287, 293, 299, 305, 311, 317, 323, 329, 335, 341, 347, 353, 359, 1291, 1301, 1311, 1321, 1331, 1341, and 1351; the CDRL3 comprises a sequence selected from the group consisting of SEQ ID NOs: 6, 12, 18, 24, 30, 36, 42, 48, 54, 60, 66, 72, 78, 84, 90, 96, 102, 108, 114, 120, 126, 132, 138, 144, 150, 156, 162, 168, 174, 180, 186, 192, 198, 204, 210, 216, 222, 228, 234, 240, 246, 252, 258, 264, 270, 276, 282, 288, 294, 300, 306, 312, 318, 324, 330, 336, 342, 348, 354, 360, 1292, 1302, 1312, 1322, 1332, 1342, and 1352; the CDRH1 comprises a sequence selected from the group consisting of SEQ ID NOs: 364, 370, 376, 382, 388, 394, 400, 406, 412, 418, 424, 430, 436, 442, 448, 454, 460, 466, 472, 478, 484, 490, 496, 502, 508, 514, 520, 526, 532, 538, 544, 550, 556, 562, 568, 574, 580, 586, 592, 598, 604, 610, 616, 622, 628, 634, 640, 646, 652, 658, 664, 670, 676, 682, 688, 694, 700, 706, 712, 718, 1293, 1303, 1313, 1323, 1333, 1343, and 1353; the CDRH2 comprises a sequence selected from the group consisting of SEQ ID NOs: 365, 371, 377, 383, 389, 395, 401, 407, 413, 419, 425, 431, 437, 443, 449, 455, 461, 467, 473, 479, 485, 491, 497, 503, 509, 515, 521, 527, 533, 539, 545, 551, 557, 563, 569, 575, 581, 587,

593, 599, 605, 611, 617, 623, 629, 635, 641, 647, 653, 659, 665, 671, 677, 683, 689, 695, 701, 707, 713, 719, 1294, 1304, 1314, 1324, 1334, 1344, and 1354; and the CDRH3 comprises a sequence selected from the group consisting of SEQ ID NOs: 366, 372, 378, 384, 390, 396, 402, 408, 414, 420, 426, 432, 438, 444, 450, 456, 462, 468, 474, 480, 486, 492, 498, 504, 510, 516, 522, 528, 534, 540, 546, 552, 558, 564, 570, 576, 582, 588, 594, 600, 606, 612, 618, 624, 630, 636, 642, 648, 654, 660, 666, 672, 678, 684, 690, 696, 702, 708, 714, 720, 1295, 1305, 1315, 1325, 1335, 1345, and 1355.

62. The composition of claim 53, wherein the antigen binding protein is an antibody or a fragment thereof, and wherein the antibody comprises a CDRL1, a CDRL2, a CDRL3, a CDRH1, a CDRH2, and a CDRH3, wherein each CDRL1, CDRL2, CDRL3, CDRH1, CDRH2, and CDRH3, respectively, comprises a sequence selected from the group consisting of SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 364, SEQ ID NO: 365, and SEQ ID NO: 366; SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 370, SEQ ID NO: 371, and SEQ ID NO: 372; SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 376, SEQ ID NO: 377, and SEQ ID NO: 378; SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 382, SEQ ID NO: 383, and SEQ ID NO: 384; SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 388, SEQ ID NO: 389, and SEQ ID NO: 390; SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 394, SEQ ID NO: 395, and SEQ ID NO: 396; SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 400, SEQ ID NO: 401, and SEQ ID NO: 402; SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 406, SEQ ID NO: 407, and SEQ ID NO: 408; SEQ ID NO: 52, SEQ ID NO: 53, SEQ ID NO: 54, SEQ ID NO: 412, SEQ ID NO: 413, and SEQ ID NO: 414; SEQ ID NO: 58, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 418, SEQ ID NO: 419, and SEQ ID NO: 420; SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 424, SEQ ID NO: 425, and SEQ ID NO: 426; SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 72, SEQ ID NO: 430, SEQ ID NO: 431, and SEQ ID NO: 432; SEQ ID NO: 76, SEQ ID NO: 77, SEQ ID NO: 78, SEQ ID NO: 436, SEQ ID NO: 437, and SEQ ID NO: 438; SEQ ID NO: 82, SEQ ID NO: 83, SEQ ID NO: 84, SEQ ID NO: 442, SEQ ID NO: 443, and SEQ ID NO: 444; SEQ ID NO: 88, SEQ ID NO: 89, SEQ ID NO: 90, SEQ ID NO: 448, SEQ ID NO: 449, and SEQ ID NO: 450; SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 454, SEQ ID NO: 455, and SEQ ID NO: 456; SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 460, SEQ ID NO: 461, and SEQ ID NO: 462; SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 466, SEQ ID NO: 467, and SEQ ID NO: 468; SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 472, SEQ ID NO: 473, and SEQ ID NO: 474; SEQ ID

NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 478, SEQ ID NO: 479, and SEQ ID NO: 480; SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 484, SEQ ID NO: 485, and SEQ ID NO: 486; SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 132, SEQ ID NO: 490, SEQ ID NO: 491, and SEQ ID NO: 492; SEQ ID NO: 136, SEQ ID NO: 137, SEQ ID NO: 138, SEQ ID NO: 496, SEQ ID NO: 497, and SEQ ID NO: 498; SEQ ID NO: 142, SEQ ID NO: 143, SEQ ID NO: 144, SEQ ID NO: 502, SEQ ID NO: 503, and SEQ ID NO: 504; SEQ ID NO: 148, SEQ ID NO: 149, SEQ ID NO: 150, SEQ ID NO: 508, SEQ ID NO: 509, and SEQ ID NO: 510; SEQ ID NO: 154, SEQ ID NO: 155, SEQ ID NO: 156, SEQ ID NO: 514, SEQ ID NO: 515, and SEQ ID NO: 516; SEQ ID NO: 160, SEQ ID NO: 161, SEQ ID NO: 162, SEQ ID NO: 520, SEQ ID NO: 521, and SEQ ID NO: 522; SEQ ID NO: 166, SEQ ID NO: 167, SEQ ID NO: 168, SEQ ID NO: 526, SEQ ID NO: 527, and SEQ ID NO: 528; SEQ ID NO: 172, SEQ ID NO: 173, SEQ ID NO: 174, SEQ ID NO: 532, SEQ ID NO: 533, and SEQ ID NO: 534; SEQ ID NO: 178, SEQ ID NO: 179, SEQ ID NO: 180, SEQ ID NO: 538, SEQ ID NO: 539, and SEQ ID NO: 540; SEQ ID NO: 184, SEQ ID NO: 185, SEQ ID NO: 186, SEQ ID NO: 544, SEQ ID NO: 545, and SEQ ID NO: 546; SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 550, SEQ ID NO: 551, and SEQ ID NO: 552; SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 556, SEQ ID NO: 557, and SEQ ID NO: 558; SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 562, SEQ ID NO: 563, and SEQ ID NO: 564; SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 568, SEQ ID NO: 569, and SEQ ID NO: 570; SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 574, SEQ ID NO: 575, and SEQ ID NO: 576; SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 580, SEQ ID NO: 581, and SEQ ID NO: 582; SEQ ID NO: 226, SEQ ID NO: 227, SEQ ID NO: 228, SEQ ID NO: 586, SEQ ID NO: 587, and SEQ ID NO: 588; SEQ ID NO: 232, SEQ ID NO: 233, SEQ ID NO: 234, SEQ ID NO: 592, SEQ ID NO: 593, and SEQ ID NO: 594; SEQ ID NO: 238, SEQ ID NO: 239, SEQ ID NO: 240, SEQ ID NO: 598, SEQ ID NO: 599, and SEQ ID NO: 600; SEQ ID NO: 244, SEQ ID NO: 245, SEQ ID NO: 246, SEQ ID NO: 604, SEQ ID NO: 605, and SEQ ID NO: 606; SEQ ID NO: 250, SEQ ID NO: 251, SEQ ID NO: 252, SEQ ID NO: 610, SEQ ID NO: 611, and SEQ ID NO: 612; SEQ ID NO: 256, SEQ ID NO: 257, SEQ ID NO: 258, SEQ ID NO: 616, SEQ ID NO: 617, and SEQ ID NO: 618; SEQ ID NO: 262, SEQ ID NO: 263, SEQ ID NO: 264, SEQ ID NO: 622, SEQ ID NO: 623, and SEQ ID NO: 624; SEQ ID NO: 268, SEQ ID NO: 269, SEQ ID NO: 270, SEQ ID NO: 628, SEQ ID NO: 629, and SEQ ID NO: 630; SEQ ID NO: 274, SEQ ID NO: 275, SEQ ID NO: 276, SEQ ID NO: 634, SEQ ID NO: 635, and SEQ ID NO: 636; SEQ ID NO: 280, SEQ ID NO:

