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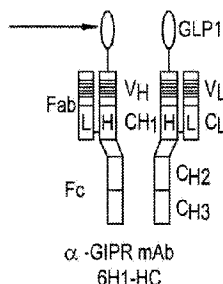
(54) Titre : METHODE DE TRAITEMENT OU D'AMELIORATION DES TROUBLES METABOLIQUES A L'AIDE DE
PROTEINES DE LIAISON ANTAGONISTES POUR PROTEINES DE FUSION AGONISTES DU RECEPTEUR DU
PEPTIDE INHIBITEUR GASTRIQUE (GIPR)/RECEPTEUR GLP-1
(54) Title: METHOD OF TREATING OR AMELIORATING METABOLIC DISORDERS USING ANTAGONISTIC BINDING
PROTEINS FOR GASTRIC INHIBITORY PEPTIDE RECEPTOR (GIPR)/GLP-1 RECEPTOR AGONIST FUSION
PROTEINS

FIG. 3

Ab: 6H1 HC

Linker: 1Kmod

GLP1: (A2G/E3H/R30G), (A2V/E3H/R30G), (A2S/E3H/R30G), (A2G/E3D/R30G),
(A2V/E3D/R30G), (A2S/E3D/R30G), (DA/A2G/R30G), (A2V/R30G), (A2S/R30G),
(A2G/E3Q/R30G), (A2V/E3Q/R30G), (A2S/E3Q/R30G)



(57) **Abrégé/Abstract:**

Method of treating metabolic diseases and disorders using a composition comprising a GLP-1/GIPR antigen binding protein fusion protein are provided. In various embodiments the metabolic disease or disorder is type 2 diabetes, obesity, dyslipidemia, elevated glucose levels, elevated insulin levels and diabetic nephropathy. In certain embodiments the composition comprises the C-terminus of a GLP-1 analog fused to the N-terminus of the light chain variable or heavy chain variable region of an antibody or functional fragment thereof that binds GIPR, optionally with a linker in between.

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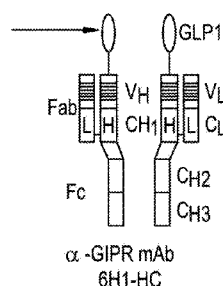
(54) Title: METHOD OF TREATING OR AMELIORATING METABOLIC DISORDERS USING ANTAGONISTIC BINDING PROTEINS FOR GASTRIC INHIBITORY PEPTIDE RECEPTOR (GIPR)/GLP-1 RECEPTOR AGONIST FUSION PROTEINS

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Ab: 6H1 HC

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GLP1: (A2G/E3H/R30G), (A2V/E3H/R30G), (A2S/E3H/R30G), (A2G/E3D/R30G), (A2V/E3D/R30G), (A2S/E3D/R30G), (0A/A2G/R30G), (A2V/R30G), (A2S/R30G), (A2G/E3Q/R30G), (A2V/E3Q/R30G), (A2S/E3Q/R30G)



(57) Abstract: Method of treating metabolic diseases and disorders using a composition comprising a GLP-1/GIPR antigen binding protein fusion protein are provided. In various embodiments the metabolic disease or disorder is type 2 diabetes, obesity, dyslipidemia, elevated glucose levels, elevated insulin levels and diabetic nephropathy. In certain embodiments the composition comprises the C-terminus of a GLP-1 analog fused to the N-terminus of the light chain variable or heavy chain variable region of an antibody or functional fragment thereof that binds GIPR, optionally with a linker in between.

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WO 2018/237095 A1

WO 2018/237095 A1

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CECI EST LE TOME 1 DE 3
CONTENANT LES PAGES 1 À 242

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JUMBO APPLICATIONS/PATENTS

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

THIS IS VOLUME 1 OF 3
CONTAINING PAGES 1 TO 242

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NOM DU FICHIER / FILE NAME :

NOTE POUR LE TOME / VOLUME NOTE:

**METHOD OF TREATING OR AMELIORATING METABOLIC DISORDERS USING
ANTAGONISTIC BINDING PROTEINS FOR GASTRIC INHIBITORY PEPTIDE
RECEPTOR (GIPR)/GLP-1 RECEPTOR AGONIST FUSION PROTEINS**

5 **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, cardiovascular diseases or diabetic nephropathy, using GLP-1 receptor agonists fused via a peptide linker to an antigen binding protein specific for the
10 gastric inhibitory peptide receptor (GIPR).

BACKGROUND OF THE INVENTION

[0002] Glucose-dependent insulintropic 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

15 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
20 (GLP-1) are known insulintropic factors ("incretins"). Intact GIP is rapidly degraded by DPPIV to an inactive form. The insulintropic 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
25 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
30 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, 5 44th EASD Annual meeting poster).

[0006] Collectively, these links to obesity and insulin resistance imply GIPR inhibition is a useful approach for therapeutic intervention.

[0007] Glucagon-like peptide-1 is a 31-amino acid peptide derived from the proglucagon gene. It is secreted by intestinal L-cells and released in response to food ingestion to induce 10 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

15 degradation by the DPP-IV enzyme, resulting in a half-life of approximately 2 minutes. Recently, long-lasting GLP-1 receptor agonists (GLP-1 RAs) such as exenatide, liraglutide, dulaglutide have been developed and are now being used clinically to improve glycemic control in patients with type 2 diabetes. Furthermore, GLP-1RAs also promote body weight reduction as well as reduction in blood pressure and plasma cholesterol levels in patients 20 (Bioorg. Med. Chem.Lett 2013, 23:4011-4018).

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 25 effective amount of a composition comprising a) an antibody or functional fragment thereof that specifically binds to human GIPR, wherein the antibody or functional fragment thereof comprises a light chain variable region and a heavy chain variable region; and b) a GLP-1 receptor agonist, wherein the C-terminus of the GLP-1 receptor agonist is fused to N-terminus of either the light chain variable region or the heavy chain variable region. In one 30 embodiment, the GLP-1 receptor agonist can be fused via a peptide linker.

[0009] 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 composition reduces body weight in an obese subject. In another embodiment, administering the composition reduces body weight gain in an obese subject. In another embodiment, administering the composition reduces fat mass in an obese subject. In another embodiment, the glucose metabolism disorder comprises insulin resistance and administering the composition reduces insulin resistance in an obese subject. In another embodiment, administering the composition reduces liver steatosis in an obese subject having increased liver steatosis. In another embodiment, administering the composition reduces liver fat content in an obese subject having increased liver fat content.

[0010] In one aspect, the composition comprises an antibody or functional fragment thereof 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 human GIPR.

[0011] In one embodiment, the human GIPR has a sequence comprising a sequence selected from the group consisting of SEQ ID NO: 3141, SEQ ID NO: 3143, and SEQ ID NO: 3145. In one embodiment, the antibody or functional fragment thereof is a monoclonal antibody, a recombinant antibody, a human antibody, a humanized antibody, a chimeric antibody, a multispecific antibody, or an antibody fragment thereof. In one embodiment, the antibody fragment is a Fab fragment, a Fab' fragment, or a F(ab')₂ fragment. In one embodiment, the antibody or functional fragment thereof is of the IgG1-, IgG2-, IgG3- or IgG4-type. In one embodiment, the antibody or functional fragment thereof inhibits binding of GIP to the extracellular portion of human GIPR.

[0012] In one embodiment, the GLP-1 receptor agonist is GLP-1(7-37) or a GLP-1(7-37) analog. In one embodiment, the GLP-1 receptor agonist is selected from the group consisting of GLP-1(7-37) (SEQ ID NO: 3184);

[0013] Exendin-4 (SEQ ID NO: 3163);

[0014] Exendin-3 (SEQ ID NO: 3164);

[0015] Leu¹⁴-exendin-4 (SEQ ID NO: 3165);

[0016] Leu¹⁴,Phe²⁵-exendin-4 (SEQ ID NO: 3166);

- [0017] Leu¹⁴,Ala¹⁹,Phe²⁵-exendin-4 (SEQ ID NO: 3167);
- [0018] exendin-4(1-30) (SEQ ID NO: 3168);
- [0019] Leu¹⁴-exendin-4(1-30) (SEQ ID NO: 3169);
- [0020] Leu¹⁴,Phe²⁵-exendin-4(1-30) (SEQ ID NO: 3170);
- 5 [0021] Leu¹⁴,Ala¹⁹,Phe²⁵-exendin-4(1-30) (SEQ ID NO: 3171);
- [0022] exendin-4(1-28) (SEQ ID NO: 3172);
- [0023] Leu¹⁴-exendin-4(1-28) (SEQ ID NO: 3173);
- [0024] Leu¹⁴,Phe²⁵-exendin-4(1-28) (SEQ ID NO: 3174);
- [0025] Leu¹⁴,Ala¹⁹,Phe²⁵-exendin-4 (1-28) (SEQ ID NO: 3175);
- 10 [0026] Leu¹⁴,Lys^{17,20},Ala¹⁹,Glu²¹,Phe²⁵,Gln²⁸-exendin-4 (SEQ ID NO: 3176);
- [0027] Leu¹⁴,Lys^{17,20},Ala¹⁹,Glu²¹,Gln²⁸-exendin-4 (SEQ ID NO: 3177);
- [0028] Phe⁴,Leu¹⁴,Gln²⁸,Lys³³,Glu³⁴, Ile^{35,36},Ser³⁷-exendin-4(1-37) (SEQ ID NO: 3178);
- [0029] Phe⁴,Leu¹⁴,Lys^{17,20},Ala¹⁹,Glu²¹,Gln²⁸-exendin-4 (SEQ ID NO: 3179);
- [0030] Val¹¹,Ile¹³,Leu¹⁴,Ala¹⁶,Lys²¹,Phe²⁵-exendin-4 (SEQ ID NO: 3180);
- 15 [0031] exendin-4-Lys⁴⁰ (SEQ ID NO: 3181);
- [0032] GLP-1(7-37) (SEQ ID NO: 3182);
- [0033] 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:
- 20 3183);
- [0034] Arg³⁴-GLP-1(7-37) (SEQ ID NO: 3184);
- [0035] Glu³⁰-GLP-1(7-37) (SEQ ID NO: 3185);
- [0036] Lys²²-GLP-1(7-37) (SEQ ID NO: 3186);
- [0037] Gly^{8,36},Glu²²-GLP-1(7-37) (SEQ ID NO: 3187);
- 25 [0038] Val⁸,Glu²²,Gly³⁶-GLP-1(7-37) (SEQ ID NO: 3188);
- [0039] Gly^{8,36},Glu²²,Lys³³,Asn³⁴-GLP-1(7-37) (SEQ ID NO: 3189);
- [0040] Val⁸,Glu²²,Lys³³,Asn³⁴,Gly³⁶-GLP-1(7-37) (SEQ ID NO: 3190);
- [0041] Gly^{8,36},Glu²²,Pro³⁷-GLP-1(7-37) (SEQ ID NO: 3191);
- [0042] Val⁸,Glu²²,Gly³⁶,Pro³⁷-GLP-1(7-37) (SEQ ID NO: 3192);
- 30 [0043] Gly^{8,36},Glu²²,Lys³³, Asn³⁴,Pro³⁷-GLP-1(7-37) (SEQ ID NO: 3193);
- [0044] Val⁸,Glu²²,Lys³³,Asn³⁴,Gly³⁶,Pro³⁷-GLP-1(7-37) (SEQ ID NO: 3194);
- [0045] Gly^{8,36},Glu²²-GLP-1(7-36) (SEQ ID NO: 3195);
- [0046] Val⁸,Glu²²,Gly³⁶-GLP-1(7-36) (SEQ ID NO: 3196);
- [0047] Val⁸,Glu²²,Asn³⁴,Gly³⁶-GLP-1(7-36) (SEQ ID NO: 3197);

- [0048] Gly^{8,36},Glu²²,Asn³⁴-GLP-1(7-36) (SEQ ID NO: 3198);
- [0049] GLP-1 analog (SEQ ID NO: 3199);
- [0050] GLP-1 analog (SEQ ID NO: 3200);
- [0051] [Gly^{8,36},Glu²²]GLP-1(7-37) (SEQ ID NO: 3201);
- 5 [0052] HAEGTFTSDVSSYLEGQAAKEFIAWLVKGRG (SEQ ID NO: 3202);
- [0053] AEGTFTSDVSSYLEGQAAKEFIAWLVKGRG (SEQ ID NO: 3203);
- [0054] EGTFTSDVSSYLEGQAAKEFIAWLVKGRG (SEQ ID NO: 3204);
- [0055] HEGTFTSDVSSYLEGQAAKEFIAWLVKGRG (SEQ ID NO: 3205);
- [0056] HEGTFTSDVSSYLEGQAAKEFIAWLVKGR (SEQ ID NO: 3206);
- 10 [0057] HLEGTFTSDVSSYLEGQAAKEFIAWLVKGRG (SEQ ID NO: 3207);
- [0058] HEGTFTSDLSKQMEEEAVRLF (SEQ ID NO: 3208);
- [0059] HEGTFTSDLSKQMEEEAVRLFI (SEQ ID NO: 3209);
- [0060] HEGTFTSDVSSYLEGQAAKEFIAWLVKGGG (SEQ ID NO: 3210);
- [0061] HEGTFTSDLSKQMEEEAVRLAAQAAQQGGG (SEQ ID NO: 3211);
- 15 [0062] HSEGTFTSDVSSYLEEQAAKEFIAWLVKGGG (SEQ ID NO: 3212);
- [0063] HSQGTFTSDVSSYLEEQAAKEFIAWLVKGGG (SEQ ID NO: 3213);
- [0064] HGDGTFTSDVSSYLEEQAAKEFIAWLVKGGG (SEQ ID NO: 3214);
- [0065] HSDGTFTSDVSSYLEEQAAKEFIAWLVKGGG (SEQ ID NO: 3215);
- [0066] HSEGTFTSDVSSYLEEQAAKEFIEWLVKGGG (SEQ ID NO: 3216);
- 20 [0067] HSQGTFTSDVSSYLEEQAAKEFIEWLVKGGG (SEQ ID NO: 3217);
- [0068] HGDGTFTSDVSSYLEEQAAKEFIEWLVKGGG (SEQ ID NO: 3218);
- [0069] HSDGTFTSDVSSYLEEQAAKEFIEWLVKGGG (SEQ ID NO: 3219);
- [0070] HEGTFTSDVSSYLEEQAAKEFIAWLKNNGG (SEQ ID NO: 3220);
- [0071] HSEGTFTSDVSSYLEEQAAKEFIAWLKNNGG (SEQ ID NO: 3221);
- 25 [0072] HSQGTFTSDVSSYLEEQAAKEFIAWLKNNGG (SEQ ID NO: 3222);
- [0073] HGDGTFTSDVSSYLEEQAAKEFIAWLKNNGG (SEQ ID NO: 3223);
- [0074] HSDGTFTSDVSSYLEEQAAKEFIAWLKNNGG (SEQ ID NO: 3224);
- [0075] HSEGTFTSDVSSYLEEQAAKEFIEWLKNNGG (SEQ ID NO: 3225);
- [0076] HSQGTFTSDVSSYLEEQAAKEFIEWLKNNGG (SEQ ID NO: 3226);
- 30 [0077] HGDGTFTSDVSSYLEEQAAKEFIEWLKNNGG (SEQ ID NO: 3227);
- [0078] HSDGTFTSDVSSYLEEQAAKEFIEWLKNNGG (SEQ ID NO: 3228);
- [0079] HEGTFTSDVSSYLEEQAAKEFIEWLKNNEG (SEQ ID NO: 3229);
- [0080] HSEGTFTSDVSSYLEEQAAKEFIEWLKNNEG (SEQ ID NO: 3230);
- [0081] HEGTFTSDVSSYLEEQAAKEFIEWLKNPGG (SEQ ID NO: 3231);

- [0082] HSEGTFTSDVSSYLEEQAAKEFIEWLKNPGG (SEQ ID NO: 3232);
- [0083] HSEGTFTSDVSSYLEEQAAKEFIEWLKNQGG (SEQ ID NO: 3233);
- [0084] HSEGTFTSDVSSYLEEQAAKEFIEWLKNQGG (SEQ ID NO: 3234);
- [0085] HSEGTFTSDVSSYLEEQAAKEFIEWLKNNTGG (SEQ ID NO: 3235);
- 5 [0086] HSEGTFTSDVSSYLEEQAAKEFIEWLKNNTGG (SEQ ID NO: 3236);
- [0087] HSEGTFTSDVSSYLEEQAAKEFIEWLKNVGG (SEQ ID NO: 3237);
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- [0089] HSEGTFTSDVSSYLEEQAAKEFIEWLKQGGG (SEQ ID NO: 3239);
- [0090] HSEGTFTSDVSSYLEEQAAKEFIEWLKQGGG (SEQ ID NO: 3240);
- 10 [0091] HSEGTFTSDVSSYLEEQAAKEFIAWLKGGG (SEQ ID NO: 3241);
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- 15 [0096] HVQGTFTSDVSSYLEGQAAKEFIAWLKGGG (SEQ ID NO: 3246);
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- [0098] HVDGTFTSDVSSYLEGQAAKEFIAWLKGGG (SEQ ID NO: 3248);
- [0099] HGHGTFTSDVSSYLEGQAAKEFIAWLKGGG (SEQ ID NO: 3249);
- [0100] HVHGTFTSDVSSYLEGQAAKEFIAWLKGGG (SEQ ID NO: 3250);
- 20 [0101] HSHGTFTSDVSSYLEGQAAKEFIAWLKGGG (SEQ ID NO: 3251);
- [0102] HGDGTFTSDVSSYLEGQAAKEFIAWLKGGG (SEQ ID NO: 3252);
- [0103] HSDGTFTSDVSSYLEGQAAKEFIAWLKGGG (SEQ ID NO: 3253);
- [0104] HSEGTFTSDVSSYLEEQAAKEFIEWLKNNGG (SEQ ID NO: 3254);
- [0105] HSEGTFTSDVSSYLEEQAAKEFIEWLVKGGG (SEQ ID NO: 3255);
- 25 [0106] HSEGTFTSDYSSYLEEQAAKEFIEWLKNNGG (SEQ ID NO: 3256);
- [0107] HSEGTFTSEVSSYLEGQAAKEFIEWLKNNGG (SEQ ID NO: 3257);
- [0108] HSEGTFTSDLKQMEEEEAVRLF AAQAAQQGGG (SEQ ID NO: 3258);
- [0109] HSQGTFTSDLKQMEEEEAVRLF AAQAAQQGGG (SEQ ID NO: 3259);
- [0110] HGDGTFTSDLKQMEEEEAVRLF AAQAAQQGGG (SEQ ID NO: 3260);
- 30 [0111] HSDGTFTSDLKQMEEEEAVRLF AAQAAQQGGG (SEQ ID NO: 3261);
- [0112] HSEGTFTSDLKQMEEEEAVRLF AAQAAQQGGG (SEQ ID NO: 3262);
- [0113] HSEGTFTSDLKQMEEEEAVRLFIEWLKNNGG (SEQ ID NO: 3263);
- [0114] HSEGTFTSDVSSYLEGEAVRLFIEWLKNNGG (SEQ ID NO: 3264);
- [0115] HSEGTFTSDLKQMEEEEAVRLFIEWLKNNGPSSGAPPPS (SEQ ID NO: 3265);

- [0116] HGEGTFTSDVSSYLEGEAVRLFIEWLKNGGPSSGAPPPS (SEQ ID NO: 3266);
- [0117] HHGEGTFTSDVSSYLEEQAAKEFIEWLKNGGG (SEQ ID NO: 3267);
- [0118] HHGEGTFTSDVSSYLEEQAAKEFIEWLKDGGG (SEQ ID NO: 3268);
- [0119] HHGEGTFTSDVSSYLEEQAAKEFIEWLKQGGG (SEQ ID NO: 3269);
- 5 [0120] HHGEGTFTSDVSSYLEEQAAKEFIEWLKNQGG (SEQ ID NO: 3270);
- [0121] HHGEGTFTSDVSSYLEEQAAKEFIEWLKNTGG (SEQ ID NO: 3271);
- [0122] HHGEGTFTSDVSSYLEEQAAKEFIEWLKNVGG (SEQ ID NO: 3272);
- [0123] HHGEGTFTSDVSSYLEEQAAKEFIEWLKNPGG (SEQ ID NO: 3273);
- [0124] HHGEGTFTSDVSSYLEEQAAKEFIEWLKNEGG (SEQ ID NO: 3274);
- 10 [0125] HGAGTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3275);
- [0126] HGDGTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3276);
- [0127] HGLGTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3277);
- [0128] HGVGTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3278);
- [0129] HGFGTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3279);
- 15 [0130] HGYGTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3280);
- [0131] HGTGTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3281);
- [0132] HGNGTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3282);
- [0133] HGHGTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3283);
- [0134] HGKGTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3284);
- 20 [0135] HGIGTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3285);
- [0136] HGWGTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3286);
- [0137] HPGGTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3287);
- [0138] HSGGTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3288);
- [0139] HGRGTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3289);
- 25 [0140] AHGEGTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3290);
- [0141] GHGEGTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3291);
- [0142] HHGEGTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3292);
- [0143] HHEGTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3293);
- [0144] HGEATFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3294);
- 30 [0145] HGESTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3295);
- [0146] HGEVTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3296);
- [0147] HGEKTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3297);
- [0148] HGEETFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3298);
- [0149] HGEGTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3299);

[0150] HVEGTFTSDVSSYLEGQAAKEFIAWLVKGRG (SEQ ID NO: 3300);

[0151] HSEGTFTSDVSSYLEGQAAKEFIAWLVKGRG (SEQ ID NO: 3301); and

[0152] HGQGTFTSDVSSYLEGQAAKEFIAWLVKGRG (SEQ ID NO: 3302).

[0153] In one embodiment, the peptide linker comprises a sequence selected from the group

5 consisting of (Gly₃Ser)₂ (SEQ ID NO: 3303), (Gly₄Ser)₂ (SEQ ID NO: 3304), (Gly₃Ser)₃ (SEQ ID NO: 3305), (Gly₄Ser)₃ (SEQ ID NO: 3306), (Gly₃Ser)₄ (SEQ ID NO: 3307), (Gly₄Ser)₄ (SEQ ID NO: 3308), (Gly₃Ser)₅ (SEQ ID NO: 3309), (Gly₄Ser)₅ (SEQ ID NO: 3310), (Gly₃Ser)₆ (SEQ ID NO: 3311), (Gly₄Ser)₆, GGEGGG (SEQ ID NO: 3312);

[0154] GEEEEGGG (SEQ ID NO: 3313);

10 [0155] GEEEG (SEQ ID NO: 3314);

[0156] GEEE (SEQ ID NO: 3315);

[0157] GGDGGG (SEQ ID NO: 3316);

[0158] GGDDDGG (SEQ ID NO: 3317);

[0159] GDDDG (SEQ ID NO: 3318);

15 [0160] GDDD (SEQ ID NO: 3319);

[0161] GGGGSDDSDEGSDGEDGGGGS (SEQ ID NO: 3320);

[0162] WEWEW (SEQ ID NO: 3321);

[0163] FEFEF (SEQ ID NO: 3322);

[0164] EEEWWW (SEQ ID NO: 3323);

20 [0165] EEEFFF (SEQ ID NO: 3324);

[0166] WEEEEWW (SEQ ID NO: 3325);

[0167] FFEEFF (SEQ ID NO: 3326).

[0168] GGGG (SEQ ID NO: 3327);

[0169] GGGGSGGGG (SEQ ID NO: 3328);

25 [0170] GAPAPAPAPG (SEQ ID NO: 3329);

[0171] GGGGAGGGGAGGGG (SEQ ID NO: 3330);

[0172] GAPAPAPAPAPAPG (SEQ ID NO: 3331);

[0173] GAPAPAPAPAPAPAPAPG (SEQ ID NO: 3332);

[0174] GGGGAGGGGAGGGGAGGGG (SEQ ID NO: 3333);

30 [0175] GAPAPAPAPAPAPAPAPAPAPG (SEQ ID NO: 3334);

[0176] GSGSATGGSGSVASSGSGSATGS (SEQ ID NO: 3335); and

[0177] GSGSATGGSGSVASSGSGSATHL (SEQ ID NO: 3336).

BRIEF DESCRIPTION OF THE DRAWINGS

- [0178] FIG. 1A-1B: Synthetic Peptides
- [0179] FIG. 2: Results initial GLP-1 SAR screen: Expressible Series
- [0180] FIG. 3: Recombinant N-terminal Analogues
- 5 [0181] FIG. 4: GLP1 N-terminal Variants Summary HC of 6H1 Ab with 1Kmod Linker
- [0182] FIG. 5A-5C: In vivo pharmacodynamic evaluation of GLP1 variants and linkers in mice
- [0183] FIG. 6A-6C: In vivo pharmacodynamic evaluation of GLP1 variants in mice
- [0184] FIG. 7A-7E: PK N-terminal Variants
- 10 [0185] FIG. 8: Recombinant Linker Analogues
- [0186] FIG. 9: GLP1 Linker Variants Summary HC of 6H1 Ab GLP1(A2G/R30G)
- [0187] FIG. 10A-10E: GLP1 Linker Variants Fused to HC of 6H1 Ab in Mice
- [0188] FIG. 11A-11C: In vivo pharmacodynamic evaluation of linker variants in mice
- [0189] FIG. 12A-12E: PK Linker Variants
- 15 [0190] FIG. 13: Recombinant N-term & C-term GLP1 Analogues and Linkers
- [0191] FIG. 14: 1K Linker Variants
- [0192] FIG. 15: (G4A)3G4 Linker Variants
- [0193] FIG. 16: G(AP)10G Linker Variants
- [0194] FIG. 17: GLP1 N-terminal Variants Summary Fused to HC of 6H1 Ab
- 20 [0195] FIG. 18: Signal Sequence Processing May Be Responsible for Observed HG/E Cleavage
- [0196] FIG. 19: GLP1 C-terminal Variants Summary Fused to HC of 6H1 Ab
- [0197] FIG. 20A-20D: 1Kmod Linker
- [0198] FIG. 21A-21D: (G4A)3G4 Linker
- 25 [0199] FIG. 22A-22D: G(AP)10G Linker
- [0200] FIG. 23: GLP1 Linkers Summary Fused to HC of 6H1 Ab
- [0201] FIG. 24A-24D: linker comparison with A24E/V27K/K28N
- [0202] FIG. 25: Recombinant C-term GLP1 Analogues and Linkers
- [0203] FIG. 26: Mouse PK study
- 30 [0204] FIG. 27A-27D: Concentration-time data and PK
- [0205] FIG. 28: Recombinant C-term GLP1 Analogues and Linkers
- [0206] FIG. 29: GLP1 2G10 Fusions In Vitro Activity
- [0207] FIG. 30: Mouse PK study

- [0208] FIG. 31A-31D: Concentration-time data and PK Single
- [0209] FIG. 32: Study design to confirm potency of triple mutants on glp-1 activity
- [0210] FIG. 33A-33D: Confirmation of GLP-1 activity in vivo
- [0211] FIG. 34: Study design to confirm potency of single mutants on glp-1 activity
- 5 [0212] FIG. 35A-35D: Confirmation of GLP-1 activity in vivo
- [0213] FIG. 36A-36B: GLP1-GIPR Activity In Vivo 5G12 Ab Single Injection
- [0214] FIG. 37A-37D: Concentration-time data and PK parameters

DETAILED DESCRIPTION OF THE INVENTION

- 10 [0215] 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, diabetic neuropathy, diabetic nephropathy, diabetic retinopathy, diabetic cardiomyopathy, Type 1 diabetes, obesity and conditions
- 15 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.
- [0216] Recombinant polypeptide and nucleic acid methods used herein, including in the
- 20 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.
- [0217] The section headings used herein are for organizational purposes only and are not to
- 25 be construed as limiting the subject matter described.
- [0218] 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.
- 30 [0219] 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),
5 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
10 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.

15 **[0220]** 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.

[0221] Other than in the operating examples, or where otherwise indicated, all numbers
20 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 $\pm 1\%$.

[0222] Following convention, as used herein "a" and "an" mean "one or more" unless specifically indicated otherwise.

25 **[0223]** 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.

[0224] A "naturally occurring amino acid" is an amino acid that is encoded by the genetic
30 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.

5 [0225] An “amino acid mimetic” is a chemical compound that has a structure that is different from the general chemical structure of an amino acid, but that functions in a manner similar to a naturally occurring amino acid. Examples include a methacryloyl or acryloyl derivative of an amide, β -, γ -, δ -imino acids (such as piperidine-4-carboxylic acid) and the like.

[0226] A “non-naturally occurring amino acid” is a compound that has the same basic
10 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
15 polypeptide chain by the translation complex. A non-limiting list of examples of non-naturally occurring amino acids that can be inserted into a polypeptide sequence or substituted for a wild-type residue in polypeptide sequence include β -amino acids, homoamino acids, cyclic amino acids and amino acids with derivatized side chains. Examples include (in the L-form or D-form; abbreviated as in parentheses): citrulline (Cit),
20 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-
25 tetrahydroisoquinoline (Tic), Octahydroindole-2-carboxylic acid (Oic), 3-(1-naphthyl)alanine (1-Nal), 3-(2-naphthyl)alanine (2-Nal), 1,2,3,4-tetrahydroisoquinoline (Tic), 2-indanylglycine (IgI), para-iodophenylalanine (pI-Phe), para-aminophenylalanine (4AmP or 4-Amino-Phe), 4-guanidino phenylalanine (Guf), glycyllsine (abbreviated “K(N ϵ -glycyl)” or “K(glycyl)” or “K(gly)”), nitrophenylalanine (nitrophe), aminophenylalanine (aminophe or Amino-Phe),
30 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), acetylarginine (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.

[0227] 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.

[0228] 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.

[0229] A composition of the present invention that includes a GLP-1 receptor agonist of the present invention fused via a peptide bond of its C-terminus to the N-terminus of an anti-GIPR antigen binding protein of the invention or is a “fusion protein” or “fusion molecule”, or simply “fusion” of the present invention. A peptide linker sequence may be interposed between the GLP-1 receptor agonist peptide and the anti-GIPR antigen binding protein such that the GLP-1 receptor agonist of the present invention is fused via a peptide bond of its C-

terminus to the N-terminus of the linker peptide, and the C-terminus of the linker peptide is fused via a peptide bond to the N-terminus of the light chain variable region or to the N-terminus of the heavy chain variable region of the anti-GIPR antigen binding protein.

Although the GLP-1 receptor agonists and/or linker peptides can be fused to the anti-GIPR antigen binding protein after translation or purification of the anti-GIPR antigen binding protein, in one embodiment the fusion proteins of the present invention can be produced via expression of the full length fusion protein in a suitable cell type without a further conjugation reaction.

[0230] The term “encoding” refers to a polynucleotide sequence encoding one or more amino acids. The term does not require a start or stop codon.

[0231] 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.

[0232] 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.

[0233] Recommended parameters for determining percent identity for polypeptides or nucleotide sequences using the GAP program are the following:

[0234] Algorithm: Needleman et al., 1970, J. Mol. Biol. 48:443-453;

[0235] Comparison matrix: BLOSUM 62 from Henikoff et al., 1992, supra;

[0236] Gap Penalty: 12 (but with no penalty for end gaps)

[0237] Gap Length Penalty: 4

[0238] Threshold of Similarity: 0

[0239] 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.

[0240] 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: 3141, which consists of 466 amino acid residues and which is encoded by the nucleotide sequence SEQ ID NO: 3142, or SEQ ID NO: 3143, which consists of 430 amino acid residues and which is encoded by the nucleic acid sequence SEQ ID NO: 3144, or SEQ ID NO: 3145, which consists of 493 amino acid residues and which is encoded by the nucleic acid sequence of SEQ ID NO: 3146, or SEQ ID NO: 3147, which consists of 460 amino acids residues and which is encoded by the nucleic acid sequence of SEQ ID NO: 3148, or SEQ ID NO: 3149, which consists of 230 amino acids residues and which is encoded by the nucleic acid sequence of SEQ ID NO: 3150.

[0241] The term “GIPR polypeptide” also encompasses a GIPR polypeptide in which a naturally occurring GIPR polypeptide sequence (e.g., SEQ ID NOs: 3141, 3143 or 3145) 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-
5 occurring amino acid analogs and amino acid mimetics.

[0242] 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: 3141, 3143 or 3145). 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
10 to a naturally-occurring GIPR polypeptide amino acid sequence (e.g., SEQ ID NOs: 3141, 3143 or 3145). 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.

[0243] 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
20 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
25 Research Communications (2002) 290:1420–1426).

[0244] 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
30 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).

[0245] The terms “GIP”, “Gastric inhibitory polypeptide”, “glucose-dependent insulinitropic 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.

[0246] The 42 amino acid sequence of mature human GIP is:

[0247] 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: 3151)

[0248] and is encoded by the DNA sequence:

[0249] 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: 3152).

[0250] The 42 amino acid sequence of mature murine GIP is:

[0251] 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: 3153)

[0252] and is encoded by the DNA sequence:

[0253] 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: 3154).

[0254] The 42 amino acid sequence of mature rat GIP is:

[0255] 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: 3155)

[0256] and is encoded by the DNA sequence:

[0257] 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 c g c a g a a a g g c a a a a a a a
c g a t t g g a a a c a t a a c t g a c c c a g (SEQ ID NO: 3156).

[0258] 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: 3141, 3143 or 3145). 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.

[0259] 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, Sapidyne, 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.

[0260] “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.

[0261] 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.

[0262] 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.

[0263] 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.

[0264] 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.

[0265] 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.

[0266] 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.

[0267] In another embodiment, Fvs, domain antibodies and scFvs, and may be derived from an antibody of the present invention.

[0268] 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.

[0269] 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
5 another heavy chain molecule.

[0270] 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.

[0271] An “Fab' fragment” contains one light chain and a portion of one heavy chain that
10 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.

[0272] 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
15 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.

[0273] The “Fv region” comprises the variable regions from both the heavy and light chains, but lacks the constant regions.

[0274] “Single chain antibodies” or “scFvs” are Fv molecules in which the heavy and light
20 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.

[0275] A “domain antibody” or “single chain immunoglobulin” is an immunologically
25 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
30 the same or different antigens.

[0276] 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.

[0277] A multispecific antigen binding protein” or “multispecific antibody” is one that targets more than one antigen or epitope.

[0278] 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.

[0279] 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., Stahl 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 unlabelled 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.

[0280] 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.

[0281] 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.

[0282] 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.

[0283] 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.

[0284] 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.

[0285] 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.

[0286] 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.

[0287] 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.

[0288] 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.

[0289] 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."

[0290] 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.

[0291] 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.

[0292] 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.

[0293] 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.

[0294] 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.

[0295] 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.

[0296] 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.

[0297] 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.

[0298] 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.

[0299] A “subject” or “patient” as used herein can be any mammal. In a typical embodiment, the subject or patient is a human.

[0300] 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:1, 3 or 5, 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.

[0301] 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.

[0302] The 466 amino acid sequence of human GIPR is (Volz et al., FEBS Lett. 373:23-29 (1995); NCBI Reference Sequence: NP_0001555):

[0303] 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 RSTLTLLVPLL
 GVHEVVFAPV TEEQARGALR FAKLGFEIFL SSFQGFVLSV LYCFINKEVQ
 SEIRRGWHHC RLRRSLGEEQ RQLPERAFRA LPSGSGPGEV PTSRGLSSGT
 LPGPGNEASR ELESYC (SEQ ID NO: 3141)

[0304] and is encoded by the DNA sequence (NCBI Reference Sequence: NM_000164):

[0305] 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 ggcctcgcct gtaacgggtc cttcgatatg
 tacgtctgct gggactatgc tgcacccaat gccactgcc gccgctcctg

ccctggtac ctgccctggc accaccatgt ggctgcaggt ttcgtcctcc
 gccagtgtgg cagtgatggc caatggggac tttggagaga ccatacacia
 tgtgagaacc cagagaagaa tgaggccttt ctggaccaa ggctcatctt
 ggagcggttg caggatcatgt aactgtcgg ctactccctg tctctcgcca
 5 cactgctgct agccctgctc atcttgagtt tgttcaggcg gctacattgc
 actagaaact atatccacat caacctgttc acgtctttca tgctgcgagc
 tgcggccatt ctacgccgag accgtctgct acctcgacct ggcccctacc
 ttggggacca ggcccttgcg ctgtggaacc aggcctcgc tgctgcccgc
 acggcccaga tcgtgaccca gtactgcgtg ggtgccaact acacgtggct
 10 gctggtggag ggctctacc tgcacagtct cctggtgctc gtgggaggct
 ccgaggaggg ccacttccgc tactacctgc tcctcggtcg gggggccccc
 gcgcttttcg tcattccctg ggtgatcgtc aggtacctgt acgagaacac
 gcagtgctgg gagcgcaacg aagtcaaggc catttggtgg attatacggg
 ccccatcct catgaccatc ttgattaatt tcctcatttt tatccgcatt
 15 cttggcattc tcctgtccaa gctgaggaca cggcaaattgc gctgccggga
 ttaccggctg aggttggtc gctccacgct gacgctgggtg cccctgctgg
 gtgtccacga ggtggtgttt gctcccgta cagaggaaca ggccggggc
 gccctgcgtc tcgccaagct cggctttgag atcttcctca gtccttcca
 gggcttcctg gtcagcgtcc tctactgctt catcaacaag gaggtgcagt
 20 cggagatccg ccgtggctgg caccactgcc gcctgcgccg cagcctgggc
 gaggagcaac gccagctccc ggagcgcgcc ttccggggcc tgccctccgg
 ctccggcccc ggagaggtcc ccaccagccg cggcttgtcc tcggggaccc
 tcccagggcc tgggaatgag gccagccggg agttggaaag ttactgctag
 ggggcgggat ccccggtgtc gttcagttag catggattta ttgagtcca
 25 actgcgtgcc aggccagta cggaggacgc tggggaaatg gtgaaggaaa
 cagaaaaaag gtccctgccc ttctggagat gacaactgag tggggaaaac
 agaccgtgaa cacaaaacat caagtccac acacgctatg gaatggttat
 gaagggaagc gagaaggggg cctaggggtg tctgggaggc gtctccaagg
 aggtgacact taagccatcc ccgaaagagg tgaaagagat cactttgggg
 30 agagctggag aacaggattc taggcggaag cgatagcata ggcaaaggcc
 cttgggcagg aaggcgtca gccttggctg gagtagaatt aagtcagagc
 caacagggtg ggagagacag agaagtgggc aggggcaccc aagttgggat
 ttcatcttcag gtgcattgga gattcttagg agtgtctctt gggggtaata
 ttttattttt taaaaaatga ggat (SEQ ID NO: 3142).

[0306] A 430 amino acid isoform of human GIPR (isoform X1), predicted by automated computational analysis, has the sequence (NCBI Reference Sequence XP_005258790):

[0307] MTTSPILQLL LRLSLCGLLL QRAETGSKGQ TAGELYQRWE RYRRECQETL
 AAAEPPSVAA GFVLRQCGSD GQWGLWRDHT QCENPEKNEA FLDQRLILER
 5 LQVMYTVGYS LSLATLLLAL LILSLFRRRLH CTRNYIHINL FTSFMLRAAA
 ILSRDRLLP RGPYLGDAQAL ALWNQALAAC RTAQIVTQYC VGANYTWLLV
 EGVYLHSLLV LVGGSEEGHF RYLLLLGWGA PALFVIPWVI VRYLYENTQC
 WERNEVKAIW WIIRTPILMT ILINFLIFIR ILGILLSKLR TRQMRCRDYR
 LRLARSTLTL VPLLGVHEVV FAPVTEEQAR GALRFAKLGF EIFLSSFQGF
 10 LVSVLYCFIN KEVQSEIRRG WHHCRLRRSL GEEQRQLPER AFRALPSGSG
 PGEVPTSRGL SSGTLPGPNG EASRELESYC (SEQ ID NO: 3143)

[0308] and is encoded by the DNA sequence:

[0309] atgaccacca gcccgattct gcagctgctg ctgcgcctga gcctgtgcgg
 cctgctgctg cagcgcgcgg aaaccggcag caaaggccag accgcggggc
 15 aactgtatca gcgctgggaa cgctatcgcc gcgaatgcca ggaaaccctg
 gcggcgggcg aaaccgccgag cgtggcgggc ggctttgtgc tgcgccagt
 cggcagcgat ggccagtggg gcctgtggcg cgatcatacc cagtgcgaaa
 acccggaaaa aaacgaagcg tttctggatc agcgctgat tctggaacgc
 ctgcaggtga tgtataccgt gggctatagc ctgagcctgg cgaccctgct
 20 gctggcgctg ctgattctga gcctgtttcg ccgcctgcat tgcaccgcga
 actatattca tattaacctg tttaccagct ttatgctgcg cgcgggcgcg
 attctgagcc gcgatcgct gctgccgcgc ccgggcccgt atctgggcga
 tcaggcgctg gcgctgtgga accaggcgct ggcggcgtgc cgcaccgcgc
 agattgtgac ccagtattgc gtgggcgcga actataacctg gctgctgggtg
 25 gaaggcggtg atctgcatag cctgctgggtg ctgggtgggcg gcagcgaaga
 aggccatttt cgctattatc tgctgctggg ctggggcgcg ccggcgctgt
 ttgtgattcc gtgggtgatt gtgcgctatc tgtatgaaaa caccagtg
 tgggaacgca acgaagtga agcgatttgg tggattattc gcaccccgat
 tctgatgacc attctgatta actttctgat ttttattcgc attctgggca
 30 ttctgctgag caaactgcgc acccgccaga tgcgctgccg cgattatcgc
 ctgcgcctgg cgcgcagcac cctgaccctg gtgccgctgc tgggcgtgca
 tgaagtgggtg tttgcgccgg tgaccgaaga acaggcgcg gcgcgctgc
 gctttgcgaa actgggcttt gaaatttttc tgagcagctt tcagggcttt
 ctgggtgagcg tgctgtattg ctttattaac aaagaagtgc agagcgaaat

tcgccgcggc tggcatcatt gccgcctgcg ccgcagcctg ggcaagaac
 agcggcagct gccggaacgc gcgtttcgcg cgctgccgag cggcagcggc
 ccgggcgaag tgccgaccag ccgcggcctg agcagcggca ccctgccggg
 cccgggcaac gaagcgagcc gcgaactgga aagctattgc (SEQ ID NO: 3144).

- 5 **[0310]** 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):

[0311] MTTSPILQLL LRLSLCGLLL QRAETGSKGQ TAGELYQRWE RYRRECQETL
 AAAEPPSGLA CNGSFDMYVC WDYAAPNATA RASCPWYLPW HHHVAAGFVL
 10 RQCGSDGQWG LWRDHTQCEN PEKNEAFLDQ RLILERLQVM YTVGYSLSLA
 TLLLALLILS LFRRLLHCTR N YIHINLFTSF MLRAAAILSR DRLLPRPGPY
 LGDQALALWN QALAACRTAQ IVTQYCVGAN YTWLLVEGVY LHSLLVLVGG
 SEEGHFRYYL LLGWGAPALF VIPWVIVRYL YENTQCWERN EVKAIWWIIR
 TPILMTILIN FLIFIRILGI LLSKLRTRQM RCRDYRLRLA RSTLTIVPLL
 15 GVHEVVFAPV TEEQARGALR FAKLGFEIFL SSFQGFVSV LYCFINKEVG
 RDPAAAPALW RRRGTAPPLS AIVSQVQSEI RRGWHHCRLR RSLGEEQRQL
 PERAFRALPS GSGPGEVPTS RGLSSGTLPG PGNEASRELE SYC (SEQ ID NO: 3145)

[0312] and is encoded by the DNA sequence:

[0313] atgaccacca gcccgattct gcagctgctg ctgcgcctga gcctgtgcgg
 20 cctgctgctg cagcgcgcgg aaaccggcag caaaggccag accgcggggc
 aactgtatca gcgctgggaa cgctatcgcc gcgaatgcca ggaaaccctg
 gcggcggcgg aaccgccgag cggcctggcg tgcaacggca gctttgatat
 gtatgtgtgc tgggattatg cggcgccgaa cgcgaccgcg cgcgcgagct
 gcccgtagta tctgccgtgg catcatcatg tggcggcggg ctttgtgctg
 25 cgccagtgcg gcagcgatgg ccagtggggc ctgtggcgcg atcataccca
 gtgcgaaaac ccggaaaaaa acgaagcgtt tctggatcag gcctgattc
 tggaacgcct gcaggtgatg tataccgtgg gctatagcct gagcctggcg
 accctgctgc tggcgctgct gattctgagc ctgtttcgcc gcctgcattg
 caccgcgaac tatattcata ttaacctgtt taccagcttt atgctgcgcg
 30 cggcggcgat tctgagccgc gatcgccctgc tgccgcgccc gggcccgat
 ctgggcgatc aggcgctggc gctgtggaac caggcgctgg cggcgtgccg
 caccgcgcag attgtgaccc agtattgcgt gggcgcgaaac tatacctggc
 tgctggtgga aggcgtgtat ctgcatagcc tgctggtgct ggtgggcggc
 agcgaagaag gccattttcg ctattatctg ctgctgggct ggggcgcgcc

ggcgctgttt gtgattccgt ggggtgattgt gcgctatctg tatgaaaaca
 cccagtgtctg ggaacgcaac gaagtgaag cgatttggtg gattattcgc
 accccgattc tgatgaccat tctgattaac tttctgattt ttattcgc
 tctgggcatt ctgctgagca aactgcgcac ccgccagatg cgctgccgcg
 5 attatcgctt gcgcctggcg cgcagcacc tgacctgggt gccgctgctg
 ggcgtgcatg aagtgggtgtt tgcgccgggtg accgaagaac aggcgcgcg
 cgcgctgcgc tttgcgaaac tgggctttga aatttttctg agcagctttc
 agggctttct ggtgagcgtg ctgtattgct ttattaacaa agaagtgggc
 cgcgatccgg cggcggcgcc ggcgctgtgg cgccgccgcg gcaccgcgc
 10 gccgctgagc gcgattgtga gccagggtgca gagcgaaatt cgccgcggct
 ggcatcattg ccgcctgcgc cgcagcctgg gcgaagaaca gcgccagctg
 ccggaacgcg cgtttcgcgc gctgccgagc ggcagcggcc cgggcgaagt
 gccgaccagc cgcggcctga gcagcggcac cctgccgggc cggggcaacg
 aagcgagccg cgaactggaa agctattgct aa (SEQ ID NO: 3146)
 15 **[0314]** 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.
[0315] MPLRLLLLLL WLWGLQWAET DSEGQTTTGE LYQRWEHYGQ ECQKMLETTE
 PPSGLACNGS FDMYACWNYT AANTTARVSC PWYLPWFRQV SAGFVFRQCG
 20 SDGQWGSWRD HTQCENPEKN GAFQDQTLIL ERLQIMYTVG YSLSLTTLIL
 ALLILSLFRR LHCTRNYIHM NLFTSFMLRA AAILTRDQLL PPLGPYTGQDQ
 APTPWNQALA ACRTAQIMTQ YCVGANYTWL LVEGVYLHHL LVIVGRSEKG
 HFRCYLLLGW GAPALFVIPW VIVRYLRENT QCWERNEVKA IWWIIRTPIL
 ITILINFLIF IRILGILVSK LRTRQMRCPD YRLRLARSTL TLVPLLGVHE
 25 VVFAPVTEEQ VEGSLRFAKL AFEIFLSSFQ GFLVSVLYCFINKEVQSEIRQ
 GWRHRRLRLS LQEQRPRPHQ ELAPRAVPLS SACREAAVGN ALPSGMLHVP
 GDEVLESYC (SEQ ID NO: 3147)
[0316] and is encoded by the DNA sequence (NCBI Reference Sequence: NM_001080815):
[0317] atgccgctgc gcctgctgct gctgctgctg tggctgtggg gcctgcagtg
 30 ggcggaaacc 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 ctggcgcgat catacccagt gcgaaaaccc
 ggaaaaaac ggcgcgtttc aggatcagac cctgattctg gaacgcctgc
 agattatgta taccgtgggc tatagcctga gcctgaccac cctgctgctg
 gcgctgctga ttctgagcct gtttcgccgc ctgcattgca cccgcaacta
 5 tattcatatg aacctgttta ccagctttat gctgcgcgcg gcggcgattc
 tgacccgcga tcagctgctg ccgccgctgg gcccgtatac cggcgatcag
 gcgccgaccc cgtggaacca ggcgctggcg gcgtgccgca ccgcgcagat
 tatgacccag tattgcgtgg gcgcgaacta tacctggctg ctggtggaag
 gcgtgtatct gcatcatctg ctggtgattg tgggccgcag cgaaaaaggc
 10 cattttcgct gctatctgct gctgggctgg ggcgcgccgg cgctgtttgt
 gattccgtgg gtgattgtgc gctatctgcg cgaaaacacc cagtgtctggg
 aacgcaacga agtgaaagcg atttggtgga ttattcgac cccgattctg
 attaccattc tgattaactt tctgattttt attcgattc tgggcattct
 ggtgagcaaa ctgcgcaccc gccagatgcg ctgcccggat tatcgccctgc
 15 gcctggcgcg cagcaccttg accctgggtgc cgctgctggg cgtgcatgaa
 gtggtgtttg cgccggtgac cgaagaacag gtggaaggca gcctgcgctt
 tgcgaaactg gcgtttgaaa tttttctgag cagctttcag ggctttctgg
 tgagcgtgct gtattgcttt attaacaaag aagtgcagag cgaaattcgc
 cagggctggc gccatcgccg cctgcgcctg agcctgcagg aacagcgccc
 20 gcgcccgcag caggaactgg cgccgcgcgc ggtgccgctg agcagcgctg
 gccgcgaagc ggcggtgggc aacgcgctgc cgagcggcat gctgcatgtg
 ccgggcgatg aagtgtgga aagctattgc taa (SEQ ID NO: 3148)

[0318] 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:

25 AAI20674):

[0319] MPLRLLLLLL WLWGLQWAET DSEGQTTTGE LYQRWEHYGQ ECQKMLETTE
 PPSGLACNGS FDMYACWNYT AANTTARVSC PWYLPWFRQV SAGFVFRQCG
 SDGQWGSWRD HTQCENPEKN GAFQDQTLIL ERLQIMYTVG YSLSLTLLLL
 ALLILSLFRR LHCTRNYIHM NLFTSFMLRA AAILTRDQLL PPLGPYTGDO

30 APTPNQVLH RLLPGGTKTF PIYFRTPPHH (SEQ ID NO: 3149)

[0320] and is encoded by the DNA sequence:

[0321] atgccgctgc gcctgctgct gctgctgctg tggctgtggg gcctgcagtg
 ggcggaaacc gatagcgaag gccagaccac caccggcgaa ctgtatcagc
 gctgggaaca ttatggccag gaatgccaga aaatgctgga aaccaccgaa

ccgccgagcg gcctggcgtg caacggcagc tttgatatgt atgcgtgctg
 gaactatacc gcggcgaaca ccaccgcgcg cgtgagctgc ccgtgggtatc
 tgccgtgggtt tcgccaggtg agcgcgggct ttgtgtttcg ccagtgcggc
 agcgatggcc agtggggcag ctggcgcgat catacccagt gcgaaaaccc
 5 ggaaaaaac ggcgcgtttc aggatcagac cctgattctg gaacgcctgc
 agattatgta taccgtgggc tatagcctga gcctgaccac cctgctgctg
 gcgctgctga ttctgagcct gtttcgccgc ctgcattgca cccgcaacta
 tattcatatg aacctgttta ccagctttat gctgcgcgcg gcggcgattc
 tgaccgcga tcagctgctg ccgccgctgg gcccgatac cggcgatcag
 10 gcgccgaccc cgtggaacca ggtgctgcat cgctgctgc cgggcggcac
 caaaccttt ccgatttatt ttgcacctt tccgcatcat taa (SEQ ID NO: 3150).

[0322] As stated herein, the term “GIPR polypeptide” encompasses naturally occurring GIPR polypeptide sequences, e.g., human amino acid sequences SEQ ID NOs: 3141, 3143 or 3145. 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: 3141, 3143 or 3145, by one or more amino acids, such that the sequence is at least 85% identical to SEQ ID NOs: 3141, 3143 or 3145. 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.

[0323] 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.

[0324] Naturally occurring residues can be divided into classes based on common side chain properties:

[0325] (1) hydrophobic: norleucine, Met, Ala, Val, Leu, Ile;

[0326] (2) neutral hydrophilic: Cys, Ser, Thr;

[0327] (3) acidic: Asp, Glu;

[0328] (4) basic: Asn, Gln, His, Lys, Arg;

[0329] (5) residues that influence chain orientation: Gly, Pro; and

[0330] (6) aromatic: Trp, Tyr, Phe.

[0331] Additional groups of amino acids can also be formulated using the principles described in, e.g., Creighton (1984) **PROTEINS: STRUCTURE AND MOLECULAR**
5 **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).

[0332] Conservative substitutions can involve the exchange of a member of one of these
10 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.

[0333] 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-
15 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
20 properties to such residues meeting both definitions).

[0334] Nucleic acid sequences encoding a GIPR polypeptide provided herein, including those degenerate to SEQ ID NOs: 3141, 3143 or 3145, and those encoding polypeptide variants of SEQ ID NOs: 3141, 3143 or 3145 form other aspects of the instant disclosure.

[0335] In order to express the GIPR nucleic acid sequences provided herein, the appropriate
25 coding sequences, e.g., SEQ ID NOs: 3141, 3143 or 3145, 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
30 Laboratory Press, Cold Spring Harbor, N.Y., 1989). The invention also relates to such vectors comprising a nucleic acid sequence according to the invention.

[0336] 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

5 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.

10 **[0337]** 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,

15 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.

20 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.

[0338] Thus, provided herein are vectors comprising a nucleic acid sequence encoding GIPR

25 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

30 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.

5 [0339] 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.

[0340] 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
10 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.

[0341] 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
15 transforming a cell with an expression vector are well known.

[0342] 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
20 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
25 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
30 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.

[0343] 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
5 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.

[0344] 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
10 as Bootcov MR, 1997, Proc. Natl. Acad. Sci. USA 94:11514-9, Fairlie WD, 2000, Gene 254: 67-76.

[0345] 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: 3141. In another embodiment, the human GIPR has the sequence as
15 such set forth in SEQ ID NO: 3143. In another embodiment, the human GIPR has the sequence as such set forth in SEQ ID NO: 3145.

[0346] 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,
20 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.

[0347] The antigen binding proteins that are disclosed herein have a variety of utilities. The
25 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
30 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.

[0348] 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.

[0349] 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.

[0350] 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.

[0351] 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: 3141. 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: 3143. 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: 3145.

[0352] 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:

[0353] (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: 3141, 3143 or 3145 under comparable conditions.

[0354] (b) ability to decrease blood glucose;

[0355] (c) ability to increase glucose tolerance;

[0356] (d) ability to increase insulin sensitivity;

[0357] (e) ability to decrease body weight or reduce body weight gain;

[0358] (f) ability to decrease fat mass or decrease inflammation in fat tissue;

[0359] (g) ability to decrease fasting insulin levels;

[0360] (h) ability to decrease circulating cholesterol levels;

[0361] (i) ability to decrease circulating triglyceride levels;

[0362] (j) ability to decrease liver steatosis or reduce triglyceride level in liver;

[0363] (k) decrease AST, ALT, and/or ALP levels.

[0364] In one embodiment, a GIPR antigen binding protein has one or more of the following activities:

[0365] (a) binds human GIPR such that K_D 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.

[0366] (b) has a half-life in human serum of at least 3 days;

[0367] Some antigen binding proteins that are provided have an on-rate (k_a) for GIPR of at least 10^4 /M x seconds, at least 10^5 /M x seconds, or at least 10^6 /M x 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 $1 \times 10^{-2} \text{ s}^{-1}$, or $1 \times 10^{-3} \text{ s}^{-1}$, or $1 \times 10^{-4} \text{ s}^{-1}$, or $1 \times 10^{-5} \text{ s}^{-1}$. In certain embodiments, the antigen binding protein has a K_D (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.

[0368] 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.

[0369] 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.

[0370] 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.

[0371] 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.

[0372] 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.

[0373] 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.

[0374] 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.

A-2165-WO-PCT

Table 1. Amino acid SEQ ID NOs.

Identifier	Construct	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
IPS:336175	2C2.005	1	158	315	472	629	786	943	1100	1257	1414
IPS:335914	4B1	2	159	316	473	630	787	944	1101	1258	1415
IPS:335938	6H1	3	160	317	474	631	788	945	1102	1259	1416
IPS:335941	2F11	4	161	318	475	632	789	946	1103	1260	1417
IPS:335970	5C2	5	162	319	476	633	790	947	1104	1261	1418
IPS:335978	13H12	6	163	320	477	634	791	948	1105	1262	1419
IPS:335986	11C1	7	164	321	478	635	792	949	1106	1263	1420
IPS:335994	12H11	8	165	322	479	636	793	950	1107	1264	1421
IPS:336024	18E3	9	166	323	480	637	794	951	1108	1265	1422
IPS:336041	2G10 LC1	10	167	324	481	638	795	952	1109	1266	1423
IPS:336077	4H9.004	11	168	325	482	639	796	953	1110	1267	1424
IPS:336088	6A5.004	12	169	326	483	640	797	954	1111	1268	1425
IPS:336099	17H11.004	13	170	327	484	641	798	955	1112	1269	1426
IPS:359621	17H11.004.001	14	171	328	485	642	799	956	1113	1270	1427
IPS:359781	4H9.004.001	15	172	329	486	643	800	957	1114	1271	1428
IPS:360929	4H9.004.002	16	173	330	487	644	801	958	1115	1272	1429
IPS:360936	4H9.004.003	17	174	331	488	645	802	959	1116	1273	1430
IPS:360943	4H9.004.004	18	175	332	489	646	803	960	1117	1274	1431
IPS:360949	4H9.004.005	19	176	333	490	647	804	961	1118	1275	1432
IPS:359761	4H9.004.006	20	177	334	491	648	805	962	1119	1276	1433
IPS:360955	4B1.010	21	178	335	492	649	806	963	1120	1277	1434
IPS:360962	4B1.011	22	179	336	493	650	807	964	1121	1278	1435
IPS:360968	4B1.012	23	180	337	494	651	808	965	1122	1279	1436
IPS:360974	4B1.013	24	181	338	495	652	809	966	1123	1280	1437
IPS:360978	4B1.014	25	182	339	496	653	810	967	1124	1281	1438
IPS:359785	4B1.015	26	183	340	497	654	811	968	1125	1282	1439
IPS:360982	4B1.016	27	184	341	498	655	812	969	1126	1283	1440
IPS:335922	18F2	28	185	342	499	656	813	970	1127	1284	1441
IPS:360986	18F2.002	29	186	343	500	657	814	971	1128	1285	1442
IPS:360995	18F2.003	30	187	344	501	658	815	972	1129	1286	1443
IPS:360999	18F2.004	31	188	345	502	659	816	973	1130	1287	1444
IPS:361005	18F2.005	32	189	346	503	660	817	974	1131	1288	1445

A-2165-WO-PCT

IPS:361009	18F2.006	33	190	347	504	661	818	975	1132	1289	1446
IPS:361013	18F2.007	34	191	348	505	662	819	976	1133	1290	1447
IPS:361017	18F2.008	35	192	349	506	663	820	977	1134	1291	1448
IPS:361021	18F2.009	36	193	350	507	664	821	978	1135	1292	1449
IPS:361028	18F2.010	37	194	351	508	665	822	979	1136	1293	1450
IPS:360535	18F2.011	38	195	352	509	666	823	980	1137	1294	1451
IPS:361035	18F2.012	39	196	353	510	667	824	981	1138	1295	1452
IPS:359940	2F11.002	40	197	354	511	668	825	982	1139	1296	1453
IPS:361039	2F11.003	41	198	355	512	669	826	983	1140	1297	1454
IPS:361043	2F11.004	42	199	356	513	670	827	984	1141	1298	1455
IPS:361049	2F11.005	43	200	357	514	671	828	985	1142	1299	1456
IPS:361055	2F11.006	44	201	358	515	672	829	986	1143	1300	1457
IPS:361059	2F11.007	45	202	359	516	673	830	987	1144	1301	1458
IPS:361063	2F11.008	46	203	360	517	674	831	988	1145	1302	1459
IPS:359949	2F11.009	47	204	361	518	675	832	989	1146	1303	1460
IPS:359956	2F11.010	48	205	362	519	676	833	990	1147	1304	1461
IPS:359865	6H1.002	49	206	363	520	677	834	991	1148	1305	1462
IPS:359869	6H1.003	50	207	364	521	678	835	992	1149	1306	1463
IPS:359873	6H1.004	51	208	365	522	679	836	993	1150	1307	1464
IPS:359877	6H1.005	52	209	366	523	680	837	994	1151	1308	1465
IPS:361067	6H1.006	53	210	367	524	681	838	995	1152	1309	1466
IPS:361071	6H1.007	54	211	368	525	682	839	996	1153	1310	1467
IPS:361075	6H1.008	55	212	369	526	683	840	997	1154	1311	1468
IPS:361079	6A5.004.001	56	213	370	527	684	841	998	1155	1312	1469
IPS:361085	6A5.004.002	57	214	371	528	685	842	999	1156	1313	1470
IPS:361091	6A5.004.003	58	215	372	529	686	843	1000	1157	1314	1471
IPS:361095	6A5.004.004	59	216	373	530	687	844	1001	1158	1315	1472
IPS:361101	6A5.004.005	60	217	374	531	688	845	1002	1159	1316	1473
IPS:361105	6A5.004.006	61	218	375	532	689	846	1003	1160	1317	1474
IPS:361109	6A5.004.007	62	219	376	533	690	847	1004	1161	1318	1475
IPS:361113	6A5.004.008	63	220	377	534	691	848	1005	1162	1319	1476
IPS:361120	6A5.004.009	64	221	378	535	692	849	1006	1163	1320	1477
IPS:359896	6A5.004.010	65	222	379	536	693	850	1007	1164	1321	1478
IPS:359890	6A5.004.011	66	223	380	537	694	851	1008	1165	1322	1479
IPS:359567	2A11.002	67	224	381	538	695	852	1009	1166	1323	1480

A-2165-WO-PCT

IPS:335965	2A11.003	68	225	382	539	696	853	1010	1167	1324	1481
IPS:361158	2A11.004	69	226	383	540	697	854	1011	1168	1325	1482
IPS:361165	2A11.005	70	227	384	541	698	855	1012	1169	1326	1483
IPS:361172	2G10 LC1.003	71	228	385	542	699	856	1013	1170	1327	1484
IPS:361178	2G10 LC1.004	72	229	386	543	700	857	1014	1171	1328	1485
IPS:361185	2G10 LC1.005	73	230	387	544	701	858	1015	1172	1329	1486
IPS:361192	2G10 LC1.006	74	231	388	545	702	859	1016	1173	1330	1487
IPS:359609	2G10 LC1.007	75	232	389	546	703	860	1017	1174	1331	1488
IPS:359615	2G10 LC1.008	76	233	390	547	704	861	1018	1175	1332	1489
IPS:361196	2G10 LC1.009	77	234	391	548	705	862	1019	1176	1333	1490
IPS:361202	2G10 LC1.010	78	235	392	549	706	863	1020	1177	1334	1491
IPS:359644	18E3.002	79	236	393	550	707	864	1021	1178	1335	1492
IPS:361206	18E3.003	80	237	394	551	708	865	1022	1179	1336	1493
IPS:359628	18E3.004	81	238	395	552	709	866	1023	1180	1337	1494
IPS:359637	18E3.005	82	239	396	553	710	867	1024	1181	1338	1495
IPS:361210	18E3.006	83	240	397	554	711	868	1025	1182	1339	1496
IPS:361214	18E3.007	84	241	398	555	712	869	1026	1183	1340	1497
IPS:361218	18E3.008	85	242	399	556	713	870	1027	1184	1341	1498
IPS:361222	5C2.006	86	243	400	557	714	871	1028	1185	1342	1499
IPS:361229	5C2.007	87	244	401	558	715	872	1029	1186	1343	1500
IPS:361236	5C2.008	88	245	402	559	716	873	1030	1187	1344	1501
IPS:359685	5C2.009	89	246	403	560	717	874	1031	1188	1345	1502
IPS:361240	5C2.010	90	247	404	561	718	875	1032	1189	1346	1503
IPS:361247	5C2.011	91	248	405	562	719	876	1033	1190	1347	1504
IPS:361254	5C2.012	92	249	406	563	720	877	1034	1191	1348	1505
IPS:361261	5C2.013	93	250	407	564	721	878	1035	1192	1349	1506
IPS:361268	5C2.014	94	251	408	565	722	879	1036	1193	1350	1507
IPS:359669	5C2.015	95	252	409	566	723	880	1037	1194	1351	1508
IPS:359678	5C2.016	96	253	410	567	724	881	1038	1195	1352	1509
IPS:361275	11C1.002	97	254	411	568	725	882	1039	1196	1353	1510
IPS:361282	11C1.003	98	255	412	569	726	883	1040	1197	1354	1511
IPS:361289	11C1.004	99	256	413	570	727	884	1041	1198	1355	1512
IPS:359712	11C1.005	100	257	414	571	728	885	1042	1199	1356	1513
IPS:361293	11C1.006	101	258	415	572	729	886	1043	1200	1357	1514
IPS:361297	11C1.007	102	259	416	573	730	887	1044	1201	1358	1515

A-2165-WO-PCT

IPS:361301	11C1.008	103	260	417	574	731	888	1045	1202	1359	1516
IPS:359703	11C1.009	104	261	418	575	732	889	1046	1203	1360	1517
IPS:361305	11C1.010	105	262	419	576	733	890	1047	1204	1361	1518
IPS:361312	13H12.002	106	263	420	577	734	891	1048	1205	1362	1519
IPS:359744	13H12.003	107	264	421	578	735	892	1049	1206	1363	1520
IPS:361319	13H12.004	108	265	422	579	736	893	1050	1207	1364	1521
IPS:359737	13H12.005	109	266	423	580	737	894	1051	1208	1365	1522
IPS:361326	13H12.006	110	267	424	581	738	895	1052	1209	1366	1523
IPS:361330	12H11.002	111	268	425	582	739	896	1053	1210	1367	1524
IPS:361337	12H11.003	112	269	426	583	740	897	1054	1211	1368	1525
IPS:361344	12H11.004	113	270	427	584	741	898	1055	1212	1369	1526
IPS:361351	12H11.005	114	271	428	585	742	899	1056	1213	1370	1527
IPS:361358	12H11.006	115	272	429	586	743	900	1057	1214	1371	1528
IPS:361365	12H11.007	116	273	430	587	744	901	1058	1215	1372	1529
IPS:361372	12H11.008	117	274	431	588	745	902	1059	1216	1373	1530
IPS:361379	12H11.009	118	275	432	589	746	903	1060	1217	1374	1531
IPS:361383	12H11.010	119	276	433	590	747	904	1061	1218	1375	1532
IPS:361387	12H11.011	120	277	434	591	748	905	1062	1219	1376	1533
IPS:361391	12H11.012	121	278	435	592	749	906	1063	1220	1377	1534
IPS:361395	12H11.013	122	279	436	593	750	907	1064	1221	1378	1535
IPS:361402	12H11.014	123	280	437	594	751	908	1065	1222	1379	1536
IPS:361406	2C2.005.001	124	281	438	595	752	909	1066	1223	1380	1537
IPS:361412	2C2.005.002	125	282	439	596	753	910	1067	1224	1381	1538
IPS:361418	2C2.005.003	126	283	440	597	754	911	1068	1225	1382	1539
IPS:361424	2C2.005.004	127	284	441	598	755	912	1069	1226	1383	1540
IPS:361430	2C2.005.005	128	285	442	599	756	913	1070	1227	1384	1541
IPS:361436	2C2.005.006	129	286	443	600	757	914	1071	1228	1385	1542
IPS:361442	2C2.005.007	130	287	444	601	758	915	1072	1229	1386	1543
IPS:361448	2C2.005.008	131	288	445	602	759	916	1073	1230	1387	1544
IPS:361454	2C2.005.009	132	289	446	603	760	917	1074	1231	1388	1545
IPS:361460	2C2.005.010	133	290	447	604	761	918	1075	1232	1389	1546
IPS:361466	2C2.005.011	134	291	448	605	762	919	1076	1233	1390	1547
IPS:361472	2C2.005.012	135	292	449	606	763	920	1077	1234	1391	1548
IPS:361478	2C2.005.013	136	293	450	607	764	921	1078	1235	1392	1549
IPS:361485	2C2.005.014	137	294	451	608	765	922	1079	1236	1393	1550

A-2165-WO-PCT

IPS:361845	18F2.013	138	295	452	609	766	923	1080	1237	1394	1551
IPS:361851	6H1.009	139	296	453	610	767	924	1081	1238	1395	1552
IPS:361855	2C2.005.015	140	297	454	611	768	925	1082	1239	1396	1553
IPS:336067	5G12.006	141	298	455	612	769	926	1083	1240	1397	1554
IPS:336169	17B11.002	142	299	456	613	770	927	1084	1241	1398	1555
IPS:361127	5G12.006.001	143	300	457	614	771	928	1085	1242	1399	1556
IPS:361136	5G12.006.002	144	301	458	615	772	929	1086	1243	1400	1557
IPS:361140	5G12.006.003	145	302	459	616	773	930	1087	1244	1401	1558
IPS:359919	5G12.006.004	146	303	460	617	774	931	1088	1245	1402	1559
IPS:361144	5G12.006.005	147	304	461	618	775	932	1089	1246	1403	1560
IPS:361151	5G12.006.006	148	305	462	619	776	933	1090	1247	1404	1561
IPS:361491	17B11.002.001	149	306	463	620	777	934	1091	1248	1405	1562
IPS:361499	17B11.002.002	150	307	464	621	778	935	1092	1249	1406	1563
IPS:361503	17B11.002.003	151	308	465	622	779	936	1093	1250	1407	1564
IPS:361507	17B11.002.004	152	309	466	623	780	937	1094	1251	1408	1565
IPS:361514	17B11.002.005	153	310	467	624	781	938	1095	1252	1409	1566
IPS:360582	17B11.002.006	154	311	468	625	782	939	1096	1253	1410	1567
IPS:361518	17B11.002.007	155	312	469	626	783	940	1097	1254	1411	1568
IPS:360570	17B11.002.008	156	313	470	627	784	941	1098	1255	1412	1569
IPS:362051	5G12.005.001	157	314	471	628	785	942	1099	1256	1413	1570

Table 2. Nucleic acid SEQ ID NOs.

Identifier	Construct	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
IPS:336175	2C2.005	1571	1728	1885	2042	2199	2356	2513	2670	2827	2984
IPS:335914	4B1	1572	1729	1886	2043	2200	2357	2514	2671	2828	2985
IPS:335938	6H1	1573	1730	1887	2044	2201	2358	2515	2672	2829	2986
IPS:335941	2F11	1574	1731	1888	2045	2202	2359	2516	2673	2830	2987
IPS:335970	5C2	1575	1732	1889	2046	2203	2360	2517	2674	2831	2988
IPS:335978	13H12	1576	1733	1890	2047	2204	2361	2518	2675	2832	2989
IPS:335986	11C1	1577	1734	1891	2048	2205	2362	2519	2676	2833	2990
IPS:335994	12H11	1578	1735	1892	2049	2206	2363	2520	2677	2834	2991
IPS:336024	18E3	1579	1736	1893	2050	2207	2364	2521	2678	2835	2992
IPS:336041	2G10_LC1	1580	1737	1894	2051	2208	2365	2522	2679	2836	2993

A-2165-WO-PCT

IPS:336077	4H9.004	1581	1738	1895	2052	2209	2366	2523	2680	2837	2994
IPS:336088	6A5.004	1582	1739	1896	2053	2210	2367	2524	2681	2838	2995
IPS:336099	17H11.004	1583	1740	1897	2054	2211	2368	2525	2682	2839	2996
IPS:359621	17H11.004.001	1584	1741	1898	2055	2212	2369	2526	2683	2840	2997
IPS:359781	4H9.004.001	1585	1742	1899	2056	2213	2370	2527	2684	2841	2998
IPS:360929	4H9.004.002	1586	1743	1900	2057	2214	2371	2528	2685	2842	2999
IPS:360936	4H9.004.003	1587	1744	1901	2058	2215	2372	2529	2686	2843	3000
IPS:360943	4H9.004.004	1588	1745	1902	2059	2216	2373	2530	2687	2844	3001
IPS:360949	4H9.004.005	1589	1746	1903	2060	2217	2374	2531	2688	2845	3002
IPS:359761	4H9.004.006	1590	1747	1904	2061	2218	2375	2532	2689	2846	3003
IPS:360955	4B1.010	1591	1748	1905	2062	2219	2376	2533	2690	2847	3004
IPS:360962	4B1.011	1592	1749	1906	2063	2220	2377	2534	2691	2848	3005
IPS:360968	4B1.012	1593	1750	1907	2064	2221	2378	2535	2692	2849	3006
IPS:360974	4B1.013	1594	1751	1908	2065	2222	2379	2536	2693	2850	3007
IPS:360978	4B1.014	1595	1752	1909	2066	2223	2380	2537	2694	2851	3008
IPS:359785	4B1.015	1596	1753	1910	2067	2224	2381	2538	2695	2852	3009
IPS:360982	4B1.016	1597	1754	1911	2068	2225	2382	2539	2696	2853	3010
IPS:335922	18F2	1598	1755	1912	2069	2226	2383	2540	2697	2854	3011
IPS:360986	18F2.002	1599	1756	1913	2070	2227	2384	2541	2698	2855	3012
IPS:360995	18F2.003	1600	1757	1914	2071	2228	2385	2542	2699	2856	3013
IPS:360999	18F2.004	1601	1758	1915	2072	2229	2386	2543	2700	2857	3014
IPS:361005	18F2.005	1602	1759	1916	2073	2230	2387	2544	2701	2858	3015
IPS:361009	18F2.006	1603	1760	1917	2074	2231	2388	2545	2702	2859	3016
IPS:361013	18F2.007	1604	1761	1918	2075	2232	2389	2546	2703	2860	3017
IPS:361017	18F2.008	1605	1762	1919	2076	2233	2390	2547	2704	2861	3018
IPS:361021	18F2.009	1606	1763	1920	2077	2234	2391	2548	2705	2862	3019
IPS:361028	18F2.010	1607	1764	1921	2078	2235	2392	2549	2706	2863	3020
IPS:360535	18F2.011	1608	1765	1922	2079	2236	2393	2550	2707	2864	3021
IPS:361035	18F2.012	1609	1766	1923	2080	2237	2394	2551	2708	2865	3022
IPS:359940	2F11.002	1610	1767	1924	2081	2238	2395	2552	2709	2866	3023
IPS:361039	2F11.003	1611	1768	1925	2082	2239	2396	2553	2710	2867	3024
IPS:361043	2F11.004	1612	1769	1926	2083	2240	2397	2554	2711	2868	3025
IPS:361049	2F11.005	1613	1770	1927	2084	2241	2398	2555	2712	2869	3026
IPS:361055	2F11.006	1614	1771	1928	2085	2242	2399	2556	2713	2870	3027
IPS:361059	2F11.007	1615	1772	1929	2086	2243	2400	2557	2714	2871	3028

A-2165-WO-PCT

IPS:361063	2F11.008	1616	1773	1930	2087	2244	2401	2558	2715	2872	3029
IPS:359949	2F11.009	1617	1774	1931	2088	2245	2402	2559	2716	2873	3030
IPS:359956	2F11.010	1618	1775	1932	2089	2246	2403	2560	2717	2874	3031
IPS:359865	6H1.002	1619	1776	1933	2090	2247	2404	2561	2718	2875	3032
IPS:359869	6H1.003	1620	1777	1934	2091	2248	2405	2562	2719	2876	3033
IPS:359873	6H1.004	1621	1778	1935	2092	2249	2406	2563	2720	2877	3034
IPS:359877	6H1.005	1622	1779	1936	2093	2250	2407	2564	2721	2878	3035
IPS:361067	6H1.006	1623	1780	1937	2094	2251	2408	2565	2722	2879	3036
IPS:361071	6H1.007	1624	1781	1938	2095	2252	2409	2566	2723	2880	3037
IPS:361075	6H1.008	1625	1782	1939	2096	2253	2410	2567	2724	2881	3038
IPS:361079	6A5.004.001	1626	1783	1940	2097	2254	2411	2568	2725	2882	3039
IPS:361085	6A5.004.002	1627	1784	1941	2098	2255	2412	2569	2726	2883	3040
IPS:361091	6A5.004.003	1628	1785	1942	2099	2256	2413	2570	2727	2884	3041
IPS:361095	6A5.004.004	1629	1786	1943	2100	2257	2414	2571	2728	2885	3042
IPS:361101	6A5.004.005	1630	1787	1944	2101	2258	2415	2572	2729	2886	3043
IPS:361105	6A5.004.006	1631	1788	1945	2102	2259	2416	2573	2730	2887	3044
IPS:361109	6A5.004.007	1632	1789	1946	2103	2260	2417	2574	2731	2888	3045
IPS:361113	6A5.004.008	1633	1790	1947	2104	2261	2418	2575	2732	2889	3046
IPS:361120	6A5.004.009	1634	1791	1948	2105	2262	2419	2576	2733	2890	3047
IPS:359896	6A5.004.010	1635	1792	1949	2106	2263	2420	2577	2734	2891	3048
IPS:359890	6A5.004.011	1636	1793	1950	2107	2264	2421	2578	2735	2892	3049
IPS:359567	2A11.002	1637	1794	1951	2108	2265	2422	2579	2736	2893	3050
IPS:335965	2A11.003	1638	1795	1952	2109	2266	2423	2580	2737	2894	3051
IPS:361158	2A11.004	1639	1796	1953	2110	2267	2424	2581	2738	2895	3052
IPS:361165	2A11.005	1640	1797	1954	2111	2268	2425	2582	2739	2896	3053
IPS:361172	2G10_LC1.003	1641	1798	1955	2112	2269	2426	2583	2740	2897	3054
IPS:361178	2G10_LC1.004	1642	1799	1956	2113	2270	2427	2584	2741	2898	3055
IPS:361185	2G10_LC1.005	1643	1800	1957	2114	2271	2428	2585	2742	2899	3056
IPS:361192	2G10_LC1.006	1644	1801	1958	2115	2272	2429	2586	2743	2900	3057
IPS:359609	2G10_LC1.007	1645	1802	1959	2116	2273	2430	2587	2744	2901	3058
IPS:359615	2G10_LC1.008	1646	1803	1960	2117	2274	2431	2588	2745	2902	3059
IPS:361196	2G10_LC1.009	1647	1804	1961	2118	2275	2432	2589	2746	2903	3060
IPS:361202	2G10_LC1.010	1648	1805	1962	2119	2276	2433	2590	2747	2904	3061
IPS:359644	18E3.002	1649	1806	1963	2120	2277	2434	2591	2748	2905	3062
IPS:361206	18E3.003	1650	1807	1964	2121	2278	2435	2592	2749	2906	3063

A-2165-WO-PCT

IPS:359628	18E3.004	1651	1808	1965	2122	2279	2436	2593	2750	2907	3064
IPS:359637	18E3.005	1652	1809	1966	2123	2280	2437	2594	2751	2908	3065
IPS:361210	18E3.006	1653	1810	1967	2124	2281	2438	2595	2752	2909	3066
IPS:361214	18E3.007	1654	1811	1968	2125	2282	2439	2596	2753	2910	3067
IPS:361218	18E3.008	1655	1812	1969	2126	2283	2440	2597	2754	2911	3068
IPS:361222	5C2.006	1656	1813	1970	2127	2284	2441	2598	2755	2912	3069
IPS:361229	5C2.007	1657	1814	1971	2128	2285	2442	2599	2756	2913	3070
IPS:361236	5C2.008	1658	1815	1972	2129	2286	2443	2600	2757	2914	3071
IPS:359685	5C2.009	1659	1816	1973	2130	2287	2444	2601	2758	2915	3072
IPS:361240	5C2.010	1660	1817	1974	2131	2288	2445	2602	2759	2916	3073
IPS:361247	5C2.011	1661	1818	1975	2132	2289	2446	2603	2760	2917	3074
IPS:361254	5C2.012	1662	1819	1976	2133	2290	2447	2604	2761	2918	3075
IPS:361261	5C2.013	1663	1820	1977	2134	2291	2448	2605	2762	2919	3076
IPS:361268	5C2.014	1664	1821	1978	2135	2292	2449	2606	2763	2920	3077
IPS:359669	5C2.015	1665	1822	1979	2136	2293	2450	2607	2764	2921	3078
IPS:359678	5C2.016	1666	1823	1980	2137	2294	2451	2608	2765	2922	3079
IPS:361275	11C1.002	1667	1824	1981	2138	2295	2452	2609	2766	2923	3080
IPS:361282	11C1.003	1668	1825	1982	2139	2296	2453	2610	2767	2924	3081
IPS:361289	11C1.004	1669	1826	1983	2140	2297	2454	2611	2768	2925	3082
IPS:359712	11C1.005	1670	1827	1984	2141	2298	2455	2612	2769	2926	3083
IPS:361293	11C1.006	1671	1828	1985	2142	2299	2456	2613	2770	2927	3084
IPS:361297	11C1.007	1672	1829	1986	2143	2300	2457	2614	2771	2928	3085
IPS:361301	11C1.008	1673	1830	1987	2144	2301	2458	2615	2772	2929	3086
IPS:359703	11C1.009	1674	1831	1988	2145	2302	2459	2616	2773	2930	3087
IPS:361305	11C1.010	1675	1832	1989	2146	2303	2460	2617	2774	2931	3088
IPS:361312	13H12.002	1676	1833	1990	2147	2304	2461	2618	2775	2932	3089
IPS:359744	13H12.003	1677	1834	1991	2148	2305	2462	2619	2776	2933	3090
IPS:361319	13H12.004	1678	1835	1992	2149	2306	2463	2620	2777	2934	3091
IPS:359737	13H12.005	1679	1836	1993	2150	2307	2464	2621	2778	2935	3092
IPS:361326	13H12.006	1680	1837	1994	2151	2308	2465	2622	2779	2936	3093
IPS:361330	12H11.002	1681	1838	1995	2152	2309	2466	2623	2780	2937	3094
IPS:361337	12H11.003	1682	1839	1996	2153	2310	2467	2624	2781	2938	3095
IPS:361344	12H11.004	1683	1840	1997	2154	2311	2468	2625	2782	2939	3096
IPS:361351	12H11.005	1684	1841	1998	2155	2312	2469	2626	2783	2940	3097
IPS:361358	12H11.006	1685	1842	1999	2156	2313	2470	2627	2784	2941	3098

A-2165-WO-PCT

IPS:361365	12H11.007	1686	1843	2000	2157	2314	2471	2628	2785	2942	3099
IPS:361372	12H11.008	1687	1844	2001	2158	2315	2472	2629	2786	2943	3100
IPS:361379	12H11.009	1688	1845	2002	2159	2316	2473	2630	2787	2944	3101
IPS:361383	12H11.010	1689	1846	2003	2160	2317	2474	2631	2788	2945	3102
IPS:361387	12H11.011	1690	1847	2004	2161	2318	2475	2632	2789	2946	3103
IPS:361391	12H11.012	1691	1848	2005	2162	2319	2476	2633	2790	2947	3104
IPS:361395	12H11.013	1692	1849	2006	2163	2320	2477	2634	2791	2948	3105
IPS:361402	12H11.014	1693	1850	2007	2164	2321	2478	2635	2792	2949	3106
IPS:361406	2C2.005.001	1694	1851	2008	2165	2322	2479	2636	2793	2950	3107
IPS:361412	2C2.005.002	1695	1852	2009	2166	2323	2480	2637	2794	2951	3108
IPS:361418	2C2.005.003	1696	1853	2010	2167	2324	2481	2638	2795	2952	3109
IPS:361424	2C2.005.004	1697	1854	2011	2168	2325	2482	2639	2796	2953	3110
IPS:361430	2C2.005.005	1698	1855	2012	2169	2326	2483	2640	2797	2954	3111
IPS:361436	2C2.005.006	1699	1856	2013	2170	2327	2484	2641	2798	2955	3112
IPS:361442	2C2.005.007	1700	1857	2014	2171	2328	2485	2642	2799	2956	3113
IPS:361448	2C2.005.008	1701	1858	2015	2172	2329	2486	2643	2800	2957	3114
IPS:361454	2C2.005.009	1702	1859	2016	2173	2330	2487	2644	2801	2958	3115
IPS:361460	2C2.005.010	1703	1860	2017	2174	2331	2488	2645	2802	2959	3116
IPS:361466	2C2.005.011	1704	1861	2018	2175	2332	2489	2646	2803	2960	3117
IPS:361472	2C2.005.012	1705	1862	2019	2176	2333	2490	2647	2804	2961	3118
IPS:361478	2C2.005.013	1706	1863	2020	2177	2334	2491	2648	2805	2962	3119
IPS:361485	2C2.005.014	1707	1864	2021	2178	2335	2492	2649	2806	2963	3120
IPS:361845	18F2.013	1708	1865	2022	2179	2336	2493	2650	2807	2964	3121
IPS:361851	6H1.009	1709	1866	2023	2180	2337	2494	2651	2808	2965	3122
IPS:361855	2C2.005.015	1710	1867	2024	2181	2338	2495	2652	2809	2966	3123
IPS:336067	5G12.006	1711	1868	2025	2182	2339	2496	2653	2810	2967	3124
IPS:336169	17B11.002	1712	1869	2026	2183	2340	2497	2654	2811	2968	3125
IPS:361127	5G12.006.001	1713	1870	2027	2184	2341	2498	2655	2812	2969	3126
IPS:361136	5G12.006.002	1714	1871	2028	2185	2342	2499	2656	2813	2970	3127
IPS:361140	5G12.006.003	1715	1872	2029	2186	2343	2500	2657	2814	2971	3128
IPS:359919	5G12.006.004	1716	1873	2030	2187	2344	2501	2658	2815	2972	3129
IPS:361144	5G12.006.005	1717	1874	2031	2188	2345	2502	2659	2816	2973	3130
IPS:361151	5G12.006.006	1718	1875	2032	2189	2346	2503	2660	2817	2974	3131
IPS:361491	17B11.002.001	1719	1876	2033	2190	2347	2504	2661	2818	2975	3132
IPS:361499	17B11.002.002	1720	1877	2034	2191	2348	2505	2662	2819	2976	3133

WO 2018/237095

PCT/US2018/038634

A-2165-WO-PCT

IPS:361503	17B11.002.003	1721	1878	2035	2192	2349	2506	2663	2820	2977	3134
IPS:361507	17B11.002.004	1722	1879	2036	2193	2350	2507	2664	2821	2978	3135
IPS:361514	17B11.002.005	1723	1880	2037	2194	2351	2508	2665	2822	2979	3136
IPS:360582	17B11.002.006	1724	1881	2038	2195	2352	2509	2666	2823	2980	3137
IPS:361518	17B11.002.007	1725	1882	2039	2196	2353	2510	2667	2824	2981	3138
IPS:360570	17B11.002.008	1726	1883	2040	2197	2354	2511	2668	2825	2982	3139
IPS:362051	5G12.005.001	1727	1884	2041	2198	2355	2512	2669	2826	2983	3140

A-2165-WO-PCT

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

iPS #	Ab	Type	VL	VH
iPS:336175	2C2.005	NA	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG GGACCCCGGGCAGAGGTCACCATCTCTTGT CTGGAAGTAGCTCCAACATCGGAAGTAATACTG TAAACTGGTACCAGCACCTCCCAGGAACGGCCC CCAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATGACAGCCTGAATGTCGGGTAT TCGGCGGAGGGACCAAGCTGACCGTCTCTAGGT	CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCCGGATACACCTTACCGGGTACTAT ATGCATTGGTGCAGACGGCCCTGGACAAGGG CTTGAGTGGATGGATGATCAACCTAACAGT GGTGGCACAACCTATGCACAGAAGTTTCAGGGC AGGTCACCATGACCAAGGACACGTCCATCAGT ACAGCTACATGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGATTACTGTGCGAGAGGG GGGGATTACGTTTGGGGACTTATCGGCTCAC TACTACTACGGTATGGAGCTCTGGGGCCCAAGGG ACCACGGTCACCGTCTCCTCA
			SEQ ID NO: 1571	SEQ ID NO: 1728
		AA	QSVLTQPPSASGTPGQRVTISCSGSSNIGSNTVNW YQHLPGTAPKLLIYTNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDDSLNPGPVFGGGTK LTVLG	QMQRVQSGAEVKKPGASVKVSKASGYTFTGYY MHWVRQAPGQGLEWMGWNPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSLRSDDTAVYYCARG GDYVWGTYPHYYYGMDVWVGQTTVTVSS
iPS:335914	4B1	NA	SEQ ID NO: 1	SEQ ID NO: 158
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGATCACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACCAAGGAAAGCCCCA AGCGCTGATCTATGGTGCATCCAGTTTGCAA GTGGGTCCCTTCAAGTTACGCGGCACTGGAT CTGGGACAGAAATTCACCTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCACTTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAGTGGATATCAACCA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCACTTTCAGTAACCTTTGGCA TGCACCTGGTCCCGCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGGAA GTAAATGAAAACCTATGCAGACTCCGTGAAGGGCC GATTACCATCTCCAGAGACAATTCACAAGAATA CGTGTATCTGCACATGAACAGCTGAGAGTCG CGGACACGGCTGTGATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGAACCTGGTCAACCGTCTCCTCA
			SEQ ID NO: 1572	SEQ ID NO: 1729

A-2165-WO-PCT

		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLWY QQKPGKAPKRLIYGASSLQSGVPSRFSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVWYDGSNENYADSVKG RFTISRDN SKNTLYLHMNSLRVADTAVYYCARDG TIFGVLLGDYWGQGTLVTVSS
			SEQ ID NO: 2	SEQ ID NO: 159
		NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACAGGGAAGCCCCA AGCCCTGATCTATGGTGCAATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTACGCGCAGTGGAT CTGGGACAGAAATTCACCTCTCAAAATCAGCAGCC TGACGCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAAATAATACCCCTTCACCTTCGGGCCCT GGGACCAAAGTGGATATCAAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCACTTCCAGTTACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGGAA GTAATAATACTATGCAGACTCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCACAAGACA CGCTGTATCTGCAATGAACAGCTGAGAGCCG AGGACACGGCTGTGTTACTGTGCGCGAGATG GGACGATTTTGGAGTGCTCTTGGGGGACTACT GGGCCAGGGAACCTGGTGCAACCGTCTCCTCA
	IP:335938	6H1	SEQ ID NO: 1573	SEQ ID NO: 1730
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLWY QQKPGKAPKRLIYGASSLQSGVPSRFSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAIVWYDGSNKYYADSVKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSS
			SEQ ID NO: 3	SEQ ID NO: 160
		NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTAA ATTGGTATCAGCAGAAACAGGGAAGCCCCA AGCTCCTGATCTACGATGCATCCAAATTTGGAA CAGGGGTCCCATCAAGGTTCAAGTGAAGTGGAT CTGGGACAGATTTAGTTTCAACCATCAGCAGCCT GCAGCCTGAAGATATTGCAACATATTACTGTCA ACAGTATGATATCTCCTCACTTTCGGCGGAGG GACCAAAGGTGGAGATCAAGCGA	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCACTTCCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGGA AGTAATAATACTATGCAGACTCCGTGAAGGGC CGATTCAACCATCTCCAGCGACAATTCACAAGAAC ACGCTGTATCTGCAAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTTACTGTGCGGAGAGAT AGGACGATTTTGGAGTGGTCTTGAAGTACTGG GGCCAGGGAACCTGGTGCAACCGTCTCCTCA
	IP:335941	2F11	SEQ ID NO: 1574	SEQ ID NO: 1731

A-2165-WO-PCT

		AA	DIQMTQSPSSLSASVGDRAVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGTD FSFTISLQPEDIAITYYCQYDILLTFGGGKVEIKR	SEQ ID NO: 4	QVQLVESGGGVVQGRSLRLSCAASGFTFSYGM HWVRQAPGKGLEWVAIVYDGSNKYYADSVKG RFTISDINSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLDYWGQGTLVTVSS
		NA		SEQ ID NO: 161	SEQ ID NO: 161
	5C2	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCCTCTGGCGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTATCCAGCTCC AACAATAAGAACTACATAGCTTGTACCAAGCAG CAACCAGGACATCCTCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGTCCCTGACC GATTCAGTGGCAGCGGTCTGGACAGATTCA CTCTACCATCAGCAGCTGCAAGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTTCGGCCAAAGGACCAAGGTGGA AATCAAAACGA	SEQ ID NO: 1732	CAGGTGCCGTGGTGCAAGTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCGACAGGCCCTGGACAAGG CTTGAGTGGATGGGTGGATCAACCTGACAGT GGTGGCACAGACTATTCACAGAGTTTCAGGGC AGGTTCAACCATGACCAAGGACACGTCATCAGC ACAGCTACATGAACTGAGCAGGCTGAGATCT GACGACACGGCCGTGATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCGTCT CCTCA
	13H12	AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQPGHPPKLLIYWASTRESGVPDFRSGS GSGTDFLTISLQAEDVAVFYCQYYSTPWTFGQ GTKVEIKR	SEQ ID NO: 1575	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYI HWVRQAPGQGLEWMGWINPDSGGTDYSQRFQGR FTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGTLVTVSS
	13H12	NA		SEQ ID NO: 162	SEQ ID NO: 162
	13H12	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCCTCTGGCGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTATCCAGCTCC AACAATAAGAACTACATAGCTTGTACCAAGCAG AAACCAGGACATCCTCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGTCCCTGACC GATTCAGTGGCAGCGGTCTGGACAGATTCA CTCTACCATCAGCAGCTGCAAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTTCGGCCAAAGGACCAAGGTGGA AATCAAAACGA	SEQ ID NO: 1733	CAGGTGCCGTGGTGCAAGTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCGACAGGCCCTGGACAAGG CTTGAGTGGATGGGTGGATCAACCTGACAGT GGTGGCACAGACTATTCACAGAGTTTCAGGGC AGGTTCAACCATGACCAAGGACACGTCATCAGC ACAGCTACATGAACTGAGCAGGCTGAGATCT GACGACACGGCCGTGATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCGTCT CCTCA
	13H12	NA		SEQ ID NO: 1576	SEQ ID NO: 1733

A-2165-WO-PCT

			DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQKPGHPPKLLIYWASTRESGVDPDRFSGS GSGTDFLTIISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR	SEQ ID NO: 6	QVPLVQSGAEVKKPGASVKVSKASGYTFTGYI HWVRQAPGQGLEWMGWINPDSGGTDYSQRFQGR FTMTRDTSISTAYMELSRLSDDTAVYYCAREATI FGMLIVPFDYWGGQTLVTVSS
		AA		SEQ ID NO: 163	SEQ ID NO: 163
		NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAACAG AACCAAGGACAGCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTACGCAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCAAGGTGG AAATCAAACGA	SEQ ID NO: 1577	CAGGTGCCGTGGTACAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCGTCAGGCCCTGGACAAAGG CTTGTGTGGATGGGTGGATCAGCCCTAACAGT GGTGACAAAGCTATGCACAGAAATTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCTATATGGAGCTGAGCAGACTGAGATCT GACGACACGGCCGTGATTTCTGTACGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCAACCGTCT CCTCA
		AA		SEQ ID NO: 1734	SEQ ID NO: 1734
		NA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQKPGQPPNLLIYWSTRDSGVDPDRFSG SAGTDFLTINSLQAEDVAVYYCQQYYRTPTWTF GQGTKVEIKR	SEQ ID NO: 164	QVPLVQSGAEVKKPGASVKVSKASGYTFTGYI HWVRQAPGQGLVWMGWISPNSGDTSYAQKFQDR VTMTRDTSISTAYMELSRLSDDTAVYYFCTREATI FGMLIVPFDYWGGQTLVTVSS
		AA		SEQ ID NO: 1735	SEQ ID NO: 1735
		NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAAGCAG AACCAAGGACAGCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAAGAT GTGGCTGTTTATTACTGTACGCAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCAAGGTGG AAATCAAACGA	SEQ ID NO: 1578	CAGGTGCCGTGGTGCAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCGTCAGGCCCTGGACAAAGG CTTGTGTGGATGGGTGGATAAGCCCTAACCAAT GGTGACAAAACTATGCACAGAAATTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCTATATGGAGCTGAGCAGGCTGAGATCT GACGACACGGCCGTGATTTACTGTACGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCAACCGTCT CCTCA

A-2165-WO-PCT

		AA	DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRDSGVPRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF QGQTKVEIKR SEQ ID NO: 8	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVVRQAPGQGLEWMGWISPNNGDITNYAQKFQD RVTMTDRDTSISTAYMELSLRLRSDDTAVYYCTREA TIFGMILIVPFDYWGQGLVTIVSS SEQ ID NO: 165
	18E3	NA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCAGACAGGTTCAAGTGGCAGTG GGTCTGGGACAGACTTCACTCTCACCATCAGCA GACAGGAGCCTGATGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGTTCAACCGTCACTTTCCGG CGGAGGGACCAAGGTGGAGATCAAAACGA SEQ ID NO: 1579	CAGGTGCAGTTGCAGGAGTGGGGCCAGGACTG GTGAAGCCTTACAGACCCCTGTCCCTCACCTGC ACTGTCTCTGGTGAAGTCCATCAGAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCACCCAGGGA AGGGCTGGAGTGGATTGGGTACATCTATTACA GTGGGAGCACCTACTACAAACCCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGTCTAAGA ACCAAGTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGGACACGGCCGTGTATTACTGTGCGAGAGA TCGTATTACGATTTTGGAGTGGTTATGGGGGGC GGTATGGACGTCTGGGGCCAAAGGGACACCGGTC ACCGTCTCCTCA SEQ ID NO: 1736
		AA	EIVLTQSPGTLSPGERATLSCRASQISYSYLAW YQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDF TLTISRQEPDDFAVYYCQYQGSSPLTFGGGKVEI KR SEQ ID NO: 9	QVQLQESGPGLVKPSQTLSTCTVSGDSISSGGYY WSWIRQHPGKGLEWIGYIYSGSTYYNPSLKSRT ISVDTSKNQFSLKLSSVTAAADTAVYYCARDRIITFG VVMGGGMDVWGQGLTIVTVSS SEQ ID NO: 166
	2G10_LC1	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCCTG TCTGTGTCTCCAGGGGAAAGAGCCACCCCTCTCC TGCAGGGCCAGTCAGAGTGTAGCAGCAACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACAGGGCC ACTGGTATCCAGCCAGGTCAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGCAGTCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTGGCTCTCACTTTTCGGCG GAGGGACCAAGGTGGAGATCAAAACGA SEQ ID NO: 1580	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACTTCCAGTAAGTATGCG ATGCACTGGGTCCGCCAGGCTCCAGGCGAGGGG CTGGAGTGGGTGGCAGCTATATGGTTTGATGGA AGTGATAAATACTATGCAGACTCCGTGAAGGGC CGATTACCATCTCCAGAGACAACTCCAAAGAAC ACGCTGTATCTGCAAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAAACCCCTGGTCAACCGTCTCCTCA SEQ ID NO: 1737

A-2165-WO-PCT

	IP:336077	4H9.004	AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQKPGQAPRLLIYGAAATRATGIPARVSGSGSGTE FTLTISLQSEDFAVYYCQQYNWPLTFGGGKVE IKR	QVQLVESGGGVVQPRSLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAIWFDGSKYYADSVKG RFTISRDNSKNTLYQMNSLRAEDTAVYYCARDQ AIFGVDPDYWGQGLVTVSS
			NA	SEQ ID NO: 10 GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACAGGGAAGCCCCCTA AACGCTGATCTATGGTGCATCCAGTTTGCAA GTGGGTCCCATCAAGGTTACGCGGCAGTGGAT CTGGGACAGAGTTCATCTCAATCAGCAGCC TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAATAGTTACCCATTCACTTTCGGCCCT GGGACCAAAGTGGATGTCAAACGA	SEQ ID NO: 167 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCACTTCACTTACTTTGGCA TGCACCTGGTCCCGCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGGAA GTAATAATACATATGCAGACTCCGTGAAGGGCC GCTTCAACCATCTCCAGAGACAATTCGAAGAACA CGCTGATCTGCAATGAACAGCTGAGAGCCG AGGACACGGCTGTGTTACTGTGCGCGAGATG GGACGATTTTGGAGTGTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
	IP:336088	6A5.004	AA	DIQMTQSPSSLSASVGDRTVITCRASQGIRNELGW YQKPGKAPKRLIYGASLSQGVPSRFSGSGSGTE FTLTISLQPEDFVITYYCLQHNSYPFTFGPGTKVDV KR	SEQ ID NO: 1738 QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKLEWVAIVYDGSNKYYADSVKG RFTISRDNSKNTLYQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGLVTVSS
			NA	SEQ ID NO: 11 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGACAGAGTCACCATCACTT GCCAGCGAGTCAGGACATTACCAACTATTAA ATTGGTATCAGCAGAAACAGGGAAGCCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGTCCCATCAAGGTTCAAGTGAAGTGGATC TGGGACAGATTTTACTTTCACCATCAGCAGCCTG CAGCCTGAAGATATTGCAACATATTACTGTCAA CAGTATGATGATCTATTCACTTTCGGCCCTGGGA CCAAAGTGGATATCAAACGA	SEQ ID NO: 168 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCTCCTTCAAGTAGCTATGGCA TGCACCTGGTCCCGCAGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGCTATATGGTATGATGGAA ATAATAATACATATGCAGACTCCGTGAAGGGCC GATTCAACCATCTCCAGAGACAATTCGAAGAACA CGCTGATCTGCAATGAACAGCTGAGAGCCG AGGACACGGCTGTGTTACTGTGCGGAGAGATC GGACGATTTTGGAGTGTCTTGAAGTACCTCG GCCAGGGAACCTGGTCAACCGTCTCCTCA
			AA	DIQMTQSPSSLSASVGDRTVITITCQASQDITNLYNW YQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD	SEQ ID NO: 1739 QVQLVESGGGVVQPRSLRLSCAASGFSFSYGM HWVRQPPGKLEWVAIWYDGNKNKYADSVKG
				SEQ ID NO: 1582	

A-2165-WO-PCT

			FTFTISSLPEDIATYYCQYDDLLFTFGPGTKVDIK R	RTFISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYLGQGTLLVTVSS
			SEQ ID NO: 12	SEQ ID NO: 169
		NA	GACATCCAGATGACCCAGTCTCCATCTTCCGTGT CTGCATCTGTAGGAGACAGAGTCAACCATCACTT GTCGGCGAGTCAAGGTCTTATCATCTGGTTAG CCTGGTATCAGCAGAAACCGGGGAAAGCCCTA AACTCCTGATCTATGCTGCATCCAGTTTGCAAAG TGGGTCCCATCAAGGTTCAAGCGGCAAGTGGCTC TGGGACAGATTTCACTCTCAACCATCAGCAGCCT ACAGCCTGAAGATTTTGCAACTTACTATTGTCAA CAGACTAACAGTTTCCCTCCGACGTTCCGGCCAA GGGACCAAGGTGGAATCAAAACGA	CAGGTGCAGCTGCAGGAGTCGGGGCCCAAGGACTG GTGAAGCCTTCGGAGACCCCTGTCCCTCACCTGC ACTGTCTCTCAGGGCTCCATCAGTAGTTACTACT GGAGCTGGATCCGGCAGCCCGCCGGGAAGGGA CTAGAGTGGATTGGCCGTATCTATACCAAGTGGG AGCAACAACTACAACCCCTCCCTCAAGAGTCGA GTCACCATGTCAATAGACACGTCCAAAGAACCA TTCTCCCTGAAACTGAACCTGTGTGACCGCCGCG GACACGGCCGTGTATTACTGTGCGAGAGATGTA GCAGTGGCTGGCTTTGACTACTGGGGCCAGGGA ACCTGTGCACCGTCTCTCTCA
		AA	SEQ ID NO: 1583	SEQ ID NO: 1740
		AA	DIQMTQSPSSVSASVGDRTVTITCRASQGLIWLAW YQKPGKAPKLLIYAASLQSGVPSRFSGSGTD FTLTISLQPEDFATYYCQQTNSFPPTFGQTKVEI KR	QVQLQESGPGLVKPSSETLSLTCTVSQGISYYWS WIRQPAKGLEWIGRIYTSNSTNYPNPSLKSRVTMS IDTSKNQFSLKLSVTAAADTAVYYCARDVAVAGF DYWGQGTLLVTVSS
		NA	SEQ ID NO: 13	SEQ ID NO: 170
		NA	GACATCCAGATGACCCAGTCTCCATCTTCCGTGT CTGCATCTGTAGGAGACAGAGTCAACCATCACTT GTCGGCGAGTCAAGGTCTTATCATCTGGTTAG CCTGGTATCAGCAGAAACCGGGGAAAGCCCTA AACTCCTGATCTATGCTGCATCCAGTTTGCAAAG TGGGTCCCATCAAGGTTCAAGCGGCAAGTGGCTC TGGGACAGATTTCACTCTCAACCATCAGCAGCCT ACAGCCTGAAGATTTTGCAACTTACTATTGTCAA CAGACTAACAGTTTCCCTCCGACGTTCCGGCCAA GGGACCAAGGTGGAATCAAAACGA	CAGGTGCAGCTGCAGGAGTCGGGGCCCAAGGACTG GTGAAGCCTTCGGAGACCCCTGTCCCTCACCTGC ACTGTCTCTGCGGGCTCCATCAGTAGTTACTACT GGAGCTGGATCCGGCAGCCCGCCGGGAAGGGA CTAGAGTGGATTGGCCGTATCTATACCAAGTGGG AGCAACAACTACAACCCCTCCCTCAAGAGTCGA GTCACCATGTCAATAGACACGTCCAAAGAACCA TTCTCCCTGAAACTGAACCTGTGTGACCGCCGCG GACACGGCCGTGTATTACTGTGCGAGAGATGTA GCAGTGGCTGGCTTTGACTACTGGGGCCAGGGA ACCTGTGCACCGTCTCTCTCA
		AA	SEQ ID NO: 1584	SEQ ID NO: 1741
		AA	DIQMTQSPSSVSASVGDRTVTITCRASQGLIWLAW YQKPGKAPKLLIYAASLQSGVPSRFSGSGTD	QVQLQESGPGLVKPSSETLSLTCTVSQGISYYWS WIRQPAKGLEWIGRIYTSNSTNYPNPSLKSRVTMS

A-2165-WO-PCT

			FTLTISSLQPEDFATYYCQQTNSFPPTFGQGTKEI KR	IDTSKNQFSLKLSVTAADTAVYYCARDVA VAGF DYWGQGLVT VSS
			SEQ ID NO: 14	SEQ ID NO: 171
		4H9.004.001	GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCAACCATCACTT GCCGGCAAGTCAGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACAGGAAAGCCCCCTA AACTCCTGATCTATGTTGATCCAGTTTGCAA GTGGGTCCTCATCAAGGTTACGCGCAGTGGAT CTGGGACAGAGTTCACCTCTCAAAATCAGCAGCC TGACGCTGAAGATTTGTAACTTATTACTGTCT ACAGCATAAATAGTTACCCATTCACTTTTCGGCCA AGGGACCAAAGTGGATGTCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCCTGT GCAGCTCTGGATTCACTTACAGTTACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCACAAGACA CGCTGTATCTGCAAATGAACAGCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTGGAGTGCTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
			SEQ ID NO: 1585	SEQ ID NO: 1742
		AA	DIQMTQSPSSLSASVDRVTITCRASQGI RNELGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGTE FTLTISSLQPEDFVITYYCLQHNSYPFTFGQGT KVD VKR	QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIYDASNKYYADAVKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGLVT VSS
			SEQ ID NO: 15	SEQ ID NO: 172
		4H9.004.002	GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCAACCATCACTT GCCGGCAAGTCAGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACAGGAAAGCCCCCTA AACTCCTGATCTATGTTGATCCAGTTTGCAA GTGGGTCCTCATCAAGGTTACGCGCAGTGGAT CTGGGACAGAGTTCACCTCTCAAAATCAGCAGCC TGACGCTGAAGATTTGTAACTTATTACTGTCT ACAGCATAAATAGTTACCCATTCACTTTTCGGCCA AGGGACCAAAGTGGATGTCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCCTGT GCAGCTCTGGATTCACTTACAGTTACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACTCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCACAAGACA CGCTGTATCTGCAAATGAACAGCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTGGAGTGCTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
			SEQ ID NO: 1586	SEQ ID NO: 1743
		AA	DIQMTQSPSSLSASVDRVTITCRASQGI RNELGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGTE FTLTISSLQPEDFVITYYCLQHNSYPFTFGQGT KVD VKR	QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIYDASNKYYADSVKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGLVT VSS

			SEQ ID NO: 16	SEQ ID NO: 173

A-2165-WO-PCT

!PS:360936	4H9.004.003	NA	GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCAACCATCACTT GCCGGCAAGTCAGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACACAGGAAAGCCCCA AACTCCTGATCTATGTCATCCAGTTTGCAA GTGGGTCCCATCAAGGTTACGCGCAGTGGAT CTGGGACAGAGTTCATCTCACAATCAGCAGCC TGCAGCCTGAAGATTTGTAACTTATTACTGTCT ACAGCATAAATAGTTACCCATTCACTTTGCGCCA AGGACCAAAGTGGATGTCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGTCTGGATTCACTTCACTTCACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGGAA GTAATAATACTATATGACAGCGCTGAAGGGCC GCTTCAACCATCTCCAGAGACAATTCACAAGACA CGTGTATCTGCAATGAACAGCCTGAGAGCCG AGGACACGGCTGTATTACTGTGCGCGAGATG GGACGATTTTGGAGTGCTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
		AA	DIQMTQSPSSLSASVGDRTVTITCRASQGIRNELGW YQKPGKAPKLLIYGASSLQSGVPSRFSGSGSTE FTLTISLQPEDFVTYYCLQHNSYPFTFGQGTKVD VKR	QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAIVYDGSNKYYADAVKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGLVTVSS
!PS:360943	4H9.004.004	NA	GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCAACCATCACTT GCCGGCAAGTCAGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACACAGGAAAGCCCCA AACTCCTGATCTATGTCATCCAGTTTGCAA GTGGGTCCCATCAAGGTTACGCGCAGTGGAT CTGGGACAGAGTTCATCTCACAATCAGCAGCC TGCAGCCTGAAGATTTGTAACTTATTACTGTCT ACAGCATAAATAGTTACCCATTCACTTTGCGCCCT GGGACCAAAGTGGATGTCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGTCTGGATTCACTTCACTTCACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATAATACTATATGACAGCGCTGAAGGGCC GCTTCAACCATCTCCAGAGACAATTCACAAGACA CGTGTATCTGCAATGAACAGCCTGAGAGCCG AGGACACGGCTGTATTACTGTGCGCGAGATG GGACGATTTTGGAGTGCTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
		AA	DIQMTQSPSSLSASVGDRTVTITCRASQGIRNELGW YQKPGKAPKLLIYGASSLQSGVPSRFSGSGSTE FTLTISLQPEDFVTYYCLQHNSYPFTFGPGTKVDV KR	QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAIVYDASNKYYADAVKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGLVTVSS

A-2165-WO-PCT

!PS:360949	4H9.004.005	NA	SEQ ID NO: 18 GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCAACCATCACTT GCCGGCAAGTCAGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACCCAGGAAAGCCCCA AACGCTGATCTATGGTGCATCCAGTTTGCAA GTGGGTCCTCCATCAAGGTTACGCGCAGTGGAT CTGGGACAGAGTTCATCTCACAATCAGCAGCC TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAAATAGTTACCCATTCACTTTTCGGCCA AGGGACCAAAGTGGATGTCAAACGA	SEQ ID NO: 175 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTCCAGTTACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATAATACTATATGACAGCGCTGAAGGGCC GCTTACCATCTCCAGAGACAATTCACAAGACA CGTGTATCTGCAATGAACAGCTGAGAGCCG AGGACACGGCTGTATTACTGTGCGCGAGATG GGACGATTTTGGAGTGCTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
			SEQ ID NO: 1589 DIQMTQSPSSLSASVGDRTVTITCRASQGIRNELGW YQKPGKAPKRLIYGASSLQSGVPSRFSGSGSTE FTLTISLQPEDFVTYYCLQHNSYPFTFGQGTKVD VKR	SEQ ID NO: 1746 QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAIVWYDASNKYADAVKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGLVTVSS
!PS:359761	4H9.004.006	NA	SEQ ID NO: 19 GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCAACCATCACTT GCCGGCAAGTCAGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACCCAGGAAAGCCCCA AACTCCTGATCTATGTGTCATCCAGTTTGCAA GTGGGTCCTCCATCAAGGTTACGCGCAGTGGAT CTGGGACAGAGTTCATCTCACAATCAGCAGCC TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAAATAGTTACCCATTCACTTTTCGGCCA AGGGACCAAAGTGGATGTCAAACGA	SEQ ID NO: 176 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTCCAGTTACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATAATACTATATGACAGCGCTGAAGGGCC GCTTACCATCTCCAGAGACAATTCACAAGACA CGTGTATCTGCAATGAACAGCTGAGAGCCG AGGACACGGCTGTATTACTGTGCGCGAGATA GGACGATTTTGGAGTGCTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
			SEQ ID NO: 1590 DIQMTQSPSSLSASVGDRTVTITCRASQGIRNELGW YQKPGKAPKRLIYGASSLQSGVPSRFSGSGSTE FTLTISLQPEDFVTYYCLQHNSYPFTFGQGTKVD VKR	SEQ ID NO: 1747 QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAIVWYDASNKYADAVKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLLGDYWGQGLVTVSS

A-2165-WO-PCT

IPS:360955	4B1.010	NA	SEQ ID NO: 20 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTAG GCTGTATCAGCAGAAACCAAGGAAAGCCCTA AGTCTCTGATCTATGTCATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGACAGAAATTCATCTCACAATCAGCAGCC TGACGCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAAAACGA	SEQ ID NO: 1591 DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK R	SEQ ID NO: 177 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAAGAATA CGCTGTATCTGCAAAATGAACAGCCTGAGAGTCG CGGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA
		AA	SEQ ID NO: 1748 QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVWYDASNENYADAVKVG RFTISRDN SKNTLYLQMNSLRVADTAVYYCARDG TIFGVVLGDYWGQGGLVTVSS	SEQ ID NO: 178 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAAGAATA CGCTGTATCTGCAAAATGAACAGCCTGAGAGTCG CGGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA	
	4B1.011	NA	SEQ ID NO: 21 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTAG GCTGTATCAGCAGAAACCAAGGAAAGCCCTA AGCGCTGATCTATGTCATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGACAGAAATTCATCTCACAATCAGCAGCC TGACGCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAAAACGA	SEQ ID NO: 1592 DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLQSGVPSRFSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK R	SEQ ID NO: 1749 QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVWYDASNENYADAVKVG RFTISRDN SKNTLYLQMNSLRVADTAVYYCARDG TIFGVVLGDYWGQGGLVTVSS
		AA	SEQ ID NO: 1749 QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVWYDASNENYADAVKVG RFTISRDN SKNTLYLQMNSLRVADTAVYYCARDG TIFGVVLGDYWGQGGLVTVSS	SEQ ID NO: 1749 QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVWYDASNENYADAVKVG RFTISRDN SKNTLYLQMNSLRVADTAVYYCARDG TIFGVVLGDYWGQGGLVTVSS	
IPS:360962	4B1.011	NA	SEQ ID NO: 20 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTAG GCTGTATCAGCAGAAACCAAGGAAAGCCCTA AGTCTCTGATCTATGTCATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGACAGAAATTCATCTCACAATCAGCAGCC TGACGCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAAAACGA	SEQ ID NO: 1591 DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK R	SEQ ID NO: 177 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAAGAATA CGCTGTATCTGCAAAATGAACAGCCTGAGAGTCG CGGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA
		AA	SEQ ID NO: 1748 QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVWYDASNENYADAVKVG RFTISRDN SKNTLYLQMNSLRVADTAVYYCARDG TIFGVVLGDYWGQGGLVTVSS	SEQ ID NO: 178 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAAGAATA CGCTGTATCTGCAAAATGAACAGCCTGAGAGTCG CGGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA	
	4B1.011	NA	SEQ ID NO: 21 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTAG GCTGTATCAGCAGAAACCAAGGAAAGCCCTA AGCGCTGATCTATGTCATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGACAGAAATTCATCTCACAATCAGCAGCC TGACGCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAAAACGA	SEQ ID NO: 1592 DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLQSGVPSRFSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK R	SEQ ID NO: 1749 QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVWYDASNENYADAVKVG RFTISRDN SKNTLYLQMNSLRVADTAVYYCARDG TIFGVVLGDYWGQGGLVTVSS
		AA	SEQ ID NO: 1749 QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVWYDASNENYADAVKVG RFTISRDN SKNTLYLQMNSLRVADTAVYYCARDG TIFGVVLGDYWGQGGLVTVSS	SEQ ID NO: 1749 QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVWYDASNENYADAVKVG RFTISRDN SKNTLYLQMNSLRVADTAVYYCARDG TIFGVVLGDYWGQGGLVTVSS	

A-2165-WO-PCT

IPS:360968	4B1.012	NA	SEQ ID NO: 22 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCAACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACCCAGGAAAGCCCCA AGCTCCTGATCTATGTCATCCAGTTTGCAA GTGGGTCCTTCAAGTTACGCGGCAAGTGAT CTGGGACAGAAATTCATCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATATAATTACCCCTTCACCTTTCGGCCCT GGGACCAAGTGGATATCAAAACGA	SEQ ID NO: 179 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCTGAGACTCTCCTGT GCAGCTCTGGATTCACTTTCAGTAACCTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGACAGCCCGTGAAGGGCC GATTCAACCATCTCCAGAGACAATTCCAAAGAATA CGCTGTATCTGCAATGAACAGCCTGAGAGTCG CGGACACGGCTGTGATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCTGGTCAACCGTCTCCTCA
			SEQ ID NO: 1593 DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	SEQ ID NO: 1750 QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVWYDASNENYADAVKVG RFTISRDN SKNTLYLQMNSLRVADTAVYYCARDG TIFGVVLGDYWGQGLVTVSS
IPS:360974	4B1.013	NA	SEQ ID NO: 23 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCAACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACCCAGGAAAGCCCCA AGCTCCTGATCTATGTCATCCAGTTTGCAA GTGGGTCCTTCAAGTTACGCGGCAAGTGAT CTGGGACAGAAATTCATCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATATAATTACCCCTTCACCTTTCGGCCAA GGGACCAAGTGGATATCAAAACGA	SEQ ID NO: 180 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCTGAGACTCTCCTGT GCAGCTCTGGATTCACTTTCAGTAACCTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGACAGCTCCGTGAAGGGCC GATTCAACCATCTCCAGAGACAATTCCAAAGAATA CGCTGTATCTGCAATGAACAGCCTGAGAGTCG CGGACACGGCTGTGATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCTGGTCAACCGTCTCCTCA
			SEQ ID NO: 1594 DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIK R	SEQ ID NO: 1751 QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVWYDASNENYADSVKVG RFTISRDN SKNTLYLHMNSLRVADTAVYYCARDG TIFGVVLGDYWGQGLVTVSS

A-2165-WO-PCT

IPS:360978	4B1.014	NA	SEQ ID NO: 24 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCAACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACCAGGGAAGCCCCCTA AGCTCCTGATCTATGTTGATCCAGTTTGCAA GTGGGTCCTTCAAGTTACGCGGCAAGTGAT CTGGGACAGAAATTCATCTCTCAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATATAATTACCCCTTCACTTTGCGCCAA GGGACCAAGTGGATATCAAAACGA	SEQ ID NO: 181 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCACTTTCAGTAACCTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGGAA GTAATGAAAACATATGACAGCCCGTGAAGGGCC GATTCAACCATCTCCAGAGACAATTCCAAAGAATA CGCTGTATCTGCACATGAACAGCCTGAGAGTCG CGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA
			SEQ ID NO: 1595 DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK R	SEQ ID NO: 1752 QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVYDGSNENYADAVKVG RFTISRDN SKNTLYLHMNSLRVADTAVYYCARDG TIFGVVLGDYWGQGLVTVSS
IPS:359785	4B1.015	NA	SEQ ID NO: 25 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCAACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACCAGGGAAGCCCCCTA AGCTCCTGATCTATGTTGATCCAGTTTGCAA GTGGGTCCTTCAAGTTCAAGCGGCAAGTGAT CTGGGACAGAAATTCATCTCTCAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATATAATTACCCCTTCACTTTGCGCCAA GGGACCAAGTGGATATCAAAACGA	SEQ ID NO: 182 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCACTTTCAGTAACCTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGACAGCCCGTGAAGGGCC GATTCAACCATCTCCAGAGACAATTCCAAAGAATA CGCTGTATCTGCAAATGAACAGCCTGAGAGTCG AGGACACGGCTGTGTATTATTGTGCGCGAGATA GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA
			SEQ ID NO: 1596 DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK R	SEQ ID NO: 1753 QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVYDASNENYADAVKVG RFTISRDN SKNTLYLQMNSLRVEDTAVYYCARDR TIFGVVLGDYWGQGLVTVSS

A-2165-WO-PCT

		SEQ ID NO: 26	GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTATAGGAGACAGAGTCACCATCACTTGCCGGCAAGTCAGGACATTAGAGATTATTTAGGCTGTATCAGCAGAAACCAAGGAAAGCCCTAAGCTCCTGATCTATGTCATCCAGTTTGCAAAGTGGGTCCCTTCAAGGTTCAGCGGCAGTGGATCTGGGACAGAAATTCATCTCACAATCAGCAGCCTGCAGCCTGAAGATTTGCAACTTATTACTGTCTACAGCATATAAATTACCCCTTCACTTTCGGCCAAAGGACCAAAGTGGATATCAAAACGA	SEQ ID NO: 183	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGTCCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGGCTCTGGATTCACTTTCAGTAACTTTGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGTGGCAGTTATATGGTATGATGCAAGTAATGAAAACATATGCAGACGCCGTGAAGGGCGATTCAACCATCTCCAGAGACAATTCCAAAGAATACGCTGTATCTGCAAAATGAACAGCCTGAGAGTCGAGGACACGGCTGTGTATTATTGTGCGCGAGATGGACGATCTTTGGAGTGGTCTTGGGGGACTACTGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA
4B1.016	!PS:360982	NA	SEQ ID NO: 1597	SEQ ID NO: 1754	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAIVWYDASNENYADAVKGRFTISRDNKNTLYLQMNSLRVEDTAVYYCARDGTIFGVVLGDYWGQGGLVTVSS
		SEQ ID NO: 27	GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTATAGGAGACAGAGTCACCATCACTTGCCGGCAAGTCAGGACCTTAGAAATTTATTTAGGCTGTATCACCAGAAACCAAGGAAAGCCCTAAGCGCTGATCTATGTCATCCAGTTTGCAAAGTGGGTCCCTTCAAGGTTCAGCGGCAGTGGATCTGGGACAGAAATTCATCTCACAATCAGCAGCCTGCAGCCTGAAGATTTGCAACTTATTACTGTCTACAGCATATAAATTACCCCTTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAAACGA	SEQ ID NO: 184	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGTCCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGGCTCTGGATTCACTTTCAGTAACTTTGGCATGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGCTGGAGTGGTGGCAGTTATATGGTATGATGGAAAGTAATGAAAACATATGCAGACTCCGTGAAGGGCGATTCAACCATCTCCAGAGACAATTCCAAAGAACACGCTGTATCTGCAATGAACAGCCTGAGAGCCGCGGACACGGCTGTGTATTACTGTGCGGAGAGATGGACGATCTTTGGAGTGGTCTTGGGGGACTACTGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA
18F2	!PS:335922	NA	SEQ ID NO: 1598	SEQ ID NO: 1755	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAIVWYDGSNENYADSVKGRFTISRDNKNTLYLHMNSLRADTAVYYCARDGTIFGVVLGDYWGQGGLVTVSS
		SEQ ID NO: 28	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGWYHQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	SEQ ID NO: 185	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGTCCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGGCTCTGGATTCACTTTCAGTAACTTTGGCATGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGCTGGAGTGGTGGCAGTTATATGGTATGATGGAAAGTAATGAAAACATATGCAGACTCCGTGAAGGGCGATTCAACCATCTCCAGAGACAATTCCAAAGAACACGCTGTATCTGCAATGAACAGCCTGAGAGCCGCGGACACGGCTGTGTATTACTGTGCGGAGAGATGGACGATCTTTGGAGTGGTCTTGGGGGACTACTGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGWYQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIKR	SEQ ID NO: 1756	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAIVWYDGSNENYADSVKGRFTISRDNKNTLYLHMNSLRADTAVYYCARDGTIFGVVLGDYWGQGGLVTVSS

A-2165-WO-PCT

!PS:360986	18F2.002	NA	SEQ ID NO: 28 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACCTTAGAAATATTAG GCTGGTATCAACAGAAACACAGGAAAGCCCTA AGCTCTGATCTATGTCATCCAGTTTGCAA GTGGGTCCTTCAAGTTACGCGCAGTGGAT CTGGGACAGAAATTCATCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTACTGTCT ACAGCATATAATTACCCCTTCACCTTCGGCCCT GGGACCAAAGTGGATATCAAAACGA	SEQ ID NO: 185 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTTCAGTAACCTTTGGCA TGCACTGGTCCGCCAGGCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGCAGACGCCGTGAAGGCC GATTCAACCATCTCCAGAGACAATTCCAAAGAACA CGCTGTATCTGCAATGAACAGCCTGAGAGCCG CGACACGGCTGTGTAATTAATGTCGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
			SEQ ID NO: 1599 DIQMTQSPSSLSASIGDRVTITCRASQDLRNLYLGW YQKPGKAPKLLIYGASSLQSGVPSRFSGSGTE FTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR	SEQ ID NO: 1756 QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVWYDASNENYADAVKG RFTISRDN SKNTLYLQMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGLVTVSS
!PS:360995	18F2.003	NA	SEQ ID NO: 29 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACCTTAGAAATATTAG GCTGGTATCAACAGAAACACAGGAAAGCCCTA AGCTCTGATCTATGTCATCCAGTTTGCAA GTGGGTCCTTCAAGTTACGCGCAGTGGAT CTGGGACAGAAATTCATCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTACTGTCT ACAGCATATAATTACCCCTTCACCTTCGGCCCT GGGACCAAAGTGGATATCAAAACGA	SEQ ID NO: 186 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTTCAGTAACCTTTGGCA TGCACTGGTCCGCCAGGCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGCAGACGCCGTGAAGGCC GATTCAACCATCTCCAGAGACAATTCCAAAGAACA CGCTGTATCTGCAATGAACAGCCTGAGAGCCG CGACACGGCTGTGTAATTAATGTCGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
			SEQ ID NO: 1600 DIQMTQSPSSLSASIGDRVTITCRASQDLRNLYLGW YQKPGKAPKLLIYGASSLQSGVPSRFSGSGTE FTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR	SEQ ID NO: 1757 QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVWYDASNENYADAVKG RFTISRDN SKNTLYLHMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGLVTVSS

A-2165-WO-PCT

!PS:360999	18F2.004	NA	SEQ ID NO: 30	SEQ ID NO: 187
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!PS:361005	18F2.005	NA	SEQ ID NO: 1601	SEQ ID NO: 1758
			DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YHQPQKAPKLLIYGASSLQSGVPSRFSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR	QVQLVESGGGVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVYDASNENYADAVKGRFTISRDNSKNTLYLQMNSLRAADTAVYYCARDGTIFGVVLGDYWGQGLVTVSS
!PS:361005	18F2.005	NA	SEQ ID NO: 31	SEQ ID NO: 188
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTATAGGAGACAGAGTCACCATCACTTGCCGGCAAGTCAGGACCTTAGAAATATTAGGCTGGTATCAACAGAAACAGGAAAGCCCCCTAAGCGCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGTCCCTTCAAAGTTACGCGGCAAGTGATCTGGGACAGAAATTCATCTCTCAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCTACAGCATAAATAATTACCCCTTCACCTTCGGGCCCT GGGACCAAAGTGGATATCAAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCTGAGACTCTCCTGT GCAGCTCTGGATTCACTTTCAGTAACCTTTGGCA TGCACCTGGTCCGCCAGGCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAAATGAAAACATATGCAGACGCCGTGAAGGCC GATTCAACCATCTCCAGAGACAATTCCAAAGAACA CGCTGTATCTGCAATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTAATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
		AA	SEQ ID NO: 1602	SEQ ID NO: 1759
			DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YQKPQKAPKRLIYGASSLQSGVPSRFSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR	QVQLVESGGGVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVYDASNENYADAVKGRFTISRDNSKNTLYLQMNSLRAADTAVYYCARDGTIFGVVLGDYWGQGLVTVSS

A-2165-WO-PCT

!PS:361009	18F2.006	NA	SEQ ID NO: 32	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACCTTAGAAATTATTAG GCTGGTATCAACAGAAACCAAGGAAAGCCCTA AGCCCTGATCTATGGTGCATCCAGTTTGCAA GTGGGTCCTTCAAGGTTACGCGGCAAGTGAT CTGGGACAGAAATTCATCTCTCAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATATAATTACCCCTTCACTTTGCGCCCT GGGACCAAGTGGATATCAAAACGA	SEQ ID NO: 189	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCTGAGACTCTCCTGT GCAGCTCTGGATTCACTTTCAGTAACCTTTGGCA TGCACTGGTCCGCCAGGCCCAAGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGCAGACGCCGTGAAGGCC GATTCAACCATCTCCAGAGACAATTCCAAAGAACA CGCTGTATCTGCACATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
			SEQ ID NO: 1603	DIQMTQSPSSLSASIGDRVTITCRASQDLRNVLGW YQKPGKAPKRLIYGASSLQSGVPSRFSGSGTE FTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR	SEQ ID NO: 1760	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVWYDASNENYADAVKVG RFTISRDN SKNTLYLHMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGLVTVSS
!PS:361013	18F2.007	NA	SEQ ID NO: 33	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACCTTAGAAATTATTAG GCTGGTATCACCAAGAACCAAGGAAAGCCCTA AGCTCCTGATCTATGTGTCATCCAGTTTGCAA GTGGGTCCTTCAAGGTTCAAGCGGCAAGTGAT CTGGGACAGAAATTCATCTCTCAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATATAATTACCCCTTCACTTTGCGCCCT GGGACCAAGTGGATATCAAAACGA	SEQ ID NO: 190	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCTGAGACTCTCCTGT GCAGCTCTGGATTCACTTTCAGTAACCTTTGGCA TGCACTGGTCCGCCAGGCCCAAGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGCAGACGCCGTGAAGGCC GATTCAACCATCTCCAGAGACAATTCCAAAGAACA CGCTGTATCTGCACATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
			SEQ ID NO: 1604	DIQMTQSPSSLSASIGDRVTITCRASQDLRNVLGW YHQPGRKAPKLLIYGASSLQSGVPSRFSGSGTE FTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR	SEQ ID NO: 1761	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVWYDASNENYADAVKVG RFTISRDN SKNTLYLHMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGLVTVSS

A-2165-WO-PCT

		SEQ ID NO: 34	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACCTTAGAAAATTATTAG GCTGGTATCACAGAAACCAGGGAAGCCCCCTA AGGCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGTCCCTTCAAGGTTTCAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTTCGCAACTTATTACTGTCT ACAGCATATAAATTACCCCTTCACTTTCGGCCCT GGGACCAAGTGGATATCAAAACGA	SEQ ID NO: 1605	DIQMTQSPSSLSASIGDRVTITCRASQDLRNLYLGW YHQP GKAPKRLIYGASSLQSGVPSRFSGSGTE FTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR	SEQ ID NO: 1605	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKVG RFTISRDN SKNTLYLQMNSLRADTA VYYCARDG TIFGVVLGDYWGQGTLVTVSS	SEQ ID NO: 191	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACCTTTGGCA TGCACTGGTCCGCCAGGCCCAAGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGCAGACGCCGTGAAGGGCC GATTCAACCATCTCCAGAGACAATTCCAAAGAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
IPS:361017	18F2.008	NA			AA				
		SEQ ID NO: 35	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACCTTAGAAAATTATTAG GCTGGTATCAACAGAAACCAGGGAAGCCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGTCCCTTCAAGGTTTCAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTTCGCAACTTATTACTGTCT ACAGCATATAAATTACCCCTTCACTTTCGGCCCT GGGACCAAGTGGATATCAAAACGA	SEQ ID NO: 1606	DIQMTQSPSSLSASIGDRVTITCRASQDLRNLYLGW YQKPGKAPKLLIYGASSLQSGVPSRFSGSGTE FTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR	SEQ ID NO: 1606	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDGSNENYADAVKVG RFTISRDN SKNTLYLQMNSLRADTA VYYCARDG TIFGVVLGDYWGOGTLVTVSS	SEQ ID NO: 192	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACCTTTGGCA TGCACTGGTCCGCCAGGCCCAAGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGGAA GTAATGAAAACATATGCAGACGCCGTGAAGGGCC GATTCAACCATCTCCAGAGACAATTCCAAAGAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
IPS:361021	18F2.009	NA							
		SEQ ID NO: 1606	DIQMTQSPSSLSASIGDRVTITCRASQDLRNLYLGW YQKPGKAPKLLIYGASSLQSGVPSRFSGSGTE FTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR	SEQ ID NO: 1606	AA				

A-2165-WO-PCT

		SEQ ID NO: 36	GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTATAGGAGACAGAGTCACCATCACTTGCCGGCAAGTCAGGACCTTAGAAATTATTAGGCTGGTATCAACAGAAACACAGGAAAGCCCCTAGCTCCTGATCTATGGTGATCCAGTTTGCAAAGTGGGTCCCTTCAAGTTTCAGCGGCAGTGGATCTGGGACAGAAATTCATCTCACAATCAGCAGCCTGCAGCCTGAAGATTCGCAACTTATTACTGTCTACAGCATATAAATTACCCCTTCACCTTCGGCCCTGGACCAAGTGGATATCAAAACGA	SEQ ID NO: 1607	DIQMTQSPSSLSASIGDRVTITCRASQDLRNLYLGWYQKPGKAPKLLIYGASSLQSGVPSRFSGSGSTEFTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	SEQ ID NO: 193	CAGGTGCAGTGGTGGAGTCTGGGGAGGCGGTGTCCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACTTTCAGTAACCTTTGGCATGCACTGGGTCCGCCAGGCCCAAGCAAGGGCGTGGAGTGGTGGCAGTTATATGGTATGATGCAAGTAATGAAAACATATGCAGACTCCGTGAAGGGCGATTCAACCATCTCCAGAGACAAATTCCAAGAACA
	18F2.010	NA				SEQ ID NO: 1608	CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCGCGACACGGCTGTGTATTACTGTGCGGAGAGATGGACGATCTTTGGAGTGGTCTTGGGGGACTACTGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA
	!PS:361028				AA	SEQ ID NO: 1609	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAWIWYDASNENYADAVKGRFTISRDNSKNTLYLQMNSLRAADTAVYYCARDGTIFGVVLGDYWGQGTLVTVSS
						SEQ ID NO: 194	
						SEQ ID NO: 37	CAGGTGCAGTGGTGGAGTCTGGGGAGGCGGTGTCCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACTTTCAGTAACCTTTGGCATGCACTGGGTCCGCCAGGCCCAAGGCGGTGGAGTGGTGGCAGTTATATGGTATGATGCAAGTAATGAAAACATATGCAGACGCCGTGAAGGGCGGATTCAACCATCTCCAGAGACAAATTCCAAGAACA
	18F2.011	NA				SEQ ID NO: 38	CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGGAGAGATAGGACGATCTTTGGAGTGGTCTTGGGGGACTACTGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA
	!PS:360535				NA	SEQ ID NO: 1608	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAWIWYDASNENYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLGDYWGQGTLVTVSS
					AA	SEQ ID NO: 1609	

		SEQ ID NO: 38	GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTATAGGAGACAGAGTCACCATCACTTGCCGGCAAGTCAGGACCTTAGAAATTATTTAGGCTGGTATCAACAGAAACCAGGGAAGCCCTAAGCTCTGATCTATGGTGATCCAGTTTGCAAGTGGGTCCCTTCAAGGTTCAAGCGCGCAGTGGATCTGGACAGAAATTCACCTTCACAAATCAGCAGCCTGACGCTGAAGATTTGCGAACTTATTACTGTCTACAGCATAATAATTACCCCTTCACTTTTCGGCCCTGGGACCAAAAGTGGATATCAAAACGA	SEQ ID NO: 1609	SEQ ID NO: 195	
	18F2.012	NA			CAGGTGCAGCTGGTGAGTCTGGGGAGGCGGTGTCCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGGCTGGAATTCACCTTTCAGTAACCTTTGGCATGCACCTGGTCCGACGCCAGCCAGCAAGGGCTGGAGTGGTGCGAGTTATATGGTATGATGCAAGTAATGAAAACTATGCAGACGCCGTGAAGGGCGGATTACCATCTCCAGAGACAATTCCAAAGAACACGCTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTATTACTGTGCGAGAGATGGACGATCTTTGGAGTGGTCTTTGGGGGACTACTGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA	SEQ ID NO: 1766
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGWYQKPGKAPKLLIYGASSLSQGVPSRFSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR		SEQ ID NO: 196	
	2F11.002	NA			CAGGTGCAACTGGTGAGTCTGGGGAGGCGGTGTCCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGGCTGGAATTCACCTTTCAGTAGCTATGGCATGCACCTGGTCCGACGCTCCAGGCAAGGGCTGGAATAAATACTATGCAGACGCCGTGAAGGGCGATTACCATCTCCAGGACAATTCCAAAGAACACGCTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTATTACTGTGCGAGAGATAGGACGATTTTGGAGTGGTCTTTGACTACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA	SEQ ID NO: 1767
		AA	DIQMTQSPSSLSASVGRVTITCQASQDISNYLNWYQKPGKAPKLLIYDASNLETGVPSPRFSGSGGTFSLTISSLQPEDFATYYCQYDILLTFGGGKVEIKR		SEQ ID NO: 197	

A-2165-WO-PCT

!PS:361039	2F11.003	NA	SEQ ID NO: 40	SEQ ID NO: 197
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCAACCATCACTTGCCAGGCGAGTCAGGACATTAGCAACTATTAAATTGGTATCAGCAGAAACAGGGAAGCCCCCTAAGCTCCTGATCTACGATGCATCCAAATTGGAAA CAGGGTCCCATCAAGGTTTCAGTGGAAAGTGGATCTGGGACAGATTTTAGTCTCAACCATCAGCAGCCTGCAGCCTGAAGATTTTGCACATATTACTGTCAACAGTATGATATTCCTCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGA	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTGTCCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGCTCTGGATTCACTTCAGTAGCTATGGCATGCACTGGTCCGCAAGGCTCCAGGCAAGGGCTGGAGTGGTGGCAGTTATATGGTATGATGCAAGTAATAAATACTATGCAGACGCCGTGAAGGGCCGATTCAACCATCTCCAGCGACAATTCCAAAGAACACGCTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGGAGAGATAGGACGATTTTGGAGTGGTTCTTGACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTCA
!PS:361043	2F11.004	NA	SEQ ID NO: 1611	SEQ ID NO: 1768
			DIQMTQSPSSLSASVGDRTVTITCQASQDISNYLNWYQKPGKAPKLLIYDASNLETGVPSRFSGSGGTD FSLTISSLQPEDFATYYCQYDILLTFGGGTKVEIKR	QVQLVESGGGVVQPRSLRLSCAASGFTFSYGMHWVRQAPGKGLEWVAIVWYDASNKYADAVKGRFTISDINSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLDYWGQGLVTVSS
		AA	SEQ ID NO: 41	SEQ ID NO: 198
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCAACCATCACTTGCCAGGCGAGTCAGGACATTAGCAACTATTAAATTGGTATCAGCAGAAACAGGGAAGCCCCCTAAGCTCCTGATCTACGATGCATCCAAATTGGAAA CAGGGTCCCATCAAGGTTTCAGTGGAAAGTGGATCTGGGACAGATTTTAGTCTCAACCATCAGCAGCCTGCAGCCTGAAGATTTTGCACATATTACTGTCAACAGTATGATATTCCTCTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAGCGA	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTGTCCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGCTCTGGATTCACTTCAGTAGCTATGGCATGCACTGGTCCGCAAGGCTCCAGGCAAGGGCTGGAGTGGTGGCAGTTATATGGTATGATGCAAGTAATAAATACTATGCAGACGCCGTGAAGGGCCGATTCAACCATCTCCAGGGAACAATTCCAAAGAACACGCTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGGAGAGATAGGACGATTTTGGAGTGGTTCTTGACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTCA
		AA	SEQ ID NO: 1612	SEQ ID NO: 1769
			DIQMTQSPSSLSASVGDRTVTITCQASQDISNYLNWYQKPGKAPKLLIYDASNLETGVPSRFSGSGGTD FSLTISSLQPEDIATYYCQYDILLTFGGGTKVEIKR	QVQLVESGGGVVQPRSLRLSCAASGFTFSYGMHWVRQAPGKGLEWVAIVWYDASNKYADAVKGRFTISDINSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLDYWGQGLVTVSS

A-2165-WO-PCT

!PS:361049	2F11.005	NA	SEQ ID NO: 42 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCAACCATCACTT GCCAGCGAGTCAGGACATTAGCAACTATTAA ATTGGTATCAGCAGAAACAGGGAAGCCCCCTA AGCTCCTGATCTACGATGCATCCAAATTGGAA CAGGGTCCCATCAAGGTTCAAGTGGAAAGTGAT CTGGGACAGATTTAGTTTCAACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATATTCCTCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGA	SEQ ID NO: 199 CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCACTTCCAGTACGTATGGC ATGCACTGGTCCGCCAGGCTCCAGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGCAGACGCCGTGAAGGGC CGATTCAACCATCTCCAGGACAAATCCCAAGAAC ACGCTGTATCTGCAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGGAGAGAT AGGACGATTTTGGAGTGGTTCTTGACTACTGG GGCCAGGGAACCCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1613 DIQMTQSPSSLSASVGDRTVTITCQASQDISNYLNW YQKPGKAPKLLIYDASNLETGVPSPFSGSGGTD FSFTISLQPEDFATYYCQYDILLTFGGGKVEIK R	SEQ ID NO: 1770 QVQLVESGGGVVQPRSLRLSCAASGFTFSYGM HWVRQAPGKGLEWVAIVWYDASNKYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLDYWGQGLVTVSS
!PS:361055	2F11.006	NA	SEQ ID NO: 43 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCAACCATCACTT GCCAGCGAGTCAGGACATTAGCAACTATTAA ATTGGTATCAGCAGAAACAGGGAAGCCCCCTA AGCTCCTGATCTACGATGCATCCAAATTGGAA CAGGGTCCCATCAAGGTTCAAGTGGAAAGTGAT CTGGGACAGATTTAGTCTCAACCATCAGCAGCC TGCAGCCTGAAGATATTGCAACATATTACTGTC AACAGTATGATATTCTCCTCACTTTCGGCGGAG GGACCAAGGTGGAGATCAAGCGA	SEQ ID NO: 200 CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCACTTCCAGTACGTATGGC ATGCACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGCAGACGCCGTGAAGGGC CGATTCAACCATCTCCAGGACAAATCCCAAGAAC ACGCTGTATCTGCAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGGAGAGAT AGGACGATTTTGGAGTGGTTCTTGACTACTGG GGCCAGGGAACCCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1614 DIQMTQSPSSLSASVGDRTVTITCQASQDISNYLNW YQKPGKAPKLLIYDASNLETGVPSPFSGSGGTD FSLTISSLQPEDIATYYCQYDILLTFGGGKVEIKR	SEQ ID NO: 1771 QVQLVESGGGVVQPRSLRLSCAASGFTFSYGM HWVRQAPGKGLEWVAIVWYDASNKYADAVKG RFTISSDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLDYWGQGLVTVSS

A-2165-WO-PCT

!PS:361059	2F11.007	NA	SEQ ID NO: 44	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCAACCATCACTT GCCAGCGAGTCAGGACATTAGCAACTATTAA ATTGGTATCAGCAGAAACAGGGAAGCCCCCTA AGCTCTGATCTACGATGCATCCAAATTGGAA CAGGGTCCCATCAAGGTTCAAGTGGAAAGTGGAT CTGGGACAGATTTAGTTTCAACCATCAGCAGCCT GCAGCCTGAAGATTTTGAACATATTACTGTCA ACAGTATGATATTCCTCCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGA	SEQ ID NO: 201	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGTCTGGATTCACTTCCAGTACGTATGGC ATGCACTGGTCCGCCAGGCTCCAGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGCAGACGCCGTGAAGGGC CGATTCAACCATCTCCAGCACAATTCCAAAGAAC ACGCTGTATCTGCAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGGAGAGAT AGGACGATTTTGGAGTGGTCTTGTGACTACTGG GGCCAGGGAACCCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1615	DIQMTQSPSSLSASVGDRTVTITCQASQDISNYLNW YQKPGKAPKLLIYDASNLETGVPSPFSGSGGTD FSFTISLQPEDFATYYCQYDILLTFGGGKVEIK R	SEQ ID NO: 1772	QVQLVESGGGVVQPRSLRLSCAASGFTFSYGM HWVRQAPGKGLEWVAIVWYDASNKYADAVKG RFTISDINSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLDYWGQGLVTVSS
!PS:361063	2F11.008	NA	SEQ ID NO: 45	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCAACCATCACTT GCCAGCGAGTCAGGACATTAGCAACTATTAA ATTGGTATCAGCAGAAACAGGGAAGCCCCCTA AGCTCTGATCTACGATGCATCCAAATTGGAA CAGGGTCCCATCAAGGTTCAAGTGGAAAGTGGAT CTGGGACAGATTTAGTTTCAACCATCAGCAGCCT GCAGCCTGAAGATATTGCAACATATTACTGTCA ACAGTATGATATTCCTCCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGA	SEQ ID NO: 202	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGTCTGGATTCACTTCCAGTACGTATGGC ATGCACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGCAGACGCCGTGAAGGGC CGATTCAACCATCTCCAGGACAATTCCAAAGAAC ACGCTGTATCTGCAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGGAGAGAT AGGACGATTTTGGAGTGGTCTTGTGACTACTGG GGCCAGGGAACCCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1616	DIQMTQSPSSLSASVGDRTVTITCQASQDISNYLNW YQKPGKAPKLLIYDASNLETGVPSPFSGSGGTD FSFTISLQPEDFATYYCQYDILLTFGGGKVEIKR	SEQ ID NO: 1773	QVQLVESGGGVVQPRSLRLSCAASGFTFSYGM HWVRQAPGKGLEWVAIVWYDASNKYADAVKG RFTISDINSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLDYWGQGLVTVSS

			SEQ ID NO: 46	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGCGAGTCAGGACATTAGCAACTATTAA ATTGGTATCAGCAGAAACCAGGAAAGCCCTA AGCTCTGATCTACGATGCATCCAAATTTGAAA CAGGGTCCCATCAAGGTTTCAGTGGAAGTGGAT CTGGACAGATTTTAGTCTCACCATCAGCAGCC TGCAGCCTGAAAGATTTTGC AACATAATTACTGTCA ACAGTATGATA TTCTCCTCACTTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGA	SEQ ID NO: 203	CAGGTGCAACTGGTGAGTCTGGGGAGGCGGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTGTGATTCACTTCAAGTAGCTATGGC ATGCATGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGCAGACTCCGTGAAGGGC CGATTCAACCATCTCCAGGGACAATTCCAAGAAC ACGCTGTATCTGCAAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGGAGAGAT AGGACGATTTTGGAGTGTCTTGACTACTGG GGCCAGGGAACCTGTACCGTCTCCTCA
	2F11.009	IPS:359949	NA	SEQ ID NO: 1617 DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQKPKGAPKLLIYDASNLETGVPSPRFGSGSGTD FSLTISSLQPEDFATYYCQQYDILLTFGGGTKEIK R	SEQ ID NO: 1774	QVQLVESGGGVVQPRSLRLSCAASGFTFSYGM HWVRQAPGKGLEWVAWIYDASNKYADSVKVG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLDYWGQGLVTVSS
			AA	SEQ ID NO: 47 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGCGAGTCAGGACATTAGCAACTATTAA ATTGGTATCAGCAGAAACCAGGAAAGCCCTA AGCTCTGATCTACGATGCATCCAAATTTGAAA CAGGGTCCCATCAAGGTTTCAGTGGAAGTGGAT CTGGACAGATTTTAGTCTCACCATCAGCAGCC TGCAGCCTGAAAGATTTTGC AACATAATTACTGTCA ACAGTATGATA TTCTCCTCACTTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGA	SEQ ID NO: 204	CAGGTGCAACTGGTGAGTCTGGGGAGGCGGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTGTGATTCACTTCAAGTAGCTATGGC ATGCATGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGGA AGTAATAAATACTATGCAGACGCCGTGAAGGGC CGATTCAACCATCTCCAGGGACAATTCCAAGAAC ACGCTGTATCTGCAAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGGAGAGAT AGGACGATTTTGGAGTGTCTTGACTACTGG GGCCAGGGAACCTGTACCGTCTCCTCA
	2F11.010	IPS:359956	NA	SEQ ID NO: 1618 DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQKPKGAPKLLIYDASNLETGVPSPRFGSGSGTD FSLTISSLQPEDFATYYCQQYDILLTFGGGTKEIK R	SEQ ID NO: 1775	QVQLVESGGGVVQPRSLRLSCAASGFTFSYGM HWVRQAPGKGLEWVAWIYDASNKYADAVKVG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLDYWGQGLVTVSS
			AA	SEQ ID NO: 1618 DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQKPKGAPKLLIYDASNLETGVPSPRFGSGSGTD FSLTISSLQPEDFATYYCQQYDILLTFGGGTKEIK R	SEQ ID NO: 1775	QVQLVESGGGVVQPRSLRLSCAASGFTFSYGM HWVRQAPGKGLEWVAWIYDASNKYADAVKVG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLDYWGQGLVTVSS

A-2165-WO-PCT

		SEQ ID NO: 48	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCAACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTAG GCTGTATCAGCAGAAACCAGGAAAGCCCCTA AGGCCTGATCTATGGTGCATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCACAATCAGCAGCC TGACGCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAGTGGATATCAAAACGA	SEQ ID NO: 1619	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLQSGVPSRFSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	SEQ ID NO: 205	CAGGTGCAGTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGTTATGATGCAA GTAATAAATACTATGACAGACGCCGTGAAGGGCC GCTTCAACCATCTCCAGAGACAAATTCCAAGAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTGGAGTGCTCTTGGGGGACTACT GGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA
IP:359865	6H1.002	NA				SEQ ID NO: 1776	QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAIVWYDASNKYYADAVKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSS
		SEQ ID NO: 49	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCAACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTAG GCTGTATCAGCAGAAACCAGGAAAGCCCCTA AGGCCTGATCTATGGTGCATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCACAATCAGCAGCC TGACGCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAGTGGATATCAAAACGA	SEQ ID NO: 49	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLQSGVPSRFSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	SEQ ID NO: 206	CAGGTGCAGTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGTTATGATGCAA GTAATAAATACTATGACAGACGCCGTGAAGGGCC GCTTCAACCATCTCCAGAGACAAATTCCAAGAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATA GGACGATTTTGGAGTGCTCTTGGGGGACTACT GGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA
IP:359869	6H1.003	NA				SEQ ID NO: 1777	QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAIVWYDASNKYYADAVKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLLGDYWGQGTLVTVSS
		SEQ ID NO: 1620	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLQSGVPSRFSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	SEQ ID NO: 1620			
		AA					