281, SEQ ID NO: 282, SEQ ID NO: 640, SEQ ID NO: 641, and SEQ ID NO: 642; SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 646, SEQ ID NO: 647, and SEQ ID NO: 648; SEQ ID NO: 292, SEQ ID NO: 293, SEQ ID NO: 294, SEQ ID NO: 652, SEQ ID NO: 653, and SEQ ID NO: 654; SEQ ID NO: 298, SEQ ID NO: 299, SEQ ID NO: 300, SEQ ID NO: 658, SEQ ID NO: 659, and SEQ ID NO: 660; SEQ ID NO: 304, SEQ ID NO: 305, SEQ ID NO: 306, SEQ ID NO: 664, SEQ ID NO: 665, and SEQ ID NO: 666; SEQ ID NO: 310, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 670, SEQ ID NO: 671, and SEQ ID NO: 672; SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 318, SEQ ID NO: 676, SEQ ID NO: 677, and SEQ ID NO: 678; SEQ ID NO: 322, SEQ ID NO: 323, SEQ ID NO: 324, SEQ ID NO: 682, SEQ ID NO: 683, and SEQ ID NO: 684; SEQ ID NO: 328, SEQ ID NO: 329, SEQ ID NO: 330, SEQ ID NO: 688, SEQ ID NO: 689, and SEQ ID NO: 690; SEQ ID NO: 334, SEQ ID NO: 335, SEQ ID NO: 336, SEQ ID NO: 694, SEQ ID NO: 695, and SEQ ID NO: 696; SEQ ID NO: 340, SEQ ID NO: 341, SEQ ID NO: 342, SEQ ID NO: 700, SEQ ID NO: 701, and SEQ ID NO: 702; SEQ ID NO: 346, SEQ ID NO: 347, SEQ ID NO: 348, SEQ ID NO: 706, SEQ ID NO: 707, and SEQ ID NO: 708; SEQ ID NO: 352, SEQ ID NO: 353, SEQ ID NO: 354, SEQ ID NO: 712, SEQ ID NO: 713, and SEQ ID NO: 714; SEQ ID NO: 358, SEQ ID NO: 359, SEQ ID NO: 360, SEQ ID NO: 718, SEQ ID NO: 719, and SEQ ID NO: 720; SEQ ID NO: 1290, SEQ ID NO: 1291, SEQ ID NO: 1292, SEQ ID NO: 1293, SEQ ID NO: 1294, and SEQ ID NO: 1295; SEQ ID NO: 1300, SEQ ID NO: 1301, SEQ ID NO: 1302, SEQ ID NO: 1303, SEQ ID NO: 1304, and SEQ ID NO: 1305; SEQ ID NO: 1310, SEQ ID NO: 1311, SEQ ID NO: 1312, SEQ ID NO: 1313, SEQ ID NO: 1314, and SEQ ID NO: 1315; SEQ ID NO: 1320, SEQ ID NO: 1321, SEQ ID NO: 1322, SEQ ID NO: 1323, SEQ ID NO: 1324, and SEQ ID NO: 1325; SEQ ID NO: 1330, SEQ ID NO: 1331, SEQ ID NO: 1332, SEQ ID NO: 1333, SEQ ID NO: 1334, and SEQ ID NO: 1335; SEQ ID NO: 1340, SEQ ID NO: 1341, SEQ ID NO: 1342, SEQ ID NO: 1343, SEQ ID NO: 1344, and SEQ ID NO: 1345; SEQ ID NO: 1350, SEQ ID NO: 1351, SEQ ID NO: 1352, SEQ ID NO: 1353, SEQ ID NO: 1354, and SEQ ID NO: 1355; and SEQ ID NO: 1360, SEQ ID NO: 1361, SEQ ID NO: 1362, SEQ ID NO: 1363, SEQ ID NO: 1364, and SEQ ID NO: 1365.