A-2165-WO-PCT

IP:359873	6H1.004	NA	SEQ ID NO: 50	SEQ ID NO: 207
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTATAGGAGACAGAGTCACCATCACTTGCCGGCAAGTCAGGACATTAGAGATTATTAGGCTGGTATCAGCAGAAACCAGGAAAGCCCCTAAGCTCTGATCTATGGTGCATCCAGTTTGCAAAGTGGGTCCCTTCAAGGTTACGCGGAGTGGATCTGGGACAGAAATCACTCTCACAATCAGCAGCCTGACGCTGAAGATTTCGCAACTTATTACTGTCTACAGCATATAATTACCCCTTCACTTTCGGCCAAAGGACCAAAGTGATATCAAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGGTGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCTCTGGATTCACTTACGTTACTTTGGCATGCACTGGTCCCGCAGGCTCCAGGCAAGGGGCTGGAGTGGTGGCAGTTATATGGTATGATGCAAATAATACTATGCAGACGCCGTGAAGGGCCGCTTCAACCATCTCCAGAGACAATTCAGAACAACGCTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTATTACTGTGCGCGAGATGGACGATTTTGGAGTGCCTTGGGGGACTACTGGGCCAGGGAACCTGGTCAACCGTCTCCTCA
IP:359877	6H1.005	NA	SEQ ID NO: 1621	SEQ ID NO: 1778
			DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKLLIYGASSLQSGVPSRFSGSGTEFTLTISLQPEDFATYYCLQHNNYPFTFGQGTKVDIKR	QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAWIYDASNKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGTIFGVLLGDYWGQGLVTVSS
IP:359877	6H1.005	NA	SEQ ID NO: 51	SEQ ID NO: 208
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTATAGGAGACAGAGTCACCATCACTTGCCGGCAAGTCAGGACATTAGAGATTATTAGGCTGGTATCAGCAGAAACCAGGAAAGCCCCTAAGCTCTGATCTATGGTGCATCCAGTTTGCAAAGTGGGTCCCTTCAAGGTTACGCGGAGTGGATCTGGGACAGAAATCACTCTCACAATCAGCAGCCTGACGCTGAAGATTTCGCAACTTATTACTGTCTACAGCATATAATTACCCCTTCACTTTCGGCCAAAGGACCAAAGTGATATCAAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGGTGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCTCTGGATTCACTTACGTTACTTTGGCATGCACTGGTCCCGCAGGCTCCAGGCAAGGGGCTGGAGTGGTGGCAGTTATATGGTATGATGCAAATAATACTATGCAGACGCCGTGAAGGGCCGCTTCAACCATCTCCAGAGACAATTCAGAACAACGCTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTATTACTGTGCGCGAGATAAGGACGATTTTGGAGTGCCTTGGGGGACTACTGGGCCAGGGAACCTGGTCAACCGTCTCCTCA
IP:359877	6H1.005	AA	SEQ ID NO: 1622	SEQ ID NO: 1779
			DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKLLIYGASSLQSGVPSRFSGSGTEFTLTISLQPEDFATYYCLQHNNYPFTFGQGTKVDIKR	QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAWIYDASNKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVLLGDYWGQGLVTVSS

A-2165-WO-PCT

	!PS:361067	6H1.006	NA	SEQ ID NO: 52	SEQ ID NO: 209
				GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTATAGGAGACAGAGTCACCATCACTTGCCGGCAAGTCAGGACATTAGAGATTATTAGGCTGGTATCAGCAGAAACCAGGAAAGCCCCAAGCTCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGTCCTTCAAGGTTACGCGCAGTGGATCTGGGACAGAAATTCATCTCAATCAGCAGCCTGACGCTGAAGATTTCGCAACTTATTACTGTCTACAGCATAAATTAACCCCTTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAAACA	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGTCCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGCTCTGGATTACCTTCAGTTACTTTGGCATGCACTGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGTGGCAGTTATATGGTATGATGGAAATAATAATACTATGCAGACTCCGTGAAGGGCCGCTTCAACATCTCCAGAGACAATCCAAAGAACACGTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTATTACTGTGCGCGAGATGGACGATTTTGGAGTGCTCTTGGGGGACTACTGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA
	AA			SEQ ID NO: 1780	SEQ ID NO: 1780
				QVQLVESGGGVVQPGSRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAIVYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGTIFGVLLGDYWGQGLVTVSS	QVQLVESGGGVVQPGSRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAIVYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGTIFGVLLGDYWGQGLVTVSS
	!PS:361071	6H1.007	NA	SEQ ID NO: 53	SEQ ID NO: 210
				GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTATAGGAGACAGAGTCACCATCACTTGCCGGCAAGTCAGGACATTAGAGATTATTAGGCTGGTATCAGCAGAAACCAGGAAAGCCCCAAGCTCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGTCCTTCAAGGTTACGCGCAGTGGATCTGGGACAGAAATTCATCTCAATCAGCAGCCTGACGCTGAAGATTTCGCAACTTATTACTGTCTACAGCATAAATTAACCCCTTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAAACA	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGTCCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGCTCTGGATTACCTTCAGTTACTTTGGCATGCACTGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGTGGCAGTTATATGGTATGATGGCAATAATAATACTATGCAGACTCCGTGAAGGGCCGCTTCAACATCTCCAGAGACAATCCAAAGAACACGTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTATTACTGTGCGCGAGATGGACGATTTTGGAGTGCTCTTGGGGGACTACTGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA
	AA			SEQ ID NO: 1624	SEQ ID NO: 1781
				DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKLLIYGASSLQSGVPSRFSGSGTEFTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	QVQLVESGGGVVQPGSRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAIVYDASNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGTIFGVLLGDYWGQGLVTVSS
				SEQ ID NO: 54	SEQ ID NO: 211

A-2165-WO-PCT

!PS:361075	6H1.008	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACCAGGAAAGCCCCA AGTCTGTATCTATGTGTCATCCAGTTTGCAA GTGGGTCCCTTCAAGTTACGCGCAGTGGAT CTGGACAGAAATTCATCTCTACAATCAGCAGCC TGACGCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGGAA GTAATAATACTATGACAGCGCCGTGAAGGGCC GCTTACCATCTCCAGAGACAATTCACAAGACA CGTGTATCTGCAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTTACTGTGCGCGAGATG GGACGATTTTGGAGTGCTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASLQSGVPSRFSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	SEQ ID NO: 1782 QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKLEWVAIVYDGSNKYYADAVKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSS
!PS:361079	6A5.004.001	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGACAGAGTCACCATCACTT GCCAGCGAGTCAGGACATTACCAACTATTAA ATTGGTATCAGCAGAAACCAGGAAAGCCCCA AACTCCTGATCTACGATGCTTCCAAATTTGGAGCC AGGGTCCCATCAAGGTTCAAGTGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAAGTGGATATCAAAACGA	SEQ ID NO: 212 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCTCTTCAAGTAGCTATGGCA TGCACTGGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGTGGCAGCTATATGGTATGATGCAA ATAATAATACTATGACAGCGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCACAAGACA CGCTGTATCTGCAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTTACTGTGCGGAGAGATC GGACGATTTTGGAGTGCTCTTGAAGTACTGGG GCCAGGGAACCTGGTCAACCGTCTCCTCA
		AA	DIQMTQSPSSLSASVGDRTVTITCAASQDITNLYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGGTD FTLTISSLQPEDFATYYCQYQYDDLFTFGPGTKVDIK R	SEQ ID NO: 1783 QVQLVESGGGVVQPRSLRLSCAASGFSYSGM HWVRQPPGKLEWVAIIWYDANNKYYADAVKG RFTISRDSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGQGLVTVSS

A-2165-WO-PCT

!PS:361085	6A5.004.002	NA	SEQ ID NO: 56	SEQ ID NO: 213
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGACAGAGTCACCATCACTT GCCAGCGAGTCAGGACATTACCACTATTAA ATTGGTATCAGCAGAAACAGGAAAGCCCCA AACTCCTGATCTACGATGCTTCCAATTGGAGCC AGGGTCCCATCAAGGTTCAAGTGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATATTGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAAGTGGATATCAAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGATTCTCCTTCAGTAGCTATGGCA TGCACCTGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGTGGCAGCTATATGATGATGCAAA ATAATAATACTATGACAGCCTCCGCTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCTCAAGAACAA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGATTACTGTGCGAGAGATC GGACGATTTTGGAGTGGTCTTGAAGTACTGGG GCCAGGGAACCTGGTCAACCGTCTCCTCA
!PS:361091	6A5.004.003	NA	SEQ ID NO: 1627	SEQ ID NO: 1784
			DIQMTQSPSSLSASVGDRTVITCQASQDITNLYNW YQKPGKAPKLLIYDASNLEPGVPSRFSGSGTD FTLTISSLQPEDIATYYCQYDDLFTFGPGTKVDIK R	QVQLVESGGGVQPGRLSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAIIWYDANNKYADAVKG RFTISRDSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGQGLVTVSS
!PS:361091	6A5.004.003	NA	SEQ ID NO: 57	SEQ ID NO: 214
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGACAGAGTCACCATCACTT GCCAGCGAGTCAGGACATTACCACTATTAA ATTGGTATCAGCAGAAACAGGAAAGCCCCA AACTCCTGATCTACGATGCTTCCAATTGGAGCC AGGGTCCCATCAAGGTTCAAGTGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAAGTGGATATCAAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGATTCTCCTTCAGTAGCTATGGCA TGCACCTGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGTGGCAGCTATATGATGATGCAAA ATAATAATACTATGACAGCCTCCGCTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCTCAAGAACAA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGATTACTGTGCGAGAGATC GGACGATTTTGGAGTGGTCTTGAAGTACTCG GCCAGGGAACCTGGTCAACCGTCTCCTCA
!PS:361091	6A5.004.003	AA	SEQ ID NO: 1628	SEQ ID NO: 1785
			DIQMTQSPSSLSASVGDRTVITCQASQDITNLYNW YQKPGKAPKLLIYDASNLEPGVPSRFSGSGTD FTLTISSLQPEDFATYYCQYDDLFTFGPGTKVDIK R	QVQLVESGGGVQPGRLSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAIIWYDANNKYADAVKG RFTISRDSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYLQGQGLVTVSS

		SEQ ID NO: 58	SEQ ID NO: 215
IPS:361095	6A5.004.004	NA	CAGTGCAGTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGTATGATGCAA ATAATAAATACTATGACAGACCGCTGAAGGGCC GATTCAACCATCTCCAGAGACAGTTCCAAAGAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGGAGAGATC GGACGATTTTGGAGTGGTCTTGAAGTACTGGG GCCAGGGAACCTGTGTACCGTCTCCTCTCA
			SEQ ID NO: 1786
		AA	QVQLVESGGGVVQPRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAIIWYDANNKYYADAVKG RFTISRDSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGQGLVTVSS
IPS:361101	6A5.004.005	NA	CAGTGCAGTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGCAA ATAATAAATACTATGACAGCCCTGAAGGGCC GATTCAACCATCTCCAGAGACAGTTCCAAAGAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGGAGAGATC GGACGATTTTGGAGTGGTCTTGAAGTACCTCG GCCAGGGAACCTGTGTACCGTCTCCTCTCA
			SEQ ID NO: 1787
		AA	QVQLVESGGGVVQPRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAIIWYDANNKYYADAVKG RFTISRDSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYLGOGTLVTVSS

A-2165-WO-PCT

IP:361105	6A5.004.006	NA	SEQ ID NO: 60	SEQ ID NO: 217
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTGGGGACAGAGTCACCATCACTTGCCAGCGAGTCAGGACATTACCACTATTAAATTGGTATCAGCAGAAACAGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTGGAGCCAGGGTCCCATCAAGGTTCAAGTGAAGTGGATCTGGGACAGATTTACTTTCACCATCAGCAGCCTGCAGCCTGAAGATTTGCAACATATTACTGTCAA CAGTATGATGATCTATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGGTGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCTCTGATTCTCCTTCAGTAGCTATGGCATGCACCTGGTCCGCCAGCCTCCAGGCAAGGGGCTGGAGTGGTGGCAGCTATATGATGATGCAATAAATAACTATATGACAGCCCTGAAGGGCCGATTACCATCTCCAGAGACAGTTCACAAGAACACGCTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTATTACTGTGCGAGAGATCGGACGATTTTGGAGTGTCTTGAAGTACCTCGGCCAGGGAACCTGGTCAACCGTCTCCTCA
IP:361109	6A5.004.007	NA	SEQ ID NO: 1631	SEQ ID NO: 1788
			DIQMTQSPSSLSASVGDRTVTITCQASQDITNLYNWYQKPGKAPKLLIYDASNLEPGVPSRFSGSGTDFTFTISLQPEDFATYYCQYDDLFTFGPGTKVDIKR	QVQLVESGGGVVQGRSLRLSCAASGFSFSSYGMHWVRQPPGKGLEWVAIWYDANNKYADAVKGRFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLEYLGQGLVTVSS
IP:361109	6A5.004.007	NA	SEQ ID NO: 61	SEQ ID NO: 218
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTGGGGACAGAGTCACCATCACTTGCCAGCGAGTCAGGACATTACCACTATTAAATTGGTATCAGCAGAAACAGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTGGAGCCAGGGTCCCATCAAGTTCAGTGAAGTGGATCTGGGACAGATTTACTTTCACCATCAGCAGCCTGCAGCCTGAAGATATTGCAACATATTACTGTCAA CAGTATGATGATCTATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGGTGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCTCTGATTCTCCTTCAGTAGCTATGGCATGCACCTGGTCCGCCAGCCTCCAGGCAAGGGGCTGGAGTGGTGGCAGCTATATGATGATGCAATAAATAACTATGACAGCCCTGAAGGGCCGATTACCATCTCCAGAGACAGTTCACAAGAACACGCTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTATTACTGTGCGAGAGATCGGACGATTTTGGAGTGTCTTGAAGTACTGGGCCAGGGAACCTGGTCAACCGTCTCCTCA
IP:361109	6A5.004.007	AA	SEQ ID NO: 1632	SEQ ID NO: 1789
			DIQMTQSPSSLSASVGDRTVTITCQASQDITNLYNWYQKPGKAPKLLIYDASNLEPGVPSRFSGSGTDFTFTISLQPEDIATYYCQYDDLFTFGPGTKVDIKR	QVQLVESGGGVVQGRSLRLSCAASGFSFSSYGMHWVRQPPGKGLEWVAIWYDANNKYADAVKGRFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLEYWGQGLVTVSS

A-2165-WO-PCT

IP:36113	6A5.004.008	NA	SEQ ID NO: 62	SEQ ID NO: 219
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTGGGGACAGAGTCACCATCACTTGCCAGGCGAGTCAGGACATTACCAACTATTAAATTGGTATCAGCAGAAACAGGGAAGCCCCATAACTCCTGATCTACGATGCTTCCAAATTGGAGCCAGGGTCCCATCAAGGTTTCAGTGGAAAGTGGATCTGGGACAGATTTTACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACATATTACTGTCAACAGTATGATGATCTATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGGTGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCTGTGATTCTCCTCAGTAGCTATGGCATGCACTGGTCCGCCAGCCTCCAGGCAAGGGGCTGGAGTGGTGGCAGCTATATGATATGATGGAAATAATAATACTATGCAGACGCCGTGAAGGGCCGATTACCATCTCCAGAGACAGTTCACAAGACAACGCTGTATCTGCAATATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATCGGACGATTTTGGAGTGGTCCCTTGAGTACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA
IP:361120	6A5.004.009	NA	SEQ ID NO: 1633	SEQ ID NO: 1790
			DIQMTQSPSSLSASVGDRTVTITCQASQDITNLYLNWYQKPGKAPKLLIYDASNLEPGVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQYDDLFITFGPGTKVDIKR	QVQLVESGGGVVQPRSLRLSCAASGFSFSSYGMHWVRQPPGKGLEWVAIWYDGNKKYYADAVKGRFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLEYWGQGLVTVSS
IP:361120	6A5.004.009	NA	SEQ ID NO: 63	SEQ ID NO: 220
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTGGGGACAGAGTCACCATCACTTGCCAGGCGAGTCAGGACATTACCAACTATTAAATTGGTATCAGCAGAAACAGGGAAGCCCCATAACTCCTGATCTACGATGCTTCCAAATTGGAGCCAGGGTCCCATCAAGTTCAGTGGAAAGTGGATCTGGGACAGATTTTACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACATATTACTGTCAACAGTATGATGATCTATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGGTGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCTGTGATTCTCCTCAGTAGCTATGGCATGCACTGGTCCGCCAGCCTCCAGGCAAGGGGCTGGAGTGGTGGCAGCTATATGATATGATGCAAATAATAATACTATGCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAGTTCACAAGACAACGCTGTATCTGCAATATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATCGGACGATTTTGGAGTGGTCCCTTGAGTACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA
IP:361120	6A5.004.009	AA	SEQ ID NO: 1634	SEQ ID NO: 1791
			DIQMTQSPSSLSASVGDRTVTITCQASQDITNLYLNWYQKPGKAPKLLIYDASNLEPGVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQYDDLFITFGPGTKVDIKR	QVQLVESGGGVVQPRSLRLSCAASGFSFSSYGMHWVRQPPGKGLEWVAIWYDANNKKYYADSVKGRFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLEYWGQGLVTVSS

A-2165-WO-PCT

IP:359890	6A5.004.011	NA	SEQ ID NO: 64	SEQ ID NO: 221
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTGGGGACAGAGTCACCATCACTTGCCAGCGAGTCAGGACATTACCACTATTAAATTGGTATCAGCAGAAACAGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTGGAGCCAGGGTCCCATCAAGGTTCAAGTGAAGTGGATCTGGGACAGATTTACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGAACATATTACTGTCAACAGTATGATGATCTATTCACTTTCGGCCAAAGGACCAAAGTGGATATCAAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGCTCTGATTCTCCTTCAGTAGCTATGGCA TGCACCTGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGTGGCAGCTATATGATGATGCAAAATAATAAATACTATGCAGACGCCGTGAAGGGCCGATTACCATCTCCAGAGACAGTTCCAAAGAACACGCTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTATTACTGTGCGAGAGATC GGACGATTTTGGAGTGTCTTGAAGTACTGGG GCCAGGGAACCTGGTCAACCGTCTCCTCA
IP:359890	6A5.004.011	NA	SEQ ID NO: 1635	SEQ ID NO: 1792
			DIQMTQSPSSLSASVGDRTVTITCQASQDITNLYNWYQKPGKAPKLLIYDASNLEPGVPSRFSGSGTDFTLTISSLQPEDFATYYCQYDDLFITFGQGTKVDIKR	QVQLVESGGGVVQGRSLRLSCAASGFSFSSYGMHWVRQPPGKGLEWVAIWYDANNKYYADAVKGRFTISRDSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLEYWGQGLVTVSS
IP:359890	6A5.004.011	NA	SEQ ID NO: 65	SEQ ID NO: 222
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTGGGGACAGAGTCACCATCACTTGCCAGCGAGTCAGGACATTACCACTATTAAATTGGTATCAGCAGAAACAGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTGGAGCCAGGGTCCCATCAAGTTCAGTGAAGTGGATCTGGGACAGATTTACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGAACATATTACTGTCAACAGTATGATGATCTATTCACTTTCGGCCAAAGGACCAAAGTGGATATCAAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGCTCTGATTCTCCTTCAGTAGCTATGGCA TGCACCTGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGTGGCAGCTATATGATGATGCAAAATAATAAATACTATGCAGACGCCGTGAAGGGCCGATTACCATCTCCAGAGACAGTTCCAAAGAACACGCTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTATTACTGTGCGAGAGATC GGACGATTTTGGAGTGTCTTGAAGTACTGGTGGCAGGGAACCTGGTCAACCGTCTCCTCA
IP:359890	6A5.004.011	AA	SEQ ID NO: 1636	SEQ ID NO: 1793
			DIQMTQSPSSLSASVGDRTVTITCQASQDITNLYNWYQKPGKAPKLLIYDASNLEPGVPSRFSGSGTDFTLTISSLQPEDFATYYCQYDDLFITFGQGTKVDIKR	QVQLVESGGGVVQGRSLRLSCAASGFSFSSYGMHWVRQPPGKGLEWVAIWYDANNKYYADAVKGRFTISRDSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLEYWGQGLVTVSS

A-2165-WO-PCT

IPS:359567	2A11.002	NA	SEQ ID NO: 66	SEQ ID NO: 223
			GAAATTGTGTTGACGCAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCT GCAGGCCAGTCAGATTTTACCAGCACCTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCAGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCAGACAGGTTCACTGTCAGTGGCAGTG GGTCTGGGACAGACTTCACTCTCACCATCAGCA GATTGGAGCCTGAAGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGCTCACCTCGCTTCGGCC AAGGGACACGACTGGAGATTAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTTCAGTAGCTATGGC ATGCATGGTCCGCCAGGCTCCAGGCAAGGGA CTGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAATACTATGAAGACGCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAAATCCAAAGAAC ACGCTGTTTCTGCAAGTGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGGG ATTACGATTTTGGTGCATGGGTTTGAATATTGGG GCCAGGGAACCCCTGGTCAACCGTCTCCTCA
IPS:335965	2A11.003	NA	SEQ ID NO: 67	SEQ ID NO: 224
			GAAATTGTGTTGACGCAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCT GCAGGCCAGTCAGATTTTACCAGCACCTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCAGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCAGACAGGTTCACTGTCAGTGGCAGTG GGTCTGGGACAGACTTCACTCTCACCATCAGCA GATTGGAGCCTGAAGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGCTCACCTCGCTTCGGCC AAGGGACACGACTGGAGATTAAACGA	QVQLVESGGGVQPGRSLRLSCAASGFSFSSYGM HWVRQAPGKGLEWVAWIYDASNKYIEDAVKGG RFTISRDN SKNTLFLQVNSLRAEDTAVYYCARGITI FGHGFYWGQGLVTVSS
		AA	SEQ ID NO: 1637	SEQ ID NO: 1794
			EIVLTQSPGTLSPGERATLSCRASQIFTSTYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDF TLTISRLEPEDFAVYYCQQYGSSPRFGQGRLEIKR	QVQLVESGGGVQPGRSLRLSCAASGFSFSSYGM HWVRQAPGKGLEWVAWIYDASNKYIEDAVKGG RFTISRDN SKNTLFLQVNSLRAEDTAVYYCARGITI FGHGFYWGQGLVTVSS
		AA	SEQ ID NO: 1638	SEQ ID NO: 1795
			EIVLTQSPGTLSPGERATLSCRASQIFTSTYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDF TLTISRLEPEDFAVYYCQQYGSSPRFGQGRLEIKR	QVQLVESGGGVQPGRSLRLSCAASGFSFSSYGM HWVRQAPGKGLEWVAWIYDGSNKYYEDSVKGG RFTISRDN SKNTLFLQVNSLRAEDTAVYYCARGITI FGHGFYWGQGLVTVSS

A-2165-WO-PCT

!PS:361158	2A11.004	NA	SEQ ID NO: 68	SEQ ID NO: 225
			GAAATTGTTGACGCAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGAAAGAGCCACCCCTCTCCT GCAGGCCAGTCAGATTTTACCAGCACCTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCAGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCAGACAGGTTCAAGTGGCAGTG GGTCTGGACAGACTTCACTCTCACCATCAGCA GATTGGAGCCTGAAGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGCTCACCTCGCTTCGGCC AAGGGACACGACTGGAGATTAAACGA	CAGGTGCAGCTGTTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTTCAGTAGCTATGGC ATGCACCTGGTCCGCCAGGCTCCAGGCAAGGGA CTGGAGTGGTGGCAGTTATATGGTATGATGGA AGTAATAAATACTATGAAGACGCCGTGAAGGCG CGATTCAACCATCTCCAGAGACAAATTCCAAAGAAC ACGCTGTTTCTGCAAGTGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGGG ATTACGATTTTGGTCAATGGGTTTGAATATTGGG GCCAGGGAACCCCTGGTCAACCGTCTCCTCA
!PS:361165	2A11.005	NA	SEQ ID NO: 1639	SEQ ID NO: 1796
			EIVLTQSPGTLSPGERATLSCRASQIFTSTYLAW YQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDF TLTISRLEPEDFAVYYCQQYGSSPRFGQGRLEIKR	QVQLVESGGGVQPGRSLRLSCAASGFSFSSYGM HWVRQAPGKGLEWVAIVWYDGSNKYYEDAVKG RFTISRDNKNTLFLQVNSLRAEDTAVYYCARGITI FGHGFYWGQGTLVTVSS
!PS:361165	2A11.005	NA	SEQ ID NO: 69	SEQ ID NO: 226
			GAAATTGTTGACGCAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGAAAGAGCCACCCCTCTCCT GCAGGCCAGTCAGATTTTACCAGCACCTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCAGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCAGACAGGTTCAAGTGGCAGTG GGTCTGGACAGACTTCACTCTCACCATCAGCA GATTGGAGCCTGAAGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGCTCACCTCGCTTCGGCC AAGGGACACGACTGGAGATTAAACGA	CAGGTGCAGCTGTTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTTCAGTAGCTATGGC ATGCACCTGGTCCGCCAGGCTCCAGGCAAGGGA CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGAAGACTCCGTGAAGGCG CGATTCAACCATCTCCAGAGACAAATTCCAAAGAAC ACGCTGTTTCTGCAAGTGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGGG ATTACGATTTTGGTCAATGGGTTTGAATATTGGG GCCAGGGAACCCCTGGTCAACCGTCTCCTCA
!PS:361165	2A11.005	AA	SEQ ID NO: 1640	SEQ ID NO: 1797
			EIVLTQSPGTLSPGERATLSCRASQIFTSTYLAW YQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDF TLTISRLEPEDFAVYYCQQYGSSPRFGQGRLEIKR	QVQLVESGGGVQPGRSLRLSCAASGFSFSSYGM HWVRQAPGKGLEWVAIVWYDASNKYYEDSVKG RFTISRDNKNTLFLQVNSLRAEDTAVYYCARGITI FGHGFYWGQGTLVTVSS

A-2165-WO-PCT

!PS:361172	2G10_LC1.003	NA	SEQ ID NO: 70	SEQ ID NO: 227
			GAAATAGTGATGACGCAGTCTCCAGCCACCCTG TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTTAGCAGCACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAAGCCACAGGGCC ACTGGTATCCCAAGCAGGTTCAAGTGCCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGCAGTCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTGGCCTCTCAGTTTCGGCG GAGGGACCAAGGTGGAGATCAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACTTCCAGTAACTATGGC ATGCAGTGGTCCGCCAGGCTCCAGGCGAGGGG CTGGAGTGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAACCTCCAAGAAC ACGCTGTATCTGCAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCTGGTCAACCGTCTCCTCA
!PS:361178	2G10_LC1.004	NA	SEQ ID NO: 1641	SEQ ID NO: 1798
			EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQKPGQAPRLLIYGAAATRTATGIPARFSGSGTE FTLTISLQSEDFAVYYCQQYNWPLTFGGGKVE IKR	QVQLVESGGGVQPGRSLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAIWFDASDKYYADA VKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGLVTVSS
!PS:361178	2G10_LC1.004	NA	SEQ ID NO: 71	SEQ ID NO: 228
			GAAATAGTGATGACGCAGTCTCCAGCCACCCTG TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTTAGCAGCACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAAGCCACAGGGCC ACTGGTATCCCAAGCAGGTTCAAGTGCCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGCAGTCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTGGCCTCTCAGTTTCGGCG GAGGGACCAAGGTGGAGATCAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACTTCCAGTAACTATGGC ATGCAGTGGTCCGCCAGGCTCCAGGCGAGGGG CTGGAGTGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACTCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAACCTCCAAGAAC ACGCTGTATCTGCAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCTGGTCAACCGTCTCCTCA
!PS:361178	2G10_LC1.004	AA	SEQ ID NO: 1642	SEQ ID NO: 1799
			EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQKPGQAPRLLIYGAAATRTATGIPARFSGSGTE FTLTISLQSEDFAVYYCQQYNWPLTFGGGKVE IKR	QVQLVESGGGVQPGRSLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAIWFDASDKYYADSVKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGLVTVSS

A-2165-WO-PCT

IPS:361185	2G10_LC1.005	NA	SEQ ID NO: 72	SEQ ID NO: 229
			GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTAGCAGCACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGACGCCACCAGGGCC ACTGGTATCCAGCCAGGTTCAAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGCAGTCTGAAGATTTTGCAAGTTTATTACTGTC AGCAGTATAATAACTGGCTCTCACTTTTCGGGG GAGGGACCAAGGTGGAGATCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAAGTATGGC ATGCACTGGTCCGCCAGGCTCCAGCGAGGGG CTGGAGTGGTGGCAGCTATATGGTTTGATGGA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAACTCCAAGAAC ACCTGTATCTGCAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTGGAGTGTCCCCGACTACTGG GGCAGGGAAACCTGTGTACCCGTCTCCTCA
IPS:361192	2G10_LC1.006	NA	SEQ ID NO: 1643	SEQ ID NO: 1800
			EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAAATRAATGIPARFSGSGTE FTLTISSLQSEDFAVYYCQQYNWPLTFGGGKVE IKR	QVQLVESGGGVVQPRSLRLSCAASGFTFSNYGM HWVRQAPGEGLWVAIWFDGSDKYADAVKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGLVTVSS
IPS:361192	2G10_LC1.006	NA	SEQ ID NO: 73	SEQ ID NO: 230
			GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTAGCAGCACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGACGCCACCAGGGCC ACTGGTATCCAGCCAGGTCAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGCAGTCTGAAGATTTTGCAAGTTTATTACTGTC AGCAGTATAATAACTGGCTCTCACTTTTCGGGG GAGGGACCAAGGTGGAGATCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAAGTATGGC ATGCACTGGTCCGCCAGGCTCCAGCGAGGGG CTGGAGTGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAACTCCAAGAAC ACCTGTATCTGCAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTGGAGTGTCCCCGACTACTGG GGCAGGGAAACCTGTGTACCCGTCTCCTCA
IPS:361192	2G10_LC1.006	AA	SEQ ID NO: 1644	SEQ ID NO: 1801
			EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAAATRAATGIPARVSGSGSGTE FTLTISSLQSEDFAVYYCQQYNWPLTFGGGKVE IKR	QVQLVESGGGVVQPRSLRLSCAASGFTFSNYGM HWVRQAPGEGLWVAIWFDASDKYADAVKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGLVTVSS

A-2165-WO-PCT

IP:359609	2G10 LC1.007	NA	SEQ ID NO: 74	SEQ ID NO: 231
			GAAATAGTGATGACGAGTCTCCAGCCACCCTG TCTGTGTCTCCAGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTAGCAGCACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGACGCCACCAGGGCC ACTGGTATCCAGCCAGGTTCAAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGGAGCCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTTCCCTCTCACTTTCGGCGG AGGGACCAAGGTGGAGATCAAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAAGTATGGC ATGCACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAACTCCAAAGAAC ACGCTGTATCTGCAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTGGAGTGTCCCCGACTACTGG GGCCAGGGAACCTGTGTACCCGTCTCCTCA
IP:359615	2G10 LC1.008	NA	SEQ ID NO: 1645	SEQ ID NO: 1802
			EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAAATRTATGIPARFSGSGTE FTLTISSELPEDFAVYYCQQYNFPLTFGGGKVEI KR	QVQLVESGGGVVQGRSLRLSCAASGFTFSNYGM HWVRQAPGKGLEWVAIWFDASDKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGLVTVSS
IP:359615	2G10 LC1.008	NA	SEQ ID NO: 75	SEQ ID NO: 232
			GAAATAGTGATGACGAGTCTCCAGCCACCCTG TCTGTGTCTCCAGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTAGCAGCACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGACGCCACCAGGGCC ACTGGTATCCAGCCAGGTTCAAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGGAGCCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTATCCTCTCACTTTCGGCGG AGGGACCAAGGTGGAGATCAAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAAGTATGGC ATGCACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAACTCCAAAGAAC ACGCTGTATCTGCAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTGGAGTGTCCCCGACTACTGG GGCCAGGGAACCTGTGTACCCGTCTCCTCA
IP:359615	2G10 LC1.008	AA	SEQ ID NO: 1646	SEQ ID NO: 1803
			EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAAATRTATGIPARFSGSGTE FTLTISSELPEDFAVYYCQQYNFPLTFGGGKVEI KR	QVQLVESGGGVVQGRSLRLSCAASGFTFSNYGM HWVRQAPGKGLEWVAIWFDASDKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGLVTVSS

A-2165-WO-PCT

IP:361196	2G10_LC1.009	NA	SEQ ID NO: 76	SEQ ID NO: 233
			GAAATAGTGATGACGAGTCTCCAGCCACCCTG TCTGTGTCTCCAGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTAGCAGCACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGACGCCACCAGGGCC ACTGGTATCCAGCCAGGTTCAAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGGAGCCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTGGCTCTCACTTTCGGCG GAGGGACCAAGGTGGAGATCAAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAAGTATGGC ATGCACTGGTCCGCCAGGCTCCAGCGAGGGG CTGGAGTGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAACTCCAAAGAAC ACGCTGTATCTGCAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTGGAGTGTCCCCGACTACTGG GGCCAGGGAACCTGTGTACCCGTCTCCTCA
IP:361202	2G10_LC1.010	NA	SEQ ID NO: 1647	SEQ ID NO: 1804
			EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAAATRTATGIPARFSGSGTE FTLTISSELPEDFAVYYCQQYNWPLTFGGGTKVE IKR	QVQLVESGGGVVQPRSLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAIWFDASDKYYADA VKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGLTVTVSS
IP:361202	2G10_LC1.010	NA	SEQ ID NO: 77	SEQ ID NO: 234
			GAAATAGTGATGACGAGTCTCCAGCCACCCTG TCTGTGTCTCCAGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTAGCAGCACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGACGCCACCAGGGCC ACTGGTATCCAGCCAGGTTCAAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGGAGCCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTGGCTCTCACTTTCGGCG GAGGGACCAAGGTGGAGATCAAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAAGTATGGC ATGCACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAACTCCAAAGAAC ACGCTGTATCTGCAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTGGAGTGTCCCCGACTACTGG GGCCAGGGAACCTGTGTACCCGTCTCCTCA
IP:361202	2G10_LC1.010	AA	SEQ ID NO: 1648	SEQ ID NO: 1805
			EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAAATRTATGIPARFSGSGTE FTLTISSELPEDFAVYYCQQYNWPLTFGGGTKVE IKR	QVQLVESGGGVVQPRSLRLSCAASGFTFSNYGM HWVRQAPGKGLEWVAIWFDASDKYYADA VKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGLTVTVSS

A-2165-WO-PCT

IP:359644	18E3.002	NA	SEQ ID NO: 78	SEQ ID NO: 235
			GAAATTGTTGACGCAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCT GCAGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACACAGCAGAAACCTGGCCAGGCTC CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCAGACAGGTTCACTGAGGAGTG GGTCTGGGACAGACTTCACTCTCACCATCAGCA GACTGGAGCCTGATGATTTGACGTGATTACTG TCAGCAGTATGGTAGTTCAACCGCTCACTTTCGGC GGAGGGACCAAGGTGGAGATCAAAACGA	CAGGTGCAGTTGCAGGAGTCGGGGCCAGGACTG GTGAAGCCTTCAGAGACCCCTGTCCCTCACCTGC ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCCCCAGGGA AGGCCCTGGAGTGGATTGGGTACATCTATTACA GTGGGAGCACCTACTACAACCCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGTCTAAGA ACCACTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGGACACGGCCGTGATTACTGTGCGAGAGA TCGTATTACGATTTTGGAGTGGTTATGGGGGGC GGTATGGACGTCTGGGGCCAAAGGACACCGGTC ACCGTCTCCTCA
IP:361206	18E3.003	NA	SEQ ID NO: 1649	SEQ ID NO: 1806
			EIVLTQSPGTLSPGERATLSCRASQISYSYLAW YQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDF TLTISRLEPDDFAVYYCQYGSSPLTFGGGKVEIK R	QVQLQESGPGLVKPSFTLSLTCTVSGDSISSGGYY WSWIRQPPGKGLEWIGYIYSGSTYYNPSLKSRT ISVDTSKNQFSLKLSSTVAADTAVYYCARDRTIFG VVMGGMDVWVGQGTITVTVSS
IP:361206	18E3.003	NA	SEQ ID NO: 79	SEQ ID NO: 236
			GAAATTGTTGACGCAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCT GCAGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACACAGCAGAAACCTGGCCAGGCTC CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCAGACAGGTTCACTGAGGAGTG GGTCTGGGACAGACTTCACTCTCACCATCAGCA GACAGGAGCCTGATGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGTTCAACCGCTCACTTTCGG CGAGGGACCAAGGTGGAGATCAAAACGA	CAGGTGCAGTTGCAGGAGTCGGGGCCAGGACTG GTGAAGCCTTCAGAGACCCCTGTCCCTCACCTGC ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCCCCAGGGA AGGCCCTGGAGTGGATTGGGTACATCTATTACA GTGGGAGCACCTACTACAACCCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGTCTAAGA ACCACTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGGACACGGCCGTGATTACTGTGCGAGAGA TCGTATTACGATTTTGGAGTGGTTATGGGGGGC GGTATGGACGTCTGGGGCCAAAGGACACCGGTC ACCGTCTCCTCA
IP:361206	18E3.003	AA	SEQ ID NO: 1650	SEQ ID NO: 1807
			EIVLTQSPGTLSPGERATLSCRASQISYSYLAW YQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDF TLTISRQEPDDFAVYYCQYGSSPLTFGGGKVEI KR	QVQLQESGPGLVKPSFTLSLTCTVSGDSISSGGYY WSWIRQPPGKGLEWIGYIYSGSTYYNPSLKSRT ISVDTSKNQFSLKLSSTVAADTAVYYCARDRTIFG VVMGGMDVWVGQGTITVTVSS

A-2165-WO-PCT

	!PS:359628	18E3.004	NA	SEQ ID NO: 80	SEQ ID NO: 237
				GAAATTGTGTTGACGCAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCAGACAGGTTCAAGTGGCAGTG GGTCTGGACAGACTTCACTCTCACCATCAGCA GACTGGAGCCTGATGATTTTGCAGTGTATTACTG TCAGCAGTATGGTAGTTCAACCGCTCACTTTCGGC GGAGGGACCAAGGTGGAGATCAAAACGA	CAGGTGCAGTTGCAGGAGTCGGGGCCAGGACTG GTGAAGCCTTACAGACCCTGTCCCTCACCTGC ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCCCCAGGGA AGGGCTGGAGTGGATTGGGTACATCTATTACA GTGGGAGCACCTACTACAACCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGTCTAAGA ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGACACGGCCGTGTATTACTGTGCGAGAGA TCGTATTACGATTTTGGAGTGGTTATGGGGGGC GGTATGGACGTCTGGGGCCAAAGGGACACCGGTC ACCGTCTCCTCA
	!PS:359637	18E3.005	NA	SEQ ID NO: 1651	SEQ ID NO: 1808
				EIVLTQSPGTLSPGERATLSCRASQISYSYLAW YQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDF TLTISRLEPDDFAVYYCQYGSSPLTFGGGKVEIK R	QVQLQESGPGLVKPSQTLSTCTVSGDSISSGGYY WSWIRQPPGKGLEWIGYIYSGSTYYPNPSLKSRVT ISVDTSKNQFSLKLSSTVAADTAVYYCARDRIITFG VVMGGMDVWGQGTITVTVSS
			AA	SEQ ID NO: 81	SEQ ID NO: 238
				GAAATTGTGTTGACGCAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCAGACAGGTTCAAGTGGCAGTG GGTCTGGACAGACTTCACTCTCACCATCAGCA GACTGGAGCCTGATGATTTTGCAGTGTATTACTG TCAGCAGTATGGTAGTTCAACCGCTCACTTTCGGC GGAGGGACCAAGGTGGAGATCAAAACGA	CAGGTGCAGTTGCAGGAGTCGGGGCCAGGACTG GTGAAGCCTTACAGACCCTGTCCCTCACCTGC ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCCCCAGGGA AGGGCTGGAGTGGATTGGGTACATCTATTACA GTGGGAGCACCTACTACAACCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGTCTAAGA ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGACACGGCCGTGTATTACTGTGCGAGAGA TCGTATTACGATTTTGGAGTGGTTATGGGGGGC GGTATGGACGTCTGGGGCCAAAGGGACACCGGTC ACCGTCTCCTCA
			AA	SEQ ID NO: 1652	SEQ ID NO: 1809
				EIVLTQSPGTLSPGERATLSCRASQISYSYLAW YQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDF TLTISRLEPDDFAVYYCQYGSSPLTFGGGKVEIK R	QVQLQESGPGLVKPSQTLSTCTVSGDSISSGGYY WSWIRQHPGKGLEWIGYIYSGSTYYPNPSLKSRVT ISVDTSKNQFSLKLSSTVAADTAVYYCARDRIITFG VVMGGMDVWGQGTITVTVSS

A-2165-WO-PCT

	!PS:361210	18E3.006	NA	SEQ ID NO: 82	SEQ ID NO: 239
				GAAATTGTGTTGACGCAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCAGACAGGTTCAAGTGGCAGTG GGTCTGGACAGACTTCACTCTCACCATCAGCA GACTGGAGCCTGATGATTTTGCAGTGTATTACTG TCAGCAGTATGGTAGTTCAACCGCTCACTTTCGGC GGAGGGACCAAGGTGGAGATCAAAACGA	CAGGTGCAGTTGCAGGAGTGGGGCCAGGACTG GTGAAGCCTTACAGACCCTGTCCCTCACCTGC ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCACCAGGGA AGGCTGGAGTGGATTGGGTACATCTATTACA GTGGAGCACCTACTACAACCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGTCTAAGA ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGACACGGCCGTGTATTACTGTGCGAGAGA TCGTATTACGATTTTGGAGTGGTTATGGGGGGC GGTATGGACGTCTGGGGCCAAAGGGACACCGGTC ACCGTCTCCTCA
	!PS:361214	18E3.007	NA	SEQ ID NO: 1653	SEQ ID NO: 1810
				EIVLTQSPGTLSPGERATLSCRASQISYSYLAW YQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDF TLTISRLEPDDFAVYYCQYQYSSPLTFGGGKVEIK R	QVQLQESGPGLVKPSQTLSTCTVSGDSISSGGYY WSWIRQHPGKGLEWIGYIYSGSTYINPSLKSRT ISVDTSKNQFSLKLSSTVAADTAVYYCARDRTITFG VVMGGMDVWGQGTITVTVSS
	!PS:361214	18E3.007	NA	SEQ ID NO: 83	SEQ ID NO: 240
				GAAATTGTGTTGACGCAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCAGACAGGTTCAAGTGGCAGTG GGTCTGGACAGACTTCACTCTCACCATCAGCA GACAGGAGCCTGATGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGTTCAACCGCTCACTTTCGG CGGAGGGACCAAGGTGGAGATCAAAACGA	CAGGTGCAGTTGCAGGAGTGGGGCCAGGACTG GTGAAGCCTTACAGACCCTGTCCCTCACCTGC ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCACCAGGGA AGGCTGGAGTGGATTGGGTACATCTATTACA GTGGAGCACCTACTACAACCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGTCTAAGA ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGACACGGCCGTGTATTACTGTGCGAGAGA TCGTATTACGATTTTGGAGTGGTTATGGGGGGC GGTATGGACGTCTGGGGCCAAAGGGACACCGGTC ACCGTCTCCTCA
	!PS:361214	18E3.007	AA	SEQ ID NO: 1654	SEQ ID NO: 1811
				EIVLTQSPGTLSPGERATLSCRASQISYSYLAW YQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDF TLTISRQEPDDFAVYYCQYQYSSPLTFGGGKVEI KR	QVQLQESGPGLVKPSQTLSTCTVSGDSISSGGYY WSWIRQHPGKGLEWIGYIYSGSTYINPSLKSRT ISVDTSKNQFSLKLSSTVAADTAVYYCARDRTITFG VVMGGMDVWGQGTITVTVSS

A-2165-WO-PCT

!PS:361218	18E3.008	NA	SEQ ID NO: 84	SEQ ID NO: 241
			GAAATTGTGTTGACGCAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCAGACAGGTTCAAGTGGCAGTG GGTCTGGACAGACTTCACTCTCACCATCAGCA GACAGAGCCTGATGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGTTCACCGCTCACTTTCCG CGGAGGGACCAAGGTGGAGATCAAAACGA	CAGGTGCAGTTGCAGGAGTGGGGCCAGGACTG GTGAAGCCTTACAGACCCTGTCCCTCACCTGC ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCCCCAGGGA AGGGCTGGAGTGGATTGGGTACATCTATTACA GTGGGAGCACCTACTACAACCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGTCTAAGA ACCACTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGACACGGCCGTGATTACTGTGCGAGAGA TCGTATTACGATTTTGGAGTGGTTATGGGGGGC GGTATGGACGTCTGGGGCCAAAGGGACACGGTC ACCGTCTCCTCA
!PS:361222	5C2.006	NA	SEQ ID NO: 1655	SEQ ID NO: 1812
			EIVLTQSPGTLSPGERATLSCRASQISYSYLAW YQKPGQAPRLIYGASSRATGIPDRFSGSGGTDF TLTISRQEPDDFAVYYCQYQSSPLTFGGGKVEI KR	QVQLQESGPGLVKPSQTLSTCTVSGDSISSGGYY WSWIRQPPGKGLEWIGYIYSGSTYYNPSLKSRVT ISVDTSKNQFSLKLSSTVAADTAVYYCARDRIITFG VVMGGMDVWGQGTITVTVSS
!PS:361222	5C2.006	NA	SEQ ID NO: 85	SEQ ID NO: 242
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTATCCAGCTCC AACAATAAGAACTACATAGCTTGTACCAAGCAG CAACCAGGACATCCTCCTAAGCTGCTCATTACT GGCATCTACCCGGGAATCCGGGTCCCTGACC GATTCAGTGGCAGCGGTCTGGACAGATTICA CTCTCACCATCAGCAGCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTTCGGCCAAAGGGACCAAGGTGGA AATCAAAACGA	CAGGTGCAGCTGGTGCAAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCGACAGGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATCAACCTGAAAGT GGTGGCACAGACTATTACAGAGGTTTCAAGGGC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCTACATGGAAGTGAACAGGCTGAGATCT GACGACACGGCCGTGATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCAACCGTCT CCTCA
!PS:361222	5C2.006	AA	SEQ ID NO: 1656	SEQ ID NO: 1813
			DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQPGHPPKLLIYWASTRESGVDPDRFSGS GSGTDFLTIISSLQAEDVAVFYCQYQYSTPWTFGQ GTKVEIKR	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYI HWVRAQPGQGLEWMGWINPESGGTDYSQRFQGR VTMTRDTSISTAYMELNRLRSDDDTAVYYCAREATI FGMVIVPFDYWGGQGLVTVSS

A-2165-WO-PCT

!PS:361229	5C2.007	NA	SEQ ID NO: 86	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG CAACCAGGACATCCTCCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGTCCTGACC GATTCAGTGGCAGCGGCTCTGGACAGATTTC CTCTACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAAAGGACCAAGGTGGA AATCAAAACGA	SEQ ID NO: 243	CAGGTGCCGTGGTGCAAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCACAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATCAACCTGAAAGT GGTGGACAGACTATTACAGAGGTTTCAGGGC AGGTTCAACCATGACCAAGGACACGTCATCAGC ACAGCTACATGGAACCTGAACAGGCTGAGATCT GACGACACGGCCGTGTTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCGTCT CCTCA
			SEQ ID NO: 1657	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQPGHPPKLLIYWASTRESGVPDFRFGS GSGTDFLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR	SEQ ID NO: 1814	QVPLVQSGAEVKKPGASVKVCKASGYTFTGYI HWVRAPGQGLEWMGWINPESGGTDYSQRFQGR FTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGLVTVSS
!PS:361236	5C2.008	NA	SEQ ID NO: 87	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG CAACCAGGACATCCTCCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGTCCTGACC GATTCAGTGGCAGCGGCTCTGGACAGATTTC CTCTACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAAAGGACCAAGGTGGA AATCAAAACGA	SEQ ID NO: 244	CAGGTGCAGCTGGTGCAAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCACAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATCAACCTGACGCT GGTGGACAGACTATTACAGAGGTTTCAGGGC AGGTTCAACCATGACCAAGGACACGTCATCAGC ACAGCTACATGGAACCTGAACAGGCTGAGATCT GACGACACGGCCGTGTTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCGTCT CCTCA
			SEQ ID NO: 1658	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQPGHPPKLLIYWASTRESGVPDFRFGS GSGTDFLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR	SEQ ID NO: 1815	QVQLVQSGAEVKKPGASVKVCKASGYTFTGYI HWVRAPGQGLEWMGWINPDAGGTDYSQRFQGR RVTMTRDTSISTAYMELNRLRSDDTAVYYCAREA TIFGMVIVPFDYWGQGLVTVSS

A-2165-WO-PCT

!PS:359685	SC2.009	NA	SEQ ID NO: 88	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG CAACAGGACATCCTCCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGTCCTGACC GATTCAGTGGCAGCGGCTCTGGACAGATTCA CTCTACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAAAGGACCAAGGTGGA AATCAAAACGA	SEQ ID NO: 245	CAGGTGCCGCTGGTGCAAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCACAGGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATCAACCTGACGCT GGTGGACAGACTATTACAGAGGTTTCAAGGGC AGGTTCAACCATGACCAAGGACACGTCCTCAGC ACAGCTACATGGAACCTGAACAGGCTGAGATCT GACGACACGGCCGTGATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCGTCT CCTCA
			SEQ ID NO: 1659	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQPGHPPKLLIYWASTRESGVPDFRFGS GSGTDFLTITSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR	SEQ ID NO: 1816	QVPLVQSGAEVKKPGASVKVCKASGYTFTGYI HWVRAQPGQGLEWMGWNPDAAGTDYSQRFQ RFTMTRDTSISTAYMELNRLRSDDTAVYYCAREA TIFGMVIVPDFYWGQGLVTVSS
!PS:361240	SC2.010	NA	SEQ ID NO: 89	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG CAACAGGACATCCTCCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGTCCTGACC GATTCAGTGGCAGCGGCTCTGGACAGATTCA CTCTACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAAAGGACCAAGGTGGA AATCAAAACGA	SEQ ID NO: 246	CAGGTGCAGCTGGTGCAAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCACAGGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATCAACCTGACAGT GGTGGACAGACTATTACAGAGGTTTCAAGGGC AGGTTCAACCATGACCAAGGACACGTCCTCAGC ACAGCTACATGGAACCTGAACAGGCTGAGATCT GACGACACGGCCGTGATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCGTCT CCTCA
			SEQ ID NO: 1660	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQPGHPPKLLIYWASTRESGVPDFRFGS GSGTDFLTITSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR	SEQ ID NO: 1817	QVQLVQSGAEVKKPGASVKVCKASGYTFTGYI HWVRAQPGQGLEWMGWNPDSGGTDYSQRFQGR VTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI FGMVIVPDFYWGQGLVTVSS

A-2165-WO-PCT

!PS:361247	SC2.011	NA	SEQ ID NO: 90	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAAGCAG CAACAGGACATCCTCCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGTCCCTGACC GATTCAGTGGCAGCGGTCTGGGACAGATTTC CTCTACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAAAGGACCAAGGTGGA AATCAAAACGA	SEQ ID NO: 247	CAGGTGCAGCTGGTGCAAGTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGGTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATCAACCTTGACAGT GGTGGACAGACTATTCACAGAGGTTTCAGGGC AGGTTCAACCATGACCAAGGACACGTCCTACAGC ACAGCTACATGGAACCTGAACAGGCTGAGATCT GACGACACGGCCGTGATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
			SEQ ID NO: 1661	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQPGHPPKLLIYWASTRESGVPDFRFGS GSGTDFLTIISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR	SEQ ID NO: 1818	QVQLVQSGAEVKKPGASVKVSKASGYTFTGYYI HWVRAPGQGLEWMGWINPDSGGTDYSQRFQGR FTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGLVTVSS
!PS:361254	SC2.012	NA	SEQ ID NO: 91	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAAGCAG CAACAGGACATCCTCCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGTCCCTGACC GATTCAGTGGCAGCGGTCTGGGACAGATTTC CTCTACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAAAGGACCAAGGTGGA AATCAAAACGA	SEQ ID NO: 248	CAGGTGCCGCTGGTGCAAGTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGGTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATCAACCTTGACAGT GGTGGACAGACTATTCACAGAGGTTTCAGGGC AGGTTCAACCATGACCAAGGACACGTCCTACAGC ACAGCTACATGGAACCTGAACAGGCTGAGATCT GACGACACGGCCGTGATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
			SEQ ID NO: 1662	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQPGHPPKLLIYWASTRESGVPDFRFGS GSGTDFLTIISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR	SEQ ID NO: 1819	QVPLVQSGAEVKKPGASVKVSKASGYTFTGYYI HWVRAPGQGLEWMGWINPDSGGTDYSQRFQGR VTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGLVTVSS

A-2165-WO-PCT

!PS:361261	SC2.013	NA	SEQ ID NO: 92	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG CAACAGGACATCCTCCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGTCCCTGACC GATTCAGTGGCAGCGGTCTGGGACAGATTCA CTCTACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAAAGGGACCAAGGTGGA AATCAAAACGA	SEQ ID NO: 249	CAGGTGCAGCTGGTGCAAGTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGGTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATCAACCTTGACGCT GGTGGACAGACTATTCACAGAGGTTTCAGGGC AGGTTCAACCATGACCAAGGACACGTCCTCAGC ACAGCTACATGGAACCTGAACAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
			SEQ ID NO: 1663	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQPGHPPKLLIYWASTRESGVPDFRFGS GSGTDFLTITSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR	SEQ ID NO: 1820	QVQLVQSGAEVKKPGASVKVSKASGYTFTGYI HWVRAPGQGLEWMGWNPDAAGTDYSQRFQG RFTMTRDTSISTAYMELNRLRSDDTAVYYCAREA TIFGMVIVPFDYWGGQTLVTVSS
!PS:361268	SC2.014	NA	SEQ ID NO: 93	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG CAACAGGACATCCTCCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGTCCCTGACC GATTCAGTGGCAGCGGTCTGGGACAGATTCA CTCTACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAAAGGGACCAAGGTGGA AATCAAAACGA	SEQ ID NO: 250	CAGGTGCCGCTGGTGCAAGTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGGTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATCAACCTTGACGCT GGTGGACAGACTATTCACAGAGGTTTCAGGGC AGGTTCAACCATGACCAAGGACACGTCCTCAGC ACAGCTACATGGAACCTGAACAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
			SEQ ID NO: 1664	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQPGHPPKLLIYWASTRESGVPDFRFGS GSGTDFLTITSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR	SEQ ID NO: 1821	QVPLVQSGAEVKKPGASVKVSKASGYTFTGYI HWVRAPGQGLEWMGWNPDAAGTDYSQRFQG RVTMTRDTSISTAYMELNRLRSDDTAVYYCAREA TIFGMVIVPFDYWGGQTLVTVSS

A-2165-WO-PCT

!PS:35969	SC2.015	NA	SEQ ID NO: 94	SEQ ID NO: 251
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAAGAACTACATAGCTTGGTACCAGCAG AACCAAGGACAACCTCCTAAGCTGCTCATTTAC TGGGCATCTACCCGGGAATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGACAGATTTC ACTCTCACCATCAGCAGCTTGCAGGCTGAAGAT GTGGCAGTTTTTTTACTGTCAACAATATTATAGTA CTCCGTGGACGTTCTGGCCAAAGGGACCAAGGTGG AAATCAAAACGA	CAGGTGCAGCTGGTGCAAGTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGGTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCGACAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATCAACCTGACGCT GGTGGACAGACTATTACAGAGGTTTCAAGGGC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCTACATGGAACCTGAACAGCCTGAGATCT GACGACACGGCCGTGATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
!PS:359678	SC2.016	NA	SEQ ID NO: 1665	SEQ ID NO: 1822
			DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQKPGQPPKLLIYWASTRESGVPDFRFGS GSGTDFLTITSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVVRAPGQGLEWMGWINPDAGGTDYSQRFQG RVMTTRDTSISTAYMELNSLRSDDTAVYYCAREA TIFGMVIVPDFYWGQGLVTVSS
!PS:359678	SC2.016	NA	SEQ ID NO: 95	SEQ ID NO: 252
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAAGAACTACATAGCTTGGTACCAGCAG AACCAAGGACAACCTCCTAAGCTGCTCATTTAC TGGGCATCTACCCGGGAATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGACAGATTTC ACTCTCACCATCAGCAGCTTGCAGGCTGAAGAT GTGGCAGTTTTTTTACTGTCAACAATATTATAGTA CTCCGTGGACGTTCTGGCCAAAGGGACCAAGGTGG AAATCAAAACGA	CAGGTGCAGCTGGTGCAAGTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGGTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCGACAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATCAACCTGAAAGT GGTGGACAGACTATTACAGAGGTTTCAAGGGC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCTACATGGAACCTGAACAGCCTGAGATCT GACGACACGGCCGTGATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
!PS:359678	SC2.016	AA	SEQ ID NO: 1666	SEQ ID NO: 1823
			DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQKPGQPPKLLIYWASTRESGVPDFRFGS GSGTDFLTITSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVVRAPGQGLEWMGWINPESGGTDYSQRFQGR VTMTTRDTSISTAYMELNSLRSDDTAVYYCAREATI FGMVIVPDFYWGQGLVTVSS

A-2165-WO-PCT

!PS:361275	11C1.002	NA	SEQ ID NO: 96	SEQ ID NO: 253
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAACAG AACCAAGGACAGCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGAAATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTGGCCAAAGGGACCAAGGTGG AAATCAAAACGA	CAGGTGCCGTGGTACAGTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGGTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCGTACGGCCCTGGACAAGGG CTTGTGTGGATGGGTGGATCAGCCCTAACAGT GGTGAACAAAGCTATGCACAGAAGTTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGAGCTGAGCAGACTGAGATCT GACGACACGGCCGTGATTTCTGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
!PS:361282	11C1.003	NA	SEQ ID NO: 1667	SEQ ID NO: 1824
			DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRESGVPDFRFG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	QVPLVQSGAEVKKPGASVKVCKASGYTFTGYI HWVRAPGQGLVWMGWISPNSETSYAQKFQDR VTMTRDTSISTAYMELSRLSRDDTAVYFCAREATI FGMLIVPFDYWGQGLVTVSS
!PS:361282	11C1.003	NA	SEQ ID NO: 97	SEQ ID NO: 254
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAACAG AACCAAGGACAGCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGAAATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTGGCCAAAGGGACCAAGGTGG AAATCAAAACGA	CAGGTGCCGTGGTACAGTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGGTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCGTACGGCCCTGGACAAGGG CTTGTGTGGATGGGTGGATCAGCCCTAACAGT GGTGAACAAAGCTATGCACAGAAGTTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGAGCTGAGCAGACTGAGATCT GACGACACGGCCGTGATTTCTGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
		AA	SEQ ID NO: 1668	SEQ ID NO: 1825
			DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRESGVPDFRFG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	QVPLVQSGAEVKKPGASVKVCKASGYTFTGYI HWVRAPGQGLVWMGWISPNSETSYAQKFQDR VTMTRDTSISTAYMELSRLSRDDTAVYFCAREATI FGMLIVPFDYWGQGLVTVSS

A-2165-WO-PCT

!PS:361289	11C1.004	NA	SEQ ID NO: 98	SEQ ID NO: 255
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAACAG AACCAAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGGACCAAGGTGG AAATCAAAACGA	CAGTGCCGCTGGTACAGTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGGTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCTCAGGCCCTGGACAAAGG CTTGTGTGGATGGGTGGATCAGCCCTAACAGT GGTGAACAAAGCTATGCACAGAAATTTCAGGAC AGGTCACCATGACCAAGGACACGTCCATCAGC ACAGCTATATGAGCTGAGCAGACTGAGATCT GACGACAGCGGCTGTATTTCTGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
!PS:359712	11C1.005	NA	SEQ ID NO: 1669	SEQ ID NO: 1826
			DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRD SGVPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	QVPLVQSGAEVKKPGASVKVSKASGYTFTGYI HWVRAPGQGLVWMGWISPNSETSYAQKFQDR VTMTRDTSISTAYMELSR LRSDDTA VYFCAREATI FGMLIVPFDYWGQGLVTVSS
!PS:359712	11C1.005	NA	SEQ ID NO: 99	SEQ ID NO: 256
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAACAG AACCAAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGAAATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGGACCAAGGTGG AAATCAAAACGA	CAGTGCCGCTGGTACAGTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGGTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCTCAGGCCCTGGACAAAGG CTTGTGTGGATGGGTGGATCAGCCCTAACAGT GGTGAACAAAGCTATGCACAGAAATTTCAGGAC AGGTCACCATGACCAAGGACACGTCCATCAGC ACAGCTATATGAGCTGAGCAGACTGAGATCT GACGACAGCGGCTGTATTTCTGTACGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
!PS:359712	11C1.005	AA	SEQ ID NO: 1670	SEQ ID NO: 1827
			DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRD SGVPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	QVPLVQSGAEVKKPGASVKVSKASGYTFTGYI HWVRAPGQGLVWMGWISPNSETSYAQKFQDR VTMTRDTSISTAYMELSR LRSDDTA VYFCAREATI FGMLIVPFDYWGQGLVTVSS

A-2165-WO-PCT

!PS:361293	11C1.006	NA	SEQ ID NO: 100 GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAACAG AACCAAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGAAATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTGGCCAAAGGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 257 CAGGTGCCGTGGTACAGTCTGGGGCTGAGGTG AAGAACGCTGGGGCTCAGTGAAGGTCTCCTGC AAGGTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCGTCAGGCCCTGGACAAGGG CTTGTGTGGATGGGTGGATCAGCCCTAACAGT GGTGACAAAGCTATGCACAGAAGTTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGAGCTGAGCAGACTGAGATCT GACGACACGGCCGTGATTTCTGTACGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
			SEQ ID NO: 1671 DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRESGVPDFRFG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1828 QVPLVQSGAEVKKPGASVKVCKASGYTFTGYI HWVRAQPGQGLVWMGWISPNSGDTSYAQKFQDR VTMTRDTSISTAYMELSRLRSDDTAVYFCTREATI FGMLIVPFDYWGQGLVTVSS
!PS:361297	11C1.007	NA	SEQ ID NO: 101 GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAACAG AACCAAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTGGCCAAAGGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 258 CAGGTGCCGTGGTACAGTCTGGGGCTGAGGTG AAGAACGCTGGGGCTCAGTGAAGGTCTCCTGC AAGGTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCGTCAGGCCCTGGACAAGGG CTTGTGTGGATGGGTGGATCAGCCCTAACAGT GGTGAAACAAAGCTATGCACAGAAGTTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGAGCTGAGCAGACTGAGATCT GACGACACGGCCGTGATTTCTGTACGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
			SEQ ID NO: 1672 DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRDSGVPDFRFG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1829 QVPLVQSGAEVKKPGASVKVCKASGYTFTGYI HWVRAQPGQGLVWMGWISPNSGDTSYAQKFQDR VTMTRDTSISTAYMELSRLRSDDTAVYFCTREATI FGMLIVPFDYWGQGLVTVSS

A-2165-WO-PCT

!PS:361301	11C1.008	NA	SEQ ID NO: 102 GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAACAG AACCAAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 259 CAGGTGCCGCTGGTACAGTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGGTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCGTCAAGCCCTGGACAAAGG CTTGTGTGGATGGGTGGATCAGCCCTAACAGT GGTGACAAAGCTATGCACAGAAGTTTCAGGAC AGGTCACCATGACCAAGGACACGTCCATCAGC ACAGCTATATGAGCTGAGCAGACTGAGATCT GACGACACGGCCGTGATTTCTGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
			SEQ ID NO: 1673 DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRD SGVPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1830 QVPLVQSGAEVKKPGASVKVCKASGYTFTGYI HWVRQAPGQGLVWMGWISPNSGDTSYAQKFQDR VTMTRDTSISTAYMELSLRSDDTAVYFCAREATI FGMLIVPFDYWGQGTLVTVSS
!PS:359703	11C1.009	NA	SEQ ID NO: 103 GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAACAG AAACCAGGACAGCCTCCTAAACTGCTCATTTAC TGGACTTCTACCCGAGAAATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 260 CAGGTGCAGCTGGTACAGTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGGTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCGTCAAGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATCAGCCCTAACAGT GGTGAAACAAAGCTATGCACAGAAGTTTCAGGAC AGGTCACCATGACCAAGGACACGTCCATCAGC ACAGCTATATGAGCTGAGCAGCCTGAGATCT GACGACACGGCCGTGATTTCTGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
			SEQ ID NO: 1674 DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRD SGVPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1831 QVQLVQSGAEVKKPGASVKVCKASGYTFTGYI HWVRQAPGQGLEWMGWISPNSETSYAQKFQDR VTMTRDTSISTAYMELSLRSDDTAVYFCAREATI FGMLIVPFDYWGQGTLVTVSS

A-2165-WO-PCT

!PS:361305	11C1.010	SEQ ID NO: 104	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAACAG AACCAAGGACAGCTCTTAACCTGCTCATTTAC TGGACTTCTACCCGAGAAATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCAAGGTGG AATCAAAACGA	SEQ ID NO: 261	CAGGTGCAGCTGGTACAGTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGGTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGTGGTCAAGCCCTTGACAAAGG CTTGAGTGGATGGGTGGATCAGCCCTAACAGT GGTGAACAAAGCTATGCACAGAAGTTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGAGCTGAGCAGACTGAGATCT GACGACACGGCCGTGATTTCTGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
		SEQ ID NO: 1675	DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRESGVPDFRSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPTWTF GQGTKVEIKR	SEQ ID NO: 1832	QVQLVQSGAEVKKPGASVKVSKASGYTFTGYYI HWVRAPGQGLEWMGWISPNSETSYAQKFQDR VTMTRDTSISTA YMELSRLSRDDTA VYFCAREATI FGMLIVPFDYWGQGTLVTVSS
!PS:361312	13H12.002	SEQ ID NO: 105	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGCTCTGGGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACATAGCTTGGTACCAGCAG AAACCAGGACATCCTCCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGTCCCTGACC GATTCAGTGGCAGCGGTCTGGGACAGATTTC CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAAAGGACCAAGGTGGA AATCAAAACGA	SEQ ID NO: 262	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGGTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCGACAGGCCCTGGACAAAGGA CTTGAGTGGATGGGTGGATCAACCCGTGAAAGT GGTGGCACAGACTATTACAGAGGTTTCAGGGC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTACATGGAAGTGAAGAGGCTGAGATCT GACGACACGGCCGTGATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
		SEQ ID NO: 1676	DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGHPPKLLIYWASTRESGVPDFRSGS GSGTDFLTITSLQAEDVAVFYCQQYYSTPTWTFGQ GTKVEIKR	SEQ ID NO: 1833	QVPLVQSGAEVKKPGASVKVSKASGYTFTGYYI HWVRAPGQGLEWMGWINPESGGTDYSQRFQGR VTMTRDTSISTA YMELSRLSRDDTA VYYCAREATI FGMVIVPFDYWGQGTLVTVSS

A-2165-WO-PCT

	!PS:359744	13H12.003	NA	SEQ ID NO: 106 GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG AACCAAGGACATCCTCCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGTCCTGACC GATTCAGTGGCAGCGGCTCTGGGACAGATTCA CTCTACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAAAGGGACCAAGGTGGA AATCAAAACGA	SEQ ID NO: 263 CAGGTGCCGTGGTGCAAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCGACAGGCCCTGGACAAGGA CTTGAGTGGATGGGTGGATCAACCTGAAAGT GGTGGACAGACTATTCACAGAGGTTTCAGGGC AGGTTCAACCATGACCAAGGACACGTCCTCAGC ACAGCTACATGGAACCTGAGCAGGCTGAGATCT GACGACACGGCCGTGTTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
				SEQ ID NO: 1677 DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQKPGHPPKLLIYWASTRESGVPDFRFGS GSGTDFLTITSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR	SEQ ID NO: 1834 QVPLVQSGAEVKKPGASVKVCKASGYTFTGYI HWVRAPGQGLEWMGWINPESGGTDYSQRFQGR FTMTRDTSISTAYMELSRLLSDDTAVYYCAREATI FGMVIVPFDYWGQGLVTVSS
	!PS:361319	13H12.004	NA	SEQ ID NO: 107 GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG AAACCAGGACATCCTCCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGTCCTGACC GATTCAGTGGCAGCGGCTCTGGGACAGATTCA CTCTACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAAAGGGACCAAGGTGGA AATCAAAACGA	SEQ ID NO: 264 CAGGTGCCGTGGTGCAAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCGACAGGCCCTGGACAAGGA CTTGAGTGGATGGGTGGATCAACCTGACAGT GGTGGACAGACTATTCACAGAGGTTTCAGGGC AGGTTCAACCATGACCAAGGACACGTCCTCAGC ACAGCTACATGGAACCTGAGCAGGCTGAGATCT GACGACACGGCCGTGTTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
				SEQ ID NO: 1678 DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQKPGHPPKLLIYWASTRESGVPDFRFGS GSGTDFLTITSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR	SEQ ID NO: 1835 QVPLVQSGAEVKKPGASVKVCKASGYTFTGYI HWVRAPGQGLEWMGWINPDSGGTDYSQRFQGR VTMTRDTSISTAYMELSRLLSDDTAVYYCAREATI FGMVIVPFDYWGQGLVTVSS

A-2165-WO-PCT

	!PS:359737	13H12.005	NA	SEQ ID NO: 108 GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACATAGCTTGGTACCAAGCAG AACCAAGGACAACCTCCTAAGCTGCTCATTTAC TGGGCATCTACCCGGGAATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGCTCTGGACAGATTTC ACTCTACCATCAAGCAGCTGCGAGGCTGAAGAT GTGGCAGTTTTTTACTGTCAACAATATTATAGTA CTCCGTGGACGTTGGCCAAAGGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 265 CAGGTGCAGCTGGTGCAAGTCTGGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGGTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCGACAGGCCCTGGACAAGGA CTTGAGTGGATGGGTGGATCAACCTGAAAGT GGTGGACAGACTATTCACAGAGGTTTCAGGGC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTACATGGAACCTGAGCAGCCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
				SEQ ID NO: 1679 DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQKPGQPPKLLIYWASTRESGVPDFRFGS GSGTDFLTITSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR	SEQ ID NO: 1836 QVQLVQSGAEVKKPGASVKVSKASGYTFTGYYI HWVRAPGQGLEWMGWINPESGGTDYSQRFQGR VTMTRDTSISTA YMELSSLRSDDTAVYYCAREATI FGMVIVPFDYWGQGLVTVSS
	!PS:361326	13H12.006	NA	SEQ ID NO: 109 GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACATAGCTTGGTACCAAGCAG AACCAAGGACAACCTCCTAAGCTGCTCATTTAC TGGGCATCTACCCGGGAATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGCTCTGGACAGATTTC ACTCTACCATCAAGCAGCTGCGAGGCTGAAGAT GTGGCAGTTTTTTACTGTCAACAATATTATAGTA CTCCGTGGACGTTGGCCAAAGGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 266 CAGGTGCCGCTGGTGCAAGTCTGGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGGTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCGACAGGCCCTGGACAAGGA CTTGAGTGGATGGGTGGATCAACCTGAAAGT GGTGGACAGACTATTCACAGAGGTTTCAGGGC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTACATGGAACCTGAGCAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
				SEQ ID NO: 1680 DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQKPGQPPKLLIYWASTRESGVPDFRFGS GSGTDFLTITSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR	SEQ ID NO: 1837 QVPLVQSGAEVKKPGASVKVSKASGYTFTGYYI HWVRAPGQGLEWMGWINPESGGTDYSQRFQGR VTMTRDTSISTA YMELSSLRSDDTAVYYCAREATI FGMVIVPFDYWGQGLVTVSS

A-2165-WO-PCT

!PS:361330	12H11.002	NA	SEQ ID NO: 110 GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAGCAG AACCAAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAAGTGCGAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 267 CAGGTGCCGCTGGTGCAAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCGTCAGGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATAAGCCCTAACCAA GGTGAACAAACTATGCACAGAAATTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGAGCTGAGCAGGCTGAGATCT GACGACACGGCCGTGTTACTGTGCGGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
		AA	SEQ ID NO: 1681 DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRD SGVPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1838 QVPLVQSGAEVKKPGASVKVCKASGYTFTGYI HWVRAPGQGLEWMGWISPNQGETNYAQKFQD RVTMTDRDTSISTAYMELSLRSDDTAVYYCAREA TIFGMLIVPFDYWGQGLTVTVSS
!PS:361337	12H11.003	NA	SEQ ID NO: 111 GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAGCAG AAACCAAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAAGTGCGAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 268 CAGGTGCCGCTGGTGCAAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCGTCAGGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATAAGCCCTAACCAA GGTGAACAAACTATGCACAGAAATTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGAGCTGAGCAGGCTGAGATCT GACGACACGGCCGTGTTACTGTGCGGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
		AA	SEQ ID NO: 1682 DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRD SGVPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1839 QVPLVQSGAEVKKPGASVKVCKASGYTFTGYI HWVRAPGQGLEWMGWISPNQGETNYAQKFQD RVTMTDRDTSISTAYMELSLRSDDTAVYYCAREA TIFGMLIVPFDYWGQGLTVTVSS

A-2165-WO-PCT

!PS:361344	12H11.004	NA	SEQ ID NO: 112 GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAGCAG AACCAAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 269 CAGGTGCCGCTGGTGCAAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCGTCAGGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATAAGCCCTAACCAA GGTGAACAAACTATGCACAGAAGTTTCAGGAC AGGTCACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGAGCTGAGCAGGCTGAGATCT GACGACACGGCCGTGTTACTGTACGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
		AA	SEQ ID NO: 1683 DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRDSGVPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1840 QVPLVQSGAEVKKPGASVKVCKASGYTFTGYI HWVRAPGQGLEWMGWISPNQGETNYAQKFQD RVTMTDRDTSISTAYMELSLRSDDTAVYYCTREA TIFGMLIVPFDYWGQGLVTVSS
!PS:361351	12H11.005	NA	SEQ ID NO: 113 GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAGCAG AACCAAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 270 CAGGTGCCGCTGGTGCAAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCGTCAGGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATAAGCCCTAACCAAT GGTGAACAAACTATGCACAGAAGTTTCAGGAC AGGTCACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGAGCTGAGCAGGCTGAGATCT GACGACACGGCCGTGTTACTGTGCGGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
		AA	SEQ ID NO: 1684 DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRDSGVPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1841 QVPLVQSGAEVKKPGASVKVCKASGYTFTGYI HWVRAPGQGLEWMGWISPNQGETNYAQKFQD RVTMTDRDTSISTAYMELSLRSDDTAVYYCAREA TIFGMLIVPFDYWGQGLVTVSS

A-2165-WO-PCT

!PS:361358	12H11.006	NA	SEQ ID NO: 114 GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGCGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAAGAACTACTTAGCTTGGTACCAGCAG AAACCAGGACAGCTCCTAACTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAAGTGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTTCGGCCAAGGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 271 CAGGTGCCGCTGGTGCAAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCGTCAAGGCCCTGGACAAGGG CTTGAGTGGATGGGGTGGATAAGCCCTAACAAAT GGTGACACAAACTATGCACAGAAGTTTTCAGGAC AGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
		AA	SEQ ID NO: 1685 DIVMTQSPDLSVSLGERATINCKSSQSVLSSSNK NYLAWYQQKPGQPPNLLIYWTSRDSGVPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1842 QVPLVQSGAEVKPGASVKVSCKASGYTFTGYVI HWVRQAPGQGLEWMGWISPNNGDTNYAQKFQD RVMTTRDTSISTAYMELSLRSDDTAVYYCAREA TIFGMLIVPFDYWGQGLTVTVSS
!PS:361365	12H11.007	NA	SEQ ID NO: 115 GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGCGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAAGAACTACTTAGCTTGGTACCAGCAG AAACCAGGACAGCTCCTAACTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAAGTGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTTCGGCCAAGGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 272 CAGGTGCCGCTGGTGCAAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCGTCAAGGCCCTGGACAAGGG CTTGAGTGGATGGGGTGGATAAGCCCTAACCAA GGTGACACAAACTATGCACAGAAGTTTTCAGGAC AGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTACGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
		AA	SEQ ID NO: 1686 DIVMTQSPDLSVSLGERATINCKSSQSVLSSSNK NYLAWYQQKPGQPPNLLIYWTSRDSGVPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1843 QVPLVQSGAEVKPGASVKVSCKASGYTFTGYVI HWVRQAPGQGLEWMGWISPNQGDNTY AQKFQD RVMTTRDTSISTAYMELSLRSDDTAVYYCTREA TIFGMLIVPFDYWGQGLTVTVSS