63. The composition of claim 53, wherein the antigen binding protein is an antibody or a fragment thereof, and wherein the antibody or fragment thereof comprises a light chain variable region comprising a sequence selected from the group consisting of SEQ ID NOs: 723, 727, 731, 735, 739, 743, 747, 751, 755, 759, 763, 767, 771, 775, 779, 783, 787, 791, 795, 799, 803, 807, 811, 815, 819, 823, 827, 831, 835, 839, 843, 847, 851, 855, 859, 863, 867, 871, 875, 879, 883, 887, 891, 895, 899, 903, 907, 911, 915, 919, 923, 927, 931,

935, 939, 943, 947, 951, 955, 959, 1286, 1296, 1306, 1316, 1326, 1336, 1346, and 1356 and a heavy chain variable region comprising a sequence selected from the group consisting of SEQ ID NOs: 724, 728, 732, 736, 740, 744, 748, 752, 756, 760, 764, 768, 772, 776, 780, 784, 788, 792, 796, 800, 804, 808, 812, 816, 820, 824, 828, 832, 836, 840, 844, 848, 852, 856, 860, 864, 868, 872, 876, 880, 884, 888, 892, 896, 900, 904, 908, 912, 916, 920, 924, 928, 932, 936, 940, 944, 948, 952, 956, 960, 1287, 1297, 1307, 1317, 1327, 1337, 1347, and 1357.

64. The composition of claim 53, wherein the antigen binding protein is an antibody or a fragment thereof, and wherein the antibody or fragment thereof comprises a combination of a 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: 723 and a heavy chain variable region comprising SEQ ID NO: 724; a light chain variable region comprising SEQ ID NO: 727 and a heavy chain variable region comprising SEQ ID NO: 728; a light chain variable region comprising SEQ ID NO: 731 and a heavy chain variable region comprising SEQ ID NO: 732; a light chain variable region comprising SEQ ID NO: 735 and a heavy chain variable region comprising SEQ ID NO: 736; a light chain variable region comprising SEQ ID NO: 739 and a heavy chain variable region comprising SEQ ID NO: 740; a light chain variable region comprising SEQ ID NO: 743 and a heavy chain variable region comprising SEQ ID NO: 744; a light chain variable region comprising SEQ ID NO: 747 and a heavy chain variable region comprising SEQ ID NO: 748; a light chain variable region comprising SEQ ID NO: 751 and a heavy chain variable region comprising SEQ ID NO: 752; a light chain variable region comprising SEQ ID NO: 755 and a heavy chain variable region comprising SEQ ID NO: 756; a light chain variable region comprising SEQ ID NO: 759 and a heavy chain variable region comprising SEQ ID NO: 760; a light chain variable region comprising SEQ ID NO: 763 and a heavy chain variable region comprising SEQ ID NO: 764; a light chain variable region comprising SEQ ID NO: 767 and a heavy chain variable region comprising SEQ ID NO: 768; a light chain variable region comprising SEQ ID NO: 771 and a heavy chain variable region comprising SEQ ID NO: 772; a light chain variable region comprising SEQ ID NO: 775 and a heavy chain variable region comprising SEQ ID NO: 776; a light chain variable region comprising SEQ ID NO: 779 and a heavy chain variable region comprising SEQ ID NO: 780; a light chain variable region comprising SEQ ID NO: 783 and a heavy chain variable region comprising SEQ ID NO: 784; a light chain variable region comprising SEQ ID NO: 787 and a heavy chain variable region comprising SEQ ID NO: 788; a light chain variable region comprising SEQ ID NO: 791 and a heavy chain variable region comprising SEQ ID NO: 792; a light chain variable region comprising SEQ ID NO: 795 and

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65. The composition of claim 53, wherein the antigen binding protein is an antibody, and wherein the antibody comprises a light chain comprising a sequence selected from the group consisting of SEQ ID NOs: 963, 967, 971, 975, 979, 983, 987, 991, 995, 999, 1003, 1007, 1011, 1015, 1019, 1023, 1027, 1031, 1035, 1039, 1043, 1047, 1051, 1055, 1059, 1063, 1067, 1071, 1075, 1079, 1083, 1087, 1091, 1095, 1099, 1103, 1107, 111 and a heavy chain comprising a sequence selected from the group consisting of SEQ ID NOs: 964, 968, 972, 976, 980, 984, 988, 992, 996, 1000, 1004, 1008, 1012, 1016, 1020, 1024, 1028, 1032, 1036, 1040, 1044, 1048, 1052, 1056, 1060, 1064, 1068, 1072, 1076, 1080, 1084, 1088, 1092, 1096, 1100, 1104, 1108, 1112, 1116, 1120, 1124, 1128, 1132, 1136, 1140, 1144, 1148, 1152, 1156, 1160, 1164, 1168, 1172, 1176, 1180, 1184, 1188, 1192, 1196, 1200, 1289, 1299, 1309, 1319, 1329, 1339, 1349, and 1359.