A-2165-WO-PCT

!PS:361372	12H11.008	NA	SEQ ID NO: 116 GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCCTGGGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAGCAG AACCAAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGGCCAAGGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 116 CAGTGCCGCTGGTGCAAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCGTCAGGCCCTGGACAAGGG CTTGAGTGATGGGTGGATAGCCCTAACAAAT GGTGAACAAACTATGCACAGAAGTTTCAGGAC AGGTCACCATGACCAAGGACACGTCCATCAGC ACAGCTATATGAGCTGAGCAGGCTGAGATCT GACGACACGGCCGTGTTACTGTACGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA	SEQ ID NO: 273
		AA	SEQ ID NO: 1687 DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRD SGVPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1844 QVPLVQSGAEVKKPGASVKVSKASGYTFTGYI HWVRAPGQGLEWMGWISPNNGETNYAQKFQD RVTMTDRDTSISTAYMELSLRSDDTAVYYCTREA TIFGMLIVPFDYWGQGLVTVSS	SEQ ID NO: 274
!PS:361379	12H11.009	NA	SEQ ID NO: 117 GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCCTGGGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAGCAG AACCAAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGAAATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGGCCAAGGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 274 CAGTGCCGCTGGTGCAAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCGTCAGGCCCTGGACAAGGG CTTGAGTGATGGGTGGATAGCCCTAACCAA GGTGAACAAACTATGCACAGAAGTTTCAGGAC AGGTCACCATGACCAAGGACACGTCCATCAGC ACAGCTATATGAGCTGAGCAGGCTGAGATCT GACGACACGGCCGTGTTACTGTGCGGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA	SEQ ID NO: 274
		AA	SEQ ID NO: 1688 DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRD SGVPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1845 QVPLVQSGAEVKKPGASVKVSKASGYTFTGYI HWVRAPGQGLEWMGWISPNNGETNYAQKFQD RVTMTDRDTSISTAYMELSLRSDDTAVYYCAREA TIFGMLIVPFDYWGQGLVTVSS	SEQ ID NO: 1845

A-2165-WO-PCT

!PS:361383	12H11.010	SEQ ID NO: 118	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAGCAG AACCAAGGACAGCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGAAATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTGGCCAAAGGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 275	CAGGTGCCGTGGTGCAAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCGTCAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATAAGCCCTAACAAAT GGTGACACAAACTATGCACAGAAGTTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGAGCTGAGCAGGCTGAGATCT GACGACACGGCCGTGTTACTGTGCGGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
		SEQ ID NO: 1689	DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRESGVDPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1846	QVPLVQSGAEVKKPGASVKVSKASGYTFTGYI HWVRAPGQGLEWMGWISPNNGDNTYAQKFQD RVTMTDRDTSISTAYMELSLRSDDTAVYYCAREA TIFGMLIVPFDYWGQGLVTVSS
!PS:361387	12H11.011	SEQ ID NO: 119	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAGCAG AAACCAGGACAGCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGAAATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTGGCCAAAGGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 276	CAGGTGCCGTGGTGCAAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCGTCAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATAAGCCCTAACCAA GGTGACACAAACTATGCACAGAAGTTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGAGCTGAGCAGGCTGAGATCT GACGACACGGCCGTGTTACTGTGCGGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
		SEQ ID NO: 1690	DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRESGVDPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1847	QVPLVQSGAEVKKPGASVKVSKASGYTFTGYI HWVRAPGQGLEWMGWISPNNGDNTYAQKFQD RVTMTDRDTSISTAYMELSLRSDDTAVYYCAREA TIFGMLIVPFDYWGQGLVTVSS

A-2165-WO-PCT

!PS:361391	12H11.012	SEQ ID NO: 120	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAGCAG AACCAAGGACAGCTCTTAACCTGCTCATTTAC TGGACTTCTACCCGAGAAATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTGGCCAAAGGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 277	CAGGTGCCGCTGGTGCAAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCGTCAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATAAGCCCTAACAAAT GGTGAACAAACTATGCACAGAAGTTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGAGCTGAGCAGGCTGAGATCT GACGACACGGCCGTGTTACTGTGCGGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
		SEQ ID NO: 1691	DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRESGVDPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1848	QVPLVQSGAEVKKPGASVKVCKASGYTFTGYI HWVRAPGQGLEWMGWISPNNGETNYAQKFQD RVTMTDRDTSISTAYMELSLRSDDTAVYYCAREA TIFGMLIVPFDYWGQGLVTVSS
!PS:361395	12H11.013	SEQ ID NO: 121	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAGCAG AAACCAGGACAGCTCTCTAAACTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTGGCCAAAGGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 278	CAGGTGCAGCTGGTGCAAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCGTCAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATAAGCCCTAACCAA GGTGAACAAACTATGCACAGAAGTTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGAGCTGAGCAGCCTGAGATCT GACGACACGGCCGTGTTACTGTGCGGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
		SEQ ID NO: 1692	DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRDSGVDPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1849	QVQLVQSGAEVKKPGASVKVCKASGYTFTGYI HWVRAPGQGLEWMGWISPNNGETNYAQKFQD RVTMTDRDTSISTAYMELSLRSDDTAVYYCAREA TIFGMLIVPFDYWGQGLVTVSS

A-2165-WO-PCT

!PS:361402	12H11.014	NA	SEQ ID NO: 122 GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAGCAG AACCAAGGACAGCCTCCTAAACTGCTCATTTAC TGGACTTCTACCCGAGAAATCCGGGTCCTGAC CGATTCAAGTGGCAGCGGCTCTGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTGGCCAAAGGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 279 CAGGTGCAGCTGGTGCAAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCGTCAAGCCCCCTGGACAAGGG CTTGAGTGGATGGGTGGATAAGCCCTAACCAA GGTGAACAAACTATGCACAGAAGTTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGAGCTGAGCAGCCTGAGATCT GACGACACGGCCGTGTTACTGTGCGGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCGTCT CCTCA
		AA	SEQ ID NO: 1693 DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPKLLIYWTSRESGVPDFRSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1850 QVQLVQSGAEVKKPGASVKVSKASGYTFTGYYI HWVRAPGQGLEWMGWISPNQGETNYAQKFQD RVMTMTRDTSISTAYMELSLRSDDTAVYYCAREA TIFGMLIVPFEDYWGQGLVTVSS
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			SEQ ID NO: 1696 QSVLTQPPSASGTPGQRVTISCSGSSNIGSNYVNW YQHLPGTAPKLLIYTNNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDES LSGPVFGGGTK LTVLG	SEQ ID NO: 1853 QMQVVQSGAEVKKPGASVKVSKASGYTFTGY MHWVRQAPQGQLEWGMWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWVGQGTITVTVSS	

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	!PS:361436	2C2.005.006	NA	SEQ ID NO: 128 CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGGTCACCATCTCTTGT CTGGAAGTAGCTCCAACATCGGAAGTAATTATG TAACTGGTACAGCACCTCCAGGAACGGCCC CCAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATGACAGCTGAATGGTCCGGTAT TCGGCGGAGGACCAAGCTGACCGTCTCCTAGGT	SEQ ID NO: 1285 CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGTCTCCTGC AAGCTTCCGGATACACCTTCAACCGGCTACTAT ATGCATTGGTGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGCAACAATATGCACAGAAGTTTCAGGGC AGGGTCAACATGACCAAGGACACGTCCATCAGT ACAGCTACATGAGCTGAGCAGGCTGAGGTCT GACGACAGCGCGTGTATTACTGTGCGAGAGGG GGGATTACGTTTGGGGGACTTATCGGCCCTCAC TACTACTACGGTATGGACGTCTGGGGCCAAGGG ACCACGGTCACCGTCTCCTCA
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!PS:361448	2C2.005.008	NA	SEQ ID NO: 130 CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGTCACCATCTCTTGT CTGGAAGTAGCTCCAACATCGGAAGTAATACTG TAACTGGTACAGCACCTCCAGGAACGGCCC CCAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATGACAGCTGCAAGTCCGGTAT TCGGCGGAGGACCAAGCTGACCGTCTCCTAGGT	SEQ ID NO: 287 CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGTCTCCTGC AAGCTTCCGGATACACCTTCAACCGGCTACTAT ATGCATTGGTGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGGCAAACTATGCACAGAAGTTTCAGGGC AGGGTCAACATGACCAAGGACACGTCCATCAGT ACAGCTACATGAGCTGAGCAGGCTGAGGTCT GACGACAGCGCGTGTATTACTGTGCGAGAGGG GGGATTACGTTTGGGGGACTTATCGGCCCTCAC TACTACTACGGTATGGACGTCTGGGGCCAAGGG ACCACGGTCACCGTCTCCTCA
			SEQ ID NO: 1701 QSVLTQPPSASGTPGQRVTISCSGSSNIGSNTVNW YQHLPGTAPKLLIYTNNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDDSLQGPVFGGGTK LTVLG	SEQ ID NO: 1858 QMVVQSGAEVKKPGASVKVSKASGYTFTGY MHWVQAPQGQLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWVGQGTITVTVSS
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!PS:361466	2C2.005.011	NA	SEQ ID NO: 133 CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGGTCACCATCTCTTGT CTGGAAGTAGCTCCAACATCGGAAGTAATACTG TAACTGGTACAGCACCTCCAGGAACGGCCC CCAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATGACAGCCTGAATGCTCCGGTAT TCGGCGGAGGACCAAGCTGACCGTCTCTAGGT	SEQ ID NO: 290 CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGTCTCCTGC AAGCTTCCGGATACACCTTCAACCGGCTACTAT ATGCATTGGTGGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGGCAAACTATGCACAGAAGTTTCAGGGC AGGGTCAACATGACCAAGGACACGTCCATCAGT ACAGCTACATGAGCTGAGCAGGCTGAGGTCT GACGACAGCGCGTGTATTACTGTGCGAGAGGG GGGATTACGTTTGGGGGACTTATCGGCCCTCAC TACTACTACGGTATGGACGTCTGGGGCCAAGGG ACCACGGTCACCGTCTCCTCA
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	!PS:361472	2C2.005.012	NA	SEQ ID NO: 134 CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG GGACCCCGGGCAGAGGTCACCATCTCTTGT CTGGAAGTAGCTCCAACATCGGAAGTAATTATG TAACTGGTACAGCACCTCCAGGAACGGCCC CCAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATAGCAGCTGAATGCTCCGGTAT TCGGCGGAGGACCAAGCTGACCGTCTCTAGGT	SEQ ID NO: 134 CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGTCTCCTGC AAGCTTCCGGATACACCTTCAACCGGCTACTAT ATGCATTGGTGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGCAACAACATATGCACAGAAGTTTCAGGGC AGGTCAACCATGACCAAGGACACGTCCATCAGT ACAGCTACATGAGCTGAGCAGGCTGAGGTCT GACGACAGCGCGTGTATTACTGTGCGAGAGGG GGGATTACGTTTGGGGACTTATCGGCCCTCAC TACTACTACGGTATGGACGTCTGGGGCCAAGGG ACCACGGTCACCGTCTCCTCA	SEQ ID NO: 291
				SEQ ID NO: 1705 QSVLTQPPSASGTPGQRVTISCSGSSNIGSNYVNW YQHLPGTAPKLLIYTNNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDSSLNAPVFGGGTK LTVLG	SEQ ID NO: 1862 QMQVVQSGAEVKKPGASVKVSKASGYTFTGY MHWVRAQPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSLRSDDTAVYYCARG GDYVVGTYRPHYYYGMDVWVGQGTITVTVSS	SEQ ID NO: 1862
	!PS:361478	2C2.005.013	NA	SEQ ID NO: 135 CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG GGACCCCGGGCAGAGGTCACCATCTCTTGT CTGGAAGTAGCTCCAACATCGGAAGTAATTATG TAACTGGTACAGCACCTCCAGGAACGGCCC CCAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATAGCAGCTGAATGCTCCGGTAT TCGGCGGAGGACCAAGCTGACCGTCTCTAGGT	SEQ ID NO: 292 CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGTCTCCTGC AAGCTTCCGGATACACCTTCAACCGGCTACTAT ATGCATTGGTGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGCAACAACATATGCACAGAAGTTTCAGGGC AGGTCAACCATGACCAAGGACACGTCCATCAGT ACAGCTACATGAGCTGAGCAGCCTGAGGTCT GACGACAGCGCGTGTATTACTGTGCGAGAGGG GGGATTACGTTTCCGGACTTATCGGCCCTCACT ACTACTACGGTATGGACGTCTGGGGCCAAGGGA CCACGGTCACCGTCTCCTCA	SEQ ID NO: 292
				SEQ ID NO: 1706 QSVLTQPPSASGTPGQRVTISCSGSSNIGSNYVNW YQHLPGTAPKLLIYTNNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDSSLNAPVFGGGTK LTVLG	SEQ ID NO: 1863 QMQVVQSGAEVKKPGASVKVSKASGYTFTGY MHWVRAQPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSLRSDDTAVYYCARG GDYVVGTYRPHYYYGMDVWVGQGTITVTVSS	SEQ ID NO: 1863

A-2165-WO-PCT

!PS:361485	2C2.005.014	NA	SEQ ID NO: 136 CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG GGACCCCGGGCAGAGGTCACCATCTCTTGTT CTGGAAGTAGCTCCAACATCGGAAGTCAAACTG TAACTGGTACAGCACCTCCAGGAACGGCCC CCAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATGAAAGCCTGAGTGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCTCCTAGGT	SEQ ID NO: 293 CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGCTTCCGGATACACCTTCAACCGGCTACTAT ATGCATTGGTGGCAGACAGCCCCCTGGACAAGGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGGCAAACTATGCACAGAAGTTTCAGGGC AGGGTCAACCATGACCAAGGACACGTCCATCAGT ACAGCTACATGAGCTGAGCAGGCTGAGGTCT GACGACAGCGCGTGTATTACTGTGCGAGAGGG GGGATTACGTTTTCGGGACTTATCGGCCTCACT ACTACTACGGTATGGACGTCTGGGGCCAAAGGA CCACGGTCACCGTCTCCTCA
		AA	SEQ ID NO: 1707 QSVLTQPPSASGTPGQRVTISCSGSSNIGSQTVNW YQHLPGTAPKLLIYTNNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDESLSGPVFGGGTK LTVLG	SEQ ID NO: 1864 QMVVQSGAEVKKPGASVKVSKASGYTFTGYY MHWVRQAPQGQLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSLRSDDTAVYYCARG GDYVFGTYRPHYYYGMDVWVGQGTITVTVSS
!PS:361845	18F2.013	NA	SEQ ID NO: 137 GACATCCAGATGACCCAGTCTCCATCTCCTCCTGT CTGCATCTATAGGAGACAGAGTCAACCATCACTT GCCGGCAAGTCAGGACCTTAGAAATTAATTAG GCTGGTATCAACAGAAACCAGGAAAGCCCCCTA AGCGCTGATCTATGGTGCATCCAGTTTGCAA GTGGGTCCTTCAAGGTTCAAGCGGCAAGTGGAT CTGGGACAGAAATTCACCTCTCAACATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTAATTACTGTCT ACAGCATATAAATTACCCCTTCACTTTTCGGCCAA GGGACCAAAAGTGGATATCAAAACGA	SEQ ID NO: 294 CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCACTTTCAGTAACCTTTGGCA TGCAC'TGGTCCCGCCAGGCCCAAGGCGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCACAAACA CGCTGTATCTGCAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATA GGACGATCTTTGGAGTGTCTTTGGGGACTACT GGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA
		AA	SEQ ID NO: 1708 DIQMTQSPSSLSASIGDRVTITCRASQDLRNVLGW YQQKPGKAPKRLIYGASSLQSGVPSRFSGSGSTE FTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDI KR	SEQ ID NO: 1865 QVQLVESGGGVVQPGRSRLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVWYDASNENYADAVKG RFTISRDNKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLGDYWGQGTITVTSS

A-2165-WO-PCT

IP:361851	6H1.009	NA	SEQ ID NO: 138	SEQ ID NO: 295
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACCAGGAAAGCCCCA AGCGCTGATCTATGGTGCATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTACGCGGAGTGAT CTGGGACAGAAATCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGATATCAAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCACTTCACTTACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGG TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATAATACTATGCAGACGCCGTGAAGGGCC GCTTCAACATCTCCAGAGACAATTCAGAACA CGCTGATCTGCAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGATTACTGTGCGCGAGATA GGACGATTTTGGAGTGCCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCTCTCCTCA
IP:361855	2C2.005.015	NA	SEQ ID NO: 1709	SEQ ID NO: 1866
			DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLQSGVPSRFSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK R	QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIWDASNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLLGDYWGQGLVTSS
IP:361855	2C2.005.015	NA	SEQ ID NO: 139	SEQ ID NO: 296
			CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG GGACCCCGGGCAGAGGTCAACATCTCTTGT CTGGAAGTAGCTCCAAACATCGGAAGTAATACTG TAACTGGTACCAAGCAACTCCCAAGGAACGGCCC CCAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTCTGTG CAACATTCGATAGCAGCCTGAGTGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCTCCTAGGT	CAGATGCAGTGGTGCAGTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGCTTCCGGATACACCTTCAACCGGCTACTAT ATGCATTGGGTGCGACAGGCCCTGGACAAGGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGGCACAACTATGCACAGAAATTTCAGGGC AGGGTCAACATGACCAAGGACACGTCCATCAGT ACAGCTACATGAGCTGAGCAGGCTGAGGTCT GACGACACGGCGTGTATTACTGTGCGGAGAGGG GGGATTACGTTTGGGGGACTTATCGGCCCTCAC TACTACTACGATGGACGTCTGGGGCCCAAGGG ACCACGGTCAACCTCTCCTCA
AA		AA	SEQ ID NO: 1710	SEQ ID NO: 1867
			QSVLTQPPSASGTPGQRVTISCGSSSNGSNTVNW YQQLPGTAPKLLIYTNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDSSLGSPVFGGGTK LTVLG	QMQVVSQSAEVKKPGASVKVSKASGYTFTGYY MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFK GRVTMTTRDTSISTAYMELSLRSDDTAVYYCARG GDYVVGTYRPHYYYGMDVVGQGTITVTVSS

A-2165-WO-PCT

IP:336067	5G12.006	NA	SEQ ID NO: 140	SEQ ID NO: 297
			GACATCCAGCTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGGCAAGTCAGACCATTAGCAGGTTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCCCTG AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG TGGGGTCCCATCAAGATTCAGTGGCAGTGGTTC TGGGACAGATTTCACTCTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGATCAGTTTGGCCA GGGGACCAAGCTGGAGATCACACGA	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT ACAGGTCTGGATTCACTTCACTAGTATGGC ATACACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGGA AGTAATAAGTTCCATGCAGACTCCGTGAAGGGC CGATTCACCATCTCCAGAGACAAATCCAAAGA ACAGTGTATCTGCAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCCTGAAGCTTTTGAATC TGGGGCCAAAGGACAAAGGTCACCGTCTCTTCA
IP:336169	17B11.002	NA	SEQ ID NO: 1711	SEQ ID NO: 1868
			DIQLTQSPSSLASVGDRTVTITCRASQTISRFLNWIY QKPGKAPELLIYVASSLQSGVPSRFSGSGTDFT LTISLQPEDFATYYCQQSYSTLISFGQGTKLEITR	QVQLVESGGGVVQGRSLRLSCTASGFTFSYGIH WVRQAPGKGLEWVAIVWYDGSNKFHADSVKGRF TISRDNSKNTLYLQMNSLRAEDSAMFYFCARGKVA GMPEAFEIWQQGKVTIVSS
IP:336169	17B11.002	NA	SEQ ID NO: 141	SEQ ID NO: 298
			CAGTCTGTGTTGACGCGAGCCGCCCTCAGTGTCTG CGCCCCAGGACAGAAAGGTCAACATCTCCTGTCTG CTGGAAGCAGCTCCAAACAATTGGAAATAATTATG TATCCTGGTATGAGCAGTTCCCAAGGAACAGCCC CCAAACTCCTCATTTATGACATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTACGCCACCTGGGCATCACCGG ACTCCAGACTGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGTGTGGT ATTCCGGCGGAGGACCAAACTGACCGTCTCTAGG T	CAAATGCAGCTGGTGCACTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCAAGTTATGAT ATCAACTGGGTGCGACAGGCCACTGGACAAAGG CTTGAGTGGATGGATGGATGAACCTTACAGT GGTAAACACAGGCTATGCACAGAAAGTTCCAGGGC AGAGTCAACATGACCAAGGACACCTCCATAAGC ACAGCTACATGGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGTTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCAAAG GGACCACGGTCAACCGTCTCCTCA
IP:336169	17B11.002	AA	SEQ ID NO: 1712	SEQ ID NO: 1869
			QSVLTQPPSVSAAPGQKVTISCSGSSNIGNNYVS WYEQFPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTS ATLGITGLQTGDEADYYCGTWDSSLSAVVFGGTT KLTVLG	QMQLVQSGAEVKKPGASVKVSKKASGYTFTSYDI NWVRQATGQGLEWMGMWNPNSGNTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDTAVYYCARG GDYVWGSYRPYYYYGMDVWVGQGTITVTIVSS

A-2165-WO-PCT

!PS:361127	5G12.006.001	NA	SEQ ID NO: 142	SEQ ID NO: 299
			GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGCAAGTCAGACCATTAGCAGGTTTAA ATTGGATCAGCAGAAACCTGGAAAGCCCCCTG AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG TGGGGTCCCATCAAGATTCAAGTGGCAGTGGTTC TGGGACAGATTTCACTCTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGATCAGTTTGGCCA GGGGACCAAGCTGGAGATCAAAACGA	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTCACTAGTATGGC ATACACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAAATCCAAAGAAC ACGCTGTATCTGCAAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCCTGAAGCTTTTGAATC TGGGGCCAAAGGGACAAAGGTCACCGTCTCTTCA
!PS:361136	5G12.006.002	NA	SEQ ID NO: 143	SEQ ID NO: 300
			GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGCAAGTCAGACCATTAGCAGGTTTAA ATTGGATCAGCAGAAACCTGGAAAGCCCCCTG AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG TGGGGTCCCATCAAGATTCAAGTGGCAGTGGTTC TGGGACAGATTTCACTCTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGATCAGTTTGGCCA GGGGACCAAGCTGGAGATCAAAACGA	QVQLVESGGGVVQGRSLRLSCAASGFTFSSYGIH WVRQAPGKGLEWVAIVWYDASNKPHADAVKGR FTISRDNSKNTLYLQMNSLRAEDSAMFYFCARGKV AGMPEAFEIWGQGTKVTVSS
AA		AA	SEQ ID NO: 1713	SEQ ID NO: 1870
			DIQLTQSPSSLASVGDRTVTITCRASQTISRFLNWI QQKPGKAPPELLIYVASSLQSGVPSRFSGSGTDFT LTISLQPEDFATYYCQQSYSTLISFGQGTKLEIKR	QVQLVESGGGVVQGRSLRLSCAASGFTFSSYGIH WVRQAPGKGLEWVAIVWYDASNKPHADAVKGR FTISRDNSKNTLYLQMNSLRAEDSAMFYFCARGKV AGMPEAFEIWGQGTKVTVSS
AA		AA	SEQ ID NO: 1714	SEQ ID NO: 1871
			DIQLTQSPSSLASVGDRTVTITCRASQTISRFLNWI QQKPGKAPPELLIYVASSLQSGVPSRFSGSGTDFT LTISLQPEDFATYYCQQSYSTLISFGQGTKLEIKR	QVQLVESGGGVVQGRSLRLSCTASGFTFSSYGIH WVRQAPGKGLEWVAIVWYDASNKPHADAVKGR FTISRDNSKNTLYLQMNSLRAEDSAMFYFCARGKV AGMPEAFEIWGQGTKVTVSS

A-2165-WO-PCT

IP:361140	5G12.006.003	NA	SEQ ID NO: 144	SEQ ID NO: 301
			GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGCAAGTCAGACCATTAGCAGGTTTAA ATTGGATCAGCAGAAACCTGGAAAGCCCTG AGTCTGTATCTATGTTGCATCCAGTTTGCAAAG TGGGTCCCATCAAGATTCAGTGGCAGTGGTTC TGGGACAGATTTCACTCTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGATCAGTTTGGCCA GGGGACCAAGCTGGAGATCACACGA	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACCTTCAGTAGCTATGGC ATACACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAAATTCCAAAGAAC ACGCTGTATCTGCAAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCGTGAAGCTTTTGAATC TGGGGCCAAAGGGACAAAGGTCACCGTCTCTTCA
IP:359919	5G12.006.004	NA	SEQ ID NO: 145	SEQ ID NO: 302
			GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGCAAGTCAGACCATTAGCAGGTTTAA ATTGGATCAGCAGAAACCTGGAAAGCCCTA AGTCTGTATCTATGTTGCATCCAGTTTGCAAAG TGGGTCCCATCAAGATTCAGTGGCAGTGGTTC TGGGACAGATTTCACTCTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGATCAGTTTGGCCA GGGGACCAAGCTGGAGATCAACGA	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACCTTCAGTAGCTATGGC ATACACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAAATTCCAAAGAAC ACGCTGTATCTGCAAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCGTGAAGCTTTTGAATC TGGGGCCAAAGGGACAAAGGTCACCGTCTCTTCA
IP:359919	5G12.006.004	AA	SEQ ID NO: 1715	SEQ ID NO: 1872
			DIQLTQSPSSLASVGDRTVTITCRASQTISRFLNWX QQKPGKAPELLIYVASSLQSGVPSRFSGSGTDFT LTISSLQPEDFATYYCQQSYSTLISFGQGTGLEITR	QVQLVESGGGVVQPRSLRLSCAASGFTFSYGIH WVRQAPGKGLEWVAIVWYDASNKPHADAVKGR FTISRDNSKNTLYLQMNSLRAEDSAMFYFCARGKV AGMPEAFEIWGQGTKVTVSS
IP:359919	5G12.006.004	AA	SEQ ID NO: 1716	SEQ ID NO: 1873
			DIQLTQSPSSLASVGDRTVTITCRASQTISRFLNWX QQKPGKAPKLLIYVASSLQSGVPSRFSGSGTDFT LTISSLQPEDFATYYCQQSYSTLISFGQGTGLEIKR	QVQLVESGGGVVQPRSLRLSCAASGFTFSYGIH WVRQAPGKGLEWVAIVWYDASNKPHADAVKGR FTISRDNSKNTLYLQMNSLRAEDSAMFYFCARGKV AGMPEAFEIWGQGTKVTVSS

A-2165-WO-PCT

	IP:361144	5G12.006.005	NA	SEQ ID NO: 146	SEQ ID NO: 303
				GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGCAAGTCAGACCATTAGCAGGTTTAA ATTGGATCAGCAGAAACCTGGGAAAGCCCCCTG AGTCTGTATCTATGTTGCATCCAGTTTGCAAAG TGGGTCCCATCAAGATTCAAGTGGCAGTGGTTC TGGGACAGATTTCACTCTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGATCAGTTTGGCCA GGGGACCAAGCTGGAGATCAAAACGA	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTCACTAGTATGGC ATACACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAGTTCCATGCAGACTCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAAATCCAAAGAAC ACGCTGTATCTGCAAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCGTGAAGCTTTTGAAATC TGGGGCCAAAGGACAAAGGTCACCGTCTCTTCA
	AA			SEQ ID NO: 1717	SEQ ID NO: 1874
				DIQLTQSPSSLASVGDRTVTITCRASQTISRFLNWX QQKPGKAPPELLIYVASSLQSGVPSRFSGSGTDFT LTISSLQPEDFATYYCQQSYSTLISFGQGTGLEIKR	QVQLVESGGGVVQPGRSRLRLSCAASGFTFSYGIH WVRQAPGKGLEWVAIVWYDASNKFHADS VKGRF TISRDN SKNTLYLQMNSLRAEDSAM YFCARGKVA GMPEAF EIWGGQTKVTVSS
	IP:361151	5G12.006.006	NA	SEQ ID NO: 147	SEQ ID NO: 304
				GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGCAAGTCAGACCATTAGCAGGTTTAA ATTGGATCAGCAGAAACCTGGGAAAGCCCCCTG AGTCTGTATCTATGTTGCATCCAGTTTGCAAAG TGGGTCCCATCAAGATTCAAGTGGCAGTGGTTC TGGGACAGATTTCACTCTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGATCAGTTTGGCCA GGGGACCAAGCTGGAGATCAAAACGA	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTCACTAGTATGGC ATACACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAAGTGGTGGCAGTTATATGGTATGATGGA AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAAATCCAAAGAAC ACGCTGTATCTGCAAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCGTGAAGCTTTTGAAATC TGGGGCCAAAGGACAAAGGTCACCGTCTCTTCA
	AA			SEQ ID NO: 1718	SEQ ID NO: 1875
				DIQLTQSPSSLASVGDRTVTITCRASQTISRFLNWX QQKPGKAPPELLIYVASSLQSGVPSRFSGSGTDFT LTISSLQPEDFATYYCQQSYSTLISFGQGTGLEIKR	QVQLVESGGGVVQPGRSRLRLSCAASGFTFSYGIH WVRQAPGKGLEWVAIVWYDGSNKFHADA VKGR FTISRDN SKNTLYLQMNSLRAEDSAM YFCARGKV AGMPEAF EIWGGQTKVTVSS

A-2165-WO-PCT

!PS:361491	17B11.002.001	NA	SEQ ID NO: 148	SEQ ID NO: 305
			CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG CGCCCCAGGACAGAAAGGTACCATCTCCTGCT CTGGAAGCAGCTCCAAACATTGGAATAATTATG TATCCTGGTATCAGCAGCTCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTACGCCACCCCTGGGCATCACCG ACTCCAGACTGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGTGTGGT ATTCGGCGGAGGACCAAACTGACCGTCTCTAGG T	CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCAGTTATGAT ATCAACTGGGTGCGACAGGCCACTGGACAAGG CTTGAGTGGATGGATGGATGAACCTAACAGT GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCAACCATGACAGGGACACCTCCATAAGC ACAGCTACATGGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGATTACTGTGCGAGAGGG GGTGATTACGTTGGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCAAG GGACCACGGTCACCGTCTCCTCA
AA			SEQ ID NO: 1719	SEQ ID NO: 1876
			QSVLTQPPSVSAAPGQKVTISCSGSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLGITGLQTGDEADYYCGTWDSSLSAVVFGGG TKLTVLG	QMQLVQSGAEVKKPGASVKVSKASGYTFTSYDI NWVRQATGQGLEWMGMWNPNSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDTAVYYCARG GDYVWGSYRPPYYYYGMDVWVGQGTITVTVSS
!PS:361499	17B11.002.002	NA	SEQ ID NO: 149	SEQ ID NO: 306
			CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG CGCCCCAGGACAGAAAGGTACCATCTCCTGCT CTGGAAGCAGCTCCAAACATTGGAATAATTATG TATCCTGGTATCAGCAGCTCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTACGCCACCCCTGGGCATCACCG ACTCCAGACTGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGTGTGGT ATTCGGCGGAGGACCAAACTGACCGTCTCTAGG T	CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCAGTTATGAT ATCAACTGGGTGCGACAGGCCACTGGACAAGG CTTGAGTGGATGGATGGATGAACCTAACAGT GGTAACACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCAACCATGACAGGGACACCTCCATAAGC ACAGCTACATGGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGATTACTGTGCGAGAGGG GGTGATTACGTTGGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCAAG GGACCACGGTCACCGTCTCCTCA
AA			SEQ ID NO: 1720	SEQ ID NO: 1877
			QSVLTQPPSVSAAPGQKVTISCSGSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLGITGLQTGDEADYYCGTWDSSLSAVVFGGG TKLTVLG	QMQLVQSGAEVKKPGASVKVSKASGYTFTSYDI NWVRQATGQGLEWMGMWNPNSGNTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDTAVYYCARG GDYVWGSYRPPYYYYGMDVWVGQGTITVTVSS

A-2165-WO-PCT

	!PS:361503	17B11.002.003	NA	SEQ ID NO: 150 CAGTCTGTGTTGACGCGAGCGCCCTCAGTGTCTG CGCCCCAGGACAGAAAGGTACCATCTCCTGCT CTGGAAGCAGCTCCAAACATTGGAATAATTATG TATCCTGGTATGAGCAGTTCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCAGTCAGCCACCTGGGCATCACCGG ACTCCAGACTGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGTGTGGT ATTCGGCGGAGGACCAAACTGACCCGTCTAGG T	SEQ ID NO: 307 CAAATGCAGCTGGTGCAAGTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAAGTTATGAT ATCAACTGGGTGCGACAGGCCACTGGACAAAGG CTTGAGTGGATGGATGGATGAACCCTAACAGT GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCAACCATGACCAAGGACACCTCCATAAGC ACAGCTACATGAGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGTTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCCAAG GGACCACGGTCACCGTCTCCTCA
				SEQ ID NO: 1721 QSVLTQPPSVSAAPGQKVTISCSGSSNIGNNYVS WYEQPFGTAPKLLIYDNNKRPSGIPDRFSGSKSGTS ATLGTGLQTGDEADYYCGTWDSSLSAVVFGGGT KLTVLG	SEQ ID NO: 1878 QMQLVQSGAEVKKPGASVKVSKKASGYTFTSYDI NWVRQATGQGLEWMGMWNPNSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDDTAVYYCARG GDYVWGSYRPYYYYGMDVWVGQGTITVTVSS
	!PS:361507	17B11.002.004	NA	SEQ ID NO: 151 CAGTCTGTGTTGACGCGAGCGCCCTCAGTGTCTG CGCCCCAGGACAGAAAGGTACCATCTCCTGCT CTGGAAGCAGCTCCAAACATTGGAATAATTATG TATCCTGGTATCAGCAGCTCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCAGTCAGCCACCTGGCCATCACCGG ACTCCAGACTGGGACGAGGCCGATTATTACTG CGGAACATTCGAAAGCAGCCTGAGTGTGTGGT ATTCGGCGGAGGACCAAACTGACCCGTCTAGG T	SEQ ID NO: 308 CAAATGCAGCTGGTGCAAGTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAAGTTATGAT ATCAACTGGGTGCGACAGGCCCTGGACAAAGG CTTGAGTGGATGGATGGATGAACCCTAACAGT GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCAACCATGACCAAGGACACCTCCATAAGC ACAGCTACATGAGAGCTGAGCAGCCTGAGATCT GACGACACGGCCGTGTTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCCAAG GGACCACGGTCACCGTCTCCTCA
				SEQ ID NO: 1722 QSVLTQPPSVSAAPGQKVTISCSGSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLAITGLQTGDEADYYCGTFESSLSAVVFGGGT KLTVLG	SEQ ID NO: 1879 QMQLVQSGAEVKKPGASVKVSKKASGYTFTSYDI NWVRQAPGQGLEWMGMWNPNSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDDTAVYYCARG GDYVWGSYRPYYYYGMDVWVGQGTITVTVSS

A-2165-WO-PCT

	!PS:361514	17B11.002.005	NA	SEQ ID NO: 152 CAGTCTGTGTTGACGCGAGCGCCCTCAGTGTCTG CGCCCCAGGACAGAAAGGTACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAATAATTATG TATCCTGGTATCAGCAGCTCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCAGTCAGCCACCTGGCCATCACCGG ACTCCAGACTGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGTGTGGT ATTCGGCGGAGGACCAAACTGACCGTCTCTAGG T	SEQ ID NO: 159 CAAATGCAGCTGGTGCAAGTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCAGTTATGAT ATCAACTGGGTGCGACAGGCCACTGGACAAAGG CTTGAGTGGATGGATGGATGAACCTAACAGT GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCAACATGACCAAGGACACCTCCATAAGC ACAGCTACATGGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGTTACTGTGCGAGAGGG GGTGATTACGTTTGGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGCTCTGGGGCCAAG GGACCACGGTCAACCGTCTCCTCA
				SEQ ID NO: 1723 QSVLTQPPSVSAAPGQKVITISCGSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLAITGLQTGDEADYYCGTWDSSLSAVVFGGG TKLTVLG	SEQ ID NO: 1880 QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQATGQGLEWMGWMNPNSSGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDTAVYYCARG GDYVWGSYRPYYYYGMDVWVGQGTITVTVSS
	!PS:360582	17B11.002.006	NA	SEQ ID NO: 153 CAGTCTGTGTTGACGCGAGCGCCCTCAGTGTCTG CGCCCCAGGACAGAAAGGTACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAATAATTATG TATCCTGGTATCAGCAGCTCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCAGTCAGCCACCTGGCCATCACCGG ACTCCAGACTGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGTGTGGT ATTCGGCGGAGGACCAAACTGACCGTCTCTAGG T	SEQ ID NO: 310 CAAATGCAGCTGGTGCAAGTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCAGTTATGAT ATCAACTGGGTGCGACAGGCCCTGGACAAAGG CTTGAGTGGATGGATGGATGAACCTAACAGT GGTAAACACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCAACATGACCAAGGACACCTCCATAAGC ACAGCTACATGGAGCTGAGCAGCCTGAGATCT GACGACACGGCCGTGTTACTGTGCGAGAGGG GGTGATTACGTTTGGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGCTCTGGGGCCAAG GGACCACGGTCAACCGTCTCCTCA
				SEQ ID NO: 1724 QSVLTQPPSVSAAPGQKVITISCGSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLAITGLQTGDEADYYCGTWDSSLSAVVFGGG TKLTVLG	SEQ ID NO: 1881 QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQAPGQGLEWMGWMNPNSSGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDTAVYYCARG GDYVWGSYRPYYYYGMDVWVGQGTITVTVSS

A-2165-WO-PCT

	!PS:361518	17B11.002.007	NA	SEQ ID NO: 154 CAGTCTGTGTTGACGCAGCGCCCTCAGTGTCTG CGCCCCAGGACAGAAAGGTACCATCTCCTGCT CTGGAAGCAGCTCCAAACATTGGAATAATTATG TATCCTGGTATCAGCAGCTCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCAGTCAGCCACCTGGGCATCACCGG ACTCCAGACTGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGTGTGGT ATTCGGCGGAGGACCAAACTGACCGTCTCTAGG T	SEQ ID NO: 151 CAAATGCAGCTGGTGCAAGTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAAGTTATGAT ATCAACTGGGTGCGACAGGCCACTGGACAAAGG CTTGAGTGGATGGATGGATGAACCCCTAACAGT GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCAACATGACCAAGGACACCTCCATAAGC ACAGCTACATGGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGATTACTGTGCGAGAGGG GGTGATTACGTTTTCGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCCAAG GGACCACGGTCAACCGTCTCCTCA
				SEQ ID NO: 1725 QSVLTQPPSVSAAPGQKVITISCGSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLGTGLQTGDEADYYCGTWDSSL SAVVFGGG TKLTVLG	SEQ ID NO: 1882 QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQATGQGLEWMGMWNPNSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDTAVYYCARG GDYVFGSYRPPYYYYGMDVWGQGTITVTVSS
	!PS:360570	17B11.002.008	NA	SEQ ID NO: 155 CAGTCTGTGTTGACGCAGCGCCCTCAGTGTCTG CGCCCCAGGACAGAAAGGTACCATCTCCTGCT CTGGAAGCAGCTCCAAACATTGGAATAATTATG TATCCTGGTATCAGCAGCTCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCAGTCAGCCACCTGGCCATCACCGG ACTCCAGACTGGGACGAGGCCGATTATTACTG CGGAACATTCGAAAGCAGCCTGAGTGTGTGGT ATTCGGCGGAGGACCAAACTGACCGTCTCTAGG T	SEQ ID NO: 152 CAAATGCAGCTGGTGCAAGTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAAGTTATGAT ATCAACTGGGTGCGACAGGCCCTGGACAAAGG CTTGAGTGGATGGATGGATGAACCCCTAACAGT GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCAACATGACCAAGGACACCTCCATAAGC ACAGCTACATGGAGCTGAGCAGCCTGAGATCT GACGACACGGCCGTGATTACTGTGCGAGAGGG GGTGATTACGTTTTCGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCCAAG GGACCACGGTCAACCGTCTCCTCA
				SEQ ID NO: 1726 QSVLTQPPSVSAAPGQKVITISCGSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLGTGLQTGDEADYYCGTFESSLSAVVFGGGT KLTVLG	SEQ ID NO: 1883 QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQAPGQGLEWMGMWNPNSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDTAVYYCARG GDYVFGSYRPPYYYYGMDVWGQGTITVTVSS

A-2165-WO-PCT

		SEQ ID NO: 156	SEQ ID NO: 313
!PS:362051	5G12.005.001	NA	CAGTGCAAGTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTCCAGTACGTATGGC ATACACTGGTCCGCCAGGCTCCAGCAAGGGG CTGAGTGGTGGCAGTTATATGATGATGCA AGTAATAGTTCCATGCAGACGCCGTGAAGGC CGATTCAACCATCTCCAGAGACAATTCACAAGAC ACGCTGTATCTGCAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCAGGCTTTTGAATC TGGGGCCAAAGGACATTGGTCACCGTCTCTTCA
			SEQ ID NO: 1884
!PS:362051	5G12.005.001	AA	QVQLVESGGGVQPGRLSLRSLSCAASGFTSSYGIH WVRQAPGKGLEWVAIVYDASNKPHADAVKGR FTISRDNSKNTLYLQMNSLRRAEDSAMYPFCARGKV AGMPEAFEIWGGQTLVTVSS
			SEQ ID NO: 314

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

IPS#	Ab	Type	CDRL1	CDRL2	CDRL3
!PS:336175	2C2.005	NA	TCTGGAAGTAGCTCCCAACATCG GAAGTAATACTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGACAGCCTG AATGGTCCGTA
			SEQ ID NO: 2199	SEQ ID NO: 2356	SEQ ID NO: 2513
		AA	SGSSNIGSNTVN	TNNQRPS	ATFDDSLNGPV
!PS:335914	4B1	NA	SEQ ID NO: 629	SEQ ID NO: 786	SEQ ID NO: 943
			CGGGCAAGTCAGGACATTAGAG ATTATTAGGC	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATATAATTACCCCT TCACT
		AA	SEQ ID NO: 2200	SEQ ID NO: 2357	SEQ ID NO: 2514
			RASQDIRDYL	GASSLQS	LQHNNYPFT
			SEQ ID NO: 630	SEQ ID NO: 787	SEQ ID NO: 944

A-2165-WO-PCT

!PS:335938	6H1	NA	CGGGCAAGTCAGGACATTAGAG ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2201 RASQDIRDYL SEQ ID NO: 631	SEQ ID NO: 2358 GASSLQS SEQ ID NO: 788	SEQ ID NO: 2515 LQHNNYPFT SEQ ID NO: 945
		NA	CAGCGAGTCAGGACATTAGCA ACTATTTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCCTCTCA CT
!PS:335941	2F11	AA	SEQ ID NO: 2202 QASQDISNYLN SEQ ID NO: 632	SEQ ID NO: 2359 DASNLET SEQ ID NO: 789	SEQ ID NO: 2516 QQYDILLT SEQ ID NO: 946
		NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
		AA	SEQ ID NO: 2203 KSSQSVLSSNNKNYIA SEQ ID NO: 633	SEQ ID NO: 2360 WASTRES SEQ ID NO: 790	SEQ ID NO: 2517 QQYYSTPWT SEQ ID NO: 947
!PS:335978	13H12	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
		AA	SEQ ID NO: 2204 KSSQSVLSSNNKNYIA SEQ ID NO: 634	SEQ ID NO: 2361 WASTRES SEQ ID NO: 791	SEQ ID NO: 2518 QQYYSTPWT SEQ ID NO: 948
		NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC	CAGCAATATTATCGTACTCCGT GGACG
!PS:335986	11C1	AA	SEQ ID NO: 2205 KSSQSVLSSNNKNYLA SEQ ID NO: 635	SEQ ID NO: 2362 WTSTRDS SEQ ID NO: 792	SEQ ID NO: 2519 QQYVRTPWT SEQ ID NO: 949
		NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC	CAGCAATATTATCGTACTCCGT GGACG
		NA	SEQ ID NO: 2206	SEQ ID NO: 2363	SEQ ID NO: 2520

A-2165-WO-PCT

		AA	KSSQSVLSSNNKNLYLA SEQ ID NO: 636	WTSTRDS SEQ ID NO: 793	QQYYRTPWWT SEQ ID NO: 950
!PS:336024	18E3	NA	AGGGCCAGTCAGAGTATTAGTT ACAGTTACTTAGCC	GGTGCATCCAGCAGGGGCCACT	CAGCAGTATGGTAGTTACCCGC TCACT
		AA	SEQ ID NO: 2207 RASQISYSYLA	SEQ ID NO: 2364 GASSRAT	SEQ ID NO: 2521 QQYGSSPLT
!PS:336041	2G10_LC1	NA	SEQ ID NO: 637 AGGGCCAGTCAGAGTGTTAGCA GCAACTTAGCC	SEQ ID NO: 794 GGTGCAGCCACCAGGGGCCACT	SEQ ID NO: 951 CAGCAGTATAATAACTGGCCTC TCACT
		AA	SEQ ID NO: 2208 RASQSVSSNLA	SEQ ID NO: 2365 GAATRAT	SEQ ID NO: 2522 QQYNNWPLT
!PS:336077	4H9.004	NA	SEQ ID NO: 638 CGGGCAAGTCAGGGCATTAGAA ATGAGTTAGGC	SEQ ID NO: 795 GGTGCATCCAGTTTGCAAAAGT	SEQ ID NO: 952 CTACAGCATAATAGTTACCCAT TCACT
		AA	SEQ ID NO: 2209 RASQGRNELG	SEQ ID NO: 2366 GASSLQS	SEQ ID NO: 2523 LQHNSYPFT
!PS:336088	6A5.004	NA	SEQ ID NO: 639 CAGGCGAGTCAGGACATTACCA ACTATTAAAT	SEQ ID NO: 796 GATGCTTCCAATTTGGAGCCA	SEQ ID NO: 953 CAACAGTATGATGATCTATTCA CT
		AA	SEQ ID NO: 2210 QASQDITNYLN	SEQ ID NO: 2367 DASNLEP	SEQ ID NO: 2524 QQYDDLFT
!PS:336099	17H11.004	NA	SEQ ID NO: 640 CGGGCGAGTCAGGGTCTTATCA TCTGGTTAGCC	SEQ ID NO: 797 GCTGCATCCAGTTTGCAAAAGT	SEQ ID NO: 954 CAACAGACTAACAGTTTCCCTC CGACG
		AA	SEQ ID NO: 2211 RASQGLIWL	SEQ ID NO: 2368 AASSLQS	SEQ ID NO: 2525 QQTNSFPPT
			SEQ ID NO: 641	SEQ ID NO: 798	SEQ ID NO: 955

A-2165-WO-PCT

!PS:359621	17H11.004.00	NA	CGGGCAGTCAGGGTCTTATCA TCTGGTTAGCC	GCTGCATCCAGTTTGCAAAAGT	CAACAGACTAACAGTTTCCCTC CGACG
		AA	SEQ ID NO: 2212 RASQGLIWL SEQ ID NO: 642	SEQ ID NO: 2369 AASSLQS SEQ ID NO: 799	SEQ ID NO: 2526 QQTNSFPPT SEQ ID NO: 956
		NA	CGGGCAAGTCAGGGCATTAGAA ATGAGTTAGGC	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATAATAGTTACCCAT TCACT
!PS:359781	4H9.004.001	AA	SEQ ID NO: 2213 RASQGIRNELG SEQ ID NO: 643	SEQ ID NO: 2370 GASSLQS SEQ ID NO: 800	SEQ ID NO: 2527 LQHNSYPFT SEQ ID NO: 957
		NA	CGGGCAAGTCAGGGCATTAGAA ATGAGTTAGGC	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATAATAGTTACCCAT TCACT
		AA	SEQ ID NO: 2214 RASQGIRNELG SEQ ID NO: 644	SEQ ID NO: 2371 GASSLQS SEQ ID NO: 801	SEQ ID NO: 2528 LQHNSYPFT SEQ ID NO: 958
!PS:360936	4H9.004.003	NA	CGGGCAAGTCAGGGCATTAGAA ATGAGTTAGGC	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATAATAGTTACCCAT TCACT
		AA	SEQ ID NO: 2215 RASQGIRNELG SEQ ID NO: 645	SEQ ID NO: 2372 GASSLQS SEQ ID NO: 802	SEQ ID NO: 2529 LQHNSYPFT SEQ ID NO: 959
		NA	CGGGCAAGTCAGGGCATTAGAA ATGAGTTAGGC	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATAATAGTTACCCAT TCACT
!PS:360943	4H9.004.004	AA	SEQ ID NO: 2216 RASQGIRNELG SEQ ID NO: 646	SEQ ID NO: 2373 GASSLQS SEQ ID NO: 803	SEQ ID NO: 2530 LQHNSYPFT SEQ ID NO: 960
		NA	CGGGCAAGTCAGGGCATTAGAA ATGAGTTAGGC	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATAATAGTTACCCAT TCACT
		AA	SEQ ID NO: 2217 RASQGIRNELG SEQ ID NO: 647	SEQ ID NO: 2374 GASSLQS SEQ ID NO: 804	SEQ ID NO: 2531 LQHNSYPFT SEQ ID NO: 961

A-2165-WO-PCT

!PS:359761	4B1.004.006	NA	CGGGCAAGTCAGGCATTAGAA ATGAGTTAGGC	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATAATAGTTACCCCAT TCACT
		AA	SEQ ID NO: 2218 RASQDIRDLG	SEQ ID NO: 2375 GASSLQS	SEQ ID NO: 2532 LQHNNYPFT
		AA	SEQ ID NO: 648	SEQ ID NO: 805	SEQ ID NO: 962
!PS:360955	4B1.010	NA	CGGGCAAGTCAGGCATTAGAG ATTATTAGGC	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2219 RASQDIRDLG	SEQ ID NO: 2376 GASSLQS	SEQ ID NO: 2533 LQHNNYPFT
		AA	SEQ ID NO: 649	SEQ ID NO: 806	SEQ ID NO: 963
!PS:360962	4B1.011	NA	CGGGCAAGTCAGGCATTAGAG ATTATTAGGC	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2220 RASQDIRDLG	SEQ ID NO: 2377 GASSLQS	SEQ ID NO: 2534 LQHNNYPFT
		AA	SEQ ID NO: 650	SEQ ID NO: 807	SEQ ID NO: 964
!PS:360968	4B1.012	NA	CGGGCAAGTCAGGCATTAGAG ATTATTAGGC	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2221 RASQDIRDLG	SEQ ID NO: 2378 GASSLQS	SEQ ID NO: 2535 LQHNNYPFT
		AA	SEQ ID NO: 651	SEQ ID NO: 808	SEQ ID NO: 965
!PS:360974	4B1.013	NA	CGGGCAAGTCAGGCATTAGAG ATTATTAGGC	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2222 RASQDIRDLG	SEQ ID NO: 2379 GASSLQS	SEQ ID NO: 2536 LQHNNYPFT
		AA	SEQ ID NO: 652	SEQ ID NO: 809	SEQ ID NO: 966
!PS:360978	4B1.014	NA	CGGGCAAGTCAGGCATTAGAG ATTATTAGGC	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2223 RASQDIRDLG	SEQ ID NO: 2380 GASSLQS	SEQ ID NO: 2537 LQHNNYPFT
		AA	SEQ ID NO: 653	SEQ ID NO: 810	SEQ ID NO: 967

A-2165-WO-PCT

!PS:359785	4B1.015	NA	CGGGCAAGTCAGGACATTAGAG ATTATTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2224 RASQDIRDYL SEQ ID NO: 654	SEQ ID NO: 2381 GASSLQS SEQ ID NO: 811	SEQ ID NO: 2538 LQHNNYPFT SEQ ID NO: 968
		NA	CGGGCAAGTCAGGACATTAGAG ATTATTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
!PS:360982	4B1.016	AA	SEQ ID NO: 2225 RASQDIRDYL SEQ ID NO: 655	SEQ ID NO: 2382 GASSLQS SEQ ID NO: 812	SEQ ID NO: 2539 LQHNNYPFT SEQ ID NO: 969
		NA	CGGGCAAGTCAGGACCTTAGAA ATTATTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2226 RASQDLRNYLG SEQ ID NO: 656	SEQ ID NO: 2383 GASSLQS SEQ ID NO: 813	SEQ ID NO: 2540 LQHNNYPFT SEQ ID NO: 970
!PS:360986	18F2.002	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2227 RASQDLRNYLG SEQ ID NO: 657	SEQ ID NO: 2384 GASSLQS SEQ ID NO: 814	SEQ ID NO: 2541 LQHNNYPFT SEQ ID NO: 971
		NA	CGGGCAAGTCAGGACCTTAGAA ATTATTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
!PS:360995	18F2.003	AA	SEQ ID NO: 2228 RASQDLRNYLG SEQ ID NO: 658	SEQ ID NO: 2385 GASSLQS SEQ ID NO: 815	SEQ ID NO: 2542 LQHNNYPFT SEQ ID NO: 972
		NA	CGGGCAAGTCAGGACCTTAGAA ATTATTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2229 RASQDLRNYLG SEQ ID NO: 659	SEQ ID NO: 2386 GASSLQS SEQ ID NO: 816	SEQ ID NO: 2543 LQHNNYPFT SEQ ID NO: 973

A-2165-WO-PCT

!PS:361005	18F2.005	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2230	SEQ ID NO: 2387	SEQ ID NO: 2544
			RASQDLRNYLG	GASSLQS	LQHNNYPFT
!PS:361009	18F2.006	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2231	SEQ ID NO: 2388	SEQ ID NO: 2545
			RASQDLRNYLG	GASSLQS	LQHNNYPFT
!PS:361013	18F2.007	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2232	SEQ ID NO: 2389	SEQ ID NO: 2546
			RASQDLRNYLG	GASSLQS	LQHNNYPFT
!PS:361017	18F2.008	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2233	SEQ ID NO: 2390	SEQ ID NO: 2547
			RASQDLRNYLG	GASSLQS	LQHNNYPFT
!PS:361021	18F2.009	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2234	SEQ ID NO: 2391	SEQ ID NO: 2548
			RASQDLRNYLG	GASSLQS	LQHNNYPFT
!PS:361028	18F2.010	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2235	SEQ ID NO: 2392	SEQ ID NO: 2549
			RASQDLRNYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 665	SEQ ID NO: 822	SEQ ID NO: 979

A-2165-WO-PCT

!PS:360535	18F2.011	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2236	SEQ ID NO: 2393	SEQ ID NO: 2550
			RASQDLRNYLG	GASSLQS	LQHNNYPFT
!PS:361035	18F2.012	NA	SEQ ID NO: 666	SEQ ID NO: 823	SEQ ID NO: 980
		AA	CGGGCAAGTCAGGACCTTAGAA ATTATTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2237	SEQ ID NO: 2394	SEQ ID NO: 2551
!PS:359940	2F11.002	NA	RASQDLRNYLG	GASSLQS	LQHNNYPFT
		AA	SEQ ID NO: 667	SEQ ID NO: 824	SEQ ID NO: 981
			CAGGCGAGTCAGGACATTAGCA ACTATTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCCTCA CT
!PS:361039	2F11.003	NA	SEQ ID NO: 2238	SEQ ID NO: 2395	SEQ ID NO: 2552
		AA	QASQDISNYLN	DASNLET	QQYDILLT
			SEQ ID NO: 668	SEQ ID NO: 825	SEQ ID NO: 982
!PS:361043	2F11.004	NA	CAGGCGAGTCAGGACATTAGCA ACTATTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCCTCA CT
		AA	SEQ ID NO: 2239	SEQ ID NO: 2396	SEQ ID NO: 2553
			QASQDISNYLN	DASNLET	QQYDILLT
!PS:361049	2F11.005	NA	SEQ ID NO: 669	SEQ ID NO: 826	SEQ ID NO: 983
		AA	CAGGCGAGTCAGGACATTAGCA ACTATTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCCTCA CT
			SEQ ID NO: 2240	SEQ ID NO: 2397	SEQ ID NO: 2554
!PS:361049	2F11.005	NA	QASQDISNYLN	DASNLET	QQYDILLT
		AA	SEQ ID NO: 670	SEQ ID NO: 827	SEQ ID NO: 984
			CAGGCGAGTCAGGACATTAGCA ACTATTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCCTCA CT
!PS:361049	2F11.005	NA	SEQ ID NO: 2241	SEQ ID NO: 2398	SEQ ID NO: 2555
		AA	QASQDISNYLN	DASNLET	QQYDILLT
			SEQ ID NO: 671	SEQ ID NO: 828	SEQ ID NO: 985

A-2165-WO-PCT

!PS:361055	2F11.006	NA	CAGCGAGTCAGGACATTAGCA ACTATTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCCTCA CT
		AA	SEQ ID NO: 2242	SEQ ID NO: 2399	SEQ ID NO: 2556
			QASQDISNYLN	DASNLET	QQYDILLT
!PS:361059	2F11.007	NA	SEQ ID NO: 672	SEQ ID NO: 829	SEQ ID NO: 986
			CAGCGAGTCAGGACATTAGCA ACTATTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCCTCA CT
		AA	SEQ ID NO: 2243	SEQ ID NO: 2400	SEQ ID NO: 2557
!PS:361063	2F11.008	NA	QASQDISNYLN	DASNLET	QQYDILLT
			SEQ ID NO: 673	SEQ ID NO: 830	SEQ ID NO: 987
		AA	CAGCGAGTCAGGACATTAGCA ACTATTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCCTCA CT
!PS:359949	2F11.009	NA	SEQ ID NO: 2244	SEQ ID NO: 2401	SEQ ID NO: 2558
			QASQDISNYLN	DASNLET	QQYDILLT
		AA	SEQ ID NO: 674	SEQ ID NO: 831	SEQ ID NO: 988
!PS:359956	2F11.010	NA	CAGCGAGTCAGGACATTAGCA ACTATTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCCTCA CT
			SEQ ID NO: 2245	SEQ ID NO: 2402	SEQ ID NO: 2559
		AA	QASQDISNYLN	DASNLET	QQYDILLT
!PS:359865	6H1.002	NA	SEQ ID NO: 675	SEQ ID NO: 832	SEQ ID NO: 989
			CAGCGAGTCAGGACATTAGCA ACTATTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCCTCA CT
		AA	SEQ ID NO: 2246	SEQ ID NO: 2403	SEQ ID NO: 2560
!PS:359865	6H1.002	NA	QASQDISNYLN	DASNLET	QQYDILLT
			SEQ ID NO: 676	SEQ ID NO: 833	SEQ ID NO: 990
		AA	CGGCAAGTCAGGACATTAGAG ATTATTAGGC	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATAATAATTACCCCT TCACT
!PS:359865	6H1.002	NA	SEQ ID NO: 2247	SEQ ID NO: 2404	SEQ ID NO: 2561
			RASQDIRDYL	GASSLQS	LQHNNYPFT
		AA	SEQ ID NO: 677	SEQ ID NO: 834	SEQ ID NO: 991

A-2165-WO-PCT

!PS:359869	6H1.003	NA	CGGGCAAGTCAGGACATTAGAG ATTATTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2248	SEQ ID NO: 2405	SEQ ID NO: 2562
			RASQDIRDYL	GASSLQS	LQHNNYPFT
!PS:359873	6H1.004	NA	CGGGCAAGTCAGGACATTAGAG ATTATTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2249	SEQ ID NO: 2406	SEQ ID NO: 2563
			RASQDIRDYL	GASSLQS	LQHNNYPFT
!PS:359877	6H1.005	NA	CGGGCAAGTCAGGACATTAGAG ATTATTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2250	SEQ ID NO: 2407	SEQ ID NO: 2564
			RASQDIRDYL	GASSLQS	LQHNNYPFT
!PS:361067	6H1.006	NA	CGGGCAAGTCAGGACATTAGAG ATTATTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2251	SEQ ID NO: 2408	SEQ ID NO: 2565
			RASQDIRDYL	GASSLQS	LQHNNYPFT
!PS:361071	6H1.007	NA	CGGGCAAGTCAGGACATTAGAG ATTATTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2252	SEQ ID NO: 2409	SEQ ID NO: 2566
			RASQDIRDYL	GASSLQS	LQHNNYPFT
!PS:361075	6H1.008	NA	CGGGCAAGTCAGGACATTAGAG ATTATTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2253	SEQ ID NO: 2410	SEQ ID NO: 2567
			RASQDIRDYL	GASSLQS	LQHNNYPFT
			SEQ ID NO: 683	SEQ ID NO: 840	SEQ ID NO: 997

A-2165-WO-PCT

!PS:361079	6A5.004.001	NA	CAGCGAGTCAGGACATTACCA ACTATTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
		AA	SEQ ID NO: 2254	SEQ ID NO: 2411	SEQ ID NO: 2568
			QASQDITNYLN	DASNLEP	QQYDDLFT
!PS:361085	6A5.004.002	NA	CAGCGAGTCAGGACATTACCA ACTATTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
		AA	SEQ ID NO: 2255	SEQ ID NO: 2412	SEQ ID NO: 2569
			QASQDITNYLN	DASNLEP	QQYDDLFT
!PS:361091	6A5.004.003	NA	CAGCGAGTCAGGACATTACCA ACTATTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
		AA	SEQ ID NO: 2256	SEQ ID NO: 2413	SEQ ID NO: 2570
			QASQDITNYLN	DASNLEP	QQYDDLFT
!PS:361095	6A5.004.004	NA	CAGCGAGTCAGGACATTACCA ACTATTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
		AA	SEQ ID NO: 2257	SEQ ID NO: 2414	SEQ ID NO: 2571
			QASQDITNYLN	DASNLEP	QQYDDLFT
!PS:361101	6A5.004.005	NA	CAGCGAGTCAGGACATTACCA ACTATTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
		AA	SEQ ID NO: 2258	SEQ ID NO: 2415	SEQ ID NO: 2572
			QASQDITNYLN	DASNLEP	QQYDDLFT
!PS:361105	6A5.004.006	NA	CAGCGAGTCAGGACATTACCA ACTATTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
		AA	SEQ ID NO: 2259	SEQ ID NO: 2416	SEQ ID NO: 2573
			QASQDITNYLN	DASNLEP	QQYDDLFT
			SEQ ID NO: 689	SEQ ID NO: 846	SEQ ID NO: 1003

A-2165-WO-PCT

!PS:361109	6A5.004.007	NA	CAGCGAGTCAGGACATTACCA ACTATTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
		AA	SEQ ID NO: 2260	SEQ ID NO: 2417	SEQ ID NO: 2574
			QASQDITNYLN	DASNLEP	QQYDDLFT
!PS:361113	6A5.004.008	NA	SEQ ID NO: 690	SEQ ID NO: 847	SEQ ID NO: 1004
			CAGCGAGTCAGGACATTACCA ACTATTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
		AA	SEQ ID NO: 2261	SEQ ID NO: 2418	SEQ ID NO: 2575
!PS:361120	6A5.004.009	NA	QASQDITNYLN	DASNLEP	QQYDDLFT
			SEQ ID NO: 691	SEQ ID NO: 848	SEQ ID NO: 1005
		AA	CAGCGAGTCAGGACATTACCA ACTATTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
!PS:359896	6A5.004.010	NA	SEQ ID NO: 2262	SEQ ID NO: 2419	SEQ ID NO: 2576
			QASQDITNYLN	DASNLEP	QQYDDLFT
		AA	SEQ ID NO: 692	SEQ ID NO: 849	SEQ ID NO: 1006
!PS:359890	6A5.004.011	NA	CAGCGAGTCAGGACATTACCA ACTATTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
			SEQ ID NO: 2263	SEQ ID NO: 2420	SEQ ID NO: 2577
		AA	QASQDITNYLN	DASNLEP	QQYDDLFT
!PS:359567	2A11.002	NA	SEQ ID NO: 693	SEQ ID NO: 850	SEQ ID NO: 1007
			CAGCGAGTCAGGACATTACCA ACTATTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
		AA	SEQ ID NO: 2264	SEQ ID NO: 2421	SEQ ID NO: 2578
!PS:359567	2A11.002	NA	QASQDITNYLN	DASNLEP	QQYDDLFT
			SEQ ID NO: 694	SEQ ID NO: 851	SEQ ID NO: 1008
		AA	AGGCCAGTCAGATTTTACCA GCACCTACTTAGCC	GGTGCATCCAGCAGGGGCCACT	CAGCAGTATGGTAGCTCACCTC GC
!PS:359567	2A11.002	NA	SEQ ID NO: 2265	SEQ ID NO: 2422	SEQ ID NO: 2579
			RASQIFTSTYLA	GASSRAT	QQYGSSPR
		AA	SEQ ID NO: 695	SEQ ID NO: 852	SEQ ID NO: 1009

A-2165-WO-PCT

!PS:335965	2A11.003	NA	AGGGCCAGTCAGATTTTACCA GCACCTACTTAGCC	GGTGCATCCAGCAGGGGCCACT	CAGCAGTATGGTAGCTCACCTC GC
		AA	SEQ ID NO: 2266	SEQ ID NO: 2423	SEQ ID NO: 2580
			RASQIFTSTYLA	GASSRAT	QQYGSSPR
!PS:361158	2A11.004	NA	AGGGCCAGTCAGATTTTACCA GCACCTACTTAGCC	GGTGCATCCAGCAGGGGCCACT	CAGCAGTATGGTAGCTCACCTC GC
		AA	SEQ ID NO: 2267	SEQ ID NO: 2424	SEQ ID NO: 2581
			RASQIFTSTYLA	GASSRAT	QQYGSSPR
!PS:361165	2A11.005	NA	AGGGCCAGTCAGATTTTACCA GCACCTACTTAGCC	GGTGCATCCAGCAGGGGCCACT	CAGCAGTATGGTAGCTCACCTC GC
		AA	SEQ ID NO: 2268	SEQ ID NO: 2425	SEQ ID NO: 2582
			RASQIFTSTYLA	GASSRAT	QQYGSSPR
!PS:361172	2G10_LC1.00 ³	NA	AGGGCCAGTCAGAGTGTAGCA GCAACTTAGCC	GGTGCAGCCACCAGGGGCCACT	CAGCAGTATAATAACTGGCCTC TCACT
		AA	SEQ ID NO: 2269	SEQ ID NO: 2426	SEQ ID NO: 2583
			RASQSVSSNLA	GAATRAT	QQYNNWPLT
!PS:361178	2G10_LC1.00 ⁴	NA	AGGGCCAGTCAGAGTGTAGCA GCAACTTAGCC	GGTGCAGCCACCAGGGGCCACT	CAGCAGTATAATAACTGGCCTC TCACT
		AA	SEQ ID NO: 2270	SEQ ID NO: 2427	SEQ ID NO: 2584
			RASQSVSSNLA	GAATRAT	QQYNNWPLT
!PS:361185	2G10_LC1.00 ⁵	NA	AGGGCCAGTCAGAGTGTAGCA GCAACTTAGCC	GGTGCAGCCACCAGGGGCCACT	CAGCAGTATAATAACTGGCCTC TCACT
		AA	SEQ ID NO: 2271	SEQ ID NO: 2428	SEQ ID NO: 2585
			RASQSVSSNLA	GAATRAT	QQYNNWPLT
			SEQ ID NO: 701	SEQ ID NO: 858	SEQ ID NO: 1015

A-2165-WO-PCT

!PS:361192	2G10_LC1.00 6	NA	AGGGCCAGTCAGAGTGTTAGCA GCAACTTAGCC	GGTGCAGCCACCAGGGGCCACT	CAGCAGTATAATAAAGTGGCCTC TCACT
		AA	SEQ ID NO: 2272 RASQSVSSNLA	SEQ ID NO: 2429 GAATRAT	SEQ ID NO: 2586 QQYNNWPLT
		AA	SEQ ID NO: 702	SEQ ID NO: 859	SEQ ID NO: 1016
!PS:359609	2G10_LC1.00 7	NA	AGGGCCAGTCAGAGTGTTAGCA GCAACTTAGCC	GGTGCAGCCACCAGGGGCCACT	CAGCAGTATAATAAAGTGGCCTC TCACT
		AA	SEQ ID NO: 2273 RASQSVSSNLA	SEQ ID NO: 2430 GAATRAT	SEQ ID NO: 2587 QQYNNFPLT
		AA	SEQ ID NO: 703	SEQ ID NO: 860	SEQ ID NO: 1017
!PS:359615	2G10_LC1.00 8	NA	AGGGCCAGTCAGAGTGTTAGCA GCAACTTAGCC	GGTGCAGCCACCAGGGGCCACT	CAGCAGTATAATAAAGTGGCCTC TCACT
		AA	SEQ ID NO: 2274 RASQSVSSNLA	SEQ ID NO: 2431 GAATRAT	SEQ ID NO: 2588 QQYNNYPLT
		AA	SEQ ID NO: 704	SEQ ID NO: 861	SEQ ID NO: 1018
!PS:361196	2G10_LC1.00 9	NA	AGGGCCAGTCAGAGTGTTAGCA GCAACTTAGCC	GGTGCAGCCACCAGGGGCCACT	CAGCAGTATAATAAAGTGGCCTC TCACT
		AA	SEQ ID NO: 2275 RASQSVSSNLA	SEQ ID NO: 2432 GAATRAT	SEQ ID NO: 2589 QQYNNWPLT
		AA	SEQ ID NO: 705	SEQ ID NO: 862	SEQ ID NO: 1019
!PS:361202	2G10_LC1.01 0	NA	AGGGCCAGTCAGAGTGTTAGCA GCAACTTAGCC	GGTGCAGCCACCAGGGGCCACT	CAGCAGTATAATAAAGTGGCCTC TCACT
		AA	SEQ ID NO: 2276 RASQSVSSNLA	SEQ ID NO: 2433 GAATRAT	SEQ ID NO: 2590 QQYNNWPLT
		AA	SEQ ID NO: 706	SEQ ID NO: 863	SEQ ID NO: 1020
!PS:359644	18E3.002	NA	AGGGCCAGTCAGAGTATTAGTT ACAGTTACTTAGCC	GGTGCATCCAGCAGGGGCCACT	CAGCAGTATGGTAGTTACCCGC TCACT
		AA	SEQ ID NO: 2277 RASQSVSSNLA	SEQ ID NO: 2434 GASSRAT	SEQ ID NO: 2591 QQYSSSPLT
		AA	SEQ ID NO: 707	SEQ ID NO: 864	SEQ ID NO: 1021

A-2165-WO-PCT

!PS:361206	18E3.003	NA	AGGGCCAGTCAGAGTATTAGTT ACAGTTACTTAGCC	GGTGCATCCAGCAGGGGCCACT	CAGCAGTATGGTAGTTTACCCGC TCACT
		AA	SEQ ID NO: 2278	SEQ ID NO: 2435	SEQ ID NO: 2592
			RASQSISYSLA	GASSRAT	QQYGSSPLT
!PS:359628	18E3.004	NA	AGGGCCAGTCAGAGTATTAGTT ACAGTTACTTAGCC	GGTGCATCCAGCAGGGGCCACT	CAGCAGTATGGTAGTTTACCCGC TCACT
		AA	SEQ ID NO: 2279	SEQ ID NO: 2436	SEQ ID NO: 2593
			RASQSISYSLA	GASSRAT	QQYGSSPLT
!PS:359637	18E3.005	NA	AGGGCCAGTCAGAGTATTAGTT ACAGTTACTTAGCC	GGTGCATCCAGCAGGGGCCACT	CAGCAGTATGGTAGTTTACCCGC TCACT
		AA	SEQ ID NO: 2280	SEQ ID NO: 2437	SEQ ID NO: 2594
			RASQSISYSLA	GASSRAT	QQYGSSPLT
!PS:361210	18E3.006	NA	AGGGCCAGTCAGAGTATTAGTT ACAGTTACTTAGCC	GGTGCATCCAGCAGGGGCCACT	CAGCAGTATGGTAGTTTACCCGC TCACT
		AA	SEQ ID NO: 2281	SEQ ID NO: 2438	SEQ ID NO: 2595
			RASQSISYSLA	GASSRAT	QQYGSSPLT
!PS:361214	18E3.007	NA	AGGGCCAGTCAGAGTATTAGTT ACAGTTACTTAGCC	GGTGCATCCAGCAGGGGCCACT	CAGCAGTATGGTAGTTTACCCGC TCACT
		AA	SEQ ID NO: 2282	SEQ ID NO: 2439	SEQ ID NO: 2596
			RASQSISYSLA	GASSRAT	QQYGSSPLT
!PS:361218	18E3.008	NA	AGGGCCAGTCAGAGTATTAGTT ACAGTTACTTAGCC	GGTGCATCCAGCAGGGGCCACT	CAGCAGTATGGTAGTTTACCCGC TCACT
		AA	SEQ ID NO: 2283	SEQ ID NO: 2440	SEQ ID NO: 2597
			RASQSISYSLA	GASSRAT	QQYGSSPLT
			SEQ ID NO: 713	SEQ ID NO: 870	SEQ ID NO: 1027

A-2165-WO-PCT

!PS:361222	5C2.006	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
		AA	SEQ ID NO: 2284 KSSQSVLSSNNKNYIA SEQ ID NO: 714	SEQ ID NO: 2441 WASTRES SEQ ID NO: 871	SEQ ID NO: 2598 QQYYSTPWT SEQ ID NO: 1028
!PS:361229	5C2.007	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
		AA	SEQ ID NO: 2285 KSSQSVLSSNNKNYIA SEQ ID NO: 715	SEQ ID NO: 2442 WASTRES SEQ ID NO: 872	SEQ ID NO: 2599 QQYYSTPWT SEQ ID NO: 1029
!PS:361236	5C2.008	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
		AA	SEQ ID NO: 2286 KSSQSVLSSNNKNYIA SEQ ID NO: 716	SEQ ID NO: 2443 WASTRES SEQ ID NO: 873	SEQ ID NO: 2600 QQYYSTPWT SEQ ID NO: 1030
!PS:359685	5C2.009	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
		AA	SEQ ID NO: 2287 KSSQSVLSSNNKNYIA SEQ ID NO: 717	SEQ ID NO: 2444 WASTRES SEQ ID NO: 874	SEQ ID NO: 2601 QQYYSTPWT SEQ ID NO: 1031
!PS:361240	5C2.010	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
		AA	SEQ ID NO: 2288 KSSQSVLSSNNKNYIA SEQ ID NO: 718	SEQ ID NO: 2445 WASTRES SEQ ID NO: 875	SEQ ID NO: 2602 QQYYSTPWT SEQ ID NO: 1032

A-2165-WO-PCT

!PS:361247	5C2.011	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
		AA	SEQ ID NO: 2289 KSSQSVLSSNNKNYIA SEQ ID NO: 719	SEQ ID NO: 2446 WASTRES SEQ ID NO: 876	SEQ ID NO: 2603 QQYYSTPWT SEQ ID NO: 1033
!PS:361254	5C2.012	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
		AA	SEQ ID NO: 2290 KSSQSVLSSNNKNYIA SEQ ID NO: 720	SEQ ID NO: 2447 WASTRES SEQ ID NO: 877	SEQ ID NO: 2604 QQYYSTPWT SEQ ID NO: 1034
!PS:361261	5C2.013	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
		AA	SEQ ID NO: 2291 KSSQSVLSSNNKNYIA SEQ ID NO: 721	SEQ ID NO: 2448 WASTRES SEQ ID NO: 878	SEQ ID NO: 2605 QQYYSTPWT SEQ ID NO: 1035
!PS:361268	5C2.014	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
		AA	SEQ ID NO: 2292 KSSQSVLSSNNKNYIA SEQ ID NO: 722	SEQ ID NO: 2449 WASTRES SEQ ID NO: 879	SEQ ID NO: 2606 QQYYSTPWT SEQ ID NO: 1036
!PS:359669	5C2.015	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
		AA	SEQ ID NO: 2293 KSSQSVLSSNNKNYIA SEQ ID NO: 723	SEQ ID NO: 2450 WASTRES SEQ ID NO: 880	SEQ ID NO: 2607 QQYYSTPWT SEQ ID NO: 1037

A-2165-WO-PCT

!PS:359678	5C2.016	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
		AA	SEQ ID NO: 2294 KSSQSVLSSNNKNYLA SEQ ID NO: 724	SEQ ID NO: 2451 WASTRES SEQ ID NO: 881	SEQ ID NO: 2608 QQYYRTPWT SEQ ID NO: 1038
!PS:361275	11C1.002	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGAATCC	CAGCAATATTATCGTACTCCGT GGACG
		AA	SEQ ID NO: 2295 KSSQSVLSSNNKNYLA SEQ ID NO: 725	SEQ ID NO: 2452 WTSTRES SEQ ID NO: 882	SEQ ID NO: 2609 QQYYRTPWT SEQ ID NO: 1039
!PS:361282	11C1.003	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGAATCC	CAGCAATATTATCGTACTCCGT GGACG
		AA	SEQ ID NO: 2296 KSSQSVLSSNNKNYLA SEQ ID NO: 726	SEQ ID NO: 2453 WTSTRES SEQ ID NO: 883	SEQ ID NO: 2610 QQYYRTPWT SEQ ID NO: 1040
!PS:361289	11C1.004	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC	CAGCAATATTATCGTACTCCGT GGACG
		AA	SEQ ID NO: 2297 KSSQSVLSSNNKNYLA SEQ ID NO: 727	SEQ ID NO: 2454 WTSTRDS SEQ ID NO: 884	SEQ ID NO: 2611 QQYYRTPWT SEQ ID NO: 1041
!PS:359712	11C1.005	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGAATCC	CAGCAATATTATCGTACTCCGT GGACG
		AA	SEQ ID NO: 2298 KSSQSVLSSNNKNYLA SEQ ID NO: 728	SEQ ID NO: 2455 WTSTRES SEQ ID NO: 885	SEQ ID NO: 2612 QQYYRTPWT SEQ ID NO: 1042