66. The composition of claim 53, wherein the antigen binding protein is an antibody, and wherein the antibody comprises a combination of a light chain and a heavy chain selected from the group consisting of a light chain comprising SEQ ID NO: 963 and a heavy chain comprising SEQ ID NO: 964; a light chain comprising SEQ ID NO: 967 and a heavy chain comprising SEQ ID NO: 968; a light chain comprising SEQ ID NO: 971 and a heavy chain comprising SEQ ID NO: 972; a light chain comprising SEQ ID NO: 975 and a heavy chain comprising SEQ ID NO: 976; a light chain comprising SEQ ID NO: 979 and a heavy chain comprising SEQ ID NO: 980; a light chain comprising SEQ ID NO: 983 and a heavy chain comprising SEQ ID NO: 984; a light chain comprising SEQ ID NO: 987 and a heavy chain comprising SEQ ID NO: 988; a light chain comprising SEQ ID NO: 991 and a heavy chain comprising SEQ ID NO: 992; a light chain comprising SEQ ID NO: 995 and a heavy chain comprising SEQ ID NO: 996; a light chain comprising SEQ ID NO: 999 and a heavy chain comprising SEQ ID NO: 1000; a light chain comprising SEQ ID NO: 1003 and a heavy chain comprising SEQ ID NO: 1004; a light chain comprising SEQ ID NO: 1007 and a heavy chain comprising SEQ ID NO: 1008; a light chain comprising SEQ ID NO: 1011 and a heavy chain comprising SEQ ID NO: 1012; a light chain comprising SEQ ID NO: 1015 and a heavy chain comprising SEQ ID NO: 1016; a light chain comprising SEQ ID NO: 1019 and a heavy chain comprising SEQ ID NO: 1020; a light chain comprising SEQ ID NO: 1023 and a heavy chain comprising SEQ ID NO: 1024; a light chain comprising SEQ ID NO: 1027 and a heavy chain comprising SEQ ID NO: 1028; a light chain comprising SEQ ID NO: 1031 and a heavy chain comprising SEQ ID NO: 1032; a light chain comprising SEQ ID NO: 1035 and a heavy chain comprising SEQ ID NO: 1036; a light chain comprising SEQ ID NO: 1039 and a heavy chain comprising SEQ ID NO: 1040; a light chain comprising SEQ ID NO: 1043 and a

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heavy chain comprising SEQ ID NO: 1180; a light chain comprising SEQ ID NO: 1183 and a heavy chain comprising SEQ ID NO: 1184; a light chain comprising SEQ ID NO: 1187 and a heavy chain comprising SEQ ID NO: 1188; a light chain comprising SEQ ID NO: 1191 and a heavy chain comprising SEQ ID NO: 1192; a light chain comprising SEQ ID NO: 1195 and a heavy chain comprising SEQ ID NO: 1196; a light chain comprising SEQ ID NO: 1199 and a heavy chain comprising SEQ ID NO: 1200; a light chain comprising SEQ ID NO: 1288 and a heavy chain comprising SEQ ID NO: 1289; a light chain comprising SEQ ID NO: 1298 and a heavy chain comprising SEQ ID NO: 1299; a light chain comprising SEQ ID NO: 1308 and a heavy chain comprising SEQ ID NO: 1309; a light chain comprising SEQ ID NO: 1318 and a heavy chain comprising SEQ ID NO: 1319; a light chain comprising SEQ ID NO: 1328 and a heavy chain comprising SEQ ID NO: 1329; a light chain comprising SEQ ID NO: 1338 and a heavy chain comprising SEQ ID NO: 1339; a light chain comprising SEQ ID NO: 1348 and a heavy chain comprising SEQ ID NO: 1349; and a light chain comprising SEQ ID NO: 1358 and a heavy chain comprising SEQ ID NO: 1359.