A-2165-WO-PCT

!PS:361293	11C1.006	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGAATCC	CAGCAATATTATCGTACTCCGT GGACG
		AA	SEQ ID NO: 2299 KSSQSVLSSNNKNYLA SEQ ID NO: 729	SEQ ID NO: 2456 WTSTRES SEQ ID NO: 886	SEQ ID NO: 2613 QQYRTPWT SEQ ID NO: 1043
!PS:361297	11C1.007	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGAATCC	CAGCAATATTATCGTACTCCGT GGACG
		AA	SEQ ID NO: 2300 KSSQSVLSSNNKNYLA SEQ ID NO: 730	SEQ ID NO: 2457 WTSTRDS SEQ ID NO: 887	SEQ ID NO: 2614 QQYRTPWT SEQ ID NO: 1044
!PS:361301	11C1.008	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGAATCC	CAGCAATATTATCGTACTCCGT GGACG
		AA	SEQ ID NO: 2301 KSSQSVLSSNNKNYLA SEQ ID NO: 731	SEQ ID NO: 2458 WTSTRDS SEQ ID NO: 888	SEQ ID NO: 2615 QQYRTPWT SEQ ID NO: 1045
!PS:359703	11C1.009	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGAATCC	CAGCAATATTATCGTACTCCGT GGACG
		AA	SEQ ID NO: 2302 KSSQSVLSSNNKNYLA SEQ ID NO: 732	SEQ ID NO: 2459 WTSTRES SEQ ID NO: 889	SEQ ID NO: 2616 QQYRTPWT SEQ ID NO: 1046
!PS:361305	11C1.010	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGAATCC	CAGCAATATTATCGTACTCCGT GGACG
		AA	SEQ ID NO: 2303 KSSQSVLSSNNKNYLA SEQ ID NO: 733	SEQ ID NO: 2460 WTSTRES SEQ ID NO: 890	SEQ ID NO: 2617 QQYRTPWT SEQ ID NO: 1047

A-2165-WO-PCT

!PS:361312	13H12.002	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
			SEQ ID NO: 2304	SEQ ID NO: 2461	SEQ ID NO: 2618
		AA	KSSQSVLSSNNKNYIA	WASTRES	QQYYSTPWT
!PS:359744	13H12.003		SEQ ID NO: 734	SEQ ID NO: 891	SEQ ID NO: 1048
		NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
		AA	SEQ ID NO: 2305 KSSQSVLSSNNKNYIA SEQ ID NO: 735	SEQ ID NO: 2462 WASTRES SEQ ID NO: 892	SEQ ID NO: 2619 QQYYSTPWT SEQ ID NO: 1049
!PS:361319	13H12.004	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
			SEQ ID NO: 2306 KSSQSVLSSNNKNYIA	SEQ ID NO: 2463 WASTRES	SEQ ID NO: 2620 QQYYSTPWT
		AA	SEQ ID NO: 736	SEQ ID NO: 893	SEQ ID NO: 1050
!PS:359737	13H12.005	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
			SEQ ID NO: 2307 KSSQSVLSSNNKNYIA	SEQ ID NO: 2464 WASTRES	SEQ ID NO: 2621 QQYYSTPWT
		AA	SEQ ID NO: 737	SEQ ID NO: 894	SEQ ID NO: 1051
!PS:361326	13H12.006	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
			SEQ ID NO: 2308 KSSQSVLSSNNKNYIA	SEQ ID NO: 2465 WASTRES	SEQ ID NO: 2622 QQYYSTPWT
		AA	SEQ ID NO: 738	SEQ ID NO: 895	SEQ ID NO: 1052

A-2165-WO-PCT

!PS:361330	12H11.002	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC	CAGCAATATTATCGTACTCCGT GGACG
		AA	SEQ ID NO: 2309 KSSQSVLSSNNKNYLA SEQ ID NO: 739	SEQ ID NO: 2466 WTSTRDS SEQ ID NO: 896	SEQ ID NO: 2623 QQYYRTPWT SEQ ID NO: 1053
!PS:361337	12H11.003	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC	CAGCAATATTATCGTACTCCGT GGACG
		AA	SEQ ID NO: 2310 KSSQSVLSSNNKNYLA SEQ ID NO: 740	SEQ ID NO: 2467 WTSTRDS SEQ ID NO: 897	SEQ ID NO: 2624 QQYYRTPWT SEQ ID NO: 1054
!PS:361344	12H11.004	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC	CAGCAATATTATCGTACTCCGT GGACG
		AA	SEQ ID NO: 2311 KSSQSVLSSNNKNYLA SEQ ID NO: 741	SEQ ID NO: 2468 WTSTRDS SEQ ID NO: 898	SEQ ID NO: 2625 QQYYRTPWT SEQ ID NO: 1055
!PS:361351	12H11.005	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC	CAGCAATATTATCGTACTCCGT GGACG
		AA	SEQ ID NO: 2312 KSSQSVLSSNNKNYLA SEQ ID NO: 742	SEQ ID NO: 2469 WTSTRDS SEQ ID NO: 899	SEQ ID NO: 2626 QQYYRTPWT SEQ ID NO: 1056
!PS:361358	12H11.006	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC	CAGCAATATTATCGTACTCCGT GGACG
		AA	SEQ ID NO: 2313 KSSQSVLSSNNKNYLA SEQ ID NO: 743	SEQ ID NO: 2470 WTSTRDS SEQ ID NO: 900	SEQ ID NO: 2627 QQYYRTPWT SEQ ID NO: 1057

A-2165-WO-PCT

!PS:361365	12H11.007	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC	CAGCAATATTATCGTACTCCGT GGACG
		AA	SEQ ID NO: 2314 KSSQSVLSSNNKNYLA SEQ ID NO: 744	SEQ ID NO: 2471 WTSTRDS SEQ ID NO: 901	SEQ ID NO: 2628 QQYYRTPWT SEQ ID NO: 1058
!PS:361372	12H11.008	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC	CAGCAATATTATCGTACTCCGT GGACG
		AA	SEQ ID NO: 2315 KSSQSVLSSNNKNYLA SEQ ID NO: 745	SEQ ID NO: 2472 WTSTRDS SEQ ID NO: 902	SEQ ID NO: 2629 QQYYRTPWT SEQ ID NO: 1059
!PS:361379	12H11.009	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGAAATCC	CAGCAATATTATCGTACTCCGT GGACG
		AA	SEQ ID NO: 2316 KSSQSVLSSNNKNYLA SEQ ID NO: 746	SEQ ID NO: 2473 WTSTRDS SEQ ID NO: 903	SEQ ID NO: 2630 QQYYRTPWT SEQ ID NO: 1060
!PS:361383	12H11.010	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGAAATCC	CAGCAATATTATCGTACTCCGT GGACG
		AA	SEQ ID NO: 2317 KSSQSVLSSNNKNYLA SEQ ID NO: 747	SEQ ID NO: 2474 WTSTRDS SEQ ID NO: 904	SEQ ID NO: 2631 QQYYRTPWT SEQ ID NO: 1061
!PS:361387	12H11.011	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGAAATCC	CAGCAATATTATCGTACTCCGT GGACG
		AA	SEQ ID NO: 2318 KSSQSVLSSNNKNYLA SEQ ID NO: 748	SEQ ID NO: 2475 WTSTRDS SEQ ID NO: 905	SEQ ID NO: 2632 QQYYRTPWT SEQ ID NO: 1062

A-2165-WO-PCT

!PS:361391	12H11.012	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGAATCC	CAGCAATATTATCGTACTCCGT GGACG
		AA	SEQ ID NO: 2319 KSSQSVLSSNNKNYLA SEQ ID NO: 749	SEQ ID NO: 2476 WTSTRES SEQ ID NO: 906	SEQ ID NO: 2633 QQYYRTPWT SEQ ID NO: 1063
!PS:361395	12H11.013	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC	CAGCAATATTATCGTACTCCGT GGACG
		AA	SEQ ID NO: 2320 KSSQSVLSSNNKNYLA SEQ ID NO: 750	SEQ ID NO: 2477 WTSTRDS SEQ ID NO: 907	SEQ ID NO: 2634 QQYYRTPWT SEQ ID NO: 1064
!PS:361402	12H11.014	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGAATCC	CAGCAATATTATCGTACTCCGT GGACG
		AA	SEQ ID NO: 2321 KSSQSVLSSNNKNYLA SEQ ID NO: 751	SEQ ID NO: 2478 WTSTRES SEQ ID NO: 908	SEQ ID NO: 2635 QQYYRTPWT SEQ ID NO: 1065
!PS:361406	2C2.005.001	NA	TCTGGAAGTAGCTCCAACATCG GAAGTCAAACTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGAAAGCCTG AGTGGTCCGGTA
		AA	SEQ ID NO: 2322 SGSSNIGSQTVN SEQ ID NO: 752	SEQ ID NO: 2479 TNNQRPS SEQ ID NO: 909	SEQ ID NO: 2636 ATFDESLSGPV SEQ ID NO: 1066
!PS:361412	2C2.005.002	NA	TCTGGAAGTAGCTCCAACATCG GAAGTCAAACTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGAAAGCCTG CAAGGTCCGGTA
		AA	SEQ ID NO: 2323 SGSSNIGSQTVN SEQ ID NO: 753	SEQ ID NO: 2480 TNNQRPS SEQ ID NO: 910	SEQ ID NO: 2637 ATFDESLSGPV SEQ ID NO: 1067

A-2165-WO-PCT

2C2.005.003	!PS:361418	NA	TCTGGAAGTAGCTCCAACATCG GAAAGTAATTATGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCTGATGAAAGCCTG AGTGGTCCGGTA
		AA	SEQ ID NO: 2324 SGSSNIGSNYVN	SEQ ID NO: 2481 TNNQRPS	SEQ ID NO: 2638 ATFDESLSGPV
		AA	SEQ ID NO: 754	SEQ ID NO: 911	SEQ ID NO: 1068
2C2.005.004	!PS:361424	NA	TCTGGAAGTAGCTCCAACATCG GAAAGTAATTATGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCTGATGAAAGCCTG CAAGGTCCGGTA
		AA	SEQ ID NO: 2325 SGSSNIGSNYVN	SEQ ID NO: 2482 TNNQRPS	SEQ ID NO: 2639 ATFDESLSGPV
		AA	SEQ ID NO: 755	SEQ ID NO: 912	SEQ ID NO: 1069
2C2.005.005	!PS:361430	NA	TCTGGAAGTAGCTCCAACATCG GAAAGTCAAACTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCTGATGACAGCCTG AATGGTCCGGTA
		AA	SEQ ID NO: 2326 SGSSNIGSQTVN	SEQ ID NO: 2483 TNNQRPS	SEQ ID NO: 2640 ATFDDSLNGPV
		AA	SEQ ID NO: 756	SEQ ID NO: 913	SEQ ID NO: 1070
2C2.005.006	!PS:361436	NA	TCTGGAAGTAGCTCCAACATCG GAAAGTAATTATGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCTGATGACAGCCTG AATGGTCCGGTA
		AA	SEQ ID NO: 2327 SGSSNIGSNYVN	SEQ ID NO: 2484 TNNQRPS	SEQ ID NO: 2641 ATFDDSLNGPV
		AA	SEQ ID NO: 757	SEQ ID NO: 914	SEQ ID NO: 1071
2C2.005.007	!PS:361442	NA	TCTGGAAGTAGCTCCAACATCG GAAAGTAATACTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCTGATGAAAGCCTG AATGGTCCGGTA
		AA	SEQ ID NO: 2328 SGSSNIGSNYVN	SEQ ID NO: 2485 TNNQRPS	SEQ ID NO: 2642 ATFDESLSGPV
		AA	SEQ ID NO: 758	SEQ ID NO: 915	SEQ ID NO: 1072
2C2.005.008	!PS:361448	NA	TCTGGAAGTAGCTCCAACATCG GAAAGTAATACTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCTGATGACAGCCTG AAGTCCGGTA
		AA	SEQ ID NO: 2329 SGSSNIGSNYVN	SEQ ID NO: 2486 TNNQRPS	SEQ ID NO: 2643 ATFDDSLQGPV
		AA	SEQ ID NO: 759	SEQ ID NO: 916	SEQ ID NO: 1073

A-2165-WO-PCT

!PS:361454	2C2.005.009	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATACTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGACAGCCTG AGTGGTCCGGTA
		AA	SEQ ID NO: 2330 SGSSNIGSNTVN	SEQ ID NO: 2487 TNNQRPS	SEQ ID NO: 2644 ATFDDSLNAPV
		AA	SEQ ID NO: 760	SEQ ID NO: 917	SEQ ID NO: 1074
!PS:361460	2C2.005.010	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATACTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGACAGCCTG AATGCTCCGGTA
		AA	SEQ ID NO: 2331 SGSSNIGSNTVN	SEQ ID NO: 2488 TNNQRPS	SEQ ID NO: 2645 ATFDDSLNAPV
		AA	SEQ ID NO: 761	SEQ ID NO: 918	SEQ ID NO: 1075
!PS:361466	2C2.005.011	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATACTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGACAGCCTG AATGCTCCGGTA
		AA	SEQ ID NO: 2332 SGSSNIGSNTVN	SEQ ID NO: 2489 TNNQRPS	SEQ ID NO: 2646 ATFDDSLNAPV
		AA	SEQ ID NO: 762	SEQ ID NO: 919	SEQ ID NO: 1076
!PS:361472	2C2.005.012	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATACTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGACAGCCTG AATGCTCCGGTA
		AA	SEQ ID NO: 2333 SGSSNIGSNTVN	SEQ ID NO: 2490 TNNQRPS	SEQ ID NO: 2647 ATFDDSLNAPV
		AA	SEQ ID NO: 763	SEQ ID NO: 920	SEQ ID NO: 1077
!PS:361478	2C2.005.013	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATACTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGACAGCCTG AATGCTCCGGTA
		AA	SEQ ID NO: 2334 SGSSNIGSNTVN	SEQ ID NO: 2491 TNNQRPS	SEQ ID NO: 2648 ATFDDSLNAPV
		AA	SEQ ID NO: 764	SEQ ID NO: 921	SEQ ID NO: 1078
!PS:361485	2C2.005.014	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATACTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGAAAGCCTG AGTGGTCCGGTA
		AA	SEQ ID NO: 2335 SGSSNIGSNTVN	SEQ ID NO: 2492 TNNQRPS	SEQ ID NO: 2649 ATFDDSLNAPV
		AA	SEQ ID NO: 765	SEQ ID NO: 922	SEQ ID NO: 1079

A-2165-WO-PCT

!PS:361845	18F2.013	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2336	SEQ ID NO: 2493	SEQ ID NO: 2650
			RASQDLRNYLG	GASSLQS	LQHNNYPFT
!PS:361851	6H1.009	NA	SEQ ID NO: 766	SEQ ID NO: 923	SEQ ID NO: 1080
		AA	CGGGCAAGTCAGGACATTAGAG ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2337	SEQ ID NO: 2494	SEQ ID NO: 2651
!PS:361855	2C2.005.015	NA	RASQDIRDYL	GASSLQS	LQHNNYPFT
		AA	SEQ ID NO: 767	SEQ ID NO: 924	SEQ ID NO: 1081
			TCTGGAAGTAGCTCCAACATCG GAAATAATACTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATAGCAGCCTG AGTGGTCCGGTA
!PS:336067	5G12.006	NA	SEQ ID NO: 2338	SEQ ID NO: 2495	SEQ ID NO: 2652
		AA	SGSSSNIGSNTVN	TNNQRPS	ATFDSSLSGPV
			SEQ ID NO: 768	SEQ ID NO: 925	SEQ ID NO: 1082
!PS:336169	17B11.002	NA	CGGGCAAGTCAGACCATTAGCA GGTTTTAAAT	GTTGCATCCAGTTTGCAAAGT	CAACAGAGTTACAGTACCCCTG ATCAGT
		AA	SEQ ID NO: 2339	SEQ ID NO: 2496	SEQ ID NO: 2653
			RASQTISRFLN	VASSLQS	QQSYSTLIS
!PS:361127	5G12.006.001	NA	SEQ ID NO: 769	SEQ ID NO: 926	SEQ ID NO: 1083
		AA	TCTGGAAGCAGCTCCAACATTG GAAATAATTATGTATCC	GACAATAATAAGCGACCCCTCA	GGAACATGGGATAGCAGCCTG AGTGCTGTGGTA
			SEQ ID NO: 2340	SEQ ID NO: 2497	SEQ ID NO: 2654
		NA	SGSSSNIGNNYVS	DNNKRPS	GTWDSLSAVV
		AA	SEQ ID NO: 770	SEQ ID NO: 927	SEQ ID NO: 1084
			CGGGCAAGTCAGACCATTAGCA GGTTTTAAAT	GTTGCATCCAGTTTGCAAAGT	CAACAGAGTTACAGTACCCCTG ATCAGT
		NA	SEQ ID NO: 2341	SEQ ID NO: 2498	SEQ ID NO: 2655
		AA	RASQTISRFLN	VASSLQS	QQSYSTLIS
			SEQ ID NO: 771	SEQ ID NO: 928	SEQ ID NO: 1085

A-2165-WO-PCT

!PS:361136	5G12.006.002	NA	CGGGCAAGTCAGACCATTAGCA GGTTTTTAAAT	GTTGCATCCAGTTTGCAAAAGT	CAACAGAGTTACAGTACCCTG ATCAGT
		AA	SEQ ID NO: 2342 RASQTISRFLN	SEQ ID NO: 2499 VASSLQS	SEQ ID NO: 2656 QQSYSTLIS
		AA	SEQ ID NO: 772	SEQ ID NO: 929	SEQ ID NO: 1086
!PS:361140	5G12.006.003	NA	CGGGCAAGTCAGACCATTAGCA GGTTTTTAAAT	GTTGCATCCAGTTTGCAAAAGT	CAACAGAGTTACAGTACCCTG ATCAGT
		AA	SEQ ID NO: 2343 RASQTISRFLN	SEQ ID NO: 2500 VASSLQS	SEQ ID NO: 2657 QQSYSTLIS
		AA	SEQ ID NO: 773	SEQ ID NO: 930	SEQ ID NO: 1087
!PS:359919	5G12.006.004	NA	CGGGCAAGTCAGACCATTAGCA GGTTTTTAAAT	GTTGCATCCAGTTTGCAAAAGT	CAACAGAGTTACAGTACCCTG ATCAGT
		AA	SEQ ID NO: 2344 RASQTISRFLN	SEQ ID NO: 2501 VASSLQS	SEQ ID NO: 2658 QQSYSTLIS
		AA	SEQ ID NO: 774	SEQ ID NO: 931	SEQ ID NO: 1088
!PS:361144	5G12.006.005	NA	CGGGCAAGTCAGACCATTAGCA GGTTTTTAAAT	GTTGCATCCAGTTTGCAAAAGT	CAACAGAGTTACAGTACCCTG ATCAGT
		AA	SEQ ID NO: 2345 RASQTISRFLN	SEQ ID NO: 2502 VASSLQS	SEQ ID NO: 2659 QQSYSTLIS
		AA	SEQ ID NO: 775	SEQ ID NO: 932	SEQ ID NO: 1089
!PS:361151	5G12.006.006	NA	CGGGCAAGTCAGACCATTAGCA GGTTTTTAAAT	GTTGCATCCAGTTTGCAAAAGT	CAACAGAGTTACAGTACCCTG ATCAGT
		AA	SEQ ID NO: 2346 RASQTISRFLN	SEQ ID NO: 2503 VASSLQS	SEQ ID NO: 2660 QQSYSTLIS
		AA	SEQ ID NO: 776	SEQ ID NO: 933	SEQ ID NO: 1090
!PS:361491	17B11.002.001	NA	TCTGGAAGCAGCTCCAACATTG GAAATAATTATGTATCC	GACAATAATAAGCGACCCCTCA	GGAACATGGGATAGCAGCCTG AGTGCTGTGGTA
		AA	SEQ ID NO: 2347 SGSSSNIGNNYVS	SEQ ID NO: 2504 DNNKRPS	SEQ ID NO: 2661 GTWDSLSAVV
		AA	SEQ ID NO: 777	SEQ ID NO: 934	SEQ ID NO: 1091

A-2165-WO-PCT

!PS:361499	17B11.002.00	2	NA	TCTGGAAGCAGCTCCAACATTG GAAATAATTATGTATCC	GACAATAATAAGCGACCCCTCA	GGAACATGGGATAGCAGCCTG AGTGCTGTGGTA
			AA	SEQ ID NO: 2348 SGSSSNIGNNYVS	SEQ ID NO: 2505 DNNKRPS	SEQ ID NO: 2662 GTWDSSL SAVV
			AA	SEQ ID NO: 778	SEQ ID NO: 935	SEQ ID NO: 1092
!PS:361503	17B11.002.00	3	NA	TCTGGAAGCAGCTCCAACATTG GAAATAATTATGTATCC	GACAATAATAAGCGACCCCTCA	GGAACATGGGATAGCAGCCTG AGTGCTGTGGTA
			AA	SEQ ID NO: 2349 SGSSSNIGNNYVS	SEQ ID NO: 2506 DNNKRPS	SEQ ID NO: 2663 GTWDSSL SAVV
			AA	SEQ ID NO: 779	SEQ ID NO: 936	SEQ ID NO: 1093
!PS:361507	17B11.002.00	4	NA	TCTGGAAGCAGCTCCAACATTG GAAATAATTATGTATCC	GACAATAATAAGCGACCCCTCA	GGAACATTCGAAAGCAGCCTG AGTGCTGTGGTA
			AA	SEQ ID NO: 2350 SGSSSNIGNNYVS	SEQ ID NO: 2507 DNNKRPS	SEQ ID NO: 2664 GTFESSL SAVV
			AA	SEQ ID NO: 780	SEQ ID NO: 937	SEQ ID NO: 1094
!PS:361514	17B11.002.00	5	NA	TCTGGAAGCAGCTCCAACATTG GAAATAATTATGTATCC	GACAATAATAAGCGACCCCTCA	GGAACATGGGATAGCAGCCTG AGTGCTGTGGTA
			AA	SEQ ID NO: 2351 SGSSSNIGNNYVS	SEQ ID NO: 2508 DNNKRPS	SEQ ID NO: 2665 GTWDSSL SAVV
			AA	SEQ ID NO: 781	SEQ ID NO: 938	SEQ ID NO: 1095
!PS:360582	17B11.002.00	6	NA	TCTGGAAGCAGCTCCAACATTG GAAATAATTATGTATCC	GACAATAATAAGCGACCCCTCA	GGAACATGGGATAGCAGCCTG AGTGCTGTGGTA
			AA	SEQ ID NO: 2352 SGSSSNIGNNYVS	SEQ ID NO: 2509 DNNKRPS	SEQ ID NO: 2666 GTWDSSL SAVV
			AA	SEQ ID NO: 782	SEQ ID NO: 939	SEQ ID NO: 1096
!PS:361518	17B11.002.00	7	NA	TCTGGAAGCAGCTCCAACATTG GAAATAATTATGTATCC	GACAATAATAAGCGACCCCTCA	GGAACATGGGATAGCAGCCTG AGTGCTGTGGTA
			AA	SEQ ID NO: 2353 SGSSSNIGNNYVS	SEQ ID NO: 2510 DNNKRPS	SEQ ID NO: 2667 GTWDSSL SAVV
			AA	SEQ ID NO: 783	SEQ ID NO: 940	SEQ ID NO: 1097

A-2165-WO-PCT

!PS:360570	17B11.002.008	NA	TCTGGAAGCAGCTCCAACATTG GAAATAATTATGTATCC	GACAATAATAAGCGACCCCTCA	GGAACATTTCGAAAGCAGCCCTG AGTGCTGTGTA
		AA	SEQ ID NO: 2354 SGSSNIGNNYVS SEQ ID NO: 784	SEQ ID NO: 2511 DNNKRPS SEQ ID NO: 941	SEQ ID NO: 2668 GTFESSLSAVV SEQ ID NO: 1098
!PS:362051	5G12.005.001	NA	CGGGCAAGTCAGACCATTAGCA GGTTTTTAAAT	GTTGCATCCAGTTTGCAAAAGT	CAACAGAGTTACAGTACCCTGC TCAGT
		AA	SEQ ID NO: 2355 RASQTISRFLN	SEQ ID NO: 2512 VASSLQS	SEQ ID NO: 2669 QQSYSTLLS
			SEQ ID NO: 785	SEQ ID NO: 942	SEQ ID NO: 1099

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

IPS#	Ab	Type	CDRH1	CDRH2	CDRH3
!PS:336175	2C2.005	NA	GGCTACTATATGCAT	TGGATCAACCCCTAACAGTGGTG GCACAAACTATGCACAGAAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCTCACTACTACT ACGGTATGGACGTC
			SEQ ID NO: 2670 GYVMH	SEQ ID NO: 2827 WINPNSGGTNYAQKFQG	SEQ ID NO: 2984 GGDYVWGTYPHYYYGMDV
		AA	SEQ ID NO: 1100	SEQ ID NO: 1257	SEQ ID NO: 1414
!PS:335914	4B1	NA	AAC TTGGCATGCAC	GTTATATGGTATGATGGAAGTA ATGAAAACTATGCAGACTCCGT GAAGGGC	GATGGACGATCTTTGGAGTGG TC TTGGGGGACTAC
			SEQ ID NO: 2671 NFGMH	SEQ ID NO: 2828 VIWYDGSNENYADSVKG	SEQ ID NO: 2985 DGTIFGVVLGDY
		AA	SEQ ID NO: 1101	SEQ ID NO: 1258	SEQ ID NO: 1415

A-2165-WO-PCT

!PS:335938	6H1	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGGAAGTA ATAAATACTATGCAGACTCCGT GAAGGC	GATGGGACGATTTTGGAGTGC TCTTGGGGGACTAC
			SEQ ID NO: 2672	SEQ ID NO: 2829	SEQ ID NO: 2986
			YFGMH	VIWYDGSNKYYADSVKG	DGTIFGVLLGDY
!PS:335941	2F11	AA	SEQ ID NO: 1102	SEQ ID NO: 1259	SEQ ID NO: 1416
			AGCTATGGCATGCAC	GTTATATGGTATGATGGAAGTA ATAAATACTATGCAGACTCCGT GAAGGC	GATAGGACGATTTTGGAGTGG TTCTTGACTAC
			SEQ ID NO: 2673	SEQ ID NO: 2830	SEQ ID NO: 2987
!PS:335970	5C2	AA	SYGMH	VIWYDGSNKYYADSVKG	DRTIFGVVLDY
			SEQ ID NO: 1103	SEQ ID NO: 1260	SEQ ID NO: 1417
			GGCTACTATATCCAC	TGGATCAACCCCTGACAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGC	GAGGCCACGATTTTGGGAATGG TTATTGTACCGTTTGACTAC
!PS:335978	13H12	NA	SEQ ID NO: 2674	SEQ ID NO: 2831	SEQ ID NO: 2988
			GYIYH	WINPDSGGTDYSQRFG	EATIFGMVIVPFDY
			SEQ ID NO: 1104	SEQ ID NO: 1261	SEQ ID NO: 1418
!PS:335986	11C1	AA	GGCTACTATATCCAC	TGGATCAACCCCTGACAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGC	GAGGCCACGATTTTGGGAATGG TTATTGTACCGTTTGACTAC
			SEQ ID NO: 2675	SEQ ID NO: 2832	SEQ ID NO: 2989
			GYIYH	WINPDSGGTDYSQRFG	EATIFGMVIVPFDY
!PS:335986	11C1	NA	SEQ ID NO: 1105	SEQ ID NO: 1262	SEQ ID NO: 1419
			GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG ACACAAGCTATGCACAGAAAGT TTCAGGAC	GAGGCCACGATTTTGGGAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2676	SEQ ID NO: 2833	SEQ ID NO: 2990
!PS:335986	11C1	AA	GYIYH	WISPNSGDTSYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1106	SEQ ID NO: 1263	SEQ ID NO: 1420

A-2165-WO-PCT

!PS:33594	12H11	NA	GGCTACTATATACAC	TGGATAAGCCCTAACAAATGGTG ACACAAACTATGCACAGAAAGT TTCAGGAC	GAGGCCACGATTTTGGAAATGC TTATTGTACCATTTGACTAC
		AA	SEQ ID NO: 2677 GYYIH SEQ ID NO: 1107	SEQ ID NO: 2834 WISPNNGDTNYAQKFQD SEQ ID NO: 1264	SEQ ID NO: 2991 EATIFGMLIVPFDY SEQ ID NO: 1421
!PS:336024	18E3	NA	AGTGGTGGTTACTACTGGAGC	TACATCTATTACAGTGGGAGCA CCTACTACAACCCGTCCTCCTCAA GAGT	GATCGTATTACGATTTTGGAG TGGTTATGGGGGCGGTATGG ACGTC
		AA	SEQ ID NO: 2678 SGYYYS SEQ ID NO: 1108	SEQ ID NO: 2835 YIYSGSTYINPSLKS SEQ ID NO: 1265	SEQ ID NO: 2992 DRITIFGVVMGGMDV SEQ ID NO: 1422
!PS:336041	2G10_LC1	NA	AACTATGGCATGCAC	GCTATATGGTTTGATGGAAGTG ATAAATACTATGCAGACTCCGT GAAGGC	GATCAGGCGATTTTGGAGTGG TCCCCGACTAC
		AA	SEQ ID NO: 2679 NYGMH SEQ ID NO: 1109	SEQ ID NO: 2836 AIWFDGSDKYYADSVKG SEQ ID NO: 1266	SEQ ID NO: 2993 DQAIFGVVPDY SEQ ID NO: 1423
!PS:336077	4H9.004	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGGAAGTA ATAAATACTATGCAGACTCCGT GAAGGC	GATGGACGATTTTGGAGTGC TCCTTGGGGGACTAC
		AA	SEQ ID NO: 2680 YFGMH SEQ ID NO: 1110	SEQ ID NO: 2837 VIWYDGSNKYYADSVKG SEQ ID NO: 1267	SEQ ID NO: 2994 DGTIFGVLLGDY SEQ ID NO: 1424
!PS:336088	6A5.004	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGGAATA ATAAATACTATGCAGACTCCGT GAAGGC	GATCGGACGATTTTGGAGTGG TCCTTGAGTAC
		AA	SEQ ID NO: 2681 SYGMH SEQ ID NO: 1111	SEQ ID NO: 2838 AIWYDGNKNYYADSVKG SEQ ID NO: 1268	SEQ ID NO: 2995 DRTIFGVVLEY SEQ ID NO: 1425

A-2165-WO-PCT

!PS:336099	17H11.004	NA	AGTTACTACTGGAGC	CGTATCTATACCAGTGGGAGCA CCAACACTACAACCCCTCCCTCAA GAGT	GATGTAGCAGTGGCTGGCTTTG ACTAC
			SEQ ID NO: 2682	SEQ ID NO: 2839	SEQ ID NO: 2996
			SYYWS	RIYTSNSTYNPSLKS	DVA VAGFDY
!PS:359621	17H11.004.001	NA	SEQ ID NO: 1112	SEQ ID NO: 1269	SEQ ID NO: 1426
			AGTTACTACTGGAGC	CGTATCTATACCAGTGGGAGCA CCAACACTACAACCCCTCCCTCAA GAGT	GATGTAGCAGTGGCTGGCTTTG ACTAC
			SEQ ID NO: 2683	SEQ ID NO: 2840	SEQ ID NO: 2997
!PS:359781	4H9.004.001	AA	SYYWS	RIYTSNSTYNPSLKS	DVA VAGFDY
			SEQ ID NO: 1113	SEQ ID NO: 1270	SEQ ID NO: 1427
			TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGCG	GATGGGACGATTTTGGAGTGC TCTTGGGGGACTAC
!PS:360929	4H9.004.002	NA	SEQ ID NO: 2684	SEQ ID NO: 2841	SEQ ID NO: 2998
			YFGMH	VIWYDASNKYYADAVKG	DGTIFGVLLGDY
			SEQ ID NO: 1114	SEQ ID NO: 1271	SEQ ID NO: 1428
!PS:360936	4H9.004.003	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACTCCGT GAAGGCG	GATGGGACGATTTTGGAGTGC TCTTGGGGGACTAC
			SEQ ID NO: 2685	SEQ ID NO: 2842	SEQ ID NO: 2999
			YFGMH	VIWYDASNKYYADSVKG	DGTIFGVLLGDY
!PS:360936	4H9.004.003	AA	SEQ ID NO: 1115	SEQ ID NO: 1272	SEQ ID NO: 1429
			TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGCG	GATGGGACGATTTTGGAGTGC TCTTGGGGGACTAC
			SEQ ID NO: 2686	SEQ ID NO: 2843	SEQ ID NO: 3000
!PS:360936	4H9.004.003	AA	YFGMH	VIWYDASNKYYADAVKG	DGTIFGVLLGDY
			SEQ ID NO: 1116	SEQ ID NO: 1273	SEQ ID NO: 1430

A-2165-WO-PCT

!PS:360943	4H9.004.004	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGCG	GATGGGACGATTTTGGAGTGC TCTTGGGGGACTAC
			SEQ ID NO: 2687	SEQ ID NO: 2844	SEQ ID NO: 3001
			YFGMH	VIWYDASNKYYADAVKG	DGTIFGVLLGDY
!PS:360949	4H9.004.005	AA	SEQ ID NO: 1117	SEQ ID NO: 1274	SEQ ID NO: 1431
			TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGCG	GATGGGACGATTTTGGAGTGC TCTTGGGGGACTAC
			SEQ ID NO: 2688	SEQ ID NO: 2845	SEQ ID NO: 3002
!PS:359761	4H9.004.006	AA	YFGMH	VIWYDASNKYYADAVKG	DGTIFGVLLGDY
			SEQ ID NO: 1118	SEQ ID NO: 1275	SEQ ID NO: 1432
			TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGCG	GATAGGACGATTTTGGAGTGC TCTTGGGGGACTAC
!PS:360955	4B1.010	NA	SEQ ID NO: 2689	SEQ ID NO: 2846	SEQ ID NO: 3003
			YFGMH	VIWYDASNKYYADAVKG	DRTIFGVLLGDY
			SEQ ID NO: 1119	SEQ ID NO: 1276	SEQ ID NO: 1433
!PS:360962	4B1.011	AA	AACCTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACCTATGCAGACGCCG TGAAGGCG	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2690	SEQ ID NO: 2847	SEQ ID NO: 3004
			NFGMH	VIWYDASNENYADAVKG	DGTIFGVVLLGDY
!PS:360962	4B1.011	NA	SEQ ID NO: 1120	SEQ ID NO: 1277	SEQ ID NO: 1434
			AACCTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACCTATGCAGACGCCG TGAAGGCG	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2691	SEQ ID NO: 2848	SEQ ID NO: 3005
!PS:360962	4B1.011	AA	NFGMH	VIWYDASNENYADAVKG	DGTIFGVVLLGDY
			SEQ ID NO: 1121	SEQ ID NO: 1278	SEQ ID NO: 1435

A-2165-WO-PCT

!PS:360968	4B1.012	NA	AACCTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGC	GATGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2692	SEQ ID NO: 2849	SEQ ID NO: 3006
		AA	NFGMH	VIWYDASNENYADAVKG	DGTIFGVVLGDY
!PS:360974	4B1.013		SEQ ID NO: 1122	SEQ ID NO: 1279	SEQ ID NO: 1436
		NA	AACCTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACTCCGT GAAGGC	GATGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2693	SEQ ID NO: 2850	SEQ ID NO: 3007
!PS:360978	4B1.014	AA	NFGMH	VIWYDASNENYADSVKG	DGTIFGVVLGDY
			SEQ ID NO: 1123	SEQ ID NO: 1280	SEQ ID NO: 1437
		NA	AACCTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGC	GATGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
!PS:360978	4B1.014		SEQ ID NO: 2694	SEQ ID NO: 2851	SEQ ID NO: 3008
			NFGMH	VIWYDASNENYADAVKG	DGTIFGVVLGDY
		AA	SEQ ID NO: 1124	SEQ ID NO: 1281	SEQ ID NO: 1438
!PS:359785	4B1.015	NA	AACCTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGC	GATAGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2695	SEQ ID NO: 2852	SEQ ID NO: 3009
		AA	NFGMH	VIWYDASNENYADAVKG	DRTIFGVVLGDY
!PS:360982	4B1.016		SEQ ID NO: 1125	SEQ ID NO: 1282	SEQ ID NO: 1439
		NA	AACCTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGC	GATGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2696	SEQ ID NO: 2853	SEQ ID NO: 3010
!PS:360982	4B1.016	AA	NFGMH	VIWYDASNENYADAVKG	DGTIFGVVLGDY
			SEQ ID NO: 1126	SEQ ID NO: 1283	SEQ ID NO: 1440

A-2165-WO-PCT

!PS:335922	18F2	NA	AACCTTTGGCATGCAC	GTTATATGGTATGATGGAAGTA ATGAAAACTATGCAGACTCCGT GAAGGC	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2697	SEQ ID NO: 2854	SEQ ID NO: 3011
		AA	NFGMH	VIWYDGSNENYADSVKG	DGTIFGVVLGDY
!PS:360986	18F2.002		SEQ ID NO: 1127	SEQ ID NO: 1284	SEQ ID NO: 1441
		NA	AACCTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGC	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2698	SEQ ID NO: 2855	SEQ ID NO: 3012
!PS:360995	18F2.003	AA	NFGMH	VIWYDASNENYADAVKG	DGTIFGVVLGDY
			SEQ ID NO: 1128	SEQ ID NO: 1285	SEQ ID NO: 1442
		NA	AACCTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGC	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
!PS:360999	18F2.004		SEQ ID NO: 2699	SEQ ID NO: 2856	SEQ ID NO: 3013
		AA	NFGMH	VIWYDASNENYADAVKG	DGTIFGVVLGDY
			SEQ ID NO: 1129	SEQ ID NO: 1286	SEQ ID NO: 1443
!PS:361005	18F2.005	NA	AACCTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGC	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2700	SEQ ID NO: 2857	SEQ ID NO: 3014
		AA	NFGMH	VIWYDASNENYADAVKG	DGTIFGVVLGDY
!PS:361005	18F2.005		SEQ ID NO: 1130	SEQ ID NO: 1287	SEQ ID NO: 1444
		NA	AACCTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGC	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2701	SEQ ID NO: 2858	SEQ ID NO: 3015
!PS:361005	18F2.005	AA	NFGMH	VIWYDASNENYADAVKG	DGTIFGVVLGDY
			SEQ ID NO: 1131	SEQ ID NO: 1288	SEQ ID NO: 1445

A-2165-WO-PCT

!PS:361009	18F2.006	NA	AACCTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGC	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
		AA	SEQ ID NO: 2702	SEQ ID NO: 2859	SEQ ID NO: 3016
			NFGMH	VIWYDASNENYADAVKG	DGTIFGVVLGDY
!PS:361013	18F2.007	NA	AACCTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGC	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
		AA	SEQ ID NO: 2703	SEQ ID NO: 2860	SEQ ID NO: 3017
			NFGMH	VIWYDASNENYADAVKG	DGTIFGVVLGDY
!PS:361017	18F2.008	NA	AACCTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGC	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
		AA	SEQ ID NO: 2704	SEQ ID NO: 2861	SEQ ID NO: 3018
			NFGMH	VIWYDASNENYADAVKG	DGTIFGVVLGDY
!PS:361021	18F2.009	NA	AACCTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGC	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
		AA	SEQ ID NO: 2705	SEQ ID NO: 2862	SEQ ID NO: 3019
			NFGMH	VIWYDASNENYADAVKG	DGTIFGVVLGDY
!PS:361028	18F2.010	NA	AACCTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACTCCGT GAAGGC	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
		AA	SEQ ID NO: 2706	SEQ ID NO: 2863	SEQ ID NO: 3020
			NFGMH	VIWYDASNENYADSVKG	DGTIFGVVLGDY
		AA	SEQ ID NO: 1136	SEQ ID NO: 1293	SEQ ID NO: 1450

A-2165-WO-PCT

!PS:360535	18F2.011	NA	AAC	TTTGGCATGCAC		GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGC	GATAGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
		AA	SEQ ID NO: 2707		SEQ ID NO: 2864	SEQ ID NO: 3021	
			NFGMH		VIWYDASNENYADAVKG	DRTIFGVVLGDY	
!PS:361035	18F2.012	NA	AAC	TTTGGCATGCAC		GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGC	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
		AA	SEQ ID NO: 2708		SEQ ID NO: 2865	SEQ ID NO: 3022	
			NFGMH		VIWYDASNENYADAVKG	DGTIFGVVLGDY	
!PS:359940	2F11.002	NA		AGCTATGGCATGCAC		GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGC	GATAGGACGATTTTGGAGTGG TTCTTGACTAC
		AA	SEQ ID NO: 2709		SEQ ID NO: 2866	SEQ ID NO: 3023	
			SYGMH		VIWYDASNKYYADAVKG	DRTIFGVVLDY	
!PS:361039	2F11.003	NA		AGCTATGGCATGCAC		GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGC	GATAGGACGATTTTGGAGTGG TTCTTGACTAC
		AA	SEQ ID NO: 2710		SEQ ID NO: 2867	SEQ ID NO: 3024	
			SYGMH		VIWYDASNKYYADAVKG	DRTIFGVVLDY	
!PS:361043	2F11.004	NA		AGCTATGGCATGCAC		GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGC	GATAGGACGATTTTGGAGTGG TTCTTGACTAC
		AA	SEQ ID NO: 2711		SEQ ID NO: 2868	SEQ ID NO: 3025	
			SYGMH		VIWYDASNKYYADAVKG	DRTIFGVVLDY	
		AA		SEQ ID NO: 1141		SEQ ID NO: 1298	SEQ ID NO: 1455

A-2165-WO-PCT

!PS:361049	2F11.005	NA	AGCTATGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGC	GATAGGACGATTTTGGAGTGG TTCTTGACTAC
			SEQ ID NO: 2712	SEQ ID NO: 2869	SEQ ID NO: 3026
			SYGMH	VIWYDASNKYYADAVKG	DRTIFGVVLDY
!PS:361055	2F11.006	AA	SEQ ID NO: 1142	SEQ ID NO: 1299	SEQ ID NO: 1456
			AGCTATGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGC	GATAGGACGATTTTGGAGTGG TTCTTGACTAC
			SEQ ID NO: 2713	SEQ ID NO: 2870	SEQ ID NO: 3027
!PS:361059	2F11.007	AA	SYGMH	VIWYDASNKYYADAVKG	DRTIFGVVLDY
			SEQ ID NO: 1143	SEQ ID NO: 1300	SEQ ID NO: 1457
			AGCTATGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGC	GATAGGACGATTTTGGAGTGG TTCTTGACTAC
!PS:361063	2F11.008	NA	SEQ ID NO: 2714	SEQ ID NO: 2871	SEQ ID NO: 3028
			SYGMH	VIWYDASNKYYADAVKG	DRTIFGVVLDY
			SEQ ID NO: 1144	SEQ ID NO: 1301	SEQ ID NO: 1458
!PS:361063	2F11.008	AA	AGCTATGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGC	GATAGGACGATTTTGGAGTGG TTCTTGACTAC
			SEQ ID NO: 2715	SEQ ID NO: 2872	SEQ ID NO: 3029
			SYGMH	VIWYDASNKYYADAVKG	DRTIFGVVLDY
!PS:359949	2F11.009	NA	SEQ ID NO: 1145	SEQ ID NO: 1302	SEQ ID NO: 1459
			AGCTATGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACTCCGT GAAGGC	GATAGGACGATTTTGGAGTGG TTCTTGACTAC
			SEQ ID NO: 2716	SEQ ID NO: 2873	SEQ ID NO: 3030
!PS:359949	2F11.009	AA	SYGMH	VIWYDASNKYYADSVKG	DRTIFGVVLDY
			SEQ ID NO: 1146	SEQ ID NO: 1303	SEQ ID NO: 1460

A-2165-WO-PCT

!PS:359865	2F11.010	NA	AGCTATGGCATGCAC	GTTATATGGTATGATGGAAGTA ATAAATACTATGCAGACGCCGT GAAGGC	GATAGGACGATTTTGGAGTGG TTCTTGACTAC
			SEQ ID NO: 2717	SEQ ID NO: 2874	SEQ ID NO: 3031
		AA	SYGMH	VIWYDASNKYYADAVKG	DRTIFGVLLDY
!PS:359865	6H1.002		SEQ ID NO: 1147	SEQ ID NO: 1304	SEQ ID NO: 1461
		NA	TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGC	GATGGACGATTTTGGAGTGC TCTTGGGGGACTAC
			SEQ ID NO: 2718	SEQ ID NO: 2875	SEQ ID NO: 3032
!PS:359869	6H1.003	AA	YFGMH	VIWYDASNKYYADAVKG	DGTFGVLLGDY
			SEQ ID NO: 1148	SEQ ID NO: 1305	SEQ ID NO: 1462
		NA	TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGC	GATAGGACGATTTTGGAGTGC TCTTGGGGGACTAC
!PS:359873	6H1.004		SEQ ID NO: 2719	SEQ ID NO: 2876	SEQ ID NO: 3033
		AA	YFGMH	VIWYDASNKYYADAVKG	DRTIFGVLLGDY
			SEQ ID NO: 1149	SEQ ID NO: 1306	SEQ ID NO: 1463
!PS:359877	6H1.005	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGC	GATGGACGATTTTGGAGTGC TCTTGGGGGACTAC
			SEQ ID NO: 2720	SEQ ID NO: 2877	SEQ ID NO: 3034
		AA	YFGMH	VIWYDASNKYYADAVKG	DGTFGVLLGDY
!PS:359877	6H1.005		SEQ ID NO: 1150	SEQ ID NO: 1307	SEQ ID NO: 1464
		NA	TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGC	GATAGGACGATTTTGGAGTGC TCTTGGGGGACTAC
			SEQ ID NO: 2721	SEQ ID NO: 2878	SEQ ID NO: 3035
!PS:359877	6H1.005	AA	YFGMH	VIWYDASNKYYADAVKG	DRTIFGVLLGDY
			SEQ ID NO: 1151	SEQ ID NO: 1308	SEQ ID NO: 1465

A-2165-WO-PCT

!PS:361067	6H1.006	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGGAAGTA ATAAATACTATGCAGACTCCGT GAAGGC	GATGGGACGATTTTGGAGTGC TCTTGGGGGACTAC
			SEQ ID NO: 2722	SEQ ID NO: 2879	SEQ ID NO: 3036
		AA	YFGMH	VIWYDGSNKYYADSVKG	DGTIFGVLLGDY
!PS:361071	6H1.007		SEQ ID NO: 1152	SEQ ID NO: 1309	SEQ ID NO: 1466
		NA	TACTTTGGCATGCAC	GTTATATGGTATGATGGAAGTA ATAAATACTATGCAGACTCCGT GAAGGC	GATGGGACGATTTTGGAGTGC TCTTGGGGGACTAC
			SEQ ID NO: 2723	SEQ ID NO: 2880	SEQ ID NO: 3037
!PS:361075	6H1.008	AA	YFGMH	VIWYDASNKYYADSVKG	DGTIFGVLLGDY
			SEQ ID NO: 1153	SEQ ID NO: 1310	SEQ ID NO: 1467
		NA	TACTTTGGCATGCAC	GTTATATGGTATGATGGAAGTA ATAAATACTATGCAGACGCCGT GAAGGC	GATGGGACGATTTTGGAGTGC TCTTGGGGGACTAC
!PS:361079	6A5.004.001		SEQ ID NO: 2724	SEQ ID NO: 2881	SEQ ID NO: 3038
		AA	YFGMH	VIWYDGSNKYYADAVKG	DGTIFGVLLGDY
			SEQ ID NO: 1154	SEQ ID NO: 1311	SEQ ID NO: 1468
!PS:361085	6A5.004.002	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAATA ATAAATACTATGCAGACGCCGT GAAGGC	GATCGGACGATTTTGGAGTGG TCCTTGAGTAC
			SEQ ID NO: 2725	SEQ ID NO: 2882	SEQ ID NO: 3039
		AA	SYGMH	AIWYDANNKYYADAVKG	DRTIFGVVLEY
!PS:361085	6A5.004.002		SEQ ID NO: 1155	SEQ ID NO: 1312	SEQ ID NO: 1469
		NA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAATA ATAAATACTATGCAGACGCCGT GAAGGC	GATCGGACGATTTTGGAGTGG TCCTTGAGTAC
			SEQ ID NO: 2726	SEQ ID NO: 2883	SEQ ID NO: 3040
!PS:361085	6A5.004.002	AA	SYGMH	AIWYDANNKYYADAVKG	DRTIFGVVLEY
			SEQ ID NO: 1156	SEQ ID NO: 1313	SEQ ID NO: 1470

A-2165-WO-PCT

!PS:361091	6A5.004.003	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAAATA ATAAATACTATGCAGACGCCGT GAAGGC	GATCGGACGATTTTGGAGTGG TCCTTGAGTAC
			SEQ ID NO: 2727	SEQ ID NO: 2884	SEQ ID NO: 3041
			SYGMH	AIWYDANNKYYADAVKG	DRTIFGVVLEY
!PS:361095	6A5.004.004	AA	SEQ ID NO: 1157	SEQ ID NO: 1314	SEQ ID NO: 1471
			AGCTATGGCATGCAC	GCTATATGGTATGATGCAAATA ATAAATACTATGCAGACGCCGT GAAGGC	GATCGGACGATTTTGGAGTGG TCCTTGAGTAC
			SEQ ID NO: 2728	SEQ ID NO: 2885	SEQ ID NO: 3042
!PS:361101	6A5.004.005	AA	SYGMH	AIWYDANNKYYADAVKG	DRTIFGVVLEY
			SEQ ID NO: 1158	SEQ ID NO: 1315	SEQ ID NO: 1472
			AGCTATGGCATGCAC	GCTATATGGTATGATGCAAATA ATAAATACTATGCAGACGCCGT GAAGGC	GATCGGACGATTTTGGAGTGG TCCTTGAGTAC
!PS:361105	6A5.004.006	NA	SEQ ID NO: 2729	SEQ ID NO: 2886	SEQ ID NO: 3043
			SYGMH	AIWYDANNKYYADAVKG	DRTIFGVVLEY
			SEQ ID NO: 1159	SEQ ID NO: 1316	SEQ ID NO: 1473
!PS:361109	6A5.004.007	AA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAAATA ATAAATACTATGCAGACGCCGT GAAGGC	GATCGGACGATTTTGGAGTGG TCCTTGAGTAC
			SEQ ID NO: 2730	SEQ ID NO: 2887	SEQ ID NO: 3044
			SYGMH	AIWYDANNKYYADAVKG	DRTIFGVVLEY
!PS:361109	6A5.004.007	NA	SEQ ID NO: 1160	SEQ ID NO: 1317	SEQ ID NO: 1474
			AGCTATGGCATGCAC	GCTATATGGTATGATGCAAATA ATAAATACTATGCAGACGCCGT GAAGGC	GATCGGACGATTTTGGAGTGG TCCTTGAGTAC
			SEQ ID NO: 2731	SEQ ID NO: 2888	SEQ ID NO: 3045
!PS:361109	6A5.004.007	AA	SYGMH	AIWYDANNKYYADAVKG	DRTIFGVVLEY
			SEQ ID NO: 1161	SEQ ID NO: 1318	SEQ ID NO: 1475

A-2165-WO-PCT

!PS:361113	6A5.004.008	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGGAATA ATAAATACTATGCAGACGCCGT GAAGGC	GATCGGACGATTTTGGAGTGG TCCTTGAGTAC
		SEQ ID NO: 2732	SEQ ID NO: 2889	SEQ ID NO: 3046	
		SYGMH	AIWYDGNKKYYADAVKG	DRTIFGVVLEY	
!PS:361120	6A5.004.009	AA	SEQ ID NO: 1162	SEQ ID NO: 1319	SEQ ID NO: 1476
		NA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAATA ATAAATACTATGCAGACTCCGT GAAGGC	GATCGGACGATTTTGGAGTGG TCCTTGAGTAC
		SEQ ID NO: 2733	SEQ ID NO: 2890	SEQ ID NO: 3047	
!PS:359896	6A5.004.010	AA	SYGMH	AIWYDANNKYYADSVKG	DRTIFGVVLEY
		SEQ ID NO: 1163	SEQ ID NO: 1320	SEQ ID NO: 1477	
		NA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAATA ATAAATACTATGCAGACGCCGT GAAGGC	GATCGGACGATTTTGGAGTGG TCCTTGAGTAC
!PS:359890	6A5.004.011	AA	SEQ ID NO: 2734	SEQ ID NO: 2891	SEQ ID NO: 3048
		SYGMH	AIWYDANNKYYADAVKG	DRTIFGVVLEY	
		SEQ ID NO: 1164	SEQ ID NO: 1321	SEQ ID NO: 1478	
!PS:359567	2A11.002	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAATA ATAAATACTATGCAGACGCCGT GAAGGC	GATCGGACGATTTTGGAGTGG TCCTTGAGTAC
		AA	SEQ ID NO: 2735	SEQ ID NO: 2892	SEQ ID NO: 3049
		SYGMH	AIWYDANNKYYADAVKG	DRTIFGVVLEY	
!PS:359567	2A11.002	NA	SEQ ID NO: 1165	SEQ ID NO: 1322	SEQ ID NO: 1479
		NA	AGCTATGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGAAGACGCCGT GAAGGC	GGGATTACGATTTTGGTCATG GGTTTGAATAT
		SEQ ID NO: 2736	SEQ ID NO: 2893	SEQ ID NO: 3050	
!PS:359567	2A11.002	AA	SYGMH	VIWYDASNKYYEDAVKG	GITIFGHGFEY
		SEQ ID NO: 1166	SEQ ID NO: 1323	SEQ ID NO: 1480	

A-2165-WO-PCT

!PS:335965	2A11.003	NA	AGCTATGGCATGCAC	GTTATGGTATGATGGAAGTA ATAAATACTATGAAGACTCCGT GAAGGC	GGGATTACGATTTTGGTCATG GGTTTGAATAT
			SEQ ID NO: 2737	SEQ ID NO: 2894	SEQ ID NO: 3051
		AA	SYGMH	VIWYDGSNKYYEDSVKG	GITIFGHGEY
!PS:361158	2A11.004		SEQ ID NO: 1167	SEQ ID NO: 1324	SEQ ID NO: 1481
		NA	AGCTATGGCATGCAC	GTTATGGTATGATGGAAGTA ATAAATACTATGAAGACGCCGT GAAGGC	GGGATTACGATTTTGGTCATG GGTTTGAATAT
			SEQ ID NO: 2738	SEQ ID NO: 2895	SEQ ID NO: 3052
!PS:361165	2A11.005	AA	SYGMH	VIWYDGSNKYYEDAVKG	GITIFGHGEY
			SEQ ID NO: 1168	SEQ ID NO: 1325	SEQ ID NO: 1482
		NA	AGCTATGGCATGCAC	GTTATGGTATGATGCAAGTA ATAAATACTATGAAGACTCCGT GAAGGC	GGGATTACGATTTTGGTCATG GGTTTGAATAT
!PS:361172	2A11.005		SEQ ID NO: 2739	SEQ ID NO: 2896	SEQ ID NO: 3053
		AA	SYGMH	VIWYDASNKYYEDSVKG	GITIFGHGEY
			SEQ ID NO: 1169	SEQ ID NO: 1326	SEQ ID NO: 1483
!PS:361178	2G10_LC1.003	NA	AACATGGCATGCAC	GCTATATGGTTTGTGCAAGTG ATAAATACTATGCAGACGCCGT GAAGGC	GATCAGCGGATTTTGGAGTGG TCCCCGACTAC
			SEQ ID NO: 2740	SEQ ID NO: 2897	SEQ ID NO: 3054
		AA	NYGMH	AIWFDASDKYYADAVKG	DQAIFGVVPDY
!PS:361178	2G10_LC1.004		SEQ ID NO: 1170	SEQ ID NO: 1327	SEQ ID NO: 1484
		NA	AACATGGCATGCAC	GCTATATGGTTTGTGCAAGTG ATAAATACTATGCAGACTCCGT GAAGGC	GATCAGCGGATTTTGGAGTGG TCCCCGACTAC
			SEQ ID NO: 2741	SEQ ID NO: 2898	SEQ ID NO: 3055
!PS:361178	2G10_LC1.004	AA	NYGMH	AIWFDASDKYYADSVKG	DQAIFGVVPDY
			SEQ ID NO: 1171	SEQ ID NO: 1328	SEQ ID NO: 1485

A-2165-WO-PCT

!PS:361185	2G10_LC1.005	NA	AACTATGGCATGCAC	GCTATATGGTTTGATGGAAGTG ATAAATACTATGCAGACGCCGT GAAGGC	GATCAGCGGATTTTGGAGTGG TCCCCGACTAC
		SEQ ID NO: 2742	SEQ ID NO: 2899	SEQ ID NO: 3056	
		NYGMH	AIWFDGSDKYYADAVKG	DQAIFGVVPDY	
!PS:361192	2G10_LC1.006	AA	SEQ ID NO: 1172	SEQ ID NO: 1486	
		NA	AACTATGGCATGCAC	GATCAGCGGATTTTGGAGTGG TCCCCGACTAC	
		SEQ ID NO: 2743	SEQ ID NO: 2900	SEQ ID NO: 3057	
!PS:359609	2G10_LC1.007	AA	NYGMH	DQAIFGVVPDY	
		SEQ ID NO: 1173	SEQ ID NO: 1330	SEQ ID NO: 1487	
		AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTG ATAAATACTATGCAGACGCCGT GAAGGC	GATCAGCGGATTTTGGAGTGG TCCCCGACTAC	
!PS:359615	2G10_LC1.008	NA	SEQ ID NO: 2744	SEQ ID NO: 3058	
		AA	NYGMH	DQAIFGVVPDY	
		SEQ ID NO: 1174	SEQ ID NO: 1331	SEQ ID NO: 1488	
!PS:361196	2G10_LC1.009	NA	AACTATGGCATGCAC	GATCAGCGGATTTTGGAGTGG TCCCCGACTAC	
		AA	SEQ ID NO: 2745	SEQ ID NO: 3059	
		NYGMH	AIWFDGSDKYYADAVKG	DQAIFGVVPDY	
!PS:361196	2G10_LC1.009	NA	SEQ ID NO: 1175	SEQ ID NO: 1489	
		NA	AACTATGGCATGCAC	GATCAGCGGATTTTGGAGTGG TCCCCGACTAC	
		SEQ ID NO: 2746	SEQ ID NO: 2903	SEQ ID NO: 3060	
!PS:361196	2G10_LC1.009	AA	NYGMH	DQAIFGVVPDY	
		SEQ ID NO: 1176	SEQ ID NO: 1333	SEQ ID NO: 1490	

A-2165-WO-PCT

!PS:361202	2G10_LC1.010	NA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTG ATAAATACTATGCAGACGCCGT GAAGGC	GATCAGCGATTGTTTGGAGTGG TCCCCGACTAC
		SEQ ID NO: 2747	SEQ ID NO: 2904	SEQ ID NO: 3061	
!PS:359644	18E3.002	AA	NYGMH	AIWFDASDKYYADAVKG	DQAIFGVVPDY
		SEQ ID NO: 1177	SEQ ID NO: 1334	SEQ ID NO: 1491	
!PS:359628	18E3.003	NA	AGTGGTGGTTACTACTGGAGC	TACATCTATTACAGTGGGAGCA CCTACTACAACCCGTCCTCTCAA GAGT	GATCGTATTACGATTTTGGAG TGGTTATGGGGGCGGTATGG ACGTC
		SEQ ID NO: 2748	SEQ ID NO: 2905	SEQ ID NO: 3062	
!PS:359637	18E3.004	AA	SGGYYS	YIYSGSTYYNPSLKS	DRITIFGVVMGGGMDV
		SEQ ID NO: 1178	SEQ ID NO: 1335	SEQ ID NO: 1492	
!PS:359628	18E3.004	NA	AGTGGTGGTTACTACTGGAGC	TACATCTATTACAGTGGGAGCA CCTACTACAACCCGTCCTCTCAA GAGT	GATCGTATTACGATTTTGGAG TGGTTATGGGGGCGGTATGG ACGTC
		SEQ ID NO: 2749	SEQ ID NO: 2906	SEQ ID NO: 3063	
!PS:359637	18E3.005	AA	SGGYYS	YIYSGSTYYNPSLKS	DRITIFGVVMGGGMDV
		SEQ ID NO: 1179	SEQ ID NO: 1336	SEQ ID NO: 1493	
!PS:359628	18E3.005	NA	AGTGGTGGTTACTACTGGAGC	TACATCTATTACAGTGGGAGCA CCTACTACAACCCGTCCTCTCAA GAGT	GATCGTATTACGATTTTGGAG TGGTTATGGGGGCGGTATGG ACGTC
		SEQ ID NO: 2750	SEQ ID NO: 2907	SEQ ID NO: 3064	
!PS:359637	18E3.005	AA	SGGYYS	YIYSGSTYYNPSLKS	DRITIFGVVMGGGMDV
		SEQ ID NO: 1180	SEQ ID NO: 1337	SEQ ID NO: 1494	
!PS:359637	18E3.005	NA	AGTGGTGGTTACTACTGGAGC	TACATCTATTACAGTGGGAGCA CCTACTACAACCCGTCCTCTCAA GAGT	GATCGTATTACGATTTTGGAG TGGTTATGGGGGCGGTATGG ACGTC
		SEQ ID NO: 2751	SEQ ID NO: 2908	SEQ ID NO: 3065	
!PS:359637	18E3.005	AA	SGGYYS	YIYSGSTYYNPSLKS	DRITIFGVVMGGGMDV
		SEQ ID NO: 1181	SEQ ID NO: 1338	SEQ ID NO: 1495	

A-2165-WO-PCT

!PS:361210	18E3.006	NA	AGTGGTGGTTACTACTGGAGC	TACATCTATTACAGTGGGAGCA CCTACTACAACCCGTCCTCAA GAGT	GATCGTATTACGATTTTGGAG TGGTTATGGGGGCGGTATGG ACGTC
		AA	SEQ ID NO: 2752	SEQ ID NO: 2909	SEQ ID NO: 3066
			SGGYYS	YIYSGSTYYNPSLKS	DRITIFGVVMGGGMDV
!PS:361214	18E3.007	NA	AGTGGTGGTTACTACTGGAGC	TACATCTATTACAGTGGGAGCA CCTACTACAACCCGTCCTCAA GAGT	GATCGTATTACGATTTTGGAG TGGTTATGGGGGCGGTATGG ACGTC
		AA	SEQ ID NO: 2753	SEQ ID NO: 2910	SEQ ID NO: 3067
			SGGYYS	YIYSGSTYYNPSLKS	DRITIFGVVMGGGMDV
!PS:361218	18E3.008	NA	AGTGGTGGTTACTACTGGAGC	TACATCTATTACAGTGGGAGCA CCTACTACAACCCGTCCTCAA GAGT	GATCGTATTACGATTTTGGAG TGGTTATGGGGGCGGTATGG ACGTC
		AA	SEQ ID NO: 2754	SEQ ID NO: 2911	SEQ ID NO: 3068
			SGGYYS	YIYSGSTYYNPSLKS	DRITIFGVVMGGGMDV
!PS:361222	5C2.006	NA	GGCTACTATATCCAC	TGGATCAACCCCTGAAAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	SEQ ID NO: 1498 GAGGCCACGATTTTGGGAATGG TTATTGTACCGTTTGACTAC
		AA	SEQ ID NO: 2755	SEQ ID NO: 2912	SEQ ID NO: 3069
			GYIYH	WINPESGGTDYSQRFQG	EATIFGMVIVPFDY
!PS:361229	5C2.007	NA	GGCTACTATATCCAC	TGGATCAACCCCTGAAAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	SEQ ID NO: 1499 GAGGCCACGATTTTGGGAATGG TTATTGTACCGTTTGACTAC
		AA	SEQ ID NO: 2756	SEQ ID NO: 2913	SEQ ID NO: 3070
			GYIYH	WINPESGGTDYSQRFQG	EATIFGMVIVPFDY
			SEQ ID NO: 1186	SEQ ID NO: 1343	SEQ ID NO: 1500

A-2165-WO-PCT

!PS:361236	5C2.008	NA	GGCTACTATATCCAC	TGGATCAACCCCTGACGCTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGCCACGATTTTGGAAATGG TTATTGTACCGTTTGACTAC
		AA	SEQ ID NO: 2757 GYIYH SEQ ID NO: 1187	SEQ ID NO: 2914 WINPDAGGTDYSQRFQG SEQ ID NO: 1344	SEQ ID NO: 3071 EATIFGMVIVPFDY SEQ ID NO: 1501
		NA	GGCTACTATATCCAC	TGGATCAACCCCTGACGCTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGCCACGATTTTGGAAATGG TTATTGTACCGTTTGACTAC
!PS:359685	5C2.009	AA	SEQ ID NO: 2758 GYIYH SEQ ID NO: 1188	SEQ ID NO: 2915 WINPDAGGTDYSQRFQG SEQ ID NO: 1345	SEQ ID NO: 3072 EATIFGMVIVPFDY SEQ ID NO: 1502
		NA	GGCTACTATATCCAC	TGGATCAACCCCTGACAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGCCACGATTTTGGAAATGG TTATTGTACCGTTTGACTAC
		AA	SEQ ID NO: 2759 GYIYH SEQ ID NO: 1189	SEQ ID NO: 2916 WINPDSGGTDYSQRFQG SEQ ID NO: 1346	SEQ ID NO: 3073 EATIFGMVIVPFDY SEQ ID NO: 1503
!PS:361247	5C2.011	NA	GGCTACTATATCCAC	TGGATCAACCCCTGACAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGCCACGATTTTGGAAATGG TTATTGTACCGTTTGACTAC
		AA	SEQ ID NO: 2760 GYIYH SEQ ID NO: 1190	SEQ ID NO: 2917 WINPDSGGTDYSQRFQG SEQ ID NO: 1347	SEQ ID NO: 3074 EATIFGMVIVPFDY SEQ ID NO: 1504
		NA	GGCTACTATATCCAC	TGGATCAACCCCTGACAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGCCACGATTTTGGAAATGG TTATTGTACCGTTTGACTAC
!PS:361254	5C2.012	AA	SEQ ID NO: 2761 GYIYH SEQ ID NO: 1191	SEQ ID NO: 2918 WINPDSGGTDYSQRFQG SEQ ID NO: 1348	SEQ ID NO: 3075 EATIFGMVIVPFDY SEQ ID NO: 1505

A-2165-WO-PCT

!PS:361261	5C2.013	NA	GGCTACTATATCCAC	TGGATCAACCCCTGACGCTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGGCCACGATTTTGGAAATGG TTATTGTACCGTTTGACTAC
		AA	SEQ ID NO: 2762	SEQ ID NO: 2919	SEQ ID NO: 3076
			GYIYH	WINPDAGGTDYSQRFQG	EATIFGMVIVPFDY
!PS:361268	5C2.014	NA	GGCTACTATATCCAC	TGGATCAACCCCTGACGCTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGGCCACGATTTTGGAAATGG TTATTGTACCGTTTGACTAC
		AA	SEQ ID NO: 2763	SEQ ID NO: 2920	SEQ ID NO: 3077
			GYIYH	WINPDAGGTDYSQRFQG	EATIFGMVIVPFDY
!PS:359669	5C2.015	NA	GGCTACTATATCCAC	TGGATCAACCCCTGACGCTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGGCCACGATTTTGGAAATGG TTATTGTACCGTTTGACTAC
		AA	SEQ ID NO: 2764	SEQ ID NO: 2921	SEQ ID NO: 3078
			GYIYH	WINPDAGGTDYSQRFQG	EATIFGMVIVPFDY
!PS:359678	5C2.016	NA	GGCTACTATATCCAC	TGGATCAACCCCTGAAAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGGCCACGATTTTGGAAATGG TTATTGTACCGTTTGACTAC
		AA	SEQ ID NO: 2765	SEQ ID NO: 2922	SEQ ID NO: 3079
			GYIYH	WINPESGGTDYSQRFQG	EATIFGMVIVPFDY
!PS:361275	11C1.002	NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG AAACAAGCTATGCACAGAAGT TTCAGGAC	GAGGCCACGATTTTGGAAATGG TTATTGTACCATTTGACTAC
		AA	SEQ ID NO: 2766	SEQ ID NO: 2923	SEQ ID NO: 3080
			GYIYH	WISPNSGETSYAQKFQD	EATIFGMLIVPFDY
		AA	SEQ ID NO: 1196	SEQ ID NO: 1353	SEQ ID NO: 1510

A-2165-WO-PCT

!PS:361282	11C1.003	NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG ACACAAGCTATGCACAGAAGT TTCAGGAC	GAGGCCACGATTTTGGAAATGC TTATTGTACCATTTGACTAC
		AA	SEQ ID NO: 2767	SEQ ID NO: 2924	SEQ ID NO: 3081
			GYIYH	WISPSGDTSYAQKFQD	EATIFGMLIVPFDY
!PS:361289	11C1.004	NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG AAACAAGCTATGCACAGAAGT TTCAGGAC	GAGGCCACGATTTTGGAAATGC TTATTGTACCATTTGACTAC
		AA	SEQ ID NO: 2768	SEQ ID NO: 2925	SEQ ID NO: 3082
			GYIYH	WISPSGDTSYAQKFQD	EATIFGMLIVPFDY
!PS:359712	11C1.005	NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG AAACAAGCTATGCACAGAAGT TTCAGGAC	GAGGCCACGATTTTGGAAATGC TTATTGTACCATTTGACTAC
		AA	SEQ ID NO: 2769	SEQ ID NO: 2926	SEQ ID NO: 3083
			GYIYH	WISPSGDTSYAQKFQD	EATIFGMLIVPFDY
!PS:361293	11C1.006	NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG ACACAAGCTATGCACAGAAGT TTCAGGAC	GAGGCCACGATTTTGGAAATGC TTATTGTACCATTTGACTAC
		AA	SEQ ID NO: 2770	SEQ ID NO: 2927	SEQ ID NO: 3084
			GYIYH	WISPSGDTSYAQKFQD	EATIFGMLIVPFDY
!PS:361297	11C1.007	NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG AAACAAGCTATGCACAGAAGT TTCAGGAC	GAGGCCACGATTTTGGAAATGC TTATTGTACCATTTGACTAC
		AA	SEQ ID NO: 2771	SEQ ID NO: 2928	SEQ ID NO: 3085
			GYIYH	WISPSGDTSYAQKFQD	EATIFGMLIVPFDY
		AA	SEQ ID NO: 1201	SEQ ID NO: 1358	SEQ ID NO: 1515

A-2165-WO-PCT

!PS:361301	11C1.008	NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG ACACAAGCTATGCACAGAAAGT TTCAGGAC	GAGGCCACGATTTTGGAAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2772	SEQ ID NO: 2929	SEQ ID NO: 3086
		AA	GYIYH	WISPSGDTSYAQKFQD	EATIFGMLIVPFDY
!PS:359703	11C1.009		SEQ ID NO: 1202	SEQ ID NO: 1359	SEQ ID NO: 1516
		NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG AAACAAGCTATGCACAGAAAGT TTCAGGAC	GAGGCCACGATTTTGGAAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2773	SEQ ID NO: 2930	SEQ ID NO: 3087
!PS:361305	11C1.010	AA	GYIYH	WISPSGETSYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1203	SEQ ID NO: 1360	SEQ ID NO: 1517
		NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG AAACAAGCTATGCACAGAAAGT TTCAGGAC	GAGGCCACGATTTTGGAAATGC TTATTGTACCATTTGACTAC
!PS:361312	13H12.002		SEQ ID NO: 2774	SEQ ID NO: 2931	SEQ ID NO: 3088
		AA	GYIYH	WISPSGETSYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1204	SEQ ID NO: 1361	SEQ ID NO: 1518
!PS:361312	13H12.002	NA	GGCTACTATATCCAC	TGGATCAACCCCTGAAAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGGCCACGATTTTGGAAATGC TTATTGTACCGTTGACTAC
			SEQ ID NO: 2775	SEQ ID NO: 2932	SEQ ID NO: 3089
		AA	GYIYH	WINPESGGTDYSQRFQG	EATIFGMVIVPFDY
!PS:359744	13H12.003		SEQ ID NO: 1205	SEQ ID NO: 1362	SEQ ID NO: 1519
		NA	GGCTACTATATCCAC	TGGATCAACCCCTGAAAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGGCCACGATTTTGGAAATGC TTATTGTACCGTTGACTAC
			SEQ ID NO: 2776	SEQ ID NO: 2933	SEQ ID NO: 3090
!PS:359744	13H12.003	AA	GYIYH	WINPESGGTDYSQRFQG	EATIFGMVIVPFDY
			SEQ ID NO: 1206	SEQ ID NO: 1363	SEQ ID NO: 1520

A-2165-WO-PCT

!PS:361319	13H12.004	NA	GGCTACTATATCCAC	TGGATCAACCCCTGACAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGGCCACGATTTTGGAAATGG TTATTGTACCGTTTGACTAC
			SEQ ID NO: 2777	SEQ ID NO: 2934	SEQ ID NO: 3091
		AA	GYIYIH	WINPDSGGTDYSQRFGQ	EATIFGMVIVPFDY
!PS:359737	13H12.005		SEQ ID NO: 1207	SEQ ID NO: 1364	SEQ ID NO: 1521
		NA	GGCTACTATATCCAC	TGGATCAACCCCTGAAAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGGCCACGATTTTGGAAATGG TTATTGTACCGTTTGACTAC
			SEQ ID NO: 2778	SEQ ID NO: 2935	SEQ ID NO: 3092
!PS:361326	13H12.006	AA	GYIYIH	WINPESGGTDYSQRFGQ	EATIFGMVIVPFDY
			SEQ ID NO: 1208	SEQ ID NO: 1365	SEQ ID NO: 1522
		NA	GGCTACTATATCCAC	TGGATCAACCCCTGAAAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGGCCACGATTTTGGAAATGG TTATTGTACCGTTTGACTAC
!PS:361330	12H11.002		SEQ ID NO: 2779	SEQ ID NO: 2936	SEQ ID NO: 3093
		AA	GYIYIH	WINPESGGTDYSQRFGQ	EATIFGMVIVPFDY
			SEQ ID NO: 1209	SEQ ID NO: 1366	SEQ ID NO: 1523
!PS:361337	12H11.003	NA	GGCTACTATATACAC	TGGATAAGCCCTAACCAAGGT GAAACAACTATGCACAGAAG TTTCAGGAC	GAGGCCACGATTTTGGAAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2780	SEQ ID NO: 2937	SEQ ID NO: 3094
		AA	GYIYIH	WISPNQGETNYAQKFQD	EATIFGMLIVPFDY
!PS:361337	12H11.003		SEQ ID NO: 1210	SEQ ID NO: 1367	SEQ ID NO: 1524
		NA	GGCTACTATATACAC	TGGATAAGCCCTAACCAAGGT GACACAACTATGCACAGAAG TTTCAGGAC	GAGGCCACGATTTTGGAAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2781	SEQ ID NO: 2938	SEQ ID NO: 3095
!PS:361337	12H11.003	AA	GYIYIH	WISPNQGDNTY AQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1211	SEQ ID NO: 1368	SEQ ID NO: 1525

A-2165-WO-PCT

!PS:361344	12H11.004	NA	GGCTACTATATACAC	TGGATAAGCCCTAACCAAGGT GAAACAAACTATGCACAGAAG TTTCAGGAC	GAGGCCACGATTTTGGAAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2782	SEQ ID NO: 2939	SEQ ID NO: 3096
			GYIYIH	WISPNQGETNYAQKFQD	EATIFGMLIVPFDY
!PS:361351	12H11.005	AA	SEQ ID NO: 1212	SEQ ID NO: 1369	SEQ ID NO: 1526
			GGCTACTATATACAC	TGGATAAGCCCTAACCAATGGTG AAACAAACTATGCACAGAAGT TTTCAGGAC	GAGGCCACGATTTTGGAAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2783	SEQ ID NO: 2940	SEQ ID NO: 3097
!PS:361358	12H11.006	AA	GYIYIH	WISPNNGETNYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1213	SEQ ID NO: 1370	SEQ ID NO: 1527
			GGCTACTATATACAC	TGGATAAGCCCTAACCAATGGTG ACACAAACTATGCACAGAAGT TTTCAGGAC	GAGGCCACGATTTTGGAAATGC TTATTGTACCATTTGACTAC
!PS:361365	12H11.007	NA	SEQ ID NO: 2784	SEQ ID NO: 2941	SEQ ID NO: 3098
			GYIYIH	WISPNNGDTNYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1214	SEQ ID NO: 1371	SEQ ID NO: 1528
!PS:361372	12H11.008	AA	GGCTACTATATACAC	TGGATAAGCCCTAACCAAGGT GACACAAACTATGCACAGAAG TTTCAGGAC	GAGGCCACGATTTTGGAAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2785	SEQ ID NO: 2942	SEQ ID NO: 3099
			GYIYIH	WISPNQGDNTNYAQKFQD	EATIFGMLIVPFDY
!PS:361372	12H11.008	NA	SEQ ID NO: 1215	SEQ ID NO: 1372	SEQ ID NO: 1529
			GGCTACTATATACAC	TGGATAAGCCCTAACCAATGGTG AAACAAACTATGCACAGAAGT TTTCAGGAC	GAGGCCACGATTTTGGAAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2786	SEQ ID NO: 2943	SEQ ID NO: 3100
!PS:361372	12H11.008	AA	GYIYIH	WISPNNGETNYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1216	SEQ ID NO: 1373	SEQ ID NO: 1530

A-2165-WO-PCT

!PS:361379	12H11.009	NA	GGCTACTATATACAC	TGGATAAGCCCTAACCAAGGT GAAACAAACTATGCACAGAAG TTTCAGGAC	GAGGCCACGATTTTGGAAATGC TTATTGTACCATTTGACTAC
		AA	SEQ ID NO: 2787 GYYIH SEQ ID NO: 1217	SEQ ID NO: 2944 WISPNQGETNYAQKFQD SEQ ID NO: 1374	SEQ ID NO: 3101 EATIFGMLIVPFDY SEQ ID NO: 1531
!PS:361383	12H11.010	NA	GGCTACTATATACAC	TGGATAAGCCCTAACCAATGGTG ACACAAACTATGCACAGAAAGT TTTCAGGAC	GAGGCCACGATTTTGGAAATGC TTATTGTACCATTTGACTAC
		AA	SEQ ID NO: 2788 GYYIH SEQ ID NO: 1218	SEQ ID NO: 2945 WISPNNGDTNYAQKFQD SEQ ID NO: 1375	SEQ ID NO: 3102 EATIFGMLIVPFDY SEQ ID NO: 1532
!PS:361387	12H11.011	NA	GGCTACTATATACAC	TGGATAAGCCCTAACCAAGGT GACACAAACTATGCACAGAAG TTTCAGGAC	GAGGCCACGATTTTGGAAATGC TTATTGTACCATTTGACTAC
		AA	SEQ ID NO: 2789 GYYIH SEQ ID NO: 1219	SEQ ID NO: 2946 WISPNQGDNTNYAQKFQD SEQ ID NO: 1376	SEQ ID NO: 3103 EATIFGMLIVPFDY SEQ ID NO: 1533
!PS:361391	12H11.012	NA	GGCTACTATATACAC	TGGATAAGCCCTAACCAATGGTG AAACAAACTATGCACAGAAAGT TTTCAGGAC	GAGGCCACGATTTTGGAAATGC TTATTGTACCATTTGACTAC
		AA	SEQ ID NO: 2790 GYYIH SEQ ID NO: 1220	SEQ ID NO: 2947 WISPNNGETNYAQKFQD SEQ ID NO: 1377	SEQ ID NO: 3104 EATIFGMLIVPFDY SEQ ID NO: 1534
!PS:361395	12H11.013	NA	GGCTACTATATACAC	TGGATAAGCCCTAACCAAGGT GAAACAAACTATGCACAGAAG TTTCAGGAC	GAGGCCACGATTTTGGAAATGC TTATTGTACCATTTGACTAC
		AA	SEQ ID NO: 2791 GYYIH SEQ ID NO: 1221	SEQ ID NO: 2948 WISPNQGETNYAQKFQD SEQ ID NO: 1378	SEQ ID NO: 3105 EATIFGMLIVPFDY SEQ ID NO: 1535

A-2165-WO-PCT

!PS:361402	12H11.014	NA	GGCTACTATATACAC	TGGATAAGCCCTAACCAAGGT GAAACAAACTATGCACAGAAG TTTCAGGAC	GAGGCCACGATTTTGGAAATGC TTATTGTACCATTTGACTAC
		SEQ ID NO: 2792	SEQ ID NO: 2949	SEQ ID NO: 3106	SEQ ID NO: 3107
!PS:361406	2C2.005.001	AA	GYMH	WISPNQGETNYAQKFQD	EATIFGMLIVPFDY
		SEQ ID NO: 1222	SEQ ID NO: 1379	SEQ ID NO: 1536	SEQ ID NO: 1537
!PS:361412	2C2.005.002	NA	GGCTACTATATGCAT	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACAGAAAGT TTCAGGGC	GGGGGGATTACGTTTGGGGG ACTTATCGGCTCCTACTACT ACGGTATGGACGTC
		SEQ ID NO: 2793	SEQ ID NO: 2950	SEQ ID NO: 3108	SEQ ID NO: 3109
!PS:361418	2C2.005.003	AA	GYMH	WINPNSGGTNYAQKFQG	GGDYVWGTYPHYYYGMDV
		SEQ ID NO: 1223	SEQ ID NO: 1380	SEQ ID NO: 1538	SEQ ID NO: 1539
!PS:361424	2C2.005.004	NA	GGCTACTATATGCAT	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACAGAAAGT TTCAGGGC	GGGGGGATTACGTTTGGGGG ACTTATCGGCTCCTACTACT ACGGTATGGACGTC
		SEQ ID NO: 2794	SEQ ID NO: 2951	SEQ ID NO: 3109	SEQ ID NO: 3110
!PS:361418	2C2.005.003	AA	GYMH	WINPNSGGTNYAQKFQG	GGDYVWGTYPHYYYGMDV
		SEQ ID NO: 1225	SEQ ID NO: 1382	SEQ ID NO: 1539	SEQ ID NO: 1540
!PS:361424	2C2.005.004	NA	GGCTACTATATGCAT	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACAGAAAGT TTCAGGGC	GGGGGGATTACGTTTGGGGG ACTTATCGGCTCCTACTACT ACGGTATGGACGTC
		SEQ ID NO: 2796	SEQ ID NO: 2953	SEQ ID NO: 3110	SEQ ID NO: 3111
!PS:361418	2C2.005.003	AA	GYMH	WINPNSGGTNYAQKFQG	GGDYVWGTYPHYYYGMDV
		SEQ ID NO: 1226	SEQ ID NO: 1383	SEQ ID NO: 1540	SEQ ID NO: 1541

A-2165-WO-PCT

!PS:361430	2C2.005.005	NA	GGCTACTATATGCAT	TGGATCAACCCCTAACAGTGGTG GCACAAACTATGCACAGAAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGG ACTTATCGGCTCACTACTACT ACGGTATGGACGTC
		AA	SEQ ID NO: 2797 GYMH SEQ ID NO: 1227	SEQ ID NO: 2954 WINPNSGGTNYAQKFQG SEQ ID NO: 1384	SEQ ID NO: 3111 GGDYVWGTYPHYYYGMDV SEQ ID NO: 1541
!PS:361436	2C2.005.006	NA	GGCTACTATATGCAT	TGGATCAACCCCTAACAGTGGTG GCACAAACTATGCACAGAAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGG ACTTATCGGCTCACTACTACT ACGGTATGGACGTC
		AA	SEQ ID NO: 2798 GYMH SEQ ID NO: 1228	SEQ ID NO: 2955 WINPNSGGTNYAQKFQG SEQ ID NO: 1385	SEQ ID NO: 3112 GGDYVWGTYPHYYYGMDV SEQ ID NO: 1542
!PS:361442	2C2.005.007	NA	GGCTACTATATGCAT	TGGATCAACCCCTAACAGTGGTG GCACAAACTATGCACAGAAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGG ACTTATCGGCTCACTACTACT ACGGTATGGACGTC
		AA	SEQ ID NO: 2799 GYMH SEQ ID NO: 1229	SEQ ID NO: 2956 WINPNSGGTNYAQKFQG SEQ ID NO: 1386	SEQ ID NO: 3113 GGDYVWGTYPHYYYGMDV SEQ ID NO: 1543
!PS:361448	2C2.005.008	NA	GGCTACTATATGCAT	TGGATCAACCCCTAACAGTGGTG GCACAAACTATGCACAGAAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGG ACTTATCGGCTCACTACTACT ACGGTATGGACGTC
		AA	SEQ ID NO: 2800 GYMH SEQ ID NO: 1230	SEQ ID NO: 2957 WINPNSGGTNYAQKFQG SEQ ID NO: 1387	SEQ ID NO: 3114 GGDYVWGTYPHYYYGMDV SEQ ID NO: 1544
!PS:361454	2C2.005.009	NA	GGCTACTATATGCAT	TGGATCAACCCCTAACAGTGGTG GCACAAACTATGCACAGAAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGG ACTTATCGGCTCACTACTACT ACGGTATGGACGTC
		AA	SEQ ID NO: 2801 GYMH SEQ ID NO: 1231	SEQ ID NO: 2958 WINPNSGGTNYAQKFQG SEQ ID NO: 1388	SEQ ID NO: 3115 GGDYVWGTYPHYYYGMDV SEQ ID NO: 1545

A-2165-WO-PCT

!PS:361460	2C2.005.010	NA	GGCTACTATATGCAT	TGGATCAACCCCTAACAGTGGTG GCACAAACTATGCACAGAAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCTCACTACTACT ACGGTATGGACGTC
		AA	SEQ ID NO: 2802 GYVMH SEQ ID NO: 1232	SEQ ID NO: 2959 WINPNSGGTNYAQKFQG SEQ ID NO: 1389	SEQ ID NO: 3116 GGDYVWGTYPHYYYGMDV SEQ ID NO: 1546
!PS:361466	2C2.005.011	NA	GGCTACTATATGCAT	TGGATCAACCCCTAACAGTGGTG GCACAAACTATGCACAGAAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCTCACTACTACT ACGGTATGGACGTC
		AA	SEQ ID NO: 2803 GYVMH SEQ ID NO: 1233	SEQ ID NO: 2960 WINPNSGGTNYAQKFQG SEQ ID NO: 1390	SEQ ID NO: 3117 GGDYVWGTYPHYYYGMDV SEQ ID NO: 1547
!PS:361472	2C2.005.012	NA	GGCTACTATATGCAT	TGGATCAACCCCTAACAGTGGTG GCACAAACTATGCACAGAAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCTCACTACTACT ACGGTATGGACGTC
		AA	SEQ ID NO: 2804 GYVMH SEQ ID NO: 1234	SEQ ID NO: 2961 WINPNSGGTNYAQKFQG SEQ ID NO: 1391	SEQ ID NO: 3118 GGDYVWGTYPHYYYGMDV SEQ ID NO: 1548
!PS:361478	2C2.005.013	NA	GGCTACTATATGCAT	TGGATCAACCCCTAACAGTGGTG GCACAAACTATGCACAGAAAGT TTCAGGGC	GGGGGGGATTACGTTTTCGGGA CTTATCGGCTCACTACTACTA CGGTATGGACGTC
		AA	SEQ ID NO: 2805 GYVMH SEQ ID NO: 1235	SEQ ID NO: 2962 WINPNSGGTNYAQKFQG SEQ ID NO: 1392	SEQ ID NO: 3119 GGDYVFGTYPHYYYGMDV SEQ ID NO: 1549
!PS:361485	2C2.005.014	NA	GGCTACTATATGCAT	TGGATCAACCCCTAACAGTGGTG GCACAAACTATGCACAGAAAGT TTCAGGGC	GGGGGGGATTACGTTTTCGGGA CTTATCGGCTCACTACTACTA CGGTATGGACGTC
		AA	SEQ ID NO: 2806 GYVMH SEQ ID NO: 1236	SEQ ID NO: 2963 WINPNSGGTNYAQKFQG SEQ ID NO: 1393	SEQ ID NO: 3120 GGDYVFGTYPHYYYGMDV SEQ ID NO: 1550

A-2165-WO-PCT

!PS:361845	18F2.013	NA	AAC	TTTGGCATGCAC	GTTATGGTATGATGCAAGTA ATGAAACTATGCAGACGCCG TGAAGGC	GATAGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2807	SEQ ID NO: 2964	SEQ ID NO: 3121	
			NFGMH	VIWYDASNENYADAVKG	DRTIFGVVLGDY	
!PS:361851	6H1.009	AA	SEQ ID NO: 1237	SEQ ID NO: 1394	SEQ ID NO: 1551	
			TACTTTGGCATGCAC	GTTATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGC	GATAGGACGATTTTGGAGTGC TCTTGGGGGACTAC	
			SEQ ID NO: 2808	SEQ ID NO: 2965	SEQ ID NO: 3122	
!PS:361855	2C2.005.015	AA	YFGMH	VIWYDASNKYYADAVKG	DRTIFGVVLGDY	
			SEQ ID NO: 1238	SEQ ID NO: 1395	SEQ ID NO: 1552	
			GGCTACTATATGCAT	TGGATCAACCCCTAACAGTGGTG GCACAACTATGCACAGAAAGT TTCAGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCTCACTACTACT ACGGTATGGACGTC	
!PS:361855	2C2.005.015	NA	SEQ ID NO: 2809	SEQ ID NO: 2966	SEQ ID NO: 3123	
			GYYMH	WINPNSGGTNYAQKFQ	GGDYVWGTYPHYYYGMDV	
			SEQ ID NO: 1239	SEQ ID NO: 1396	SEQ ID NO: 1553	
!PS:336067	5G12.006	NA	AGCTATGGCATAAC	GTTATGGTATGATGCAAGTA ATAAGTTCCATGCAGACTCCGT GAAGGC	GGAAAAGTGGCTGGTATGCCT GAAAGCTTTTGAATC	
			SEQ ID NO: 2810	SEQ ID NO: 2967	SEQ ID NO: 3124	
			SYGIH	VIWYDGSNKFHDSVK	GKVAGMPEAFEI	
!PS:336169	17B11.002	AA	SEQ ID NO: 1240	SEQ ID NO: 1397	SEQ ID NO: 1554	
			AGTTATGATATCAAC	TGGATGAACCCCTAACAGTGGTA ACACAGGCTATGCACAGAAAGT TCCAGGC	GGGGGTGATTACGTTTGGGGG AGTTATCGTCCCTACTACTACT ACTACGGTATGGACGTC	
			SEQ ID NO: 2811	SEQ ID NO: 2968	SEQ ID NO: 3125	
!PS:336169	17B11.002	AA	SYDIN	WMNPNSGNTGYAQKFQ	GGDYVWGSYRPPYYYYGMDV	
			SEQ ID NO: 1241	SEQ ID NO: 1398	SEQ ID NO: 1555	

A-2165-WO-PCT

!PS:361127	5G12.006.001	NA	AGCTATGGCATAAC	GTTATATGGTATGATGCAAGTA ATAAGTTCCATGCAGACGCCGT GAAGGC	GGAAAAAGTGGTGGTATGCCT GAAAGCTTTTGAAATC
			SEQ ID NO: 2812	SEQ ID NO: 2969	SEQ ID NO: 3126
			SYGIH	VIWYDASNKFHADA VKG	GKVAGMPEAFEI
!PS:361136	5G12.006.002	AA	SEQ ID NO: 1242	SEQ ID NO: 1399	SEQ ID NO: 1556
			AGCTATGGCATAAC	GTTATATGGTATGATGCAAGTA ATAAGTTCCATGCAGACGCCGT GAAGGC	GGAAAAAGTGGTGGTATGCCT GAAAGCTTTTGAAATC
			SEQ ID NO: 2813	SEQ ID NO: 2970	SEQ ID NO: 3127
!PS:361140	5G12.006.003	AA	SYGIH	VIWYDASNKFHADA VKG	GKVAGMPEAFEI
			SEQ ID NO: 1243	SEQ ID NO: 1400	SEQ ID NO: 1557
			AGCTATGGCATAAC	GTTATATGGTATGATGCAAGTA ATAAGTTCCATGCAGACGCCGT GAAGGC	GGAAAAAGTGGTGGTATGCCT GAAAGCTTTTGAAATC
!PS:359919	5G12.006.004	NA	SEQ ID NO: 2814	SEQ ID NO: 2971	SEQ ID NO: 3128
			SYGIH	VIWYDASNKFHADA VKG	GKVAGMPEAFEI
			SEQ ID NO: 1244	SEQ ID NO: 1401	SEQ ID NO: 1558
!PS:361144	5G12.006.005	AA	AGCTATGGCATAAC	GTTATATGGTATGATGCAAGTA ATAAGTTCCATGCAGACGCCGT GAAGGC	GGAAAAAGTGGTGGTATGCCT GAAAGCTTTTGAAATC
			SEQ ID NO: 2815	SEQ ID NO: 2972	SEQ ID NO: 3129
			SYGIH	VIWYDASNKFHADA VKG	GKVAGMPEAFEI
!PS:361144	5G12.006.005	NA	SEQ ID NO: 1245	SEQ ID NO: 1402	SEQ ID NO: 1559
			AGCTATGGCATAAC	GTTATATGGTATGATGCAAGTA ATAAGTTCCATGCAGACTCCGT GAAGGC	GGAAAAAGTGGTGGTATGCCT GAAAGCTTTTGAAATC
			SEQ ID NO: 2816	SEQ ID NO: 2973	SEQ ID NO: 3130
!PS:361144	5G12.006.005	AA	SYGIH	VIWYDASNKFHADS VKG	GKVAGMPEAFEI
			SEQ ID NO: 1246	SEQ ID NO: 1403	SEQ ID NO: 1560

A-2165-WO-PCT

!PS:361151	5G12.006.006	NA	AGCTATGGCATAAC	GTTATATGGTATGTAAGTA ATAAGTTCCATGCAGACGCCGT GAAGGC	GGAAAAAGTGGTGGTATGCCT GAAAGCTTTTGAAATC
			SEQ ID NO: 2817	SEQ ID NO: 2974	SEQ ID NO: 3131
AA		AA	SYGIH	VIWYDGSNKFHADA VKG	GKVAGMPEAFEI
			SEQ ID NO: 1247	SEQ ID NO: 1404	SEQ ID NO: 1561
NA	17B11.002.001	NA	AGTTATGATATCAAC	TGGATGAACCCCTAACAGTGGTG GCACAGGCTATGCACAGAAAGT TCCAGGGC	GGGGTGATTACGTTTGGGGG AGTTATCGTCCCTACTACTACT ACTACGGTATGGACGTC
			SEQ ID NO: 2818	SEQ ID NO: 2975	SEQ ID NO: 3132
AA		AA	SYDIN	WMNPNSGGTGYAQKFQG	GGDYVWGSYRPPYYYGMDV
			SEQ ID NO: 1248	SEQ ID NO: 1405	SEQ ID NO: 1562
NA	17B11.002.002	NA	AGTTATGATATCAAC	TGGATGAACCCCTAACAGTGGTA ACACAGGCTATGCACAGAAAGT TCCAGGGC	GGGGTGATTACGTTTGGGGG AGTTATCGTCCCTACTACTACT ACTACGGTATGGACGTC
			SEQ ID NO: 2819	SEQ ID NO: 2976	SEQ ID NO: 3133
AA		AA	SYDIN	WMNPNSGNTGYAQKFQG	GGDYVWGSYRPPYYYGMDV
			SEQ ID NO: 1249	SEQ ID NO: 1406	SEQ ID NO: 1563
NA	17B11.002.003	NA	AGTTATGATATCAAC	TGGATGAACCCCTAACAGTGGTG GCACAGGCTATGCACAGAAAGT TCCAGGGC	GGGGTGATTACGTTTGGGGG AGTTATCGTCCCTACTACTACT ACTACGGTATGGACGTC
			SEQ ID NO: 2820	SEQ ID NO: 2977	SEQ ID NO: 3134
AA		AA	SYDIN	WMNPNSGGTGYAQKFQG	GGDYVWGSYRPPYYYGMDV
			SEQ ID NO: 1250	SEQ ID NO: 1407	SEQ ID NO: 1564
NA	17B11.002.004	NA	AGTTATGATATCAAC	TGGATGAACCCCTAACAGTGGTG GCACAGGCTATGCACAGAAAGT TCCAGGGC	GGGGTGATTACGTTTGGGGG AGTTATCGTCCCTACTACTACT ACTACGGTATGGACGTC
			SEQ ID NO: 2821	SEQ ID NO: 2978	SEQ ID NO: 3135
AA		AA	SYDIN	WMNPNSGGTGYAQKFQG	GGDYVWGSYRPPYYYGMDV
			SEQ ID NO: 1251	SEQ ID NO: 1408	SEQ ID NO: 1565

A-2165-WO-PCT

!PS:361514	17B11.002.005	NA	AGTTATGATATCAAC	TGGATGAACCCCTAACAGTGGTG GCACAGGCTATGCACAGAAAGT TCCAGGGC	GGGGGTGATTACGTTTGGGGG AGTTATCGTCCCTACTACTACT ACTACGGTATGGACGTC
			SEQ ID NO: 2822	SEQ ID NO: 2979	SEQ ID NO: 3136
			SYDIN	WMNPNSGGTGYAQKFQG	GGDYVWGSYRPPYYYYGMDV
!PS:360582	17B11.002.006	AA	SEQ ID NO: 1252	SEQ ID NO: 1409	SEQ ID NO: 1566
			AGTTATGATATCAAC	TGGATGAACCCCTAACAGTGGTA ACACAGGCTATGCACAGAAAGT TCCAGGGC	GGGGGTGATTACGTTTGGGGG AGTTATCGTCCCTACTACTACT ACTACGGTATGGACGTC
			SEQ ID NO: 2823	SEQ ID NO: 2980	SEQ ID NO: 3137
!PS:360518	17B11.002.007	AA	SYDIN	WMNPNSGNTGYAQKFQG	GGDYVWGSYRPPYYYYGMDV
			SEQ ID NO: 1253	SEQ ID NO: 1410	SEQ ID NO: 1567
			AGTTATGATATCAAC	TGGATGAACCCCTAACAGTGGTG GCACAGGCTATGCACAGAAAGT TCCAGGGC	GGGGGTGATTACGTTTTCGGGA GTTATCGTCCCTACTACTACTA CTACGGTATGGACGTC
!PS:360570	17B11.002.008	NA	SEQ ID NO: 2824	SEQ ID NO: 2981	SEQ ID NO: 3138
			SYDIN	WMNPNSGGTGYAQKFQG	GGDYVWGSYRPPYYYYGMDV
			SEQ ID NO: 1254	SEQ ID NO: 1411	SEQ ID NO: 1568
!PS:360570	17B11.002.008	NA	AGTTATGATATCAAC	TGGATGAACCCCTAACAGTGGTG GCACAGGCTATGCACAGAAAGT TCCAGGGC	GGGGGTGATTACGTTTTCGGGA GTTATCGTCCCTACTACTACTA CTACGGTATGGACGTC
			SEQ ID NO: 2825	SEQ ID NO: 2982	SEQ ID NO: 3139
			SYDIN	WMNPNSGGTGYAQKFQG	GGDYVWGSYRPPYYYYGMDV
!PS:362051	5G12.005.001	AA	SEQ ID NO: 1255	SEQ ID NO: 1412	SEQ ID NO: 1569
			AGCTATGGCATAAC	GTTATATGGTATGATGCAAGTA ATAAGTTCCATGCAGACGCCGT GAAGGC	GGAAAAGTGGCTGGTATGCCT GAAGCTTTTGAATC
			SEQ ID NO: 2826	SEQ ID NO: 2983	SEQ ID NO: 3140
!PS:362051	5G12.005.001	AA	SYGIH	VIWYDASNKFHADAVKG	GKVAGMPEAFEI
			SEQ ID NO: 1256	SEQ ID NO: 1413	SEQ ID NO: 1570

A-2165-WO-PCT

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

iPS#	Ab	Type	LC	HC
IPS:336175	2C2.005	NA	CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCCGGCAGAGGGTCACCATCTCTTGT CTGGAAGTAGCTCCAAACATCGGAAGTAATACTG TAAACTGGTACCAGCACCTCCAGGAACGGCCC CCAAACCTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTCTGTG CAACATTTCGATGACAGCCTGAATGGTCCGGTAT TCGGCGGAGGAGCCAAAGCTGACCGTCCTAGGTC AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCT GCCCTCCTCTGAGGAGCTTCAAGCCAAACAAGGC CACACTGGTGTGCTCATAGTGACTTCTACCCG GGAGCCGTGACAGTGGCTTGAAGGCAGATAG CAGCCCCGTCAGGCGGAGTGGAAGCACACCAC ACCCTCCAAACAAGCAACAACAAGTACGCGGC CAGCAGCTATCTGAGCCTGACGCTGAGCAGTG GAAGTCCACAGAAAGCTACAGCTGCCAGGTCAC GCATGAAGGAGCACCGTGGAGAGACAGTGG CCCCTACAGAATGTTC	CAGATGCAGGTGGTGCAGCTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCCGGATACACCTTACCCGGCTACTAT ATGCATTGGGTGCGACAGGCCCCCTGGACAAGGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGGCAAACTATGCACAGAAATTTTCAGGGC AGGTCAACCATGACAGGACACGTCCATCAGT ACAGCTACATGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGGGATTACGTTGGGGGACTTATCGGCCCTCAC TACTACTACGATGAGCTGACGTCTGGGGCCAAGG ACCACGGTCACCGTCTCCCTCAGCCTCCACCAAG GGCCCATCGGTCTCCCTCCCTGGCACCTCTCTCCA AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT GCCTGGTCAAGGACTACTTCCCGAACCCTGGTGA CGGTGTCGTGGAACCTCAGGCGCCCTGACCAGCG GCGTGACACCTTCCCGGTGTCTACAGTCTCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT CTGCAACGTGAATCAACAAGCCAGCAACACCAA GGTGGACAAGAAAGTTGAGCCCAATCTTGTGA CAAAACTCACACATGCCACCCGTGCCAGCACCC TGAACCTCTGGGGGACCGTCAGTCTTCTCTTC CCCCCAAACCCAAAGGACACCTCATGATCTCC CGGACCCCTGAGGTACATGCGTGGTGGTGAC GTGAGCCACGAAGACCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCC AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG CACGTACCGTTGTGTGTCAGCTCCACCGTCTCTG CACGAGGACTGGTGAATGGCAAGGAGTACAA GTGCAAGGTCTCCAAACAAGCCCTCCAGCCCC CATCGAGAAACCCTCTCCAAAGCCAAAGGGCA

A-2165-WO-PCT

			GCGCCGAGAACACAGGTGTACACCCCTGCCCC ATCCGGGAGGAGATGACCAAGAACAGGTCA GCTGACCTGCCTGGTCAAAGGCTTCTATCCCA GCGACATCGCCGTGGAGTGGGAGAGCAATGGG CAGCCGAGAACAACTACAGACACGCTCC GTGCTGACTCCGACGGCTCTTCTTCTCTATA GCAAGCTCACCGTGGACAAAGACAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAAACCACTACACGAGAGAGC CTCTCCCTGTCTCCGGTAAA
			SEQ ID NO: 1885 QSVLTQPPSASGTPGQRVITISCSGSSNIGSNTVNW YQHLPGTAPKLLIYTNNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDDSLNGPVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTTPSKQSNKYY AASSYLSLTPEQWKSRSYSCQVTHEGSTVEKTV APTECS
	AA		SEQ ID NO: 2042 QMQVVQSGAEVKKPGASVKVSCKASGYTFTGY MHWVRQAPGQGLEWMGWNPNSGGTNYAQKFQ GRVTMTTRDTSISTAYMELSRLSDDTA VYYCARG GDYVWGTYPHYYYGMDVWVWQGTTVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EYQGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LDSDGSEFLYSKLTVDKSRWQQGNVVFSCVMHEA LHNHYTQKLSLSPGK
IPS:335914	4B1	NA	SEQ ID NO: 315 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTAG GCTGTATCAGCAGAAACCAAGGAAGCCCTA AGCGCTGATCTATGTGTCATCCAGTTTGCAAA GTGGGTCCCTTCAAGGTTTCAGCGGCAGTGGAT CTGGACAGAAATTCATCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAACGAAACGGTGGCT
			SEQ ID NO: 472 CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCC TGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTTCAGTAACTTTGGCA TGC ACTGGTCCGCCAGGCTCCAGGC AAGGGC TGGAGTGGTGGCAGTTATATGGTATGATGGAA GTAATGAA AACTATGCAGACTCCGTGAAGGGCC GATTACCATCTCCAGAGACAATTCCAGAATA CGCTGTATCTGCACATGAACAGCCTGAGAGTCG CGGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTTGGGGGACTACT

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	GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAATCTGGAACCTGCCTCTGTGTGT GCCTGCTGAATACTTCTATATCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAA CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	GGGGCCAGGGAACCCCTGGTCACCCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGCTGCTTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGC CCTGACCAAGCGGCTGCACACCTTCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCACGTGAATCAACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACCC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTCCTCTTCCCCCAAAACCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGGACGTGAGCCACGAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCCTGTGTGTCAGCGT CCTCACCGTCTGCACCAAGGACTGGCTGAATGG CAAGGAGTACAAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCATCCCGGAGGAGATGACCA AGAACCAAGGTACGCTGACCTGCCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGACAACATAAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1886 DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLSQGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR TVAAPSVFIAPPPSDEQLKSGTASVVCLLNNFYPREA	SEQ ID NO: 2043 QVQLVESGGGVVQPGRSRLRSCAASGFTSFNFGM HWVRQAPGKGLEWVAVIWYDGSNENYADSVKIG RFTISRDNKNTLYLHMNSLRVADTA VYYCARDG TIFGVVLGDYWGQGTLTITVSSASTKGPSVFPLAPS

AA

A-2165-WO-PCT

			KVQWKVDNALQSGNSQESVTEQDSKDSYSTYLSST LTLKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC	SEQ ID NO: 316 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAAGGAAAGCCCTA AGCGCTGATCTATGGTGCAATCCAGTTTGCAAA GTGGGTCCCTTCAAGGTTCAAGGCGCAGTGGAT CTGGACAGAAATTCATCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAAACGAAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACCTGCCCTCTGTTGTT GCCTGCTGAATAACTTCTATCCCAAGAGAGGCCA AAGTACAGTGGAAAGTGGATAACGCCCTCCAAT CGGGTAACTCCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCAAAAGAGCTTCAACA GGGGAGAGTGT		
IPS:335938	6H1	NA		SEQ ID NO: 473 CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGATTCACTTCACTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGGAA GTAATAAATACTATGCAGACTCCGTGAAGGGCC GCTTCAACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTGGAGTGTCTTTGGGGGACTACT GGGGCCAGGGAACCTGGTCAACCTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCTCTCCAAAGAGCACCTCTGGGGGACACAGC GGCCTGGGCTGCCCTGGTCAAGGACTACTTCCC CGAAACCGGTGACGGTGTCTGTGGAACCTCAGGCGC CCTGACCAAGCGGTGTGACACACTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGGCC CAAATCTTGTGACAAAACTCACACATGCCACC GTGCCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGACGTGAGCCACGAAGACCCCTGA		

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				GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTACGGT CCTCACCGTCTGCACCAAGACTGGCTGAATGG CAAGGAGTACAAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCATCCCGGAGGAGATGACCA AGAACAGGTACGCTGACCTGCCGTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGAGACAACATAAAG ACCAGCCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA SEQ ID NO: 1887	SEQ ID NO: 2044
			AA	QVQLVESGGGVVQGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIYDGSNKYYADSVKG RFTISRDNKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGGQTLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK SEQ ID NO: 317	SEQ ID NO: 474
		2F11	941 IPS:335	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTEFT LTISLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR TVAAPSVFIIPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSITYLSST LTLISKADYEKHKVYACEVTHQGLSPVTKSFNRG EC SEQ ID NO: 317	SEQ ID NO: 474
		NA		GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCAATCTGTAGGAGACAGAGTCACCATCATT GCCAGGCGAGTCAGGACATTAGCAACTATTAA ATTGGTATCAGCAGAAACCAAGGGAAGCCCCCTA	SEQ ID NO: 474

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	AGCTCTGATCTACGATGCATCCAAATTTGGAAA CAGGGTCCCATCAAGGTTCAAGTGGAGTGGAT CTGGGACAGATTTTAGTTTCACCATCAGCAGCCT GCAGCCTGAAGATATTGCAACATATTACTGTCA ACAGTATGATATTCTCCTCACATTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGAACGGTGGCTG CACCATCTGTCTTCATCTTCCCGCCATCTGATGA GCAGTTGAAATCTGGAACCTGCCCTCTGTTGTGC CTGCTGAATAACTTCTATCCAGAGAGGCCAAA GTACAGTGAAGGTGGATAACGCCCTCCCAATCG GGTAACCTCCCAGGAGAGTGTACACAGACAGGAC AGCAAGGACAGCACCTACAGCCTCAGCAGCACC CTGACGCTGAGCAAAAGCAGACTACGAGAAACA CAAAGTCTACGCCTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCACAAAGAGCTTCAACAG GGGAGAGTGT	CTGGAGTGGGTGGCAGTTATATGGTATGATGGA AGTAATAAATACTATGCAGACTCCGTGAAGGGC CGATTACCATCTCCAGCGACAATTCCAAGAAC ACGCTGATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGACGATTTTGGAGTGGTCTTGGACTACTGG GGCCAGGGAACCTGGTCAACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGGTGCCCTGGTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCTGTGGAATCAGGCGCC CTGACCAAGGGGTGCACACCTTCCCGGCTGTC CTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACCTCACACATGCCAC GTGCCAGCACCTGAACCTCTGGGGGACCGTCT AGTCTTCTCTTCCCCCAAAACCAAGGACAC CCTCATGATCTCCCCGACCCCTGAGGTACATG CGTGGTGGTGACGTGAGCCACGAAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACCAGGTCAAGCTGACCTGCCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGACAACATAAAG ACCACGCTTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC

A-2165-WO-PCT

			SEQ ID NO: 1888	TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTAAA
			SEQ ID NO: 2045	QVQLVESGGGVVQGRSLRLSCAASGFTFSYGM HWVRQAPGKGLEWVAWIYDGSNKYYADSVKG RFTISDNSKNLTLYLQMNSLRAEDTAVYYCARDR TIFGVLDYWQGQTLVTVSSASTKGPSVFPLAPSS KSTSGGTAAALGCLVKDYFPEPTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNATKPKCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKA KQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
		AA	SEQ ID NO: 318	SEQ ID NO: 475
			DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGGTD FSFTISLQPEDIATYYCQQYDILLTFGGGTKVEIKR TVAAPSVFIIPPSDEQLKSGTASVCLLNFPYPREA KVQWKVDNALQSGNSQESVTEQDSKDSITYLSST LTLKADYEEKHKVYACEVTHQGLSSPVTKSFNRG EC	CAGTGCCGCTGGTGAGTCTGGGGCTGAGGTG AAGAAGCTGGGGCTCAGTGAAAGTCTCCTGCG AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATCCACTGGTGCGACAGGCCCTGGACAAAGGG CTTGAGTGGATGGGTGGATCAACCTGACAGT GGTGGCACAGACTATTACAGAGGTTTCAGGGC AGTTTACCATGACAGGACAGGACATCATCAGC ACAGCTACATGGAATGAACTGACAGGCTGAGATCT GACGACACGGCGGTGATTAATGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGAAACCTGGTCAACCGTCT CCTCAGCTCCACCAAGGGCCATCGGTCTTCCC CCTGGACCTCTCTCCAGAGACCTCTGGGGG CACAGCGCCCTGGGTGCTGGTCAAGGACTA CTTCCCAGAACCGGTGACGGTGTGTGGAACCTC AGCGCCCTGACCAAGCGGTGACACACCTTCCC GGGTGTCTACAGTCCCTCAGGACTCTACTCCCTC AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG
	5C2	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGCTCTGGGCGAGAGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAGAACTACATAGCTTGGTACCAGCAG CAACAGGACATCCTCCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGTCCCTGACC GATTCAAGTGGCAGCGGTCTGGGACAGATTTC CTCTCAACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGCCAAGGGACCAAGGTGGA AATCAAAACGAACGGTGGCTGCACCATCTGTCTT CATCTTCCCGCATCTGATGAGCAGTTGAAATCT GGAAGTCCCTCTGTGTGTGCTGCTGAATAACT TCTATCCAGAGAGGCCAAGTACAGTGGAAAGG TGGATAACGCCCTCCAATCGGGTAACCTCCAGG AGAGTGTACAGAGCAGGACAGCAAGGACAGC ACCTACAGCTCAGCAGCAGCCTGACGCTGAGC AAAGCAGACTACGAGAAACACAAAGTCTACGC	

A-2165-WO-PCT

		CTGCGAAGTCACCCATCAGGGCCTGAGCTCGCC CGTCACAAAGAGCTTCAACAGGGGAGAGTGT	GGACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCAATCTTGTGACAAAACTCACACATG CCCACCGTGCCAGCACCTGAACCTCTGGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGACGTGAGCCACGACAGAC CCTGAGGTCAGTTCAACTGGTACGTGGACGGC GTGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTG AGGTCCTCACCGTCTTGCACCAAGACTGGCTG AATGGCAAGGAGTCAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGCAGCCCCGAGAACCCACA GGTGACACCTGCCCATCCCGGAGGAGAT GACCAAGAACAGGTACGCTGACCTGCCTGGT CAAAGGCTTCTATCCAGCGACATCGCCGTGGA GTGGAGAGCAATGGCAGCCGAGAGACAACCT ACAAGACCAGCCTCCCGTGTGGACTCCGACG GCTCCTTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGATGAGGCTCTGCACAACCA CTACACGCAGAAAGAGCCTCTCCCCTGTCTCCGGG TAAA
	AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQPGHPPKLLIYWASTRESGVPDFSGS GSGTDFLTIISSLAEDVAIFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC	SEQ ID NO: 1889 SEQ ID NO: 2046 QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWINPDGGTDYSQRFQGR FTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI FGMVIVPFDYWQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLMISRTPETCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF

A-2165-WO-PCT

					YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK			
				SEQ ID NO: 319	SEQ ID NO: 476			
				GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGCGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAAGAACTACATAGCTTGGTACCAGCAG AAACAGGACATCCTCCTAAGCTGCTCATTTACT GGGCATCTACCCGGGAATCCGGGTCCCTGACC GATTGAGTGGCAGCGGTCTGGGACAGATTTCA CTCTCACCATCAGCAGCCTGCAGGCTGAAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAGGGACCAAGGTGGA AATCAAACGAACGGTGGCTGCACCATCTGTCTT CATCTTCCCGCCATCTGATGAGCAGTTGAAATCT GGAACTGCCCTCTGTTGTGTGCCTGCTGAATAACT TCTATCCCAGAGAGGCCAAAGTACAGTGGAAAG TGGATAACGCCCTCCAATCGGGTAACCTCCCAGG AGAGTGTCAACAGCAGGACAGCAAGGACAGC ACCTACAGCCTCAGCAGCACCCTGACGCTGAGC AAAGCAGACTACGAGAAACACAAAGTCTACGC CTGCGAAGTCAACCCATCAGGGCCTGAGCTCGCC CGTCACAAAGAGCTTCAACAGGGGAGAGTGT	NA	13H12	IPS:335978	CAGTGCCGCTGGTGCACTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGCTTCTGGATACACCTTCAACCGGCTACTAT ATCCACTGGTGCGACAGGCCCTGGACAAAGGA CTTGAGTGGATGGGTGGATCAACCTGACAGT GGTGGCACAGACTATTACAGAGGTTTTCAGGGC AGTTTACCATGACCAAGGACACGTCCATCAGC ACAGCTACATGGAACCTGAGCAGGCTGAGATCT GACGACACGGCGGTGATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTT ACTACTGGGGCCAGGAAACCTGGTCAACCGTCT CCTCAGCTCCACCAAGGGCCCATCGGTCTTCCCC CCTGGACCCCTCTCCAAAGAGCACTCTGGGGG CACAGCGGCCCTGGGTGCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCTGGAACCTC AGCGCCCTGACCAAGCGGCGTGCACACCTTCCCC GGCTGTCTACAGTCTCTCAGGACTCTACTCCCTC AGCAGCTGTGTGACCGTGCCCTCCAGCAGCTTG GGCACCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCAAAATCTTGTGACAAAACCTCACACATG CCCACCGTGCCAGCACCTGAACTCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTCT ACATGCGTGGTGGTGGACGTGAGCCACGAAAGAC CCTGAGGTCAAGTTCAAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTCTC AGCGTCTCACCGTCTCTGCACCAAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAC AAAGCCCTCCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACCCACA

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			SEQ ID NO: 1890 GGTGACACCCTGCCCATCCCGGAGGAGAT GACCAAGAACAGGTGACCTGACCTGCCTGGT CAAAGGCTTCTATCCAGCACATCGCCGTGGA GTGGAGAGCAATGGCAGCCGAGAACAACT ACAAGACCAGCCTCCCGTGTGCTGACTCCGACG GCTCTTCTTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGATGAGGCTCTGCAACAACA CTACACGAGAAAGAGCCTCTCCCCTGTCTCCCGG TAAA
			SEQ ID NO: 2047 QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYI HWVRQAPGQGLEWMGWINPDSGGTDYSQRFQGR FTMTRDTSISTAYMELSLRSDDTAVYYCAREATI FGMVIVPFDYWQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLISRTPETVTVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	AA		SEQ ID NO: 320 DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQKPGHPPKLLIYWASTRESGVPDFRFGS GSGTDFLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC
			SEQ ID NO: 477 CAGGTGCCGCTGGTACAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCCGGCTACTAT ATACACTGGTGCCTCAGGCCCTGGACAAGGG CTTGTGTGATGGGTGGATCAGCCCTAACAGT GGTGACACAAAGTATGCACAGAAATTTTCAGGAC AGGTCACCATGACCAGGGACACGTCCATCAGC ACAGCCTATATGAGCTGAGCAGACTGAGATCT GACGACACGGCGTGTATTCTGTACGAGAGAG
IPS:335986	11C1	NA	SEQ ID NO: 1890 GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTATTATCCAGCTCC AACAATAAGAACTACTTAGCTTGTAACCAACAG AAACCAGGACAGCTCCTAACCTGCTCATTAC TGGACTTCTACCCGAGATTCCGGGTCCCTGAC CGATTTCAGTGGCAGCGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTACGCAATATTATCGTA

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	CTCCGTGGACGTTTCGGCCAAAGGGACCACAGGTGG AAATCAAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAATC TGGAACCTGCCCTCTGTTGTGTCCTGCTGAATAAC TTCTATCCAGAGAGGCCAAAGTACAGTGAAG GTGGATAACGCCCTCCAAATCGGGTAACTCCAG GAGAGTGTACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCTGACGCTGAG CAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCAACCCATCAGGGCCTGAGCTCGC CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGAAACCCCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGACCCCTCCTCCAAGAGCACCTCTTGGGGG CACAGCGGCCCTGGGCTGCCGTGGTCAAGGACTA CTTCCCGAACCGGTGACGGTGTCTGTGGAATC AGCGCCCTGACCAAGCGGCGTGCACACCTTCCC GGTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCAATCTTGTGACAAACTCACACATG CCCACCGTGCCCAAGCACCTGAACCTCTGGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGGACGTGAGCCACGAAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCTCTCACCCTCTGCACCAGGACTGGCTG AATGGCAAGGAGTCAAGTGAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAGCCAAAGGGCAGCCCCGAGAACCCACA GGTGTACACCTGCCCTCCCATCCCGGAGGAGAT GACCAAGAACCAAGGTGACCTGACCTGCCCTGGT CAAAGGCTTCTATCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGACGCCGAGAGACAAT ACAAGACCAGCCCTCCCGTGTGGACTCCGACG GCTCTTCTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGATGAGGCTCTGCACAACCA CTACACGACGAAGAGCCTCTCCCCTGTCTCCGGG TAAA
	SEQ ID NO: 1891	SEQ ID NO: 2048
AA	DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDFSG	QVPLVQSGAEVKKPGASVKVSKKASGYTFTGYI HWVRRAPGQGLVWMGWISPNSGDTSYAQKFQDR

A-2165-WO-PCT

			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSYLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC	VTMTRDTSISTAYMELSRRLSDDTAVYFCTREATI FGMLIVPFEDYWGGQTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLISRTEPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFCFVSMHEALHNHYTQKS LSLSPGK
			SEQ ID NO: 321	SEQ ID NO: 478
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGCGAGAGGGCCACCAATCAAC TGCAAGTCCAGCCAGAGTGTITATCCAGCTCC AACATAAGAACTACTTAGCTTGGTACCAGCAG AAACGAGGACAGCTCTCAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTACCATCAACAGCCTGCAAGGCTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTCCGGCCAGGGACCAAGGTGG AAATCAACAGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAATC TGGAAGTCCCTCTGTGTGTGCTGCTGCTGAATAAC TTCTATCCAGAGAGGCCAAAGTACAGTGGAG GTGGATAACGCCCTCCAAATCGGGTAACTCCAG GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCCTGACGCTGAG CAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCAACCATCAGGGCCTGAGCTCGC CCGTACAAAGAGCTTCAACAGGGGAGAGTGT	CAGTGCCGCTGGTGCACTTGGGGCTGAGGTG AAGAAGCTGGGGCTCAGTGAAAGTCTCCTGC AAGCTTCTGGATACACCTTCAACCGGCTACTAT ATACACTGGTGCGTCAAGGCCCTGGACAAAGG CTTGAAGTGGTGGTGGATAGCCCTAACAAAT GGTGACACAACTATGCACAGAAATTTTCAGGAC AGGTCAACATGACAGGACACGTCCTCATCAGC ACAGCTATATGAGCTGAGCAGGCTGAGATCT GACGACACGGCGGTGATTAATGTACGAGAGAG GCCACGATTTTGGAAATGCTTATGTACCAATTTG ACTACTGGGGCCAGGGAACCCCTGGTCAACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCTCTCTCCAGAGCACTCTGGGGG CACAGCGCCCTGGGTGCTGGTCAAGGACTA CTTCCCAGAACCGGTGACGGTGTCTGGAACTC AGCGCCCTGACCAAGCGGCTGCACACCTTCCC GGGTCTCTACAGTCTCAGGACTCTACTCCCTC AGCAGGTGGTGAACGCTGCCCTCCAGCAGCTTG GGCACCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCAATCTTGTGACAAACTCACACATG CCCACCGTGGCCAGCACCTGAACCTCTGGGGG ACCGTCAGTCTCTCTCTTCCCCCAAAACCCAAAG
IPS:335994	12H11	NA		

A-2165-WO-PCT

					GACACCCCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGTGACGTGAGCCACGAGAC CCTGAGGTCAAGTTC AACTGGTACGTGGACGGC GTGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCGTCTCACCGTCTTGCACCAAGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAGCCAAAGGCAGCCCCGAGAACACACA GGTGACACCCCTGCCCATCCCGGAGGAGAT GACCAAGAACAGGTACGCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGAGAGCAATGGCAGCCGAGAGACAACCT ACAAGACCAGCCTCCCGTGTGCTGACTCCGACG GCTCTTCTTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGATGAGGCTCTGCACAACCA CTACACGAGAAAGAGCCTCTCCCTGTCTCCGGG TAAA
				SEQ ID NO: 1892	SEQ ID NO: 2049
				DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDFSG SGSGTDFTLTINSLQAEDVAVYQCQQYYRTPWTF GQGTKVEIKRTVAAPSVFIPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYLSSTLTLSKADYEKHKVYACEVTHQQLSS PVTKSFNRGEC	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWISPNNGDTNYAQKFQD RVTMTRDTSISTAYMELSRLSDDTA VYYCTREA TIFGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGT AALGCLVKDYFPEPTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYIC NVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLEPPPKPKDTLMISRTPEVTCVVVDVSH DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNQKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL YSKLTVDKSRWQQGNVVFSCSVMEALHNHYTQK SLSLSPGK
			AA		

A-2165-WO-PCT

			SEQ ID NO: 322	SEQ ID NO: 479
IPS:336024	18E3	NA	GAAATTGTGTGACGCAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCCGGCTCCTCATCTATGTTGCATCCAGCAGGG CCACTGGCATCCAGACAGGTTCAAGTGGCAGTG GGTCTGGGACAGACTTCACTCTCACCATCAGCA GACAGGAGCCTGATGATTTTGCAGTGATTACT GTCAGCAGTATGGTAGTTTCAACCGCTCACTTCGG CGGAGGGACCAAGGTGGAGATCAACGAACGG TGGCTGCACCATCTGTCTTCATCTTCCCGCCATC TGATGAGCAGTTGAAATCTGGAACCTGCCTCTGT TGTGTGCCTGCTGAATAACTTCTATCCAGAGA GGCCAAAGTACAGTGGAGGTGGATAACGCCCT CCAATCGGGTAACCTCCAGGAGAGTGTACACGA GCAGGACAGCAAGGACAGCACCTACAGCCTCA GCAGCACCTTGACGCTGAGCAAAAGCAGACTACG AGAAACACAAAGTCTACGCTGCGAAGTCAACC ATCAGGGCCTGAGCTCGCCCGTCCACAAAGAGCT TCAACAGGGGAGAGTGT	CAGGTGCAGTTGCAGGAGTCGGGCCAGGACTG GTGAAGCCCTTCACAGACCCCTGTCCCTCACCTGC ACTGTCTCTGGTACTCCATCAGCAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCACCCAGGGA AGGGCTGGAGTGGATTGGGTACATCTATTACA GTGGGAGCACCTACTACAACCCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGTCCTAAGA ACCAGTCTCCCTGAAGCTGAGCTCTGTGACTGC CGGGACACGGCCGTGTATTACTGTGCGAGAGA TCGTATTACGATTTTGGAGTGGTTATGGGGGGC GGATATGACGTCTGGGGCCAAAGGACCAACGGTC ACCGTCTCTCAGCCTCCACCAAGGGCCCATCG GTCCTCCCCCTGGCACCCCTCCTCCAAGAGCACCT CTGGGGGCACAGCGGCCCTGGGCTGCCCTGGTCA AGGACTACTTCCCCGAACCGGTGACGGTGTCTGT GGAAGTCAAGGCGCCCTGACCAGCGGCGTGCACA CCTCCCGGCTGTCTACAGTCTCAGGACTCTA CTCCCTCAGCAGCGTGGTGAACCGTCCCTCCAG CAGCTTGGGCACCCAGACCTACATCTGCAACGT GAATCACAAGCCCAAGCAACCAAGGTGGACA AGAAAGTTGAGCCCAATCTTGTGACAAAACCTC ACACATGCCACCCGTGCCAGCACCTGAACCTCC TGGGGGACCGTCACTCTTCTCTTCCCCCCTCAA ACCCAAGGACACCCCTCATGATCTCCCGGACCCC TGAGGTACATGCGTGGTGGTGGACGTGAGCCA CGAAGACCCCTGAGGTCAAGTTCAACTGGTACGT GGACGGCGTGGAGGTGCATAATGCCAAGACAA AGCCGTGTAGGAGCAGTACGGCAGCACGTACC GTTGTGTACGCTCTCACCGTCTCTGCACCCAGG ACTGGCTGAATGGCAAGGAGTACAAGTGCAAG GTCTCCAACAAGCCCTCCAGCCCCCATCGAG AAAACCATCTCCAAGCCAAAGGGCAGCCCCCGA GAACCCACAGGTGTACACCTGTCCCCCATCCCGG GAGGAGATGACCAAGAACCAAGGTGAGCCTGAC CTGCCTGGTCAAGGCTTCTATCCAGCGACAT

A-2165-WO-PCT

				CGCCGTGGAGTGGGAGAGCAATGGGCAGCCGG AGAACAACTACAGACCACGCTCCCGTGTGG ACTCCGACGGCTCTTCTTCTCTATAGCAAGCT CACCGTGGACAAGAGCAGGTGGCAGCAGGGGA ACGTCTTCTCATGCTCCGTGATGCATGAGGCTCT GCACAACCACTACACGAGAGAGCCTCTCCCT GTCTCCGGGTAAA
			SEQ ID NO: 1893	SEQ ID NO: 2050
			EIVLTQSPGTLSPGERATLSCRASQISYSYLA YQKPGQAPRLIYGASSRATGIPDRFSGSGTDF TLISRQEPDDFAVYYCQQYGSSPLTFGGGKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSYSL STLTLSKADYEKHKVYACEVTHQGLSPVTKSFN RGE	QVQLQESGPGLVKPSQTLSTCTVSGDSISSGGYY WSWIRHPGKGLEWIGYIYSGSTYYNPSLKSRT ISVDTSKNQFSLKLSVTAADTAVYCARDRTIFG VVMGGMDVWVGQGTTVTVSSASTKGPSVFP SSKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL GGPSVFLFPPKPKDITMISRPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
		AA	SEQ ID NO: 323	SEQ ID NO: 480
			GAAATAGTGATGACGCAGTCTCCAGCCACCCCTG TCTGTCTCTCCAGGGGAAAGAGCCACCCCTCC TGCAGGGCCAGTCAGAGTGTAGCAGCAACTTA GCCTGGTACCAGCAGAAACCTGGCCAGCTCCC AGGCTCCTCATCTATGGTGCAGCCACCAAGGCC ACTGGTATCCCAGCCAGGGTCAAGTGGCAGTGGG TCTGGGACACAGATTCACTCTACCATCAGCAGC CTGCAGTCTGAAGATTTTGCAAGTTTATTACTGTC AGCAGTATAAATCTGGCCTCTCACTTCGGCG GAGGGACCAAGGTGGAGATCAACGAAACGGTG GCTGCACCATCTGTCTTCACTTCCCGCCATCTG ATGAGCAGTTGAAATCTGGAACCTGCCTCTGTG TGTGCCCTGCTGAATACTTCTATCCCAGAGAGG	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTACCTTCACTAATATGCG ATGCACTGGTCCGCGAGGTCCAGGCGAGGGG CTGGAGTGGTGGCAGCTATATGGTTTGATGGA AGTGATAAATACTATGCAGACTCCGTGAAGGGC CGATTACCATCTCCAGAGACAATCCAAAGAAC ACGCTGATCTGCAAATGAACAGCTTGAGAGCC GAGGACACGGCTGTGTATTAATGTGCGAGAGAT CAGCGCATTTTGGAGTGTGTTCCCGCACTACTGG GGCAGGGAACCCCTGGTCAACCTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA CCCTCCTCCAAAGAGCACCTCTGGGGGCACAGCG
IPS:336041	2G10 LCI	NA		

A-2165-WO-PCT

	CCAAAGTACAGTGGAAGGTGGATAACGCCCTCC AATCGGGTAACCTCCAGGAGAGTGTCACAGAGC AGGACAGCAAGGACAGCACCTACAGCCTCAGC AGCACCTGACGCTGAGCAAGCAGACTACGAG AAACACAAAGTCTACGCCCTGCGAAGTCACCCAT CAGGGCCTGAGCTCGCCCGTCAACAAAGAGCTTC AACAGGGGAGAGTGT	GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC GAACCGGTACGGTGTCTGTGGAACCTCAGGGCC CTGACCAGCGCGTGCACACCTTCCCGGCTGTC CTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAAGCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACCTCACACATGCCACCC GTGCCAGCACCTGAACCTCTGGGGGACCCGTC AGTCTTCTCTTCCCCCAAAACCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGTGGTGACGTGAGCCACGAGAACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCAATAAGCCAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAAGACTGGCTGAATGG CAAGGAGTACAAAGTGCAAGGTCTCCACAAAGC CCTCCAGCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAAGCCCGGAGAACCCACAGGTGT ACACCTGCCCCATCCCGGAGGAGATGACCA AGAACAGGTACGCTGACCTGCTGCTGCTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGAGCCGGAGACAACATACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1894 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLIYGAAATRAATGIPARVSGSGGTE FTLTISLSQSEDFVYQCQQYNWPLTFGGGKVE IKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEN	SEQ ID NO: 2051 QVQLVESGGGVVQPGRSRLRSCAASGFTFSNYGM HWVRQAPGEGLEWVAIWFDSGDKYYADSVKGG RFTISRDNKNTLYQMNSLRAREDVAVYCARDQ AIFGVVPDYWGQGLVTVSSASTKGPSVFPLAPSS KSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNV NHPKPSNTKVDKKVEPKSCDKTHHTCPPCPAPELLG

AA

[illegible]

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				CCCTACCGTCTGCACCAAGGACTGGCTGAATGG CAAGGAGTACAAAGTGCAAGGTCTCCAAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACAGGTACGCTGACCTGCCCTGGTCAAAG GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTAAA
				SEQ ID NO: 1895 DIQMTQSPSSLSASVGDRVTITCRASQGI RNELGW YQQKPGKAPKRLIYGASSLSQSGVPSRFSGSGSTE FTLTISLQPEDFVITYCLQHNSYPFTFGPGTKVDV KRTVAAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLS STLTLSKADYEKHKVYACEVTHQGLSPVTKSFN RGE C
			AA	SEQ ID NO: 2052 QVQLVESGGGVVQPGRSRLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIYDGSNKYYADSVKG RFTISRDNKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGLTVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLISRTPETCVVDVSHED PEVKFNWYVDGVEVHNATKPKCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
				SEQ ID NO: 325 GACATCCAGATACCCAGTCTCCATCCTCCCTGT CTGCAATCTGTGGGGACAGAGTCACCATCAGCTT GCCAGGCGAGTCAGGACATTACCAACTATTAA ATTGGTATCAGCAGAAACCAAGGAAAGCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGTCCCATCAAGGTTTCAGTGGAAAGTGGATC TGGGACAGATTTTACTTTTACCATCATCAGCAGCCTG
IP:336088	6A5.004	NA		SEQ ID NO: 482 CAGTGCAAGCTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCTCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGTGGCAGCTATATGGTATGATGGAA ATAATAAATACTATGACAGACTCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTTCCAGAACA

A-2165-WO-PCT

CAGCCTGAAGATATTGCAACATATTACTGTCAA CAGTATGATGATCTATTCACTTTCGGCCCTGGGA CCAAAGTGGATATCAAACGACGGTGGCTGCAC CATCTGCTTTCATCTTCCCGCCATCTGATGAGCA GTTGAAATCTGGAACCTGCCTCTGTTGTGCTG CTGAATAACTTCTATCCCAGAGAGGCCAAAGTA CAGTGGAAGGTGGATAACGCCCTCCATCGGGT AACTCCAGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGCAGCACCT GACGCTGAGCAAAAGCAGACTACGAGAAACACA AAGTCTACGCCCTGCGAAGTCAACCCATCAGGGC TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGG GAGAGTGT	CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTGGAGTGGTCTTGAGTACCTCG GCCAGGAACCTGGTCAACCGTCTCTCAGCCT CCACCAAGGGCCATCGGTCTTCCCCCTGGCAC CCTCTCCAAGAGCACCTCTGGGGGACAGGG CCCTGGGCTGCCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCTGGAACCTCAGGCGCC TGACCAGCGGCTGCACACCTTCCCCGGCTGTCC TACAGTCTCAGGACTCTACTCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAAGCCAG CAACACCAAGGTGGACAAAGATTGAGCCCA AATCTGTGACAAAACTCACACATGCCACCCGT GCCCAGCACCTGAACCTCTGGGGGACCGTCAG TCTTCTCTTCCCCCAAAACCAAGGACACCT CATGATCTCCGGACCCCTGAGGTACATGCGT GGTGGTGGACGTGAGCCACGAAGACCTGAGGT CAAGTTCAACTGTACGTGGACGGCTGGAGGT GCATAATGCCAAGACAAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTACGCGTCC TCACCGTCTGCACCAAGGACTGGGTGAATGGCA AGGAGTACAAGTGCAAGTCTCCAACAAAGCCC TCCCAGCCCCCATCGAGAAAACCATCTCCAAAG CCAAAGGCGAGCCCCGAGAACCCACAGGTGTAC ACCTGCCCCCATCCCCGGGAGGAGATGACCAAG AACAGGTACGCTGACCTGCCCTGGTCAAAAGGC TTCTATCCCAGCGACATCGCCGTGGAGTGGGAG AGCAATGGGCAAGCGGAGAACAACTACAAGAC CAGCCTCCCTGCTGGACTCCGACGGCTCCTTC TTCCTCTATAGCAAGCTCACCGTGGACAAAGC AGTGGCAGCAGGGGACGTCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACAG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
SEQ ID NO: 1896	SEQ ID NO: 2053

A-2165-WO-PCT

		AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNLYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGGTD FTFTISLQPEDIATYYCQQYDDLFTFGPGTKVDIK RTVAAPSFIIPPSPDEQLKSGTASVCLLNFFPRE AKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS TLTLKADYEEKHKVYACEVTHQGLSSPVTKSFNR GEC	QVQLVESGGGVVQPGRLRLSCAASGFSFSSYGM HWVRQPPGKGLVWVAIWDGNKKYYADSVKG RFTISRDSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYLGQGLVVDYFPEPVTVSWNSGALTSGV STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP SVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAAKTKPCEEQYGSTYRCVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYITLPPSRREEMTKNQVSLTCLVKGFYPS DIAVEVESNGQPENNYKTTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL SPGK
			SEQ ID NO: 326 GACATCCAGATGACCCAGTCTCCATCTTCCGTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GTCGGCGAGTCAGGGTCTTATCATCTGGTTAG CCTGGTATCAGCAGAAACCGGGAAAGCCCCCTA AACTCTGATCTATGCTGCATCCAGTTTGCAAG TGGGTCCCATCAAGGTTCAAGCGGCGAGTGGCTC TGGGACAGATTTCACCTCTCACCATCAGCAGCCT ACAGCCTGAAGATTTTGCAACTTACTATTGTCAA CAGACTAACAGTTTCCCTCCGACGTTCCGGCCAA GGGACCAAGGTGGAAATCAACGAAACGGTGGC TGCAACCATCTGTCTTCATCTTCCCGCCATCTGAT GAGCAGTTGAAATCTGGAACTGCCTCTGTTGTG TGCTGTGCTGAATAACTTCTATCCAGAGAGGCC AAAGTACAGTGGAAAGGTGGATAACGCCCTCCAA TCGGGTAACTCCAGGAGAGTGTACAGAGCAG GACAGCAAGGACAGCACCTACAGCCTCAGCAGC ACCTTGACGCTGAGCAAGCAGACTACGAGAA ACACAAAGTCTACGCTGCGAAGTCAACCCATCA GGCCTGAGCTCGCCCGTCACAAAGAGCTTCAA CAGGGGAGAGTGT	SEQ ID NO: 483 CAGTGCAGCTGCAGGAGTCGGGCCAGGACTG GTGAAGCCTTCGGAGAGCCCTGTCCCTCACCTGC ACTGTCTCAGGGTCCATCAGTAGTTACTACT GGAGCTGGATCCGCAGCCCGCGGGAAGGGA CTAGAGTGGATTGCCGTATCTATACAGTGGG AGCACCAACTACAACCCCTCCCTCAAGAGTCA GTCACCATGTCAATAGACACGTCCCAAGAACCA TTCTCCCTGAACCTGAACCTGTGACCCGCCGCG GACACGGCCGTGATTAATCTGTGCGAGAGATGTA GCAGTGGCTGGCTTTGACTACTGGGGCCAGGGA ACCTGGTCAACGCTCTCCTCAGCTCCACCAAG GGCCATCGGTCTTCCCTCCCTGGCACCTCTCCCA AGAGCACCTCTGGGGGACAGCGGCCCTGGGCT GCCTGGTCAAGGACTACTTCCCGCAACCGGTGA CGGTGTGCTGGAACTCAGGGGCCCTGACCAGCG GCGTGACACACCTTCCCGGCTGTCTACAGTCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT GCCCTCCAGCAGTTGGGACCCAGACCTACAT CTGCAACGTGAATCAAGCCCAAGCAACACCAA GGTGGACAAGAAAGTTGAGCCCAATCTTGTGA CAAACCTCACACATGCCCCACCGTGCCCAAGCACC
IPS:336099	17H11.004	NA	SEQ ID NO: 326 GACATCCAGATGACCCAGTCTCCATCTTCCGTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GTCGGCGAGTCAGGGTCTTATCATCTGGTTAG CCTGGTATCAGCAGAAACCGGGAAAGCCCCCTA AACTCTGATCTATGCTGCATCCAGTTTGCAAG TGGGTCCCATCAAGGTTCAAGCGGCGAGTGGCTC TGGGACAGATTTCACCTCTCACCATCAGCAGCCT ACAGCCTGAAGATTTTGCAACTTACTATTGTCAA CAGACTAACAGTTTCCCTCCGACGTTCCGGCCAA GGGACCAAGGTGGAAATCAACGAAACGGTGGC TGCAACCATCTGTCTTCATCTTCCCGCCATCTGAT GAGCAGTTGAAATCTGGAACTGCCTCTGTTGTG TGCTGTGCTGAATAACTTCTATCCAGAGAGGCC AAAGTACAGTGGAAAGGTGGATAACGCCCTCCAA TCGGGTAACTCCAGGAGAGTGTACAGAGCAG GACAGCAAGGACAGCACCTACAGCCTCAGCAGC ACCTTGACGCTGAGCAAGCAGACTACGAGAA ACACAAAGTCTACGCTGCGAAGTCAACCCATCA GGCCTGAGCTCGCCCGTCACAAAGAGCTTCAA CAGGGGAGAGTGT	SEQ ID NO: 483 CAGTGCAGCTGCAGGAGTCGGGCCAGGACTG GTGAAGCCTTCGGAGAGCCCTGTCCCTCACCTGC ACTGTCTCAGGGTCCATCAGTAGTTACTACT GGAGCTGGATCCGCAGCCCGCGGGAAGGGA CTAGAGTGGATTGCCGTATCTATACAGTGGG AGCACCAACTACAACCCCTCCCTCAAGAGTCA GTCACCATGTCAATAGACACGTCCCAAGAACCA TTCTCCCTGAACCTGAACCTGTGACCCGCCGCG GACACGGCCGTGATTAATCTGTGCGAGAGATGTA GCAGTGGCTGGCTTTGACTACTGGGGCCAGGGA ACCTGGTCAACGCTCTCCTCAGCTCCACCAAG GGCCATCGGTCTTCCCTCCCTGGCACCTCTCCCA AGAGCACCTCTGGGGGACAGCGGCCCTGGGCT GCCTGGTCAAGGACTACTTCCCGCAACCGGTGA CGGTGTGCTGGAACTCAGGGGCCCTGACCAGCG GCGTGACACACCTTCCCGGCTGTCTACAGTCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT GCCCTCCAGCAGTTGGGACCCAGACCTACAT CTGCAACGTGAATCAAGCCCAAGCAACACCAA GGTGGACAAGAAAGTTGAGCCCAATCTTGTGA CAAACCTCACACATGCCCCACCGTGCCCAAGCACC

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					TGAACTCCTGGGGGACCGTCAGTCTTCCTCTTC CCCCAAAACCCAAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTCACATGCGTGGTGGTGAC GTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCC AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG CACGTACCCTGTGTCAAGCGTCTCACCCGTCTG CACCAGGACTGGCTGAATGGCAAGGAGTACAA GTGCAAGGTCTCCAAACAAAGCCCTCCAGCCCC CATCGAGAAACCATCTCCAAGCCAAAGGCA GCCCCGAGAACCACAGGTGTACACCTGCCCCC ATCCCGGAGGAGATGACCAAGAACACAGGTCA GCTTGACCTGCCCTGTCAAAGGCTTCTATCCCA GCGACATCGCCGTGGAGTGGGAGAGCAATGGG CAGCCGGAACAACACTACAAGACCACGCCCTCCC GTGCTGACTCCGACGGCTCCTTCTTCTCTCTATA GCAAGCTCACCGTGGACAAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACCACTACACGCAGAAAGAGC CTCTCCCTGTCTCCGGTAAA
				SEQ ID NO: 1897	SEQ ID NO: 2054
				DIQMTQSPSSVSASVGDRVTITCRASQGLIWLAW YQQKPGKAPKLLIYAASSLQSGVPSRFSGSGGTD FTLTISSLQPEDFATYYCQQTNISFPPTFGQGTKVEI KRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS STLTLSKADYEKHKVYACEVTHQGLSPVTKSFN RGEK	QVQLQESGPGLVKPSETLSLTCTVSQGSISYYWS WIRQPAKGLEWIGRIYTSGSTNYPNLSKSRVTMS IDTSKNQFSLKLSNVTADTA VYYCARDVA VAGF DYWGQGTLLVTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVTVPSSSLGTQTYICNVNHNKPSNT KVDKKVEPKSCDKTHITCPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAAKTKECEEQYGSTYRCVSVLTIVLHQ DWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKKS RWQQGNVFSCSVMHEALHNHYTQKLSLSLSPGK
			AA		

A-2165-WO-PCT

					SEQ ID NO: 327	SEQ ID NO: 484		
					GACATCCAGATGACCCAGTCTCCATCTTCCGTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GTCGGCGAGTCAGGGTCTTATCATCTGGTTAG CCTGGTATCAGCAGAAACCGGGAAAGCCCTA AACTCTGATCTATGCTGCATCCAGTTTGCAAAG TGGGTCCCATCAAGGTTACAGGGCAGTGGCTC TGGGACAGATTTTCACCTCTCACCATCAGCAGCCT ACAGCCTGAAGATTTTGCAACTTACTATTGTCAA CAGACTAACAGTTTCCCTCCGACGTTCCGGCCAA GGGACCAAGGTGGAATCAAACGAACGGTGGC TGCAACATCTGTCTTTCATCTTCCCGCCATCTGAT GAGCAGTTGAAATCTGGAACTGCCTCTGTTGTG TGCCCTGCTGAATAACTTCTATCCAGAGAGGCC AAAGTACAGTGGAAAGGTGGATAACGCCCTCCAA TCGGGTAACCTCCAGGAGAGTGTACAGAGCAG GACAGCAAGGACAGCACCTACAGCCTCAGCAGC ACCCTGACGCTGAGCAAGCAGACTACGAGAA ACACAAGTCTACGCCCTGCGAAGTCAACCCATCA GGGCTGAGCTCGCCCGTCAACAAGAGCTTCAA CAGGGGAGAGTGT	NA		CAGGTGCAGCTGCAGGAGTCGGGCCAGGACTG GTGAAGCCTTCGGAGACCTGTCCCTCACCTGC ACTGTCTCTGGGGCTCCATCAGTAGTTACTACT GGAGCTGGATCCGGCAGCCCGCCGGGAAGGGA CTAGAGTGGATTGGCCGTATCTATACCAAGTGG AGCACCAACTACAACCCCTCCCTCAAGAGTCA GTCAACCATGTCAATAGACACGTCCAAAGAACCAG TTCTCCCTGAAACTGAACTCTGTGACCCGCCGCG GACACGGCCGTGTATTACTGTGCGGAGAGATGTA GCAGTGGCTGGCTTTGACTACTTGGGGCCAGGGA ACCTGGTCAACCGTCTCCTCAGCCTCCACCAAG GGCCATCGGTCTTCCCTCCCTGGCACCTCCTCCA AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT GCCTGGTCAAAGGACTACTTCCCGCAACCGGTGA CGGTGCTGTGGAACCTCAGGCCCTGACCAAGCG GCGTGACACACTTCCCGGTGTCTACAGTCCCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT GCCCTCCAGCAGCTTGGGCACCCAGACTACAT CTGCAACGTGAATCAAGCCCAAGCAACACCAA GGTGACAAGAAAGTTGAGCCCAATCTTGTGA CAAACCTCACACATGCCACCGTGCCCAAGCAC TGAACTCTGGGGGACCGTCAGTCTTCTCTTC CCCCAAAACCAAGGACACCTCATGATCTCC CGGACCCCTGAGGTACATGCGTGGTGGTGAC GTGAGCCACGAAGACCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCC AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG CACGTACCGTTGTGTACGCTCTCACCGTCTG CACCAGGACTGGCTGAATGGCAAGGAGTACAA GTGCAAGGTCTCCAACAAGGCCCTCCAGCCCC CATCGAGAAACCATCTCCAAGCCAAAGGGA GCCCCGAGAACCAAGGTGTACACCTGCCCCC ATCCCGGAGAGATGACCAAGAACCAAGGTCA GCCTGACCTGCCTGGTCAAGGCTTCTATCCCA GCGACATCGCCGTGGAGTGGGAGAGCAATGGG

17H11.004.001

IPS:359621

NA

A-2165-WO-PCT

				SEQ ID NO: 1898 DIQMTQSPSSVSASVGDRVITITCRASQGLIWLAW YQQKPGKAPKLLIYAASSLQSGVPSRFSGSGGTD FTLTISLQPEDFATYYCQQTNFPPTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSITYSL STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEK	SEQ ID NO: 1898 DIQMTQSPSSVSASVGDRVITITCRASQGLIWLAW YQQKPGKAPKLLIYAASSLQSGVPSRFSGSGGTD FTLTISLQPEDFATYYCQQTNFPPTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSITYSL STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEK	SEQ ID NO: 2055 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWS WIRPAGKLEWIGRIYTSGTNYPNPSLKSRVTMS IDTSKNQFSKLNSVTAADTA VYCARDVA VAGF DYWGQGTLLVTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVTVPSSSLGTQTYICNVNHNKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEEQYGSTYRCVSVLTIVLHQ DWLNGKEYKCKVSNKALPAPIEKTIKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK RWQQGNVFSCSVMHEALHNHYTQKSLSPGK	SEQ ID NO: 2055 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWS WIRPAGKLEWIGRIYTSGTNYPNPSLKSRVTMS IDTSKNQFSKLNSVTAADTA VYCARDVA VAGF DYWGQGTLLVTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVTVPSSSLGTQTYICNVNHNKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEEQYGSTYRCVSVLTIVLHQ DWLNGKEYKCKVSNKALPAPIEKTIKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK RWQQGNVFSCSVMHEALHNHYTQKSLSPGK
			AA	SEQ ID NO: 328 GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCATT GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACCAAGGGAAGCCCTA AACTCCTGATCTATGGTGATCCAGTTTGCAAA GTGGGTCCCATCAAGGTTCAAGCGGCAGTGGAT CTGGGACAGAGTTCACTCTCACAAATCAGCAGCC TGACGCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAATAGTTACCCATTCACTTTCGGCCA AGGACCAAAAGTGATGTCAAAACGAACGGTGG CTGCACCATCTGTCTTCACTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGT GTGCTGCTGAATAACTTCTATCCACAGAGAGGC CAAAAGTACAGTGGAAGGTGGATAACGCCCTCCA ATCGGGTAACTCCAGGAGAGTGTACAGAGCA	SEQ ID NO: 328 GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCATT GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACCAAGGGAAGCCCTA AACTCCTGATCTATGGTGATCCAGTTTGCAAA GTGGGTCCCATCAAGGTTCAAGCGGCAGTGGAT CTGGGACAGAGTTCACTCTCACAAATCAGCAGCC TGACGCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAATAGTTACCCATTCACTTTCGGCCA AGGACCAAAAGTGATGTCAAAACGAACGGTGG CTGCACCATCTGTCTTCACTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGT GTGCTGCTGAATAACTTCTATCCACAGAGAGGC CAAAAGTACAGTGGAAGGTGGATAACGCCCTCCA ATCGGGTAACTCCAGGAGAGTGTACAGAGCA	4H9.004.001	!PS:359781

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	GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCTGACGCTGAGCAAGCAGACTACGAGA AACACAAAGTCTACGCCCTGCGAAGTCACCCATC AGGCCCTGAGCTCGCCCCGTCACAAAGAGCTTCA ACAGGGGAGAGTGT	CCTGACCAGCGGCGTGACACACCTTCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCCAAC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAAACCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGTGGTGACGTGAGCCACGAGAACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCAATATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTACGGT CCTCACCGTCTGCACCAAGACTGGCTGAATGG CAAGGAGTACAAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCATCCCGGAGGAGATGACCA AGAACAGGTACGCTGACCTGCCGTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGAGCCGGAGACAACATAAAG ACCACGCTCCCGTGCTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1899 DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFVITYYCLQHNSYPFTFGQGTKVD VKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWVKVDNALQSGNSQESVTEQDSKDSSTYS LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF NRGEC	SEQ ID NO: 2056 QVQLVESGGGVVQPGRSRLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIYDASNKYADAVKVG RFTISRDNKNTLYLQMNSLRAEDTAVYFCARDG TIFGVLLGDYWGQGTLLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLMISRPEVTCTVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV

A-2165-WO-PCT

				SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
			SEQ ID NO: 329	SEQ ID NO: 486
			GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACCAAGGGAAGCCCCCTA AACTCTGATCTATGGTGCAATCCAGTTTGCAAA GTGGGTCCCATCAAGGTTCAAGCGGCAGTGGAT CTGGGACAGAGTTCACTCTCACAAATCAGCAGCC TGACGCTGAAGATTTTGTAACTTAATTAATGCT ACAGCATAATAGTTACCCATTCACTTTCGGCCA AGGACCAAGTGGATGTCAACGAACGGTGG CTGCACCATCTGTCTTCATCTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGT GTGCTGTCTGAATACTTCTATCCCAGAGAGGC CAAAGTACAGTGGAGGTGGATAACGCCCTCCA ATCGGGTAACCTCCAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACTACAGCCTCAGCA GCACCTGACGCTGAGCAAGCAGACTACGAGA AACACAAAGTCTACGCCCTGCGAAGTCACCCATC AGGCTGAGCTCGCCCGTCAACAAAGAGCTTCA ACAGGGGAGAGTGT	CAGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGTCCCTGAGACTCTCCTGT GCAAGCTCTGGATTCACTTCAAGTTACTTTGGCA TGCACCTGGTCCGCCAGGCTCCAGGCAAGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACTCCGTGAAGGGCC GCTTCAACCATCTCCAGAGACAATTCAGAAACA CGTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGACACGGCTGTGTAATTAAGTGGCGAGATG GGACGATTTTGGAGTCTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCTCTCCTCAG CCTCCACCAAGGCCCATCGGTCTTCCCTGGC ACCCTCTCCAAGACACCTCTGGGGGCACAGC GGCCCTGGCTGCTGTGTCAGGACTACTTCCC CGAACCGGTGACGTGTCGTGGAACTCAGGCGC CCTGACCAAGCGGTGTCACACCTTCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAGCCC AGCAACACCAAGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACCC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGCTTCTCTTCCCCCCAAACCCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAGACCCCTGA GGTCAGTTCAACTGGTACGTGGACGGCGTGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTGAGCGT CCTCACCGTCTGCACCAAGGACTGGTGAATGG CAAGGAGTACAAAGTGCAAGGTCTCCACAAAGC
	4H9.004.002	NA	!PS:360929	

A-2165-WO-PCT

			SEQ ID NO: 1900 DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSTE FTLTISLQPEDFVITYYCLQHNSYPFTFGQGTKVD VKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWVKVDNALQSGNSQESVTEQDSKDSITYS LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF NRGEC		SEQ ID NO: 1900 CCTCCAGCCCCCATCGAGAAACCACATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACAGGTGAGCCTGACCTGCCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTAAA
AA			SEQ ID NO: 2057 QVQLVESGGGVVQPGRSRLRSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIYDASNKYADSVKGG RFTISRDNKNTLYQMNSLR AEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK		SEQ ID NO: 2057 QVQLVESGGGVVQPGRSRLRSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIYDASNKYADSVKGG RFTISRDNKNTLYQMNSLR AEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
NA	4H9.004.003	IPS:360936	SEQ ID NO: 330 GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTACCATCAGCTT GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG GCTGTATCAGCAGAAACCAAGGAAAGCCCTTA AACTCCTGATCTATGGTGATCCAGTTTGCAAA GTGGGTCCCATCAAGGTTTCAGCGGCAGTGGAT CTGGGACAGAGTTCACTCTCACAAATCAGCAGCC TGACGCCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAAATAGTTACCCATTCACTTTCGGCCA		SEQ ID NO: 487 CAGGTGCAGTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCAACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGC AAGGGC TGGAGTGGTGGCAGTTATATGGTATGATGGAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG

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	AGGACCAAGTGGATGTCAAACGAACGGTGG CTGCACCATCTGTCTTCATCTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCTCTGTGT GTGCTGTCTGAATAACTTCTATCCACAGAGGC CAAAGTACAGTGAAGGTGGATAACGCCCTCCA ATCGGTAACCTCCAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCTGACGCTGAGCAAGCAGACTACGAGA AACACAAAGTCTACGCCCTGCGAAGTCAACCCATC AGGCCTGAGCTCGCCCGTCAACAAAGAGCTTCA ACAGGGGAGAGTGT	GGACGATTTTGGAGTGCTCTTGGGGGACTACT GGGGCAGGGAACCCGTGTCACCGTCTCCTCAG CCTCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGCTGCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGC CCTGACCAGCGGCTGCACACCTTCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACCC GTGCCAGCACCTGAACCTCTGGGGGACCGTCTC AGTCTTCTCTTCCCCCAAAACCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAGAACCCCTGA GGTCAAGTTCAACTGTAAGTGGACGGCGTGA GGTGATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCCTGTGTGTCAGCGT CCTCACCGTCTGCACCAAGGACTGGCTGAATGG CAAGGAGTACAAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCA AGCCAAAGGCGAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACCAAGTCAAGCTGACCTGCCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGAGCGGAGACAACATAAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1901 DIQMTQSPSSLSASVGDRTVITTCRASQGIRNELGW YQQKPGKAPKLLIYGASSLSQGVPSRFSGSGSGTE FTLTISLSQPEDFVITYYCLQHNSYPFTFGQGTQVD	SEQ ID NO: 2058 QVQLVESGGGVVQPGSRSLRSLSCAASGFTFSYFGM HWVRQAPGKGLEWVAIVYDGSNKYYADA VKG RFTISRDN SKNTLYLQMNSLR AEDTAVYYCARDG

A-2165-WO-PCT

			VKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNFFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTS LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF NRGEC	SEQ ID NO: 331 GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACCAAGGAAAGCCCCTA AACTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGTCCCATCAAGGTTCAAGCGGCAAGTGGAT CTGGACAGAGTTCACTCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAATAGTTACCCATTCACTTTCGGCCCT GGGACCAAAAGTGGATGTCAAAACGAAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACCTGCCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT CGGGTAACTCCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCAACCCATCAGG GCCTGAGCTCGCCCCGTCAAAAGAGCTTCAACA GGGGAGAGTGT	SEQ ID NO: 488 CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGATTCACTTCACTTCACTTTTGGCA TGCAC TGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGATGATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCAACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTGGAGTGTCTTGGGGGACTACT GGGGCCAGGAACCTGGTCAACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCTCTCCAAAGACACCTCTGGGGGCACAGC GGCCTGGGCTGCCTGGTCAAGGACTACTTCCC CGAAACCGGTGACGGTGTCTGTGGAACCTCAGGCG CCTGACCAAGCGGTGTCAACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAACTTTGTGACAAAACTCACACATGCCACC GTGCCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACTG
IPS:360943	4H9.004.004	NA			

A-2165-WO-PCT

				SEQ ID NO: 1902	CGTGGTGGTGACGTGAGCCACGAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAAGACTGGCTGAATGG CAAGGAGTACAAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACAGGTACGCTGACCTGCTGCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGAGAGACAACATAAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCATAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTAA
				SEQ ID NO: 2059	QVQLVESGGGVVQPGRSRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAIVYDASNKYADAVKG RFTISRDNKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKS LSLSPGK
			AA	DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSTE FTLTISLQPEDFVITYYCLQHNSYPFTFGPGTKVDV KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSITYSL STLTLSKADYEKHKVYACEVTHQGLSPVTKSFN RGEC	

A-2165-WO-PCT

			SEQ ID NO: 332	SEQ ID NO: 489
			GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGGCATTAGAAAATGAGTTAG GCTGTATCAGCAGAAACCAAGGAAAGCCOCTA AACGCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGTCCCATCAAGGTTCAAGCGGCAGTGGAT CTGGACAGAGTTCACTCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTTGTAACTTAATTACTGTCT ACAGCATAATAGTTACCCATTCACTTTCGGCCA AGGACCAAAAGTGGATGTCAAACGAACGGTGG CTGCACCATCTGTCTTTCATCTTCCC GCCCATCTGA TGAGCAGTTGAAATCTGGAACCTGCCCTCTGTGT GTGCCCTGCTGAATAAATTTCTATCCCAGAGAGGC CAAAGTACAGTGGAAAGGTGGATAACGCCCTCCA ATCGGGTAACCTCCAGGAGAGTGTACACAGAGCA GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCTGACGCTGAGCAAAAGCAGACTACGAGA AACACAAAGTCTACGCCCTGCGAAGTCAACCCATC AGGCCCTGAGCTCGCCCGTCAACAAAGAGCTTCA ACAGGGGAGAGTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCAACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTGGAGTGTCTTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGCTGCCGTGTGTCAGGACTACTTCCC CGAACCCGGTGACGGTGTCTGTGGAATCAGGCGC CCTGACCAAGCGGTGTGCAACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACCTCACACATGCCACCC GTGCCAGCACCTGAACCTCTGGGGGACCCGTC AGTCTTCCTCTTCCCCCAAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGACGTGAGCCACGAAAGACCCCTGA GGTCAGTTCAACTGGTACGTGGACGGCGTGGGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAAGGACTGGCTGAATGG CAAGGAGTACAAAGTGCAAGGTCTCCAACAAGC CCTCCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACACAGGTGT ACACCTGCCCATCCCCGGGAGGAGATGACCA AGAACAGGTCAAGCTGACCTGCCCTGGTCAAAG GCTTCTATCCCAAGCGACATCGCCGTGGAGTGGG
	4H9.004.005	IP:360949	NA	

A-2165-WO-PCT

				AGAGCAATGGGAGCCGGAGAACAACTACAAG ACCACGCTCCCGTGGTGGACTCCGAGGCTCC TTCTTCTCTATAGCAAGCTCACCCTGGACAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGAGAAGAGCCTCTCCCTGTCTCCGGGTAAA SEQ ID NO: 2060 QVQLVESGGGVVQPGRSRLRSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIYDASNKYADAVKVG RFTISRDNKNTLYLQMNSLRAEDTAVYCARDG TIFGVLLGDYWGQGLTVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNATKPKCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
				DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGW YQQKPGKAPKRLIYGASSLQSGVPSRFSGSGTE FTLTISLQPEDFVITYCLQHNSYPFTFGQGTQVD VKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWVKVDNALQSGNSQESVTEQDSKDSSTYS LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF NRGEC SEQ ID NO: 1903
			AA	
				GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCACTCTGTAGGAGACAGAGTCACCATCATT GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACCAAGGAAAGCCCTA AACTCCTGATCTATGGTGATCCAGTTTGCAAA GTGGGTCCCATCAAGGTTTCAGCGGCAGTGGAT CTGGACAGAGTTCACTCTCACAAATCAGCAGCC TGACGCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAATAGTTACCATTCACCTTCGGCCA AGGACCAAAAGTGATGTCAAAACGAACGGTGG CTGCACCATCTGTCTTCACTTCCCGCCATCTGA TGAGCAGTTGAAAATCTGGAACTGCCTCTGTTGT GTGCCTGCTGAATAACTTCTATCCACAGAGAGGC CAAAAGTACAGTGGAAGGTGGATAACGCCCTCCA SEQ ID NO: 333
!PS:359761	4H9.004.006	NA		CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTCACTTACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAAA GTAATAAATACTATGCAGAGCCCGTGAAGGGCC GCTTCAACCATCTCCAGAGACAATTCCAAGAAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGACACGGCTGTGTATTACTGTGCGCGAGATA GGACGATTTTGGAGTGTCTTGGGGGACTACT GGGGCAGGGAACCTGGTCACTGCTCTCCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCC SEQ ID NO: 490

A-2165-WO-PCT

	ATCGGGTAACTCCAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCTGACGCTGAGCAAGCAGACTACGAGA AACACAAAAGTCTACGCCTGCGAAGTCAACCCATC AGGCCTGAGCTCGCCCGTCAACAAAGAGCTTCA ACAGGGGAGAGTGT	CGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGC CCTGACCAGCGCGTGCACACCTTCCCGGTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAGCCC AGCAACACCAAGGTGGAACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACCTCACACATGCCACAC GTGCCAGCACCTGAACCTCTGGGGGACCCGTC AGTCTTCTCTTCCCCCAAAACCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAGAACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCCTTGTGTACGCGT CCTCACCGTCTGACCAAGGACTGGCTGAATGG CAAGGAGTACAAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCATCCCGGAGGAGATGACCA AGAACAGGTGACCTGACCTGCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAA
	SEQ ID NO: 1904 DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISLQPEDFVITYCLQHNSYPFTFGQGTQVD VKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWVKVDNALQSGNSQESVTEQDSKDSITYS LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF NRGEC	SEQ ID NO: 2061 QVQLVESGGGVVQGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIYDASNKYADAVKVG RFTISRDNKNTLYQMNSLRAEDTAVYVCARDR TIFGVLLGDYWGQGTLLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGLVKDYFFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLMISRTPETVTCVVVDVSHED
	AA	

A-2165-WO-PCT

				PEVKFNWYVVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
				SEQ ID NO: 334 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACCAAGGAAAGCCCCTA AGCTCTGATCTATGGTGCAATCCAGTTTGCAAA GTGGGTCCCCTTCAAGGTTCAAGGCGAGTGGAT CTGGGACAGAATTCACTCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAAATAATTACCCCTCACTTTCGGCCAA GGGACCAAGTGGATATCAACGAACGGTGGCT GCACCATCTGTCTTCACTTCCCGCCATCTGATG AGCAGTTGAATACTTGAACCTGCCCTCTGTTGT GCCTGTGAATAACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAGTGGATAACGCCCTCCAAAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAGTCTACGCCTGCGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCAAAAGAGCTTCAACA GGGGAGAGTGT
				SEQ ID NO: 491 CAGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTTACAGTAACTTTGGCA TGCACCTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAAA GTAATGAAAACATATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAAATA CGTGTATCTGCAAAATGAACAGCCTGAGAGTCG CGGACACGGCTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTTGGGGGACTACT GGGCCAGGGAACCTGTGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCTCCAAGAGCACCTCTGGGGGACACAGC GGCCCTGGCTGCCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTGCGTGGAACTCAGGCGC CCTGACCAAGCGGCGTGCAACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACATCACACATGCCACAC GTGCCACGACCTGAACCTCTGGGGGACCGCTC AGCTTCTCTTCCCCCCCCAAACCCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAGACCCCTGA GGTCAGTTCAACTGGTACGTGGACGGCGTGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAAGGACTGGCTGAATGG

A-2165-WO-PCT

			CAAGGAGTACAAAGTGCAAGGTCTCTCAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCGAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACAGGTGAGCTGACCTGCCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTAAA
			SEQ ID NO: 1905 DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSITYSLSS TLTLTKADYEEKHKVYACEVTHQGLSSPVTKSFNR GEC
		AA	SEQ ID NO: 2062 QVQLVESGGGVVQPGRSRLRSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVYDASNENYADAVKG RFTISRDNKNTLYQMNSLRVADTA VYYCARDG TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLISRPEVTQVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
			SEQ ID NO: 335 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCAATCTATAGAGACAGAGTCACCATCATT GCCGGGCAAGTCAGGACATTAGAGATTATTAG GCTGTATCAGCAGAAACCAAGGAAAGCCCTA AGCGCTGATCTATGTTGATCCAGTTTGCAAA GTGGGTCCCTTCAAGGTTTCAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
IPS:360962	4B1.011	NA	SEQ ID NO: 492 CAGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGA TGCACTGGGTCCCGCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAATA CGCTGTATCTGCAAAATGAACAGCCTGAGAGTCG

A-2165-WO-PCT

	ACAGCATAAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAACGAACGGTGGCT GCACCATCTGTCTTTCATCTTCCCGCCATCTGATG AGCAGTTGAATCTGGAACCTGCCCTCTGTGTGT GCCTGCTGAATAACTTCTATATCCAGAGAGGCCA AAGTACAGTGGAAAGGTGGATAACGCCCTCCAAAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGAGAGTGT	CGGACACGGCTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCAGGGAACCCCTGGTCAACCGTCTCCTCAG CCTCCACCAAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGCTGCCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGC CCTGACCAGCGGCGTGACACACCTTCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCACGTGAATCAACAAGCCC AGCAACACCAAGGTGGACAAGAAGTTGAGCC CAAATCTTGTGACAAACCTCACACATGCCCAAC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAACCCAAAGGACAC CCTCATGATCTCCCCGACCCCTGAGGTACATG CGTGGTGGGACGTGAGCCACGAGACCCCTGA GGTCAAGTTCAACTGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTACGGT CCTCACCGTCTGCACCAAGGACTGGCTGAATGG CAAGGAGTACAAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAAGCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACCAAGGTACGCTGACCTGCCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAAGCCGGAGACAACATAAAG ACCACGCTTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1906 DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLSQSGVPSRFSGSGSGTEFT	SEQ ID NO: 2063 QVQLVESGGGVVQPGRSRLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKGG
AA		

A-2165-WO-PCT

			LTISLQPEDFATYYCLQHNNYPFTFGQGTKVDIK RTVAAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSYSLSS TLTLKADYEHKHYVACEVTHQGLSSPVTKSFNR GEC	RFTISRDN SKNTLYLQMNSLRVADTA VYYCARDG TIFGVVLGDYWGQGT LVTVSSASTKGPSVFP LAPS SKSTSGGTAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVFPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKD TLMISRTEPTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNV FSCSVMEALHNHYTQKS LSLSPGK
			SEQ ID NO: 336 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACCAAGGGAAGCCCTA AGCTCTGATCTATGGTGCAATCCAGTTTGC AAA GTGGGTCCC TTCAAAGTTTCAAGGCGAGTGGAT CTGGGACAGAAATTCATCTCACAAATCAGCAGCC TGACGCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAACGAAACGGTGGCT GCACCATCTGTCTTCACTTCCCGCCATCTGATG AGCAGTTGAATCTGGAACTGCCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAAT CGGGTAAC TCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCAAAAGAGCTTCAACA GGGAGAGTGT	SEQ ID NO: 493 CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAAA GTAATGAAAACATATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAAATA CGCTGTATCTGCAAAATGAACAGCCTGAGAGTCG CGGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCTGGTCAACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACTCTGGGGGACACAGC GGCCTGGGCTGCCGTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTGCGTGGAACTCAGGCGC CCTGACCAAGCGGTGTCACACCTTCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGGCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCACCC GTGCCCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTCCTCTTCCCCCCTCAAAACCCAAAGGACAC
IPS:360968	4B1.012	NA	SEQ ID NO: 336 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACCAAGGGAAGCCCTA AGCTCTGATCTATGGTGCAATCCAGTTTGC AAA GTGGGTCCC TTCAAAGTTTCAAGGCGAGTGGAT CTGGGACAGAAATTCATCTCACAAATCAGCAGCC TGACGCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAACGAAACGGTGGCT GCACCATCTGTCTTCACTTCCCGCCATCTGATG AGCAGTTGAATCTGGAACTGCCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAAT CGGGTAAC TCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCAAAAGAGCTTCAACA GGGAGAGTGT	SEQ ID NO: 493 CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAAA GTAATGAAAACATATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAAATA CGCTGTATCTGCAAAATGAACAGCCTGAGAGTCG CGGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCTGGTCAACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACTCTGGGGGACACAGC GGCCTGGGCTGCCGTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTGCGTGGAACTCAGGCGC CCTGACCAAGCGGTGTCACACCTTCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGGCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCACCC GTGCCCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTCCTCTTCCCCCCTCAAAACCCAAAGGACAC

A-2165-WO-PCT

		SEQ ID NO: 1907 DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QOKPGKAPKLLIYGASSLQSGVPSRFSGSGSTEFT LTISSLPEDFATYYCLQHNNYPFTFGPGTKVDIKR TVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSITYSLST LTLISKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC
	AA	SEQ ID NO: 2064 QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAWIYDASNENYADAVKVG RFTISRDNKNTLYLQMNSLRVADTA VYYCARDG TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGT AALGCLVKDYFPEPTVSWNSGALTS GVHTFPA VLQSSGLYSLSSVTVTPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKS LSLSPGK

A-2165-WO-PCT

				SEQ ID NO: 337	SEQ ID NO: 494
IPS:360974	4B1.013	NA		GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTAG GCTGTATCAGCAGAAACCAAGGAAAGCCCCTA AGCTCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGTCCCCTTCAAGGTTCAAGGCGAGTGGAT CTGGGACAGAATTCACTCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTGCAACTTATTACTGTCT ACAGCATAAATAATACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAACGAACGGTGGCT GCACCATCTGCTTTCATCTTCCCGCCATCTGATG AGCAGTTGAATCTGGAACTGCCCTCTGTTGTGT GCCTGCTGAATACTTCTATCCCAAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCAACAAGAGCTTCAACA GGGGAGAGTGT	CAGTGCAGCTGGTGGAGTCTGGGGAGGGCGTG GTCCAGCCTGGGAGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTTCACTAATTTGGCA TGCACCTGGTCCGCCAGGCTCCAGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACTCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAATA CGTGTATCTGCACATGAACAGCCTGAGAGTCG CGGACACGGCTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCTGGTCAACCGTCTCCTCAG CCTCCACCAAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGCTGCCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGC CCTGACCAAGCGGTGTGCAACCTTCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGGCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCACGTGAATCAACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCCAAC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGGTGGTGACGTGAGCCACGAAGACCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAAGTGCAAGGTCTCCAAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCA AGCCAAAGGGCAGCCCCGAGAACACAGGTGT ACACCTGCCCTTCCCGGAGGAGATGACCA AGAACAGGTCAAGCTGACCTGCCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG

A-2165-WO-PCT

				AGAGCAATGGGAGCCGGAGAACAACTACAAG ACCACGCTCCCGTGGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCCTGGACAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTAAA SEQ ID NO: 2065 QVQLVESGGGVVQPGSRSLRSCAASGFTSFNFGM HWVRQAPGKGLEWVAWIYDASNENYADSVKVG RFTISRDNKNTLYLHMNSLRVADTA VYYCARDG TIFGVVLGDYWGQGTLLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
				DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGTEFT LTISLQPEDFATYYCLQHNNYPFTFGQGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLS TLTLTKADYEKHKVYACEVTHQGLSSLSPVTKSFNR GEC SEQ ID NO: 1908
	AA			
				GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCATT GCCGGGCAAGTCAGGACATTAGAGATTATTAG GCTGTATCAGCAGAAACCAAGGAAAGCCCTA AGCTCCTGATCTATGGTGATCCAGTTTGCAAA GTGGGTCCCTTCAAGTTTCAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCACAATCAGCAGCC TGACGCTGAAGATTTCGCAACTTACTGTCT ACAGCATAATAATTACCCCTTCACTTCGGCCAA GGGACCAAAGTGGATAACAACGAACGGTGGCT GCACCATCTGTCTTCACTTCGCCCATCTGATG AGCAGTTGAATACTGGAACCTGCCTCTGTGTGT GCCTGCTGAATAACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT SEQ ID NO: 338
IPS:360978	4B1.014	NA		CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAAGTAACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGGAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAATA CGCTGTATCTGCACATGAACAGCCTGAGAGTCG CGGACACGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCCTGGTCAACGCTCTCCTCAG CCTCCACCAAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTTGGGGGCACAGC GGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCC SEQ ID NO: 495

A-2165-WO-PCT

	CGGGTAACTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCCGAAATCAGCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	CGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGC CCTGACCAGCGCGTGCACACCTTCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAAGCCC AGCAACACCAAGGTGACAAAGAAAGTTGAGCC CAAATCTTGTGACAAACCTCACACATGCCACAC GTGCCAGCACCTGAACCTCTGGGGGACCCGTC AGTCTTCTCTTCCCCCAAAACCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGTGGTGACGTGAGCCACGAGAACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCAATATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCCTGTGTGTCAGCGT CCTCACCGTCTGCACCAAGACTGGCTGAATGG CAAGGAGTACAAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCATCCCGGAGGAGATGACCA AGAACAGGTGACCTGACCTGCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAA
	SEQ ID NO: 1909 DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT LTISLQPEDFATYYCLQHNNYPFTFGQGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLS TLTSLKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC	SEQ ID NO: 2066 QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDGSNENYADAVKG RFTISRDNKNTLYLHMNSLRVADTA VYYCARDG TIFGVVLGDYWGQGTLT VTVSSASTKGPSVFLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLMISRTPETVTCVVVDVSHED

A-2165-WO-PCT

				PEVKFNWYVVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
				SEQ ID NO: 339 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACCAAGGAAAGCCCCTA AGCTCTGATCTATGGTGCAATCCAGTTTGCAAA GTGGGTCCCCTTCAAGGTTCAAGGCGAGTGGAT CTGGGACAGAATTCACTCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAGTGGATATCAACGAACGGTGGCT GCACCATCTGTCTTCACTTCCCGCCATCTGATG AGCAGTTGAATACTTGAAGTGGATACGCCCTCCAAT GCCTGCTGAATACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAAGTGGATACGCCCTCCAAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAGTCTACGCCTGCGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCAAAAGAGCTTCAACA GGGGAGAGTGT
				SEQ ID NO: 496 CAGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTTCAAGTAACTTTGGCA TGCACCTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAAA GTAATGAAAACATATGCAGACGCCGTGAAGGGCC GATTCAACCATCTCCAGAGACAATTCCAAGAAATA CGCTGATCTGCAAAATGAACAGCCTGAGAGTCG AGGACAGGCTGTGTAATTATTGCGCGAGATA GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCTGTGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCTCCAAGAGCACCTCTGGGGGACACAGC GGCCCTGGCTGCCGTGTGTCAGGACTACTTCCC CGAACCGGTGACGGTGTGTCGTAACCTCAGGCGC CCTGACCAAGCGGCGTGCAACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACATCACACATGCCACAC GTGCCACGACCTGAACCTCTGGGGGACCGTC AGCTTCTCTTCCCCCAAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAGACCCCTGA GGTCAGTTCAACTGGTACGTGGACGGCGTGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAAGGACTGGCTGAATGG

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				CAAGGAGTACAAAGTGCAAGGTCTCTCAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCGAGCCCGAGAACACACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACAGGTACGCTGACCTGCCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGACAAATGGCAGCCGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTAAA
				SEQ ID NO: 1910 DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSTEFT LTISLQPEDFATYYCLQHNHYPTFGQGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSITYSLSS TLTLTKADYEEKHKVYACEVTHQGLSSPVTKSFNR GEC
			AA	SEQ ID NO: 2067 QVQLVESGGGVVQPGRSRLRSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVYDASNENYADAVKG RFTISRDNKNTLYQMNSLRVEDTAVYCARDR TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLISRPEVTQVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
				SEQ ID NO: 497 CAGTGCAGCTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAATA CGCTGTATCTGCAAAATGAACAGCCTGAGAGTCG
				SEQ ID NO: 340 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCAATCTATAGAGACAGAGTCACCATCATT GCCGGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACCAAGGGAAGCCCTTA AGCTCCTGATCTATGGTGATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTTCAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
	4B1.016	IPS:360982	NA	

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	ACAGCATAAATAATTACCCCTTCACCTTCGGCCAA GGGACCAAAGTGGATATCAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACCTGCCCTCTGTGTGT GCCTGCTGAATAACTTCTATATCCAGAGAGGCCA AAGTACAGTGGAAAGGTGGATAACGCCCTCCAAAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGAGAGTGT	AGGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTTGGGGGACTACT GGGGCAGGGAACCCCTGGTCAACCGTCTCCTCAG CCTCCACCAAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCTCTCAAGAGACACCTCTGGGGGCACAGC GGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGC CCTGACCAGCGGCGTGACACACCTTCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGGCTTCCAGCAGCTTGGGCACC CAGACCTACATCTGCACGTGAATCAACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACCTCACACATGCCCAAC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTCTCTTCCCCCAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGGTGGGACGTGAGCCACGAGAACCCCTGA GGTCAAGTTCAACTGTGTACGTGGACGGCGTGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAAGGACTGGCTGAATGG CAAGGAGTACAAAGTGCAAGGTCTCCACAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACCAAGGTACGCTGACCTGCCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGACAACATAAAG ACCACGCTTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1911 DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QOKPGKAPKLLIYGASSLSQGVPSRFSGSGSGTEFT	SEQ ID NO: 2068 QVQLVESGGGVVQPGRSRLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKGG
AA		

A-2165-WO-PCT

			LTISLQPEDFATYYCLQHNYPFTFGQGTKVDIK RTVAAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSLSS TLTLKADYEHKHKVYACEVTHQGLSSPVTKSFNR GEC	RFTISRDN SKNTLYLQMNSLRVEDTAVYYCARDG TIFGVVLGDYWGQGT LVTVSSASTKGPSVFP LAPS SKSTSGGT AALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVFPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKD TLMISRTEPTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTKISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
			SEQ ID NO: 341 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCATT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCACAGAAACCAGGGAAAGCCCCCTA AGGCCGTGATCTATGGTGCATCCAGTTTGCAAA GTGGGTCCC TTCAAAGTTTCAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCACAAATCAGCAGCC TGACGCCCTGAAGATTTGCAACTTATTACTGTCT ACAGCATAAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAGTGGATATCAACGAAACGGTGGCT GCACCATCTGTCTTCACTTCCCGCCATCTGATG AGCAGTTGAATCTGGAACTGCCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAGTGGATAACGCCCTCCAAAT CGGGTAAC TCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGA AAC ACAAAGTCTACGCCCTGCGAAGTCA CCCCATCAGG GCCTGAGCTCGCCCGTCAAAAGAGCTTCAACA GGGGAGAGTGT	SEQ ID NO: 498 CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGTCCGCCAGGCCCAAGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGGAA GTAATGAA AACTATGCAGACTCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAAACA CGCTGATCTGCACATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCTGGTCAACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACTCTGGGGGCACAGC GGCCTGGGTGCCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTGCGTGGAACTCAGGCGC CCTGACCAAGCGGTGCACACCTTCCCGGTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGGCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAA AACTCACACATGCCACCC GTGCCAGCACCTGAACCTCTGGGGGACCGTCT AGTCTCCTCTTCCCCCACAACCCCAAGGACAC
IPS:335922	18F2	NA	SEQ ID NO: 341 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCATT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCACAGAAACCAGGGAAAGCCCCCTA AGGCCGTGATCTATGGTGCATCCAGTTTGCAAA GTGGGTCCC TTCAAAGTTTCAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCACAAATCAGCAGCC TGACGCCCTGAAGATTTGCAACTTATTACTGTCT ACAGCATAAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAGTGGATATCAACGAAACGGTGGCT GCACCATCTGTCTTCACTTCCCGCCATCTGATG AGCAGTTGAATCTGGAACTGCCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAGTGGATAACGCCCTCCAAAT CGGGTAAC TCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGA AAC ACAAAGTCTACGCCCTGCGAAGTCA CCCCATCAGG GCCTGAGCTCGCCCGTCAAAAGAGCTTCAACA GGGGAGAGTGT	SEQ ID NO: 498 CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGTCCGCCAGGCCCAAGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGGAA GTAATGAA AACTATGCAGACTCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAAACA CGCTGATCTGCACATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCTGGTCAACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACTCTGGGGGCACAGC GGCCTGGGTGCCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTGCGTGGAACTCAGGCGC CCTGACCAAGCGGTGCACACCTTCCCGGTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGGCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAA AACTCACACATGCCACCC GTGCCAGCACCTGAACCTCTGGGGGACCGTCT AGTCTCCTCTTCCCCCACAACCCCAAGGACAC

A-2165-WO-PCT

A-2165-WO-PCT

			SEQ ID NO: 342	SEQ ID NO: 499
		18F2.002	GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTATAGGAGACAGAGTCACCATCACTTGCCGGCAAGTCAGGACCTTAGAAAATTATTTAGGCTGTATCAACAGAAACCAAGGAAAGCCOCTAAGCTCTGATCTATGGTGCAATCCAGTTTGCAAA GTGGGTCCC'TTCAAGGTTTCAGGGCAGTGGATCTGGGACAGAA'TTCACTCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTGCAACTTATTACTGTCTACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAAGTGGATATCAACGAACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAC'TGCCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAAGAGAGGCCA AAGTACAGTGGAAAGTGGAATAACGCCCTCCAATCGGGTAAC'TCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCAAAAGAGCTTCAACA GGGGAGAGTGT	CAGTGCAAGCTGGTGGAGTCTGGGGAGGGCGTGTGCCAGCCTGGAGTGCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACTTTCAAGTAACTTTGGCATGCACTGGGTCCGCCAGGCCCAAGCAAGGGGTGGAGTGGCAGTTATATGGTATGATGCAAGTAAAGAAAAC'TATGCAGACGCCGTGAAGGGCCGATTCAACCATCTCCAGAGACAATTCCAAGAAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCGCGGACACGGCTGTATTACTGTGCGAGAGATGGAGCATCTTTGGAGTGGTCTTGGGGGACTACTGGGCCAGGAAACCTGGTCAACCGTCTCCTCAGCTCCAACCAAGGGCCCATCGGTCTTCCCCCTGGCACCTCTCCAAGAGCACTCTGGGGGCACAGCGCCCTGGGTGCCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTGCTGTGGAAC'TCAGGCGCCTGACCGGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAAGCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAAC'TCACACATGCCACC GTGCCAGCACCTGAAC'TCCTGGGGGACCCGTGAGTCTTCTTCCCCCAAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGAGCAGTACGGCAGCACGTACCGTTGTGTACGCGTCTCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAAGTGCAAGGTCTCCAACAAGCCCTCCAGCCCCCATCGAGAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAAACACAGGTGTACACCTGCCCATCCCGGAGGAGATGACCAAGAACCAAGGTCAAGCTGACCTGCCCTGGTCAAAGGCTTCTATCCCAAGGACATCGCCGTGGAGTGGG
		IPS:360986	NA	

A-2165-WO-PCT

			SEQ ID NO: 1913 DIQMTQSPSSLSASIGDRVTITCRASQDLRNLYLGWYQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNHYPTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNRFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC		AGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCTCCCGTGTGGACTCCGACGGCTCCTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAAA
	AA		SEQ ID NO: 343 GACATCCAGATGACCCAGTCTCCATCCTCCTGTCTGCATCTATAGGAGACAGAGTCACCATCACTTGCCGGCAAGTCAGGACCTTAGAAATTATTTAGGCTGGTATCAACAGAAACCAAGGAAAGCCCCTAAGCTCCTGATCTATGGTGATCCAGTTTGCAAA GTGGGTCCCTTCAAGGTTCAAGCGCAGTGGATCTGGGACAGAAATTCAC'TCTCACAA TCAGCAGCC TGACGCC TGAAGATTTCGCAACTTATTACTGTCTACAGCATATAATTACCCCTTCACTTTTCGGCCCTGGGACCAAAGTGGATA TCAAAACGAACGGTGGCTGCACCATCTGTCTTCAATCTTCCCGCCATCTGATGAGCAGTTGAAA TCTGGAAC TGCCTCTGTGTGTGCCTGCTGAATA ACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAAGGTGGATAACGCCCTTCCAAT		SEQ ID NO: 2070 QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAWIWDASNENYADAVKGRFTISRDNKNTLYLQMNSLRAADTA VYYCARDGTIFGVVLGDYWGQGTLLVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKTPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDSGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
IPS:360995	18F2.003	NA			SEQ ID NO: 500 CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGGTGTCCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACTTTCAGTAACTTTGGCATGCAC'TGGTCCGCCAGGCCCAAGGCAAGGGCGTGGAGTGGTGGCAGTTATATGATGATGCAAGTAATGAAAACTATGCAGACGCCGTGAAGGGCCGATTCAACCATCTCCAGAGACAATTCCAAGAAACACGCTGTATCTGCACATGAACAGCCTGAGAGCCGCGGACACGGCTGTGTATTACTGTGCGGAGAGATGGACGATCTTTGGAGTGGTCTTGGGGGACTACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCAGCCTCCACAAAGGCCCATCGGTCTTCCCCCTGGCACCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCC

A-2165-WO-PCT

	CGGGTAACTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCCGAAATCAGCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	CGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGC CCTGACCAGCGGCGTGACACACCTTCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGAACAAGATTGAGCC CAAATCTTGTGACAAAACCTCACACATGCCACAC GTGCCAGCACCTGAACCTCTGGGGGACCCGTC AGTCTTCTCTTCCCCCAAAACCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGTGGTGACGTGAGCCACGAGAACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCCTGTGTGTCAGCGT CCTCACCGTCTGACCAAGGACTGGCTGAATGG CAAGGAGTACAAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCATCCCGGAGGAGATGACCA AGAACAGGTGACCTGACCTGCCGTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGGAGACAACATACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAA
	SEQ ID NO: 1914 DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YQQKPGKAPKLLIYGASSLSQGVPSRFSGSGSGTE FTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWVKVDNALQSGNSQESVTEQDSKDSYSTLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	SEQ ID NO: 2071 QVQLVESGGGVVQPGRSRLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAWIYDASNENYADAVKG RFTISRDNKNTLYLHMNSLRAADTA VYYCARDG TIFGVVLGDYWGQGTLT VTVSSASTKGPSVFLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLMISRTPETVTVVVDVSHED
AA		

A-2165-WO-PCT

				SEQ ID NO: 344	SEQ ID NO: 501	
				GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCACACAGAAACCAAGGAAAGCCCCA AGCTCTGATCTATGGTGCAATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTCAAGGCAAGTGGAT CTGGGACAGAAATTCATCTCTCACAATCAGCAGCC TGACGCTGAAGATTTGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAGTGGATATCAACGAACGGTGGCT GCACCATCTGCTTTCATCTTCCCGCCATCTGATG AGCAGTTGAATACTTGAAGTGGATATCCAGAGAGGCCA GCCTGCTGAATACTTCTATCCAGAGAGAGGCCA AAGTACAGTGGAAAGTGGATACGCCCTCCCAAT CGGTAACCTCCAGGAGAGTGTACAGCAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT		PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
IPS:360999	18F2.004	NA			CAGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTTCAAGTAACTTTGGCA TGCACTGGTCCGCCAGGCCCAAGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAACATATGCAGACGCCGTGAAGGGCC GATTCAACCATCTCCAGAGACAATTCCAAGAAACA CGTGTATCTGCAAAATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCAGGGAACCTGGTCAACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCTGGC ACCTCTCCAGAGACCTCTGGGGGACACAGC GGCCTGGCTGCCGTGTGTCAGAGTACTTCCC CGAACCGGTGACGTGTGTCAGTGAACCTCAGGCGC CCTGACCAAGCGGTGTGCAACCTTCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGGCTTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAGCCC AGCAACACCAAGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACCTCACACATGCCACAC GTGCCACGACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGCGGTGGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTGACGCT CCTCACCGTCTGCACCAAGGACTGGCTGAATGG	

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			CAAGGAGTACAAAGTGCAAGGTCTCCAAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACAGGTGACCTGACCTGCCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGACAAATGGCAGCCGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTAAA
			SEQ ID NO: 1915 DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YHQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISLQPEDFATYYCLQHNHYPTFTGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSITYSL STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEK
		AA	SEQ ID NO: 2072 QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVYDASNENYADAVKG RFTISRDNKNTLYQMNSLRAADTA VYYCARDG TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
			SEQ ID NO: 345 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCAATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGTATCAACAGAAACCAAGGAAAGCCCTTA AGCGCTGATCTATGTTGCATCCAGTTTGCAAA GTGGGTCCCTTCAAGGTTTCAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
IPS:361005	18F2.005	NA	SEQ ID NO: 502 CAGTGCAGCTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCAAGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG

A-2165-WO-PCT

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	SEQ ID NO: 1916 DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YQOKPGKAPKRLIYGASSLSQGVPSRFSGSGSGTE	SEQ ID NO: 2073 QVQLVESGGGVVQPGRSRLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKGG
AA		

DEMANDE OU BREVET VOLUMINEUX

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

CECI EST LE TOME 1 DE 3
CONTENANT LES PAGES 1 À 242

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JUMBO APPLICATIONS/PATENTS

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

THIS IS VOLUME 1 OF 3
CONTAINING PAGES 1 TO 242

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

NOM DU FICHIER / FILE NAME :

NOTE POUR LE TOME / VOLUME NOTE:

CLAIMS

What is claimed is:

1. A composition comprising
 - a) an antibody or functional fragment thereof that specifically binds to human GIPR,
5 wherein the antibody or functional fragment thereof comprises a light chain variable region and a heavy chain variable region; and
 - b) a GLP-1 receptor agonist, wherein the C-terminus of the GLP-1 receptor agonist is fused to N-terminus of either the light chain variable region or the heavy chain variable region.
- 10 2. The composition of claim 1, wherein said human GIPR has a sequence comprising a sequence selected from the group consisting of SEQ ID NO: 3141, SEQ ID NO: 3143, and SEQ ID NO: 3145.
3. The composition of claim 1 or 2, wherein said antibody or functional fragment thereof is a monoclonal antibody, a recombinant antibody, a human antibody, a humanized
15 antibody, a chimeric antibody, a multispecific antibody, or an antibody fragment thereof.
4. The composition of claim 3, wherein said antibody fragment is a Fab fragment, a Fab' fragment, or a F(ab')₂ fragment.
5. The composition of claim 3, wherein said antibody or functional fragment thereof is a human antibody.
- 20 6. The composition of claim 3, wherein said antibody or functional fragment thereof is a monoclonal antibody.
7. The composition of claim 3, wherein said antibody or functional fragment thereof is of the IgG1-, IgG2- IgG3- or IgG4-type.
8. The composition of claim 7, wherein said antibody or functional fragment
25 thereof is of the IgG1- or the IgG2-type.
9. The composition of one of claim 3, wherein said antibody or functional fragment thereof inhibits binding of GIP to the extracellular portion of human GIPR.

10. The composition of claim 3, 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: 629-785; said CDRL2 comprises a sequence selected from the group consisting of SEQ ID NOs: 786-942; said CDRL3 comprises a sequence selected from the group consisting of SEQ ID NOs: 943-1099; said CDRH1 comprises a sequence selected from the group consisting of SEQ ID NOs: 1100-1256; said CDRH2 comprises a sequence selected from the group consisting of SEQ ID NOs: 1257-1413; and said CDRH3 comprises a sequence selected from the group consisting of SEQ ID NOs: 1414-1570

11. The composition of claim 3, 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: 629, SEQ ID NO: 786, SEQ ID NO: 943, SEQ ID NO: 1100, SEQ ID NO: 1257, and SEQ ID NO: 1414; SEQ ID NO: 630, SEQ ID NO: 787, SEQ ID NO: 944, SEQ ID NO: 1101, SEQ ID NO: 1258, and SEQ ID NO: 1415; SEQ ID NO: 631, SEQ ID NO: 788, SEQ ID NO: 945, SEQ ID NO: 1102, SEQ ID NO: 1259, and SEQ ID NO: 1416; SEQ ID NO: 632, SEQ ID NO: 789, SEQ ID NO: 946, SEQ ID NO: 1103, SEQ ID NO: 1260, and SEQ ID NO: 1417; SEQ ID NO: 633, SEQ ID NO: 790, SEQ ID NO: 947, SEQ ID NO: 1104, SEQ ID NO: 1261, and SEQ ID NO: 1418; SEQ ID NO: 634, SEQ ID NO: 791, SEQ ID NO: 948, SEQ ID NO: 1105, SEQ ID NO: 1262, and SEQ ID NO: 1419; SEQ ID NO: 635, SEQ ID NO: 792, SEQ ID NO: 949, SEQ ID NO: 1106, SEQ ID NO: 1263, and SEQ ID NO: 1420; SEQ ID NO: 636, SEQ ID NO: 793, SEQ ID NO: 950, SEQ ID NO: 1107, SEQ ID NO: 1264, and SEQ ID NO: 1421; SEQ ID NO: 637, SEQ ID NO: 794, SEQ ID NO: 951, SEQ ID NO: 1108, SEQ ID NO: 1265, and SEQ ID NO: 1422; SEQ ID NO: 638, SEQ ID NO: 795, SEQ ID NO: 952, SEQ ID NO: 1109, SEQ ID NO: 1266, and SEQ ID NO: 1423; SEQ ID NO: 639, SEQ ID NO: 796, SEQ ID NO: 953, SEQ ID NO: 1110, SEQ ID NO: 1267, and SEQ ID NO: 1424; SEQ ID NO: 640, SEQ ID NO: 797, SEQ ID NO: 954, SEQ ID NO: 1111, SEQ ID NO: 1268, and SEQ ID NO: 1425; SEQ ID NO: 641, SEQ ID NO: 798, SEQ ID NO: 955, SEQ ID NO: 1112, SEQ ID NO: 1269, and SEQ ID NO: 1426; SEQ ID NO: 642, SEQ ID NO: 799, SEQ ID NO: 956, SEQ ID NO: 1113, SEQ ID NO: 1270, and SEQ ID NO: 1427; SEQ ID NO: 643, SEQ ID NO: 800, SEQ ID NO: 957, SEQ ID NO: 1114, SEQ ID NO: 1271, and SEQ ID NO: 1428; SEQ ID NO: 644, SEQ ID NO: 801, SEQ ID NO: 958, SEQ ID NO: 1115, SEQ ID NO: 1272, and SEQ ID NO: 1429;

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 SEQ ID NO: 961, SEQ ID NO: 1118, SEQ ID NO: 1275, and SEQ ID NO: 1432; SEQ ID
 5 NO: 648, SEQ ID NO: 805, SEQ ID NO: 962, SEQ ID NO: 1119, SEQ ID NO: 1276, and
 SEQ ID NO: 1433; SEQ ID NO: 649, SEQ ID NO: 806, SEQ ID NO: 963, SEQ ID NO:
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 10 NO: 1436; SEQ ID NO: 652, SEQ ID NO: 809, SEQ ID NO: 966, SEQ ID NO: 1123, SEQ
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 15 1283, and SEQ ID NO: 1440; SEQ ID NO: 656, SEQ ID NO: 813, SEQ ID NO: 970, SEQ ID
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 20 1130, SEQ ID NO: 1287, and SEQ ID NO: 1444; SEQ ID NO: 660, SEQ ID NO: 817, SEQ
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 1293, and SEQ ID NO: 1450; SEQ ID NO: 666, SEQ ID NO: 823, SEQ ID NO: 980, SEQ ID
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 30 SEQ ID NO: 981, SEQ ID NO: 1138, SEQ ID NO: 1295, and SEQ ID NO: 1452; SEQ ID
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 1140, SEQ ID NO: 1297, and SEQ ID NO: 1454; SEQ ID NO: 670, SEQ ID NO: 827, SEQ
 ID NO: 984, SEQ ID NO: 1141, SEQ ID NO: 1298, and SEQ ID NO: 1455; SEQ ID NO:

671, SEQ ID NO: 828, SEQ ID NO: 985, SEQ ID NO: 1142, SEQ ID NO: 1299, and SEQ ID NO: 1456; SEQ ID NO: 672, SEQ ID NO: 829, SEQ ID NO: 986, SEQ ID NO: 1143, SEQ ID NO: 1300, and SEQ ID NO: 1457; SEQ ID NO: 673, SEQ ID NO: 830, SEQ ID NO: 987, SEQ ID NO: 1144, SEQ ID NO: 1301, and SEQ ID NO: 1458; SEQ ID NO: 674, SEQ ID NO: 831, SEQ ID NO: 988, SEQ ID NO: 1145, SEQ ID NO: 1302, and SEQ ID NO: 1459; SEQ ID NO: 675, SEQ ID NO: 832, SEQ ID NO: 989, SEQ ID NO: 1146, SEQ ID NO: 1303, and SEQ ID NO: 1460; SEQ ID NO: 676, SEQ ID NO: 833, SEQ ID NO: 990, SEQ ID NO: 1147, SEQ ID NO: 1304, and SEQ ID NO: 1461; SEQ ID NO: 677, SEQ ID NO: 834, SEQ ID NO: 991, SEQ ID NO: 1148, SEQ ID NO: 1305, and SEQ ID NO: 1462; SEQ ID NO: 678, SEQ ID NO: 835, SEQ ID NO: 992, SEQ ID NO: 1149, SEQ ID NO: 1306, and SEQ ID NO: 1463; SEQ ID NO: 679, SEQ ID NO: 836, SEQ ID NO: 993, SEQ ID NO: 1150, SEQ ID NO: 1307, and SEQ ID NO: 1464; SEQ ID NO: 680, SEQ ID NO: 837, SEQ ID NO: 994, SEQ ID NO: 1151, SEQ ID NO: 1308, and SEQ ID NO: 1465; SEQ ID NO: 681, SEQ ID NO: 838, SEQ ID NO: 995, SEQ ID NO: 1152, SEQ ID NO: 1309, and SEQ ID NO: 1466; SEQ ID NO: 682, SEQ ID NO: 839, SEQ ID NO: 996, SEQ ID NO: 1153, SEQ ID NO: 1310, and SEQ ID NO: 1467; SEQ ID NO: 683, SEQ ID NO: 840, SEQ ID NO: 997, SEQ ID NO: 1154, SEQ ID NO: 1311, and SEQ ID NO: 1468; SEQ ID NO: 684, SEQ ID NO: 841, SEQ ID NO: 998, SEQ ID NO: 1155, SEQ ID NO: 1312, and SEQ ID NO: 1469; SEQ ID NO: 685, SEQ ID NO: 842, SEQ ID NO: 999, SEQ ID NO: 1156, SEQ ID NO: 1313, and SEQ ID NO: 1470; SEQ ID NO: 686, SEQ ID NO: 843, SEQ ID NO: 1000, SEQ ID NO: 1157, SEQ ID NO: 1314, and SEQ ID NO: 1471; SEQ ID NO: 687, SEQ ID NO: 844, SEQ ID NO: 1001, SEQ ID NO: 1158, SEQ ID NO: 1315, and SEQ ID NO: 1472; SEQ ID NO: 688, SEQ ID NO: 845, SEQ ID NO: 1002, SEQ ID NO: 1159, SEQ ID NO: 1316, and SEQ ID NO: 1473; SEQ ID NO: 689, SEQ ID NO: 846, SEQ ID NO: 1003, SEQ ID NO: 1160, SEQ ID NO: 1317, and SEQ ID NO: 1474; SEQ ID NO: 690, SEQ ID NO: 847, SEQ ID NO: 1004, SEQ ID NO: 1161, SEQ ID NO: 1318, and SEQ ID NO: 1475; SEQ ID NO: 691, SEQ ID NO: 848, SEQ ID NO: 1005, SEQ ID NO: 1162, SEQ ID NO: 1319, and SEQ ID NO: 1476; SEQ ID NO: 692, SEQ ID NO: 849, SEQ ID NO: 1006, SEQ ID NO: 1163, SEQ ID NO: 1320, and SEQ ID NO: 1477; SEQ ID NO: 693, SEQ ID NO: 850, SEQ ID NO: 1007, SEQ ID NO: 1164, SEQ ID NO: 1321, and SEQ ID NO: 1478; SEQ ID NO: 694, SEQ ID NO: 851, SEQ ID NO: 1008, SEQ ID NO: 1165, SEQ ID NO: 1322, and SEQ ID NO: 1479; SEQ ID NO: 695, SEQ ID NO: 852, SEQ ID NO: 1009, SEQ ID NO: 1166, SEQ ID NO: 1323, and SEQ ID NO: 1480; SEQ ID NO: 696, SEQ ID NO: 853, SEQ ID NO: 1010, SEQ ID NO: 1167, SEQ ID NO: 1324, and SEQ ID NO: 1481; SEQ ID NO: 697, SEQ ID

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 5 857, SEQ ID NO: 1014, SEQ ID NO: 1171, SEQ ID NO: 1328, and SEQ ID NO: 1485; SEQ
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 and SEQ ID NO: 1486; SEQ ID NO: 702, SEQ ID NO: 859, SEQ ID NO: 1016, SEQ ID NO:
 1173, SEQ ID NO: 1330, and SEQ ID NO: 1487; SEQ ID NO: 703, SEQ ID NO: 860, SEQ
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 10 704, SEQ ID NO: 861, SEQ ID NO: 1018, SEQ ID NO: 1175, SEQ ID NO: 1332, and SEQ
 ID NO: 1489; SEQ ID NO: 705, SEQ ID NO: 862, SEQ ID NO: 1019, SEQ ID NO: 1176,
 SEQ ID NO: 1333, and SEQ ID NO: 1490; SEQ ID NO: 706, SEQ ID NO: 863, SEQ ID NO:
 1020, SEQ ID NO: 1177, SEQ ID NO: 1334, and SEQ ID NO: 1491; SEQ ID NO: 707, SEQ
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 15 1492; SEQ ID NO: 708, SEQ ID NO: 865, SEQ ID NO: 1022, SEQ ID NO: 1179, SEQ ID
 NO: 1336, and SEQ ID NO: 1493; SEQ ID NO: 709, SEQ ID NO: 866, SEQ ID NO: 1023,
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 20 1339, and SEQ ID NO: 1496; SEQ ID NO: 712, SEQ ID NO: 869, SEQ ID NO: 1026, SEQ
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 and SEQ ID NO: 1499; SEQ ID NO: 715, SEQ ID NO: 872, SEQ ID NO: 1029, SEQ ID NO:
 25 1186, SEQ ID NO: 1343, and SEQ ID NO: 1500; SEQ ID NO: 716, SEQ ID NO: 873, SEQ
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 30 1033, SEQ ID NO: 1190, SEQ ID NO: 1347, and SEQ ID NO: 1504; SEQ ID NO: 720, SEQ
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 NO: 1349, and SEQ ID NO: 1506; SEQ ID NO: 722, SEQ ID NO: 879, SEQ ID NO: 1036,
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 5 883, SEQ ID NO: 1040, SEQ ID NO: 1197, SEQ ID NO: 1354, and SEQ ID NO: 1511; SEQ
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 and SEQ ID NO: 1512; SEQ ID NO: 728, SEQ ID NO: 885, SEQ ID NO: 1042, SEQ ID NO:
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 10 730, SEQ ID NO: 887, SEQ ID NO: 1044, SEQ ID NO: 1201, SEQ ID NO: 1358, and SEQ
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 15 1518; SEQ ID NO: 734, SEQ ID NO: 891, SEQ ID NO: 1048, SEQ ID NO: 1205, SEQ ID
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 20 1365, and SEQ ID NO: 1522; SEQ ID NO: 738, SEQ ID NO: 895, SEQ ID NO: 1052, SEQ
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 and SEQ ID NO: 1525; SEQ ID NO: 741, SEQ ID NO: 898, SEQ ID NO: 1055, SEQ ID NO:
 25 1212, SEQ ID NO: 1369, and SEQ ID NO: 1526; SEQ ID NO: 742, SEQ ID NO: 899, SEQ
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 30 1059, SEQ ID NO: 1216, SEQ ID NO: 1373, and SEQ ID NO: 1530; SEQ ID NO: 746, SEQ
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 NO: 1375, and SEQ ID NO: 1532; SEQ ID NO: 748, SEQ ID NO: 905, SEQ ID NO: 1062,
 SEQ ID NO: 1219, SEQ ID NO: 1376, and SEQ ID NO: 1533; SEQ ID NO: 749, SEQ ID

NO: 906, SEQ ID NO: 1063, SEQ ID NO: 1220, SEQ ID NO: 1377, and SEQ ID NO: 1534;
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 5 909, SEQ ID NO: 1066, SEQ ID NO: 1223, SEQ ID NO: 1380, and SEQ ID NO: 1537; SEQ
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 and SEQ ID NO: 1538; SEQ ID NO: 754, SEQ ID NO: 911, SEQ ID NO: 1068, SEQ ID NO:
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 10 756, SEQ ID NO: 913, SEQ ID NO: 1070, SEQ ID NO: 1227, SEQ ID NO: 1384, and SEQ
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 15 1544; SEQ ID NO: 760, SEQ ID NO: 917, SEQ ID NO: 1074, SEQ ID NO: 1231, SEQ ID
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 20 1391, and SEQ ID NO: 1548; SEQ ID NO: 764, SEQ ID NO: 921, SEQ ID NO: 1078, SEQ
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 922, SEQ ID NO: 1079, SEQ ID NO: 1236, SEQ ID NO: 1393, and SEQ ID NO: 1550; SEQ
 ID NO: 766, SEQ ID NO: 923, SEQ ID NO: 1080, SEQ ID NO: 1237, SEQ ID NO: 1394,
 and SEQ ID NO: 1551; SEQ ID NO: 767, SEQ ID NO: 924, SEQ ID NO: 1081, SEQ ID NO:
 25 1238, SEQ ID NO: 1395, and SEQ ID NO: 1552; SEQ ID NO: 768, SEQ ID NO: 925, SEQ
 ID NO: 1082, SEQ ID NO: 1239, SEQ ID NO: 1396, and SEQ ID NO: 1553; SEQ ID NO:
 769, SEQ ID NO: 926, SEQ ID NO: 1083, SEQ ID NO: 1240, SEQ ID NO: 1397, and SEQ
 ID NO: 1554; SEQ ID NO: 770, SEQ ID NO: 927, SEQ ID NO: 1084, SEQ ID NO: 1241,
 SEQ ID NO: 1398, and SEQ ID NO: 1555; SEQ ID NO: 771, SEQ ID NO: 928, SEQ ID NO:
 30 1085, SEQ ID NO: 1242, SEQ ID NO: 1399, and SEQ ID NO: 1556; SEQ ID NO: 772, SEQ
 ID NO: 929, SEQ ID NO: 1086, SEQ ID NO: 1243, SEQ ID NO: 1400, and SEQ ID NO:
 1557; SEQ ID NO: 773, SEQ ID NO: 930, SEQ ID NO: 1087, SEQ ID NO: 1244, SEQ ID
 NO: 1401, and SEQ ID NO: 1558; SEQ ID NO: 774, SEQ ID NO: 931, SEQ ID NO: 1088,
 SEQ ID NO: 1245, SEQ ID NO: 1402, and SEQ ID NO: 1559; SEQ ID NO: 775, SEQ ID

NO: 932, SEQ ID NO: 1089, SEQ ID NO: 1246, SEQ ID NO: 1403, and SEQ ID NO: 1560;
 SEQ ID NO: 776, SEQ ID NO: 933, SEQ ID NO: 1090, SEQ ID NO: 1247, SEQ ID NO:
 1404, and SEQ ID NO: 1561; SEQ ID NO: 777, SEQ ID NO: 934, SEQ ID NO: 1091, SEQ
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 5 935, SEQ ID NO: 1092, SEQ ID NO: 1249, SEQ ID NO: 1406, and SEQ ID NO: 1563; SEQ
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 and SEQ ID NO: 1564; SEQ ID NO: 780, SEQ ID NO: 937, SEQ ID NO: 1094, SEQ ID NO:
 1251, SEQ ID NO: 1408, and SEQ ID NO: 1565; SEQ ID NO: 781, SEQ ID NO: 938, SEQ
 ID NO: 1095, SEQ ID NO: 1252, SEQ ID NO: 1409, and SEQ ID NO: 1566; SEQ ID NO:
 10 782, SEQ ID NO: 939, SEQ ID NO: 1096, SEQ ID NO: 1253, SEQ ID NO: 1410, and SEQ
 ID NO: 1567; SEQ ID NO: 783, SEQ ID NO: 940, SEQ ID NO: 1097, SEQ ID NO: 1254,
 SEQ ID NO: 1411, and SEQ ID NO: 1568; SEQ ID NO: 784, SEQ ID NO: 941, SEQ ID NO:
 1098, SEQ ID NO: 1255, SEQ ID NO: 1412, and SEQ ID NO: 1569; and SEQ ID NO: 785,
 SEQ ID NO: 942, SEQ ID NO: 1099, SEQ ID NO: 1256, SEQ ID NO: 1413, and SEQ ID
 15 NO: 1570.

12. The composition of claim 3, wherein said antibody or functional fragment
 thereof 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: 1-157 and a heavy chain variable region comprising a sequence
 20 selected from the group consisting of SEQ ID NOs: 158-31.

13. The composition of claim 3, wherein said antibody or functional fragment
 thereof 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: 1
 25 and a heavy chain variable region comprising SEQ ID NO: 158; a light chain variable region
 comprising SEQ ID NO: 2 and a heavy chain variable region comprising SEQ ID NO: 159; a
 light chain variable region comprising SEQ ID NO: 3 and a heavy chain variable region
 comprising SEQ ID NO: 160; a light chain variable region comprising SEQ ID NO: 4 and a
 heavy chain variable region comprising SEQ ID NO: 161; a light chain variable region
 30 comprising SEQ ID NO: 5 and a heavy chain variable region comprising SEQ ID NO: 162; a
 light chain variable region comprising SEQ ID NO: 6 and a heavy chain variable region
 comprising SEQ ID NO: 163; a light chain variable region comprising SEQ ID NO: 7 and a
 heavy chain variable region comprising SEQ ID NO: 164; a light chain variable region
 comprising SEQ ID NO: 8 and a heavy chain variable region comprising SEQ ID NO: 165; a

light chain variable region comprising SEQ ID NO: 9 and a heavy chain variable region comprising SEQ ID NO: 166; a light chain variable region comprising SEQ ID NO: 10 and a heavy chain variable region comprising SEQ ID NO: 167; a light chain variable region comprising SEQ ID NO: 11 and a heavy chain variable region comprising SEQ ID NO: 168;

5 a light chain variable region comprising SEQ ID NO: 12 and a heavy chain variable region comprising SEQ ID NO: 169; a light chain variable region comprising SEQ ID NO: 13 and a heavy chain variable region comprising SEQ ID NO: 170; a light chain variable region comprising SEQ ID NO: 14 and a heavy chain variable region comprising SEQ ID NO: 171;

10 a light chain variable region comprising SEQ ID NO: 15 and a heavy chain variable region comprising SEQ ID NO: 172; a light chain variable region comprising SEQ ID NO: 16 and a heavy chain variable region comprising SEQ ID NO: 173; a light chain variable region comprising SEQ ID NO: 17 and a heavy chain variable region comprising SEQ ID NO: 174;

a light chain variable region comprising SEQ ID NO: 18 and a heavy chain variable region comprising SEQ ID NO: 175; a light chain variable region comprising SEQ ID NO: 19 and a heavy chain variable region comprising SEQ ID NO: 176; a light chain variable region comprising SEQ ID NO: 20 and a heavy chain variable region comprising SEQ ID NO: 177;

15 a light chain variable region comprising SEQ ID NO: 21 and a heavy chain variable region comprising SEQ ID NO: 178; a light chain variable region comprising SEQ ID NO: 22 and a heavy chain variable region comprising SEQ ID NO: 179; a light chain variable region comprising SEQ ID NO: 23 and a heavy chain variable region comprising SEQ ID NO: 180;

20 a light chain variable region comprising SEQ ID NO: 24 and a heavy chain variable region comprising SEQ ID NO: 181; a light chain variable region comprising SEQ ID NO: 25 and a heavy chain variable region comprising SEQ ID NO: 182; a light chain variable region comprising SEQ ID NO: 26 and a heavy chain variable region comprising SEQ ID NO: 183;

25 a light chain variable region comprising SEQ ID NO: 27 and a heavy chain variable region comprising SEQ ID NO: 184; a light chain variable region comprising SEQ ID NO: 28 and a heavy chain variable region comprising SEQ ID NO: 185; a light chain variable region comprising SEQ ID NO: 29 and a heavy chain variable region comprising SEQ ID NO: 186;

a light chain variable region comprising SEQ ID NO: 30 and a heavy chain variable region comprising SEQ ID NO: 187; a light chain variable region comprising SEQ ID NO: 31 and a heavy chain variable region comprising SEQ ID NO: 188; a light chain variable region comprising SEQ ID NO: 32 and a heavy chain variable region comprising SEQ ID NO: 189;

30 a light chain variable region comprising SEQ ID NO: 33 and a heavy chain variable region comprising SEQ ID NO: 190; a light chain variable region comprising SEQ ID NO: 34 and a

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a light chain variable region comprising SEQ ID NO: 60 and a heavy chain variable region comprising SEQ ID NO: 217; a light chain variable region comprising SEQ ID NO: 61 and a heavy chain variable region comprising SEQ ID NO: 218; a light chain variable region comprising SEQ ID NO: 62 and a heavy chain variable region comprising SEQ ID NO: 219;

5 a light chain variable region comprising SEQ ID NO: 63 and a heavy chain variable region comprising SEQ ID NO: 220; a light chain variable region comprising SEQ ID NO: 64 and a heavy chain variable region comprising SEQ ID NO: 221; a light chain variable region comprising SEQ ID NO: 65 and a heavy chain variable region comprising SEQ ID NO: 222;

10 a light chain variable region comprising SEQ ID NO: 66 and a heavy chain variable region comprising SEQ ID NO: 223; a light chain variable region comprising SEQ ID NO: 67 and a heavy chain variable region comprising SEQ ID NO: 224; a light chain variable region comprising SEQ ID NO: 68 and a heavy chain variable region comprising SEQ ID NO: 225;

a light chain variable region comprising SEQ ID NO: 69 and a heavy chain variable region comprising SEQ ID NO: 226; a light chain variable region comprising SEQ ID NO: 70 and a heavy chain variable region comprising SEQ ID NO: 227; a light chain variable region comprising SEQ ID NO: 71 and a heavy chain variable region comprising SEQ ID NO: 228;

15 a light chain variable region comprising SEQ ID NO: 72 and a heavy chain variable region comprising SEQ ID NO: 229; a light chain variable region comprising SEQ ID NO: 73 and a heavy chain variable region comprising SEQ ID NO: 230; a light chain variable region comprising SEQ ID NO: 74 and a heavy chain variable region comprising SEQ ID NO: 231;

20 a light chain variable region comprising SEQ ID NO: 75 and a heavy chain variable region comprising SEQ ID NO: 232; a light chain variable region comprising SEQ ID NO: 76 and a heavy chain variable region comprising SEQ ID NO: 233; a light chain variable region comprising SEQ ID NO: 77 and a heavy chain variable region comprising SEQ ID NO: 234;

25 a light chain variable region comprising SEQ ID NO: 78 and a heavy chain variable region comprising SEQ ID NO: 235; a light chain variable region comprising SEQ ID NO: 79 and a heavy chain variable region comprising SEQ ID NO: 236; a light chain variable region comprising SEQ ID NO: 80 and a heavy chain variable region comprising SEQ ID NO: 237;

30 a light chain variable region comprising SEQ ID NO: 81 and a heavy chain variable region comprising SEQ ID NO: 238; a light chain variable region comprising SEQ ID NO: 82 and a heavy chain variable region comprising SEQ ID NO: 239; a light chain variable region comprising SEQ ID NO: 83 and a heavy chain variable region comprising SEQ ID NO: 240;

a light chain variable region comprising SEQ ID NO: 84 and a heavy chain variable region comprising SEQ ID NO: 241; a light chain variable region comprising SEQ ID NO: 85 and a

654

a light chain variable region comprising SEQ ID NO: 111 and a heavy chain variable region comprising SEQ ID NO: 268; a light chain variable region comprising SEQ ID NO: 112 and a heavy chain variable region comprising SEQ ID NO: 269; a light chain variable region comprising SEQ ID NO: 113 and a heavy chain variable region comprising SEQ ID NO: 270;

5 a light chain variable region comprising SEQ ID NO: 114 and a heavy chain variable region comprising SEQ ID NO: 271; a light chain variable region comprising SEQ ID NO: 115 and a heavy chain variable region comprising SEQ ID NO: 272; a light chain variable region comprising SEQ ID NO: 116 and a heavy chain variable region comprising SEQ ID NO: 273;

10 a light chain variable region comprising SEQ ID NO: 117 and a heavy chain variable region comprising SEQ ID NO: 274; a light chain variable region comprising SEQ ID NO: 118 and a heavy chain variable region comprising SEQ ID NO: 275; a light chain variable region comprising SEQ ID NO: 119 and a heavy chain variable region comprising SEQ ID NO: 276;

a light chain variable region comprising SEQ ID NO: 120 and a heavy chain variable region comprising SEQ ID NO: 277; a light chain variable region comprising SEQ ID NO: 121 and

15 a heavy chain variable region comprising SEQ ID NO: 278; a light chain variable region comprising SEQ ID NO: 122 and a heavy chain variable region comprising SEQ ID NO: 279; a light chain variable region comprising SEQ ID NO: 123 and a heavy chain variable region comprising SEQ ID NO: 280; a light chain variable region comprising SEQ ID NO: 124 and a heavy chain variable region comprising SEQ ID NO: 281; a light chain variable region

20 comprising SEQ ID NO: 125 and a heavy chain variable region comprising SEQ ID NO: 282; a light chain variable region comprising SEQ ID NO: 126 and a heavy chain variable region comprising SEQ ID NO: 283; a light chain variable region comprising SEQ ID NO: 127 and a heavy chain variable region comprising SEQ ID NO: 284; a light chain variable region comprising SEQ ID NO: 128 and a heavy chain variable region comprising SEQ ID NO: 285;

25 a light chain variable region comprising SEQ ID NO: 129 and a heavy chain variable region comprising SEQ ID NO: 286; a light chain variable region comprising SEQ ID NO: 130 and a heavy chain variable region comprising SEQ ID NO: 287; a light chain variable region comprising SEQ ID NO: 131 and a heavy chain variable region comprising SEQ ID NO: 288;

a light chain variable region comprising SEQ ID NO: 132 and a heavy chain variable region

30 comprising SEQ ID NO: 289; a light chain variable region comprising SEQ ID NO: 133 and a heavy chain variable region comprising SEQ ID NO: 290; a light chain variable region comprising SEQ ID NO: 134 and a heavy chain variable region comprising SEQ ID NO: 291;

a light chain variable region comprising SEQ ID NO: 135 and a heavy chain variable region comprising SEQ ID NO: 292; a light chain variable region comprising SEQ ID NO: 136 and

a heavy chain variable region comprising SEQ ID NO: 293; a light chain variable region comprising SEQ ID NO: 137 and a heavy chain variable region comprising SEQ ID NO: 294; a light chain variable region comprising SEQ ID NO: 138 and a heavy chain variable region comprising SEQ ID NO: 295; a light chain variable region comprising SEQ ID NO: 139 and a heavy chain variable region comprising SEQ ID NO: 296; a light chain variable region comprising SEQ ID NO: 140 and a heavy chain variable region comprising SEQ ID NO: 297; a light chain variable region comprising SEQ ID NO: 141 and a heavy chain variable region comprising SEQ ID NO: 298; a light chain variable region comprising SEQ ID NO: 142 and a heavy chain variable region comprising SEQ ID NO: 299; a light chain variable region comprising SEQ ID NO: 143 and a heavy chain variable region comprising SEQ ID NO: 300; a light chain variable region comprising SEQ ID NO: 144 and a heavy chain variable region comprising SEQ ID NO: 301; a light chain variable region comprising SEQ ID NO: 145 and a heavy chain variable region comprising SEQ ID NO: 302; a light chain variable region comprising SEQ ID NO: 146 and a heavy chain variable region comprising SEQ ID NO: 303; a light chain variable region comprising SEQ ID NO: 147 and a heavy chain variable region comprising SEQ ID NO: 304; a light chain variable region comprising SEQ ID NO: 148 and a heavy chain variable region comprising SEQ ID NO: 305; a light chain variable region comprising SEQ ID NO: 149 and a heavy chain variable region comprising SEQ ID NO: 306; a light chain variable region comprising SEQ ID NO: 150 and a heavy chain variable region comprising SEQ ID NO: 307; a light chain variable region comprising SEQ ID NO: 151 and a heavy chain variable region comprising SEQ ID NO: 308; a light chain variable region comprising SEQ ID NO: 152 and a heavy chain variable region comprising SEQ ID NO: 309; a light chain variable region comprising SEQ ID NO: 153 and a heavy chain variable region comprising SEQ ID NO: 310; a light chain variable region comprising SEQ ID NO: 154 and a heavy chain variable region comprising SEQ ID NO: 311; a light chain variable region comprising SEQ ID NO: 155 and a heavy chain variable region comprising SEQ ID NO: 312; a light chain variable region comprising SEQ ID NO: 156 and a heavy chain variable region comprising SEQ ID NO: 313; and a light chain variable region comprising SEQ ID NO: 157 and a heavy chain variable region comprising SEQ ID NO: 314.

14. The composition of claim 3, wherein said antibody or functional fragment thereof is an antibody, and wherein said antibody comprises a light chain comprising a sequence selected from the group consisting of SEQ ID NOs: 315-471 and a heavy chain comprising a sequence selected from the group consisting of SEQ ID NOs: 472-628.

15. The composition of claim 3, wherein said antibody or functional fragment thereof 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: 315 and a heavy chain comprising SEQ ID NO: 472; a light chain comprising SEQ ID NO: 316 and a heavy chain comprising SEQ ID NO: 473; a light chain comprising SEQ ID NO: 317 and a heavy chain comprising SEQ ID NO: 474; a light chain comprising SEQ ID NO: 318 and a heavy chain comprising SEQ ID NO: 475; a light chain comprising SEQ ID NO: 319 and a heavy chain comprising SEQ ID NO: 476; a light chain comprising SEQ ID NO: 320 and a heavy chain comprising SEQ ID NO: 477; a light chain comprising SEQ ID NO: 321 and a heavy chain comprising SEQ ID NO: 478; a light chain comprising SEQ ID NO: 322 and a heavy chain comprising SEQ ID NO: 479; a light chain comprising SEQ ID NO: 323 and a heavy chain comprising SEQ ID NO: 480; a light chain comprising SEQ ID NO: 324 and a heavy chain comprising SEQ ID NO: 481; a light chain comprising SEQ ID NO: 325 and a heavy chain comprising SEQ ID NO: 482; a light chain comprising SEQ ID NO: 326 and a heavy chain comprising SEQ ID NO: 483; a light chain comprising SEQ ID NO: 327 and a heavy chain comprising SEQ ID NO: 484; a light chain comprising SEQ ID NO: 328 and a heavy chain comprising SEQ ID NO: 485; a light chain comprising SEQ ID NO: 329 and a heavy chain comprising SEQ ID NO: 486; a light chain comprising SEQ ID NO: 330 and a heavy chain comprising SEQ ID NO: 487; a light chain comprising SEQ ID NO: 331 and a heavy chain comprising SEQ ID NO: 488; a light chain comprising SEQ ID NO: 332 and a heavy chain comprising SEQ ID NO: 489; a light chain comprising SEQ ID NO: 333 and a heavy chain comprising SEQ ID NO: 490; a light chain comprising SEQ ID NO: 334 and a heavy chain comprising SEQ ID NO: 491; a light chain comprising SEQ ID NO: 335 and a heavy chain comprising SEQ ID NO: 492; a light chain comprising SEQ ID NO: 336 and a heavy chain comprising SEQ ID NO: 493; a light chain comprising SEQ ID NO: 337 and a heavy chain comprising SEQ ID NO: 494; a light chain comprising SEQ ID NO: 338 and a heavy chain comprising SEQ ID NO: 495; a light chain comprising SEQ ID NO: 339 and a heavy chain comprising SEQ ID NO: 496; a light chain comprising SEQ ID NO: 340 and a heavy chain comprising SEQ ID NO: 497; a light chain comprising SEQ ID NO: 341 and a heavy chain comprising SEQ ID NO: 498; a light chain comprising SEQ ID NO: 342 and a heavy chain comprising SEQ ID NO: 499; a light chain comprising SEQ ID NO: 343 and a heavy chain comprising SEQ ID NO: 500; a light chain comprising SEQ ID NO: 344 and a heavy chain comprising SEQ ID NO: 501; a light chain comprising SEQ ID NO: 345 and a heavy chain comprising SEQ ID NO: 502; a light chain comprising SEQ ID

NO: 346 and a heavy chain comprising SEQ ID NO: 503; a light chain comprising SEQ ID
 NO: 347 and a heavy chain comprising SEQ ID NO: 504; a light chain comprising SEQ ID
 NO: 348 and a heavy chain comprising SEQ ID NO: 505; a light chain comprising SEQ ID
 NO: 349 and a heavy chain comprising SEQ ID NO: 506; a light chain comprising SEQ ID
 5 NO: 350 and a heavy chain comprising SEQ ID NO: 507; a light chain comprising SEQ ID
 NO: 351 and a heavy chain comprising SEQ ID NO: 508; a light chain comprising SEQ ID
 NO: 352 and a heavy chain comprising SEQ ID NO: 509; a light chain comprising SEQ ID
 NO: 353 and a heavy chain comprising SEQ ID NO: 510; a light chain comprising SEQ ID
 NO: 354 and a heavy chain comprising SEQ ID NO: 511; a light chain comprising SEQ ID
 10 NO: 355 and a heavy chain comprising SEQ ID NO: 512; a light chain comprising SEQ ID
 NO: 356 and a heavy chain comprising SEQ ID NO: 513; a light chain comprising SEQ ID
 NO: 357 and a heavy chain comprising SEQ ID NO: 514; a light chain comprising SEQ ID
 NO: 358 and a heavy chain comprising SEQ ID NO: 515; a light chain comprising SEQ ID
 NO: 359 and a heavy chain comprising SEQ ID NO: 516; a light chain comprising SEQ ID
 15 NO: 360 and a heavy chain comprising SEQ ID NO: 517; a light chain comprising SEQ ID
 NO: 361 and a heavy chain comprising SEQ ID NO: 518; a light chain comprising SEQ ID
 NO: 362 and a heavy chain comprising SEQ ID NO: 519; a light chain comprising SEQ ID
 NO: 363 and a heavy chain comprising SEQ ID NO: 520; a light chain comprising SEQ ID
 NO: 364 and a heavy chain comprising SEQ ID NO: 521; a light chain comprising SEQ ID
 20 NO: 365 and a heavy chain comprising SEQ ID NO: 522; a light chain comprising SEQ ID
 NO: 366 and a heavy chain comprising SEQ ID NO: 523; a light chain comprising SEQ ID
 NO: 367 and a heavy chain comprising SEQ ID NO: 524; a light chain comprising SEQ ID
 NO: 368 and a heavy chain comprising SEQ ID NO: 525; a light chain comprising SEQ ID
 NO: 369 and a heavy chain comprising SEQ ID NO: 526; a light chain comprising SEQ ID
 25 NO: 370 and a heavy chain comprising SEQ ID NO: 527; a light chain comprising SEQ ID
 NO: 371 and a heavy chain comprising SEQ ID NO: 528; a light chain comprising SEQ ID
 NO: 372 and a heavy chain comprising SEQ ID NO: 529; a light chain comprising SEQ ID
 NO: 373 and a heavy chain comprising SEQ ID NO: 530; a light chain comprising SEQ ID
 NO: 374 and a heavy chain comprising SEQ ID NO: 531; a light chain comprising SEQ ID
 30 NO: 375 and a heavy chain comprising SEQ ID NO: 532; a light chain comprising SEQ ID
 NO: 376 and a heavy chain comprising SEQ ID NO: 533; a light chain comprising SEQ ID
 NO: 377 and a heavy chain comprising SEQ ID NO: 534; a light chain comprising SEQ ID
 NO: 378 and a heavy chain comprising SEQ ID NO: 535; a light chain comprising SEQ ID
 NO: 379 and a heavy chain comprising SEQ ID NO: 536; a light chain comprising SEQ ID

NO: 380 and a heavy chain comprising SEQ ID NO: 537; a light chain comprising SEQ ID
NO: 381 and a heavy chain comprising SEQ ID NO: 538; a light chain comprising SEQ ID
NO: 382 and a heavy chain comprising SEQ ID NO: 539; a light chain comprising SEQ ID
NO: 383 and a heavy chain comprising SEQ ID NO: 540; a light chain comprising SEQ ID
5 NO: 384 and a heavy chain comprising SEQ ID NO: 541; a light chain comprising SEQ ID
NO: 385 and a heavy chain comprising SEQ ID NO: 542; a light chain comprising SEQ ID
NO: 386 and a heavy chain comprising SEQ ID NO: 543; a light chain comprising SEQ ID
NO: 387 and a heavy chain comprising SEQ ID NO: 544; a light chain comprising SEQ ID
NO: 388 and a heavy chain comprising SEQ ID NO: 545; a light chain comprising SEQ ID
10 NO: 389 and a heavy chain comprising SEQ ID NO: 546; a light chain comprising SEQ ID
NO: 390 and a heavy chain comprising SEQ ID NO: 547; a light chain comprising SEQ ID
NO: 391 and a heavy chain comprising SEQ ID NO: 548; a light chain comprising SEQ ID
NO: 392 and a heavy chain comprising SEQ ID NO: 549; a light chain comprising SEQ ID
NO: 393 and a heavy chain comprising SEQ ID NO: 550; a light chain comprising SEQ ID
15 NO: 394 and a heavy chain comprising SEQ ID NO: 551; a light chain comprising SEQ ID
NO: 395 and a heavy chain comprising SEQ ID NO: 552; a light chain comprising SEQ ID
NO: 396 and a heavy chain comprising SEQ ID NO: 553; a light chain comprising SEQ ID
NO: 397 and a heavy chain comprising SEQ ID NO: 554; a light chain comprising SEQ ID
NO: 398 and a heavy chain comprising SEQ ID NO: 555; a light chain comprising SEQ ID
20 NO: 399 and a heavy chain comprising SEQ ID NO: 556; a light chain comprising SEQ ID
NO: 400 and a heavy chain comprising SEQ ID NO: 557; a light chain comprising SEQ ID
NO: 401 and a heavy chain comprising SEQ ID NO: 558; a light chain comprising SEQ ID
NO: 402 and a heavy chain comprising SEQ ID NO: 559; a light chain comprising SEQ ID
NO: 403 and a heavy chain comprising SEQ ID NO: 560; a light chain comprising SEQ ID
25 NO: 404 and a heavy chain comprising SEQ ID NO: 561; a light chain comprising SEQ ID
NO: 405 and a heavy chain comprising SEQ ID NO: 562; a light chain comprising SEQ ID
NO: 406 and a heavy chain comprising SEQ ID NO: 563; a light chain comprising SEQ ID
NO: 407 and a heavy chain comprising SEQ ID NO: 564; a light chain comprising SEQ ID
NO: 408 and a heavy chain comprising SEQ ID NO: 565; a light chain comprising SEQ ID
30 NO: 409 and a heavy chain comprising SEQ ID NO: 566; a light chain comprising SEQ ID
NO: 410 and a heavy chain comprising SEQ ID NO: 567; a light chain comprising SEQ ID
NO: 411 and a heavy chain comprising SEQ ID NO: 568; a light chain comprising SEQ ID
NO: 412 and a heavy chain comprising SEQ ID NO: 569; a light chain comprising SEQ ID
NO: 413 and a heavy chain comprising SEQ ID NO: 570; a light chain comprising SEQ ID

NO: 414 and a heavy chain comprising SEQ ID NO: 571; a light chain comprising SEQ ID
 NO: 415 and a heavy chain comprising SEQ ID NO: 572; a light chain comprising SEQ ID
 NO: 416 and a heavy chain comprising SEQ ID NO: 573; a light chain comprising SEQ ID
 NO: 417 and a heavy chain comprising SEQ ID NO: 574; a light chain comprising SEQ ID
 5 NO: 418 and a heavy chain comprising SEQ ID NO: 575; a light chain comprising SEQ ID
 NO: 419 and a heavy chain comprising SEQ ID NO: 576; a light chain comprising SEQ ID
 NO: 420 and a heavy chain comprising SEQ ID NO: 577; a light chain comprising SEQ ID
 NO: 421 and a heavy chain comprising SEQ ID NO: 578; a light chain comprising SEQ ID
 NO: 422 and a heavy chain comprising SEQ ID NO: 579; a light chain comprising SEQ ID
 10 NO: 423 and a heavy chain comprising SEQ ID NO: 580; a light chain comprising SEQ ID
 NO: 424 and a heavy chain comprising SEQ ID NO: 581; a light chain comprising SEQ ID
 NO: 425 and a heavy chain comprising SEQ ID NO: 582; a light chain comprising SEQ ID
 NO: 426 and a heavy chain comprising SEQ ID NO: 583; a light chain comprising SEQ ID
 NO: 427 and a heavy chain comprising SEQ ID NO: 584; a light chain comprising SEQ ID
 15 NO: 428 and a heavy chain comprising SEQ ID NO: 585; a light chain comprising SEQ ID
 NO: 429 and a heavy chain comprising SEQ ID NO: 586; a light chain comprising SEQ ID
 NO: 430 and a heavy chain comprising SEQ ID NO: 587; a light chain comprising SEQ ID
 NO: 431 and a heavy chain comprising SEQ ID NO: 588; a light chain comprising SEQ ID
 NO: 432 and a heavy chain comprising SEQ ID NO: 589; a light chain comprising SEQ ID
 20 NO: 433 and a heavy chain comprising SEQ ID NO: 590; a light chain comprising SEQ ID
 NO: 434 and a heavy chain comprising SEQ ID NO: 591; a light chain comprising SEQ ID
 NO: 435 and a heavy chain comprising SEQ ID NO: 592; a light chain comprising SEQ ID
 NO: 436 and a heavy chain comprising SEQ ID NO: 593; a light chain comprising SEQ ID
 NO: 437 and a heavy chain comprising SEQ ID NO: 594; a light chain comprising SEQ ID
 25 NO: 438 and a heavy chain comprising SEQ ID NO: 595; a light chain comprising SEQ ID
 NO: 439 and a heavy chain comprising SEQ ID NO: 596; a light chain comprising SEQ ID
 NO: 440 and a heavy chain comprising SEQ ID NO: 597; a light chain comprising SEQ ID
 NO: 441 and a heavy chain comprising SEQ ID NO: 598; a light chain comprising SEQ ID
 NO: 442 and a heavy chain comprising SEQ ID NO: 599; a light chain comprising SEQ ID
 30 NO: 443 and a heavy chain comprising SEQ ID NO: 600; a light chain comprising SEQ ID
 NO: 444 and a heavy chain comprising SEQ ID NO: 601; a light chain comprising SEQ ID
 NO: 445 and a heavy chain comprising SEQ ID NO: 602; a light chain comprising SEQ ID
 NO: 446 and a heavy chain comprising SEQ ID NO: 603; a light chain comprising SEQ ID
 NO: 447 and a heavy chain comprising SEQ ID NO: 604; a light chain comprising SEQ ID

NO: 448 and a heavy chain comprising SEQ ID NO: 605; a light chain comprising SEQ ID NO: 449 and a heavy chain comprising SEQ ID NO: 606; a light chain comprising SEQ ID NO: 450 and a heavy chain comprising SEQ ID NO: 607; a light chain comprising SEQ ID NO: 451 and a heavy chain comprising SEQ ID NO: 608; a light chain comprising SEQ ID NO: 452 and a heavy chain comprising SEQ ID NO: 609; a light chain comprising SEQ ID NO: 453 and a heavy chain comprising SEQ ID NO: 610; a light chain comprising SEQ ID NO: 454 and a heavy chain comprising SEQ ID NO: 611; a light chain comprising SEQ ID NO: 455 and a heavy chain comprising SEQ ID NO: 612; a light chain comprising SEQ ID NO: 456 and a heavy chain comprising SEQ ID NO: 613; a light chain comprising SEQ ID NO: 457 and a heavy chain comprising SEQ ID NO: 614; a light chain comprising SEQ ID NO: 458 and a heavy chain comprising SEQ ID NO: 615; a light chain comprising SEQ ID NO: 459 and a heavy chain comprising SEQ ID NO: 616; a light chain comprising SEQ ID NO: 460 and a heavy chain comprising SEQ ID NO: 617; a light chain comprising SEQ ID NO: 461 and a heavy chain comprising SEQ ID NO: 618; a light chain comprising SEQ ID NO: 462 and a heavy chain comprising SEQ ID NO: 619; a light chain comprising SEQ ID NO: 463 and a heavy chain comprising SEQ ID NO: 620; a light chain comprising SEQ ID NO: 464 and a heavy chain comprising SEQ ID NO: 621; a light chain comprising SEQ ID NO: 465 and a heavy chain comprising SEQ ID NO: 622; a light chain comprising SEQ ID NO: 466 and a heavy chain comprising SEQ ID NO: 623; a light chain comprising SEQ ID NO: 467 and a heavy chain comprising SEQ ID NO: 624; a light chain comprising SEQ ID NO: 468 and a heavy chain comprising SEQ ID NO: 625; a light chain comprising SEQ ID NO: 469 and a heavy chain comprising SEQ ID NO: 626; a light chain comprising SEQ ID NO: 470 and a heavy chain comprising SEQ ID NO: 627; and a light chain comprising SEQ ID NO: 471 and a heavy chain comprising SEQ ID NO: 628.

16. The composition of any one of claims 1-15, wherein the GLP-1 receptor agonist is selected from the group consisting of GLP-1(7-37) (SEQ ID NO: 3184);

Exendin-4 (SEQ ID NO: 3163);

Exendin-3 (SEQ ID NO: 3164);

Leu¹⁴-exendin-4 (SEQ ID NO: 3165);

Leu¹⁴,Phe²⁵-exendin-4 (SEQ ID NO: 3166);

Leu¹⁴,Ala¹⁹,Phe²⁵-exendin-4 (SEQ ID NO: 3167);

exendin-4(1-30) (SEQ ID NO: 3168);

Leu¹⁴-exendin-4(1-30) (SEQ ID NO: 3169);

Leu¹⁴,Phe²⁵-exendin-4(1-30) (SEQ ID NO: 3170);

- Leu¹⁴,Ala¹⁹,Phe²⁵-exendin-4(1-30) (SEQ ID NO: 3171);
 exendin-4(1-28) (SEQ ID NO: 3172);
 Leu¹⁴-exendin-4(1-28) (SEQ ID NO: 3173);
 Leu¹⁴,Phe²⁵-exendin-4(1-28) (SEQ ID NO: 3174);
 5 Leu¹⁴,Ala¹⁹,Phe²⁵-exendin-4 (1-28) (SEQ ID NO: 3175);
 Leu¹⁴,Lys^{17,20},Ala¹⁹,Glu²¹,Phe²⁵,Gln²⁸-exendin-4 (SEQ ID NO: 3176);
 Leu¹⁴,Lys^{17,20},Ala¹⁹,Glu²¹,Gln²⁸-exendin-4 (SEQ ID NO: 3177);
 Phe⁴,Leu¹⁴,Gln²⁸,Lys³³,Glu³⁴, Ile^{35,36},Ser³⁷-exendin-4(1-37) (SEQ ID NO: 3180);
 Phe⁴,Leu¹⁴,Lys^{17,20},Ala¹⁹,Glu²¹,Gln²⁸-exendin-4 (SEQ ID NO: 3181);
 10 Val¹¹,Ile¹³,Leu¹⁴,Ala¹⁶,Lys²¹,Phe²⁵-exendin-4 (SEQ ID NO: 3182);
 exendin-4-Lys⁴⁰ (SEQ ID NO: 3183);
 GLP-1(7-37) (SEQ ID NO: 3184);
 HXaa8EGTFTSDVSSYLEXaa22Xaa23AAKEFIXaa30WLXaa33Xaa34GXaa36Xaa37;
 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
 15 or K; Xaa34 is K, N, or R; Xaa36 is R or G; and Xaa37 is G, H, P, or absent (SEQ ID NO:
 3187);
 Arg³⁴-GLP-1(7-37) (SEQ ID NO: 3188);
 Glu³⁰-GLP-1(7-37) (SEQ ID NO: 3189);
 Lys²²-GLP-1(7-37) (SEQ ID NO: 3190);
 20 Gly^{8,36},Glu²²-GLP-1(7-37) (SEQ ID NO: 3191);
 Val⁸,Glu²²,Gly³⁶-GLP-1(7-37) (SEQ ID NO: 3192);
 Gly^{8,36},Glu²²,Lys³³,Asn³⁴-GLP-1(7-37) (SEQ ID NO: 3193);
 Val⁸,Glu²²,Lys³³,Asn³⁴,Gly³⁶-GLP-1(7-37) (SEQ ID NO: 3194);
 Gly^{8,36},Glu²²,Pro³⁷-GLP-1(7-37) (SEQ ID NO: 3195);
 25 Val⁸,Glu²²,Gly³⁶,Pro³⁷-GLP-1(7-37) (SEQ ID NO: 3196);
 Gly^{8,36},Glu²²,Lys³³, Asn³⁴,Pro³⁷-GLP-1(7-37) (SEQ ID NO: 3197);
 Val⁸,Glu²²,Lys³³,Asn³⁴,Gly³⁶,Pro³⁷-GLP-1(7-37) (SEQ ID NO: 3198);
 Gly^{8,36},Glu²²-GLP-1(7-36) (SEQ ID NO: 3199);
 Val⁸,Glu²²,Gly³⁶-GLP-1(7-36) (SEQ ID NO: 3200);
 30 Val⁸,Glu²²,Asn³⁴,Gly³⁶-GLP-1(7-36) (SEQ ID NO: 3201);
 Gly^{8,36},Glu²²,Asn³⁴-GLP-1(7-36) (SEQ ID NO: 3202);
 GLP-1 analog (SEQ ID NO: 3206);
 GLP-1 analog (SEQ ID NO: 3207);
 [Gly^{8,36},Glu²²]GLP-1(7-37) (SEQ ID NO: 3201);

HAEGTFTSDVSSYLEGQAAKEFIAWLVKGRG (SEQ ID NO: 3202);
AEGTFTSDVSSYLEGQAAKEFIAWLVKGRG (SEQ ID NO: 3203);
EGTFTSDVSSYLEGQAAKEFIAWLVKGRG (SEQ ID NO: 3204);
HGEFTFTSDVSSYLEGQAAKEFIAWLVKGRG (SEQ ID NO: 3205);
5 HGEFTFTSDVSSYLEGQAAKEFIAWLVKGR (SEQ ID NO: 3206);
HLEGTFTSDVSSYLEGQAAKEFIAWLVKGRG (SEQ ID NO: 3207);
HGEFTFTSDLSKQMEEEEAVRLF (SEQ ID NO: 3208);
HGEFTFTSDLSKQMEEEEAVRLFI (SEQ ID NO: 3209);
HGEFTFTSDVSSYLEGQAAKEFIAWLVKGGG (SEQ ID NO: 3210);
10 HGEFTFTSDLSKQMEEEEAVRLAAQAAQGGG (SEQ ID NO: 3211);
HSEGTFTSDVSSYLEEQAAKEFIAWLVKGGG (SEQ ID NO: 3212);
HSQGTFTSDVSSYLEEQAAKEFIAWLVKGGG (SEQ ID NO: 3213);
HGDGTFTSDVSSYLEEQAAKEFIAWLVKGGG (SEQ ID NO: 3214);
HSDGTFTSDVSSYLEEQAAKEFIAWLVKGGG (SEQ ID NO: 3215);
15 HSEGTFTSDVSSYLEEQAAKEFIEWLVKGGG (SEQ ID NO: 3216);
HSQGTFTSDVSSYLEEQAAKEFIEWLVKGGG (SEQ ID NO: 3217);
HGDGTFTSDVSSYLEEQAAKEFIEWLVKGGG (SEQ ID NO: 3218);
HSDGTFTSDVSSYLEEQAAKEFIEWLVKGGG (SEQ ID NO: 3219);
HGEFTFTSDVSSYLEEQAAKEFIAWLKNGGG (SEQ ID NO: 3220);
20 HSEGTFTSDVSSYLEEQAAKEFIAWLKNGGG (SEQ ID NO: 3221);
HSQGTFTSDVSSYLEEQAAKEFIAWLKNGGG (SEQ ID NO: 3222);
HGDGTFTSDVSSYLEEQAAKEFIAWLKNGGG (SEQ ID NO: 3223);
HSDGTFTSDVSSYLEEQAAKEFIAWLKNGGG (SEQ ID NO: 3224);
HSEGTFTSDVSSYLEEQAAKEFIEWLKNGGG (SEQ ID NO: 3225);
25 HSQGTFTSDVSSYLEEQAAKEFIEWLKNGGG (SEQ ID NO: 3226);
HGDGTFTSDVSSYLEEQAAKEFIEWLKNGGG (SEQ ID NO: 3227);
HSDGTFTSDVSSYLEEQAAKEFIEWLKNGGG (SEQ ID NO: 3228);
HGEFTFTSDVSSYLEEQAAKEFIEWLKNEGG (SEQ ID NO: 3229);
HSEGTFTSDVSSYLEEQAAKEFIEWLKNEGG (SEQ ID NO: 3230);
30 HGEFTFTSDVSSYLEEQAAKEFIEWLKNPGG (SEQ ID NO: 3231);
HSEGTFTSDVSSYLEEQAAKEFIEWLKNPGG (SEQ ID NO: 3232);
HGEFTFTSDVSSYLEEQAAKEFIEWLKNQGG (SEQ ID NO: 3233);
HSEGTFTSDVSSYLEEQAAKEFIEWLKNQGG (SEQ ID NO: 3234);
HGEFTFTSDVSSYLEEQAAKEFIEWLKNTGG (SEQ ID NO: 3235);

HSEGTFTSDVSSYLEEQAAKEFIEWLKNTGG (SEQ ID NO: 3236);
HGEFTFTSDVSSYLEEQAAKEFIEWLKNVGG (SEQ ID NO: 3237);
HSEGTFTSDVSSYLEEQAAKEFIEWLKNVGG (SEQ ID NO: 3238);
HGEFTFTSDVSSYLEEQAAKEFIEWLKQGGG (SEQ ID NO: 3239);
5 HSEGTFTSDVSSYLEEQAAKEFIEWLKQGGG (SEQ ID NO: 3240);
HGEFTFTSDVSSYLEEQAAKEFIAWLKGGG (SEQ ID NO: 3241);
HGEFTFTSDVSSYLEEQAAKEFIAWLKGGG (SEQ ID NO: 3242);
HVEGTFTSDVSSYLEGQAAKEFIAWLKGGG (SEQ ID NO: 3243);
HSEGTFTSDVSSYLEGQAAKEFIAWLKGGG (SEQ ID NO: 3244);
10 HGQGTFTSDVSSYLEGQAAKEFIAWLKGGG (SEQ ID NO: 3245);
HVQGTFTSDVSSYLEGQAAKEFIAWLKGGG (SEQ ID NO: 3246);
HSQGTFTSDVSSYLEGQAAKEFIAWLKGGG (SEQ ID NO: 3247);
HVDGTFTSDVSSYLEGQAAKEFIAWLKGGG (SEQ ID NO: 3248);
HHGTFTSDVSSYLEGQAAKEFIAWLKGGG (SEQ ID NO: 3249);
15 HVHGTFTSDVSSYLEGQAAKEFIAWLKGGG (SEQ ID NO: 3250);
HSHGTFTSDVSSYLEGQAAKEFIAWLKGGG (SEQ ID NO: 3251);
HGDGTFTSDVSSYLEGQAAKEFIAWLKGGG (SEQ ID NO: 3252);
HSDGTFTSDVSSYLEGQAAKEFIAWLKGGG (SEQ ID NO: 3253);
HGEFTFTSDVSSYLEEQAAKEFIEWLKNGG (SEQ ID NO: 3254);
20 HGEFTFTSDVSSYLEEQAAKEFIEWLKNGG (SEQ ID NO: 3255);
HGEFTFTSDVSSYLEEQAAKEFIEWLKNGG (SEQ ID NO: 3256);
HGEFTFTSEVSSYLEGQAAKEFIEWLKNGG (SEQ ID NO: 3257);
HSEGTFTSDLSKQMEEEAVRLFIAAQAQGGG (SEQ ID NO: 3258);
HSQGTFTSDLSKQMEEEAVRLFIAAQAQGGG (SEQ ID NO: 3259);
25 HGDGTFTSDLSKQMEEEAVRLFIAAQAQGGG (SEQ ID NO: 3260);
HSDGTFTSDLSKQMEEEAVRLFIAAQAQGGG (SEQ ID NO: 3261);
HGEFTFTSDLSKQMEEEAVRLFIAAQAQGGG (SEQ ID NO: 3262);
HGEFTFTSDLSKQMEEEAVRLFIEWLKNGG (SEQ ID NO: 3263);
HGEFTFTSDVSSYLEGEAVRLFIEWLKNGG (SEQ ID NO: 3264);
30 HGEFTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGAPPS (SEQ ID NO: 3265);
HGEFTFTSDVSSYLEGEAVRLFIEWLKNGGPSSGAPPS (SEQ ID NO: 3266);
HHGEFTFTSDVSSYLEEQAAKEFIEWLKNGG (SEQ ID NO: 3267);
HHGEFTFTSDVSSYLEEQAAKEFIEWLKDGGG (SEQ ID NO: 3268);
HHGEFTFTSDVSSYLEEQAAKEFIEWLKQGGG (SEQ ID NO: 3269);

HHGEGTFTSDVSSYLEEQAAKEFIEWLKNQGG (SEQ ID NO: 3270);
HHGEGTFTSDVSSYLEEQAAKEFIEWLKNTGG (SEQ ID NO: 3271);
HHGEGTFTSDVSSYLEEQAAKEFIEWLKNVGG (SEQ ID NO: 3272);
HHGEGTFTSDVSSYLEEQAAKEFIEWLKNP GG (SEQ ID NO: 3273);
5 HHGEGTFTSDVSSYLEEQAAKEFIEWLKNEGG (SEQ ID NO: 3274);
HGAGTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3275);
HGDGTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3276);
HGLGTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3277);
HGVGTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3278);
10 HGFGTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3279);
HGYGTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3280);
HGTGTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3281);
HGNGTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3282);
HHGHTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3283);
15 HGKGTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3284);
HIGTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3285);
HGWGTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3286);
HGP GTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3287);
HGS GTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3288);
20 HGR GTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3289);
AHGEGTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3290);
GHGEGTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3291);
HHGEGTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3292);
HHEGTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3293);
25 HGEATFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3294);
HGESTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3295);
HGEVTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3296);
HGEKTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3297);
HGEETFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3298);
30 HEGTFTSDVSSYLEGQAAKEFIAWL VKG (SEQ ID NO: 3299);
HVEGTFTSDVSSYLEGQAAKEFIAWL VKGRG (SEQ ID NO: 3300);
HSEGTFTSDVSSYLEGQAAKEFIAWL VKGRG (SEQ ID NO: 3301); and
HGQGTFTSDVSSYLEGQAAKEFIAWL VKGRG (SEQ ID NO: 3302).

17. The composition of any one of claims 1-16, wherein the composition further comprises a linker peptide in between the C-terminus of the GLP-1 receptor agonist and the N-terminus of the light chain variable region or heavy chain variable region.

- 5 18. The composition of claim 17, wherein the linker peptide is selected from the group consisting of (Gly₃Ser)₂ (SEQ ID NO: 3303), (Gly₄Ser)₂ (SEQ ID NO: 3304), (Gly₃Ser)₃ (SEQ ID NO: 3305), (Gly₄Ser)₃ (SEQ ID NO: 3306), (Gly₃Ser)₄ (SEQ ID NO: 3307), (Gly₄Ser)₄ (SEQ ID NO: 3308), (Gly₃Ser)₅ (SEQ ID NO: 3309), (Gly₄Ser)₅ (SEQ ID NO: 3310), (Gly₃Ser)₆ (SEQ ID NO: 3311), (Gly₄Ser)₆, GGEGGG (SEQ ID NO:3312);
- 10 GGEEEGGG (SEQ ID NO:3313); GEEEG (SEQ ID NO:3314); GEEE (SEQ ID NO:3315); GGDGGG (SEQ ID NO:3316); GGDDDG (SEQ ID NO:3317); GDDDG (SEQ ID NO:3318); GDDD (SEQ ID NO:3319); GGGGSDSDSDGEDGGGGS (SEQ ID NO:3320); WEWEW (SEQ ID NO:3321); FEFEF (SEQ ID NO:3322); EEEWW (SEQ ID NO:3323); EEEFFF (SEQ ID NO:3324); WEEEEWW (SEQ ID NO:3325); FFEFFF
- 15 (SEQ ID NO:3326). GGGG (SEQ ID NO: 3327); GGGGSGGGG (SEQ ID NO: 3328); GAPAPAPAPG (SEQ ID NO: 3329); GGGGAGGGGAGGGG (SEQ ID NO: 3330); GAPAPAPAPAPAPG (SEQ ID NO: 3331); GAPAPAPAPAPAPAPG (SEQ ID NO: 3332); GGGGAGGGGAGGGGAGGGG (SEQ ID NO: 3333); GAPAPAPAPAPAPAPAPAPG (SEQ ID NO: 3334);
- 20 GSGSATGGSGSVASSGSGSATGS (SEQ ID NO: 3335); and GSGSATGGSGSVASSGSGSATHL (SEQ ID NO: 3336).

1/48

FIG. 1A

Amgen#	GLP1 activity		H	A	E	G	T	F	T	S	D	V	S	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G
	EC50 (M)	EC50 (pM)																													
3166733#1	3.48E-10	347.9	H	G	A	G	T	F	T	S	D	V	S	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G
3166734#1	4.40E-12	4.4	H	G	D	G	T	F	T	S	D	V	S	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G
3166735#1	9.65E-11	96.5	H	G	L	G	T	F	T	S	D	V	S	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G
3166736#1	8.38E-11	83.8	H	G	V	G	T	F	T	S	D	V	S	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G
3166737#1	3.04E-09	3039	H	G	F	G	T	F	T	S	D	V	S	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G
3166738#1	2.83E-09	2831	H	G	Y	G	T	F	T	S	D	V	S	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G
3166739#1	1.62E-10	161.7	H	G	T	G	T	F	T	S	D	V	S	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G
3166740#1	2.80E-10	280.2	H	G	N	G	T	F	T	S	D	V	S	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G
3166741#1	5.37E-12	5.4	H	G	H	G	T	F	T	S	D	V	S	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G
3166742#1	6.07E-09	6070	H	G	K	G	T	F	T	S	D	V	S	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G
3166743#1	5.38E-11	53.8	H	G	I	G	T	F	T	S	D	V	S	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G
3166744#1	2.82E-09	2823	H	G	W	G	T	F	T	S	D	V	S	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G
3166745#1	3.76E-10	375.7	H	G	P	G	T	F	T	S	D	V	S	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G
3166747#1	4.26E-10	426.4	H	G	S	G	T	F	T	S	D	V	S	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G
3166748#1	1.40E-09	1395	H	G	R	G	T	F	T	S	D	V	S	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G
3166749#1	6.69E-11	66.9	A	H	G	E	G	T	F	T	S	D	V	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G
3166961#1	2.05E-10	205.2	G	H	G	E	G	T	F	T	S	D	V	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G
3166962#1	3.63E-10	363.1	H	H	G	E	G	T	F	T	S	D	V	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G
3166963#1	5.85E-10	585.2	H	H	E	G	T	F	T	S	D	V	S	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G
3166964#1	3.51E-09	3508	H	G	E	A	T	F	T	S	D	V	S	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G
3166965#1	4.98E-09	4978	H	G	E	S	T	F	T	S	D	V	S	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G
3166966#1	5.53E-08	55300	H	G	E	V	T	F	T	S	D	V	S	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G
3166967#1	~ 4.69e-005	~ 46870000	H	G	E	K	T	F	T	S	D	V	S	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G
3166968#1	9.87E-08	98710	H	G	E	E	T	F	T	S	D	V	S	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G

2/48

FIG. 1B

	GLP1 activity			H	A	E	G	T	F	T	S	D	V	S	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G		
Amgen#	EC50 (M)	EC50 (pM)	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37
3161008#1		6.2		H	G	E	G	T	F	T	S	D	V	S	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G		
3161010#1		10.7		H	V	E	G	T	F	T	S	D	V	S	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G	R	G
3161011#1		3.4		H	S	E	G	T	F	T	S	D	V	S	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G	R	G
3161012#1		4.1		H	G	Q	G	T	F	T	S	D	V	S	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G	R	G

3/48

FIG. 2

Amgen#	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	hGLP1R EC50 (pM)
3159823#1	H	A	E	G	T	F	T	S	D	V	S	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G	R	G	2.12
1119185#3	H	A	E	G	T	F	T	S	D	V	S	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G	R	G	2.35
3161005#1		A	E	G	T	F	T	S	D	V	S	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G	R	G	3005
3161006#1			E	G	T	F	T	S	D	V	S	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G	R	G	40000
1062072#3	H	G	E	G	T	F	T	S	D	V	S	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G	R	G	5.2
3161007#1	H	G	E	G	T	F	T	S	D	V	S	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G	R		6.5
3161008#1	H	G	E	G	T	F	T	S	D	V	S	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G			6.2
3161009#1	H	L	E	G	T	F	T	S	D	V	S	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G	R	G	1021
3161010#1	H	V	E	G	T	F	T	S	D	V	S	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G	R	G	10.7
3161011#1	H	S	E	G	T	F	T	S	D	V	S	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G	R	G	3.4
3161012#1	H	G	Q	G	T	F	T	S	D	V	S	S	Y	L	E	G	Q	A	A	K	E	F	I	A	W	L	V	K	G	R	G	4.1

- > 1000-fold potency decrease with truncation of single N-terminal residue.
- Truncation to Gly35 well tolerated and eliminates potential Arg36 trypsin site.
- His-Ala is the DPP-IV recognition sequence. Minimal impact when Ala8 substituted with Gly, Val, and Ser, but 500-fold decrease when substituted with Leu.
- Replacement of Glu9 with Gln does not shift potency and may reduce Gly8-Glu9 cleavage observed in vivo from mouse.

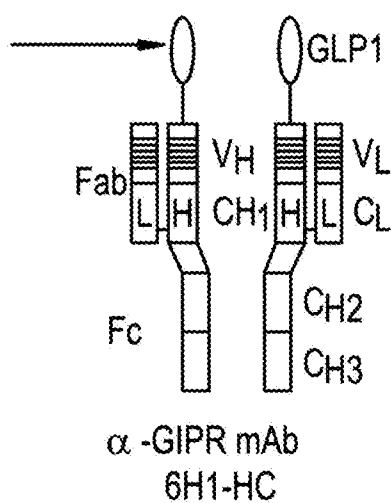
4/48

FIG. 3

Ab: 6H1 HC

Linker: 1Kmod

GLP1: (A2G/E3H/R30G), (A2V/E3H/R30G), (A2S/E3H/R30G), (A2G/E3D/R30G),
 (A2V/E3D/R30G), (A2S/E3D/R30G), (0A/A2G/R30G), (A2V/R30G), (A2S/R30G),
 (A2G/E3Q/R30G), (A2V/E3Q/R30G), (A2S/E3Q/R30G)



5/48

FIG. 4

Construct	Lot	GLP1 EC ₅₀ (pM)	GI _{PR} IC ₅₀ (nM)	Yield (g/L)	SEC (%MP)	MS Purified
(A2V/R30G)	PL-45559	126	146	148	98	NT-clip
(A2S/R30G)	PL-45560	35	189	20	97	
(A2G/E3Q/R30G)	PL-45561	37	404	36	98	
(A2V/E3Q/R30G)	PL-45562	97	221	33	98	
(A2S/E3Q/R30G)	PL-45563	56	693	98	99	
(A2G/E3H/R30G)	PL-45565	30	241	20	99	NT-clip
(A2V/E3H/R30G)	PL-45567	43	212	31	99	NT-clip
(A2S/E3H/R30G)	PL-45569	26	187	78	99	
(A2V/E3D/R30G)	PL-45564	48	273	133	99	
(A2G/E3D/R30G)	PL-45570	31	292	82	99	
(A2S/E3D/R30G)	PL-45571	21	468	107	98	
(0A/A2G/R30G)	PL-45572	88	200	146	99	



6/48

FIG. 5A

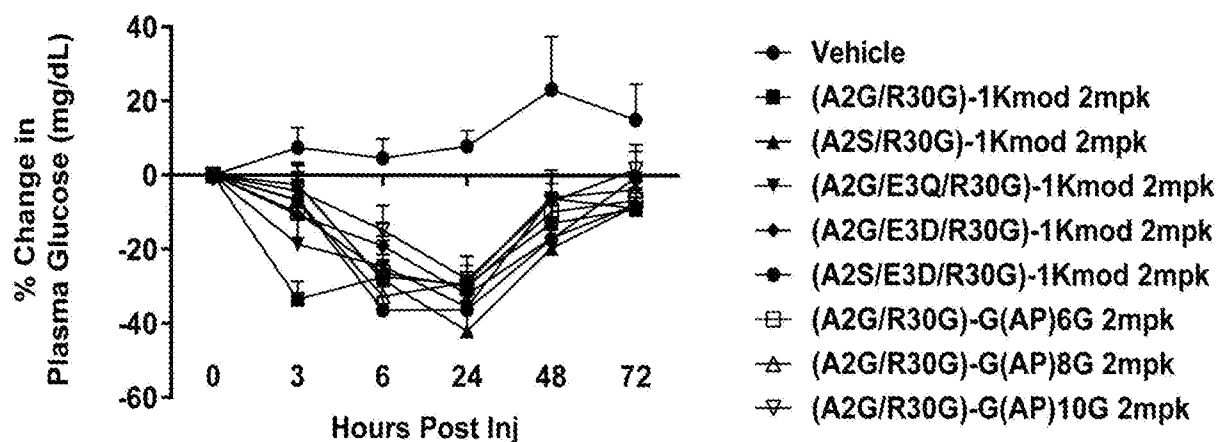


FIG. 5B

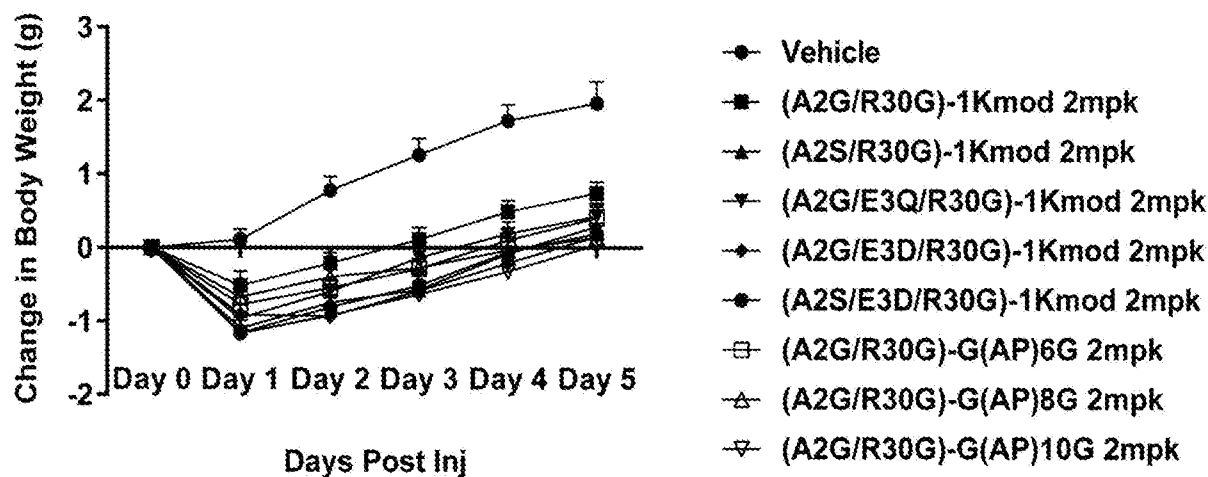


FIG. 5C

Biologic Lot or Reg #	Description	Linker / Ab Site
PL-42834	GLP1 (A2G/R30G)-1Kmod 6H1(HC)	1Kmod - 6H1-HC
PL-45560	GLP1 (A2S/R30G)-1Kmod 6H1(HC)	1Kmod - 6H1-HC
PL-45561	GLP1 (A2G/E3Q/R30G)-1Kmod 6H1(HC)	1Kmod - 6H1-HC
PL-45570	GLP1 (A2G/E3D/R30G)-1Kmod 6H1(HC)	1Kmod - 6H1-HC
PL-45571	GLP1 (A2S/E3D/R30G)-1Kmod 6H1(HC)	1Kmod - 6H1-HC
PL-45582	GLP1 (A2G/R30G)-G(AP)8G-6H1(HC)	G(AP)8G - 6H1-HC
PL-45581	GLP1 (A2G/R30G)-G(AP)6G-6H1(HC)	G(AP)6G - 6H1-HC
PL-45583	GLP1 (A2G/R30G)-G(AP)10G-6H1(HC)	G(AP)10G - 6H1-HC

7/48

FIG. 6A

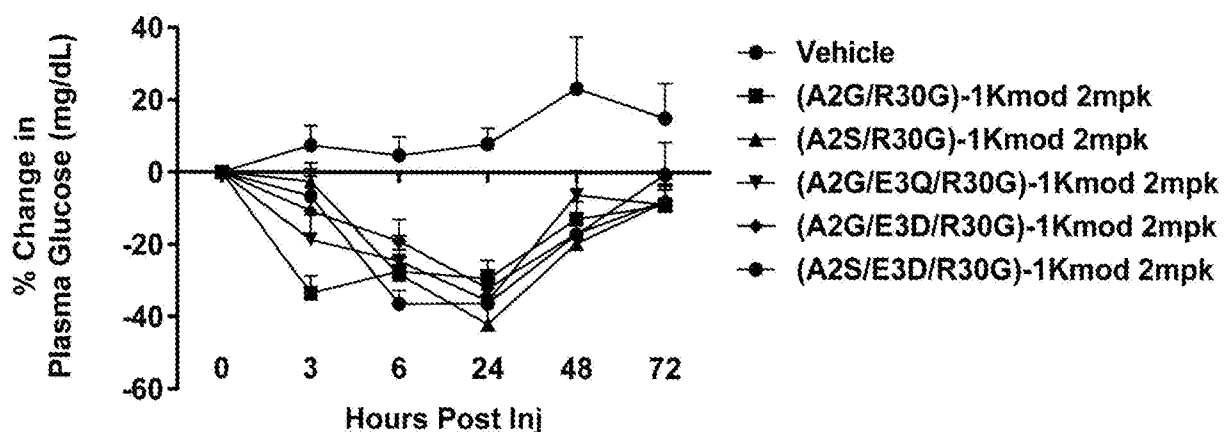


FIG. 6B

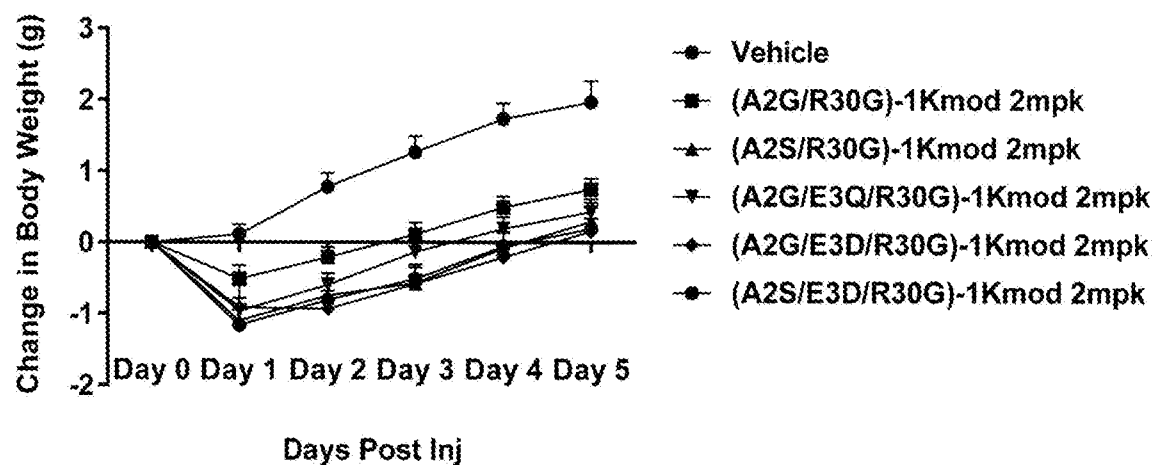


FIG. 6C

Biologic Lot or Reg #	Description	Linker / Ab Site
PL-42834	GLP1 (A2G/R30G)-1Kmod 6H1(HC)	1Kmod - 6H1-HC
PL-45560	GLP1 (A2S/R30G)-1Kmod 6H1(HC)	1Kmod - 6H1-HC
PL-45561	GLP1 (A2G/E3Q/R30G)-1Kmod 6H1(HC)	1Kmod - 6H1-HC
PL-45570	GLP1 (A2G/E3D/R30G)-1Kmod 6H1(HC)	1Kmod - 6H1-HC
PL-45571	GLP1 (A2S/E3D/R30G)-1Kmod 6H1(HC)	1Kmod - 6H1-HC

8/48

FIG. 7A

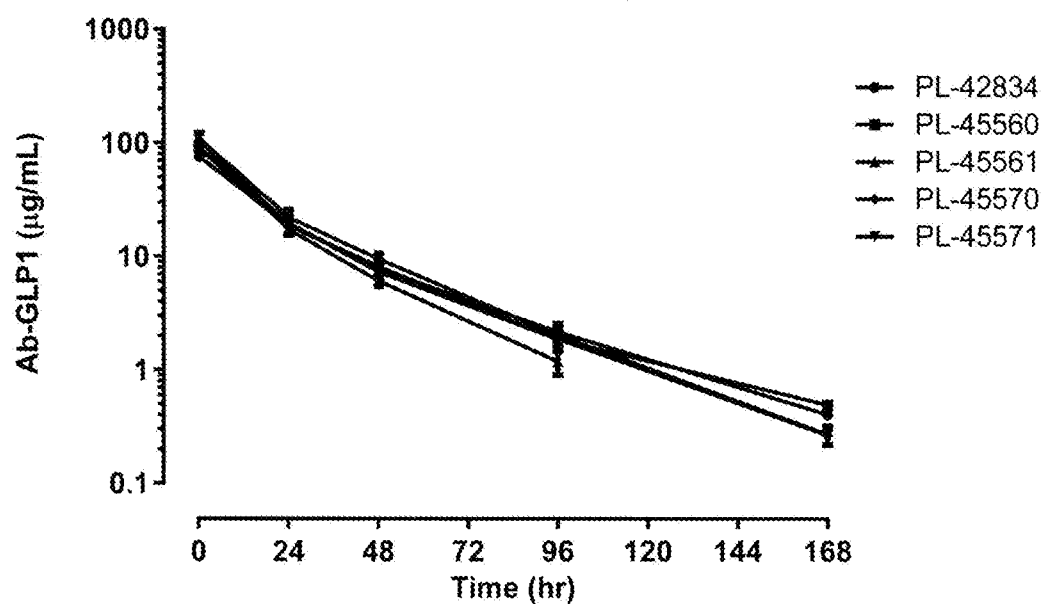
Compiled Mean ($\pm$ SD)
Intact Assay

FIG. 7B

LMR	C_0 ($\mu\text{g/mL}$)	$AUC_{0-\text{inf}}$ ($\text{hr} \cdot \mu\text{g/mL}$)	CL (mL/hr/kg)	$T_{1/2, \text{terminal}}$ (day)
PL-42834	75.5	1800	2.78	1.18
PL-45560	92.0	1990	2.52	1.30
PL-45561	90.3	1770	2.82	0.78
PL-45570	106	2150	2.33	1.02
PL-45571	110	2320	2.15	0.98

9/48

FIG. 7C

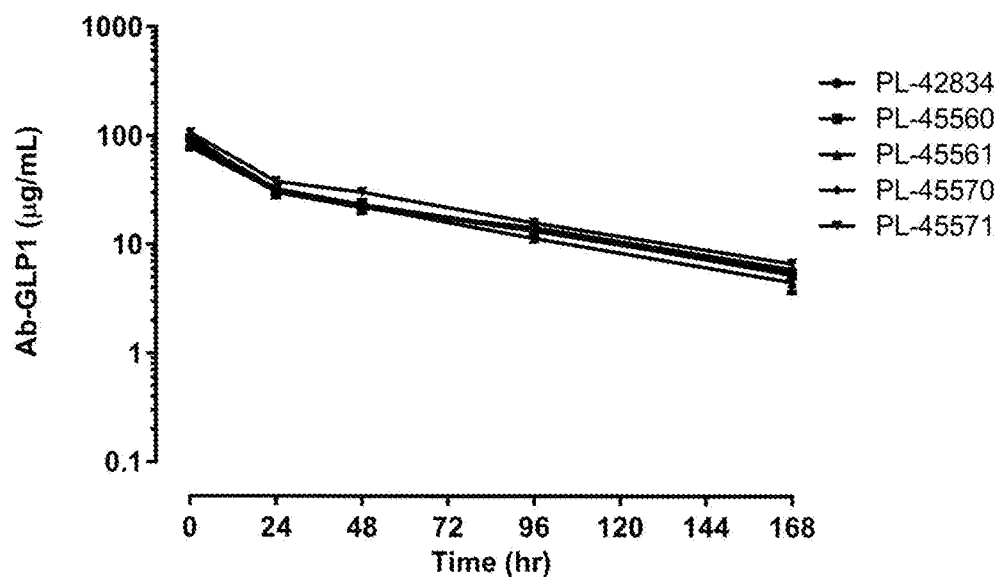
Compiled Mean ($\pm$ SD)
Total Assay

FIG. 7D

LMR	C_0 ($\mu\text{g/mL}$)	$AUC_{0-\text{inf}}$ ($\text{hr} \cdot \mu\text{g/mL}$)	CL (mL/hr/kg)	$T_{1/2, \text{terminal}}$ (day)
PL-42834	78.7	3970	1.26	2.45
PL-45560	94.9	4210	1.19	2.32
PL-45561	87.2	3780	1.32	2.16
PL-45570	99.4	4330	1.15	2.61
PL-45571	107	5030	0.99	2.37

FIG. 7E

PL-42834	GLP1(A2G/R30G)-1Kmod 6H1(HC)
PL-45560	GLP1(A2S/R30G)-1Kmod 6H1(HC)
PL-45561	GLP1(A2G/E3Q/R30G)-1Kmod 6H1(HC)
PL-45570	GLP1(A2G/E3D/R30G)-1Kmod 6H1(HC)
PL-45571	GLP1(A2S/E3D/R30G)-1Kmod 6H1(HC)

10/48

FIG. 8

Ab: 6H1 HC

GLP1 Analogue: A2G/R30G

Linkers

- Null
- G_4
- G_4SG_4
- $(G_4A)_2G_4$
- $(G_4A)_3G_4$
- $G(AP)_4G$
- $G(AP)_6G$
- $G(AP)_8G$
- $G(AP)_{10}G$

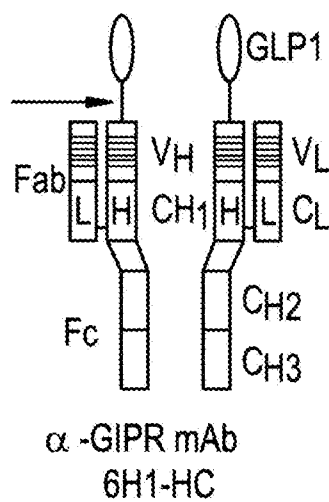


FIG. 9

Construct	Lot	GLP1 EC ₅₀ (pM)	GIPR IC ₅₀ (nM)	Yield (g/L)	SEC (%MP)	Note
No Linker	N/A	N/A	N/A	N/A	N/A	No Express
G4	PL-45578	44	183	89	100	Irreg. SEC
G4SG4	PL-45579	39	822	161	100	Irreg. SEC
{G4A}2G4	PL-45580	29	351	150	99	Irreg. SEC
{G4A}3G4	PL-45576	40	536	47	99	
G(AP)6G	PL-45581	27	292	195	99	
G(AP)8G	PL-45582	31	504	210	99	
G(AP)10G	PL-45583	23	198	163	99	



Selected linkers

- 1Kmod {GSGATGGSGSVASSGGSATHL} [23AA]
- (G₄A)₃G₄ [19AA]
- G(AP)₁₀G [22AA]

REQ-53452

12/48

FIG. 10A

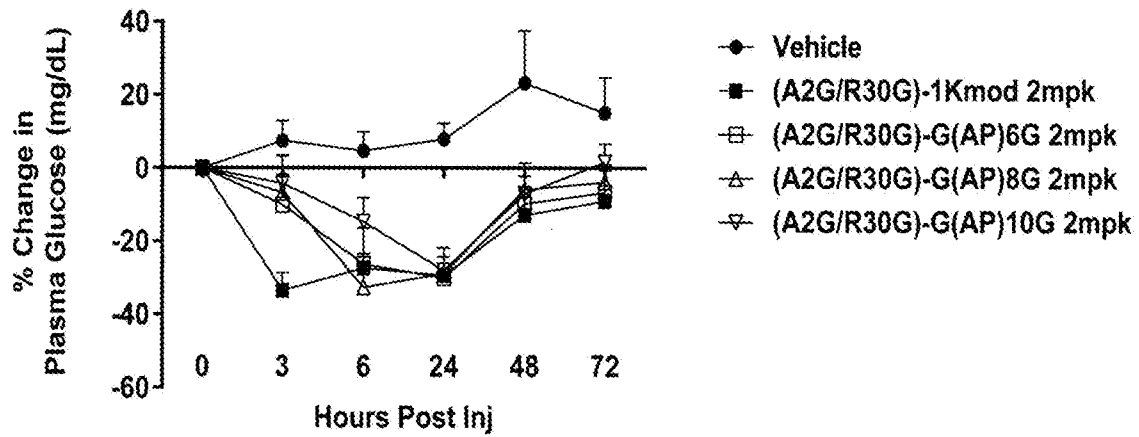


FIG. 10B

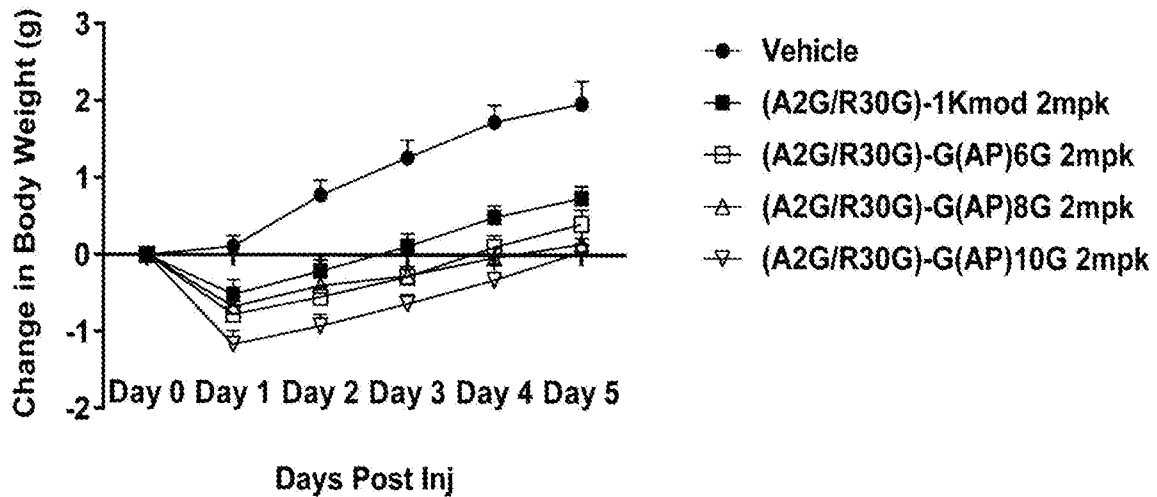
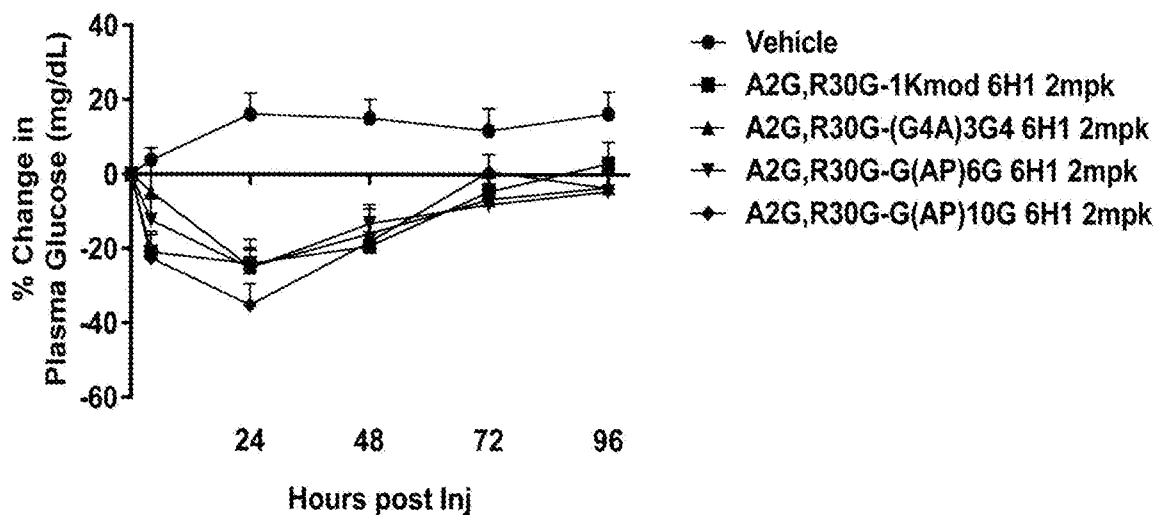


FIG. 10C



13/48

FIG. 10D

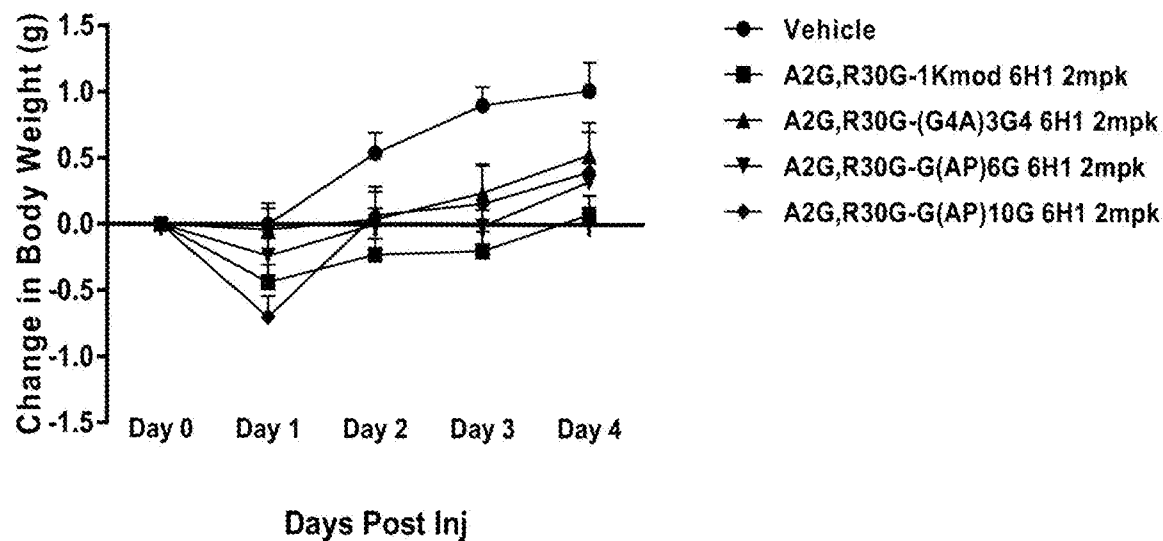


FIG. 10E

53452	GLP1 (A2G/R30G)-G(AP)6G-6H1(HC)	G(AP)6G - 6H1-HC
53452	GLP1 (A2G/R30G)-G(AP)10G-6H1(HC)	G(AP)10G - 6H1-HC
52512	GLP1 (A2G/R30G)-1Kmod 6H1(HC)	1Kmod - 6H1-HC
53452	GLP1(A2G/R30G)-(G4A)3G4 -6H1(HC)	(G4A)3G4 -6H1(HC)
53452	GLP1 (A2G/R30G)-G(AP)6G-6H1(HC)	G(AP)6G - 6H1-HC
53452	GLP1 (A2G/R30G)-G(AP)10G-6H1(HC)	G(AP)10G - 6H1-HC

14/48

FIG. 11A

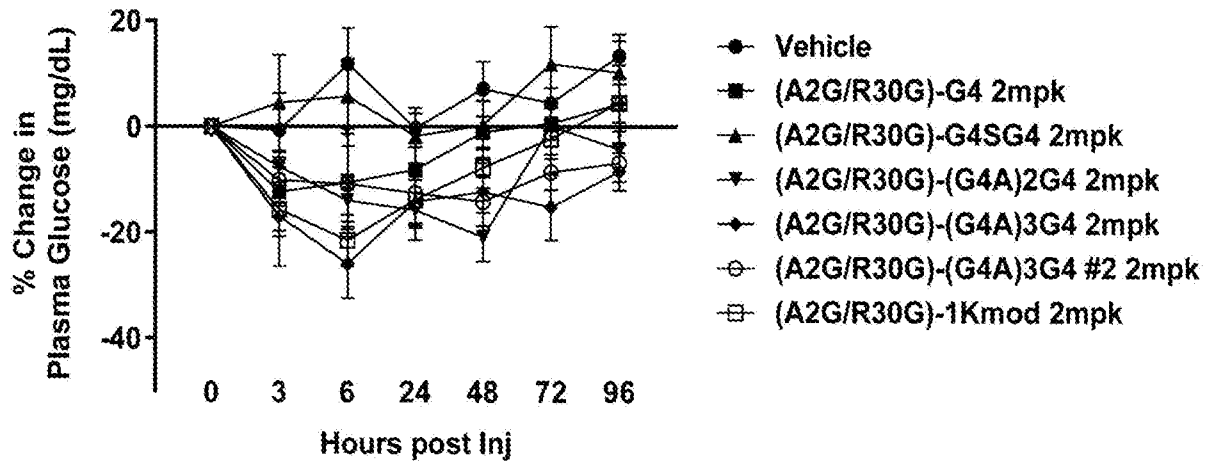


FIG. 11B

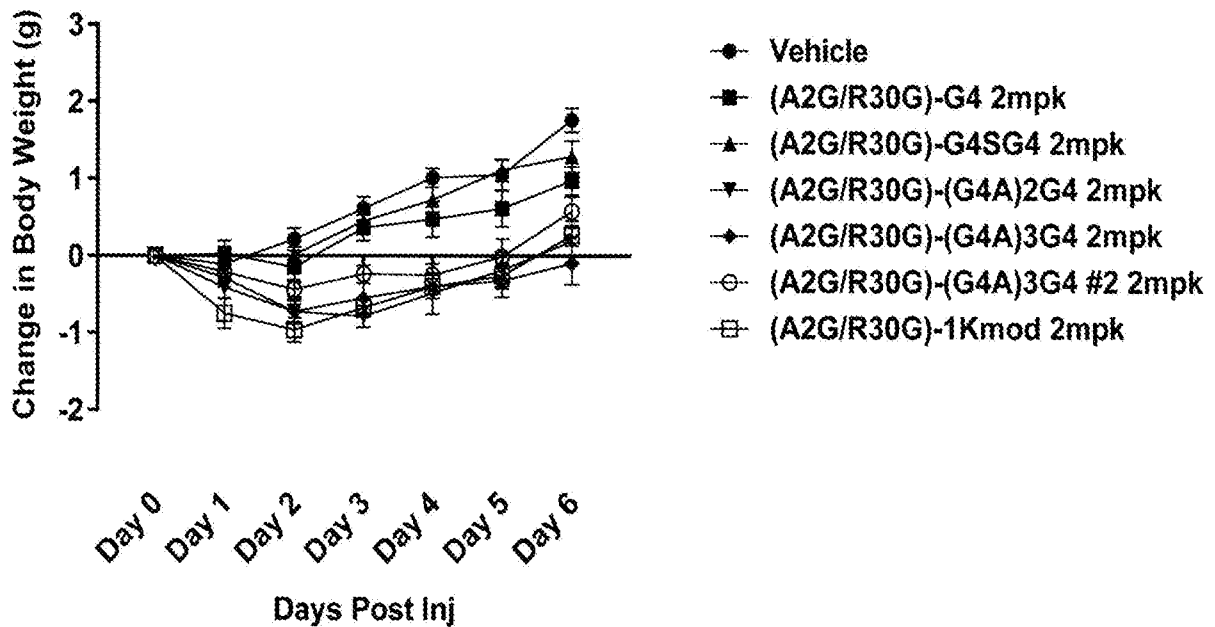


FIG. 11C

Biologic Lot or Reg #	Description	Linker / Ab Site
PL-45577	GLP1(A2G/R30G)-(G4A)3G4 #2-6H1(HC)	(G4A)3G4 #2-6H1(HC)
PL-45578	GLP1(A2G/R30G)-G4-6H1(HC)	G4-6H1(HC)
PL-45579	GLP1(A2G/R30G)-G4SG4-6H1(HC)	G4SG4-6H1(HC)
PL-45580	GLP1(A2G/R30G)-(G4A)2G4-6H1(HC)	(G4A)2G4-6H1(HC)
PL-42834	GLP1 (A2G/R30G)-1Kmod 6H1(HC)	1Kmod - 6H1-HC
PL-45576	GLP1(A2G/R30G)-(G4A)3G4 -6H1(HC)	(G4A)3G4 -6H1(HC)

15/48

FIG. 12A

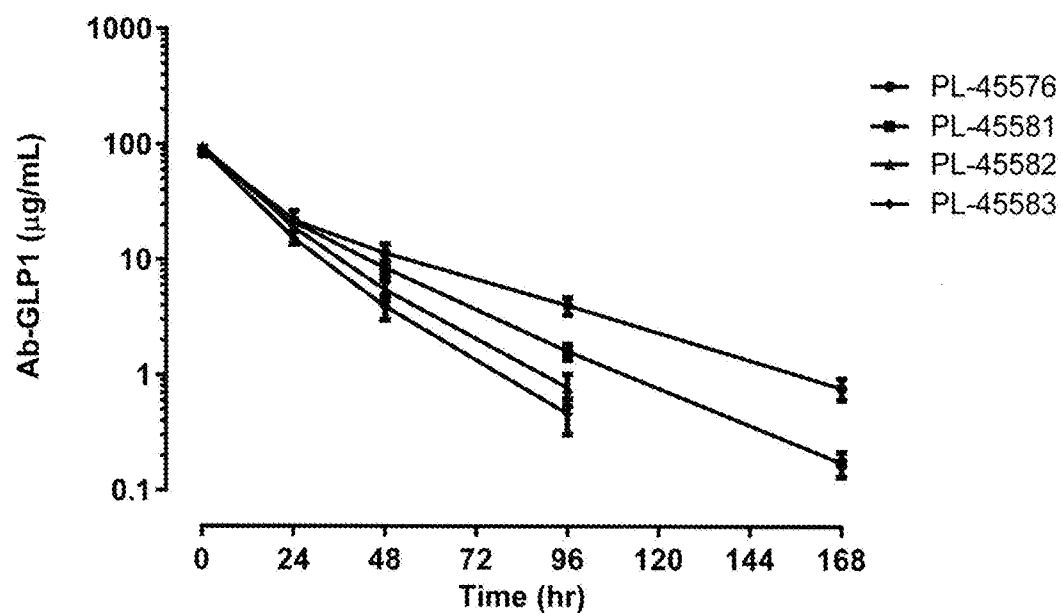
Compiled Mean ($\pm$ SD)
Intact Assay

FIG. 12B

LMR	C_0 ($\mu\text{g/mL}$)	$AUC_{0-\text{inf}}$ ($\text{hr} \cdot \mu\text{g/mL}$)	CL (mL/hr/kg)	$T_{1/2, \text{terminal}}$ (day)
PL-45576	90.5	2320	2.15	1.29
PL-45581	89.3	1990	2.52	0.89
PL-45582	96.2	1840	2.72	0.66
PL-45583	89.5	1600	3.13	0.60

16/48

FIG. 12C

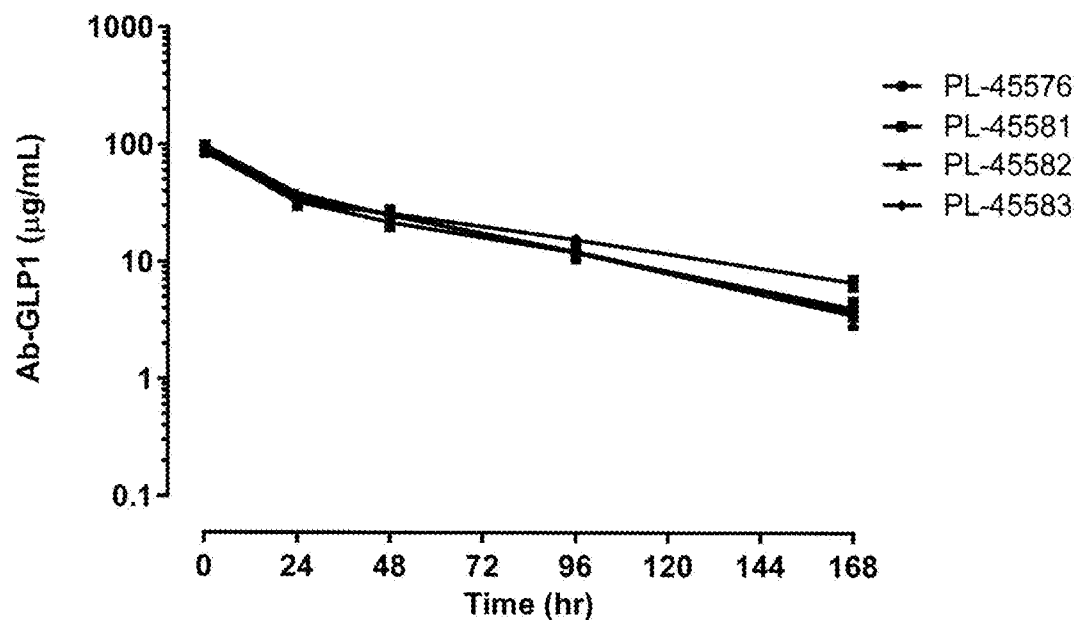
Compiled Mean ($\pm$ SD)
Total Assay

FIG. 12D

LMR	C_0 ($\mu\text{g/mL}$)	$AUC_{0-\text{inf}}$ ($\text{hr} \cdot \mu\text{g/mL}$)	CL (mL/hr/kg)	$T_{1/2, \text{terminal}}$ (day)
PL-45576	88.8	4520	1.11	2.57
PL-45581	92.2	3960	1.26	1.87
PL-45582	97.8	4050	1.23	1.76
PL-45583	86.1	3730	1.34	2.02

FIG. 12E

PL-45576	GLP1(A2G/R30G)-(G4A)3G4-6H1(HC)
PL-45581	GLP1(A2G/R30G)-G(AP)6G-6H1(HC)
PL-45582	GLP1(A2G/R30G)-G(AP)8G-6H1(HC)
PL-45583	GLP1(A2G/R30G)-G(AP)10G-6H1(HC)

17/48

FIG. 13

Ab: 6H1 HC

N-terminal substitutions (5):

A2G, A2S, A2S / E3Q, A2G / E3D, A2S / E3D

C-terminal region substitutions (4):

WT (AWLVK)

A24E (Single)

V27K/K28N (Double)

A24E/V27K/K28N (Triple)

Linkers (3):

1Kmod

(G4A)3G4

G(AP)10G

18/48

FIG. 14

ID	N-term mod	C-term mod	Linker	GIPR Activity		GLP-1 Activity	
				IC50 M	IC50 nM	EC50 M	EC50 pM
6H1.004	control			2.14E-08	21.4		
6H1.004	control			2.95E-08	29.5		
6H1.004	control			3.52E-08	35.2		
GLP-1	control					1.6E-12	1.6
GLP-1	control					2.85E-12	2.8
GLP-1	control					1.74E-12	1.7
PL-47367	A2G	WT C-term	1Kmod	2.44E-07	244	1.79E-11	17.8
PL-47368	A2S	WT C-term	1Kmod	3.51E-07	351	1.71E-11	17.1
PL-47369	A2S/E3Q	WT C-term	1Kmod	4.14E-08	41.1	2.79E-12	2.8
PL-47370	A2G/E3D	WT C-term	1Kmod	1.97E-07	197	1.11E-11	11.1
PL-47371	A2S/E3D	WT C-term	1Kmod	4.24E-07	424	1.62E-11	16.2
PL-47372	A2G	A24E	1Kmod	3.98E-08	39.8	4.46E-12	4.5
PL-47373	A2S	A24E	1Kmod	3.24E-07	324	1.63E-11	16.3
PL-47374	A2S/E3Q	A24E	1Kmod	5.35E-07	535	1.23E-11	12.3
PL-47375	A2G/E3D	A24E	1Kmod	4.88E-07	488	1.69E-11	16.9
PL-47376	A2S/E3D	A24E	1Kmod	1.98E-06	1980	5.04E-12	5
PL-47377	A2G	V27K/K28N	1Kmod	1.29E-07	129	1.97E-11	19.7
PL-47378	A2S	V27K/K28N	1Kmod	1.33E-07	133	1.58E-11	15.8
PL-47379	A2S/E3Q	V27K/K28N	1Kmod	1.49E-07	149	2.15E-11	21.5
PL-47380	A2G/E3D	V27K/K28N	1Kmod	1.29E-07	129	1.49E-11	14.9
PL-47381	A2S/E3D	V27K/K28N	1Kmod	1.41E-07	141	2.9E-11	28.9
PL-47382	A2G	A24E/V27K/K28N	1Kmod	1.58E-07	158	1.91E-11	19.1
PL-47383	A2S	A24E/V27K/K28N	1Kmod	1.62E-07	162	1.08E-11	10.8
PL-47384	A2S/E3Q	A24E/V27K/K28N	1Kmod	1.49E-07	149	1.75E-11	17.5
PL-47385	A2G/E3D	A24E/V27K/K28N	1Kmod	1.85E-07	185	3.53E-11	35.3
PL-47386	A2S/E3D	A24E/V27K/K28N	1Kmod	2.30E-07	230	1.1E-11	10.9

19/48

FIG. 15

ID	N-term mod	C-term mod	Linker	GIPR Activity		GLP-1 Activity	
				IC50 M	IC50 nM	EC50 M	EC50 pM
6H1.004	control			2.14E-08	21.4		
6H1.004	control			2.95E-08	29.5		
6H1.004	control			3.52E-08	35.2		
GLP-1	control					1.6E-12	1.6
GLP-1	control					2.85E-12	2.8
GLP-1	control					1.74E-12	1.7
PL-47387	A2G	WT C-term	(G4A)3G4	1.71E-07	171	4.39E-11	43.9
PL-47388	A2S	WT C-term	(G4A)3G4	1.91E-07	191	3.16E-11	31.6
PL-47389	A2S/E3Q	WT C-term	(G4A)3G4	3.42E-07	342	3.48E-11	34.8
PL-47390	A2G/E3D	WT C-term	(G4A)3G4	2.25E-07	225	1.59E-11	15.8
PL-47391	A2S/E3D	WT C-term	(G4A)3G4	4.07E-07	407	1.55E-11	15.5
PL-47392	A2G	A24E	(G4A)3G4	3.42E-07	342	1.39E-11	13.9
PL-47393	A2S	A24E	(G4A)3G4	2.03E-07	203	1.22E-11	12.2
PL-47394	A2S/E3Q	A24E	(G4A)3G4	3.20E-07	320	1.54E-11	15.4
PL-47395	A2G/E3D	A24E	(G4A)3G4	2.55E-07	255	1.39E-11	13.9
PL-47396	A2S/E3D	A24E	(G4A)3G4	1.21E-06	1210	1.51E-11	15.1
PL-47397	A2G	V27K/K28N	(G4A)3G4	1.78E-07	178	3.59E-11	35.9
PL-47398	A2S	V27K/K28N	(G4A)3G4	1.69E-07	169	4.17E-11	41.7
PL-47399	A2S/E3Q	V27K/K28N	(G4A)3G4	1.19E-07	119	2.75E-11	27.5
PL-47400	A2G/E3D	V27K/K28N	(G4A)3G4	1.73E-07	173	2.43E-11	24.3
PL-47401	A2S/E3D	V27K/K28N	(G4A)3G4	1.82E-07	182	2.71E-11	27.1
PL-47402	A2G	A24E/V27K/K28N	(G4A)3G4	1.45E-07	145	1.87E-11	18.7
PL-47403	A2S	A24E/V27K/K28N	(G4A)3G4	1.97E-07	197	1.12E-11	11.2
PL-47404	A2S/E3Q	A24E/V27K/K28N	(G4A)3G4	1.65E-07	165	2.32E-11	23.2
PL-47405	A2G/E3D	A24E/V27K/K28N	(G4A)3G4	1.42E-07	142	2.11E-11	21.1
PL-47406	A2S/E3D	A24E/V27K/K28N	(G4A)3G4	1.81E-07	181	3.72E-11	37.2

20/48

FIG. 16

ID	N-term mod	C-term mod	Linker	GIPR Activity		GLP-1 Activity	
				IC50 M	IC50 nM	EC50 M	EC50 pM
6H1.004	control			2.14E-08	21.4		
6H1.004	control			2.95E-08	29.5		
6H1.004	control			3.52E-08	35.2		
GLP-1	control					1.6E-12	1.6
GLP-1	control					2.85E-12	2.8
GLP-1	control					1.74E-12	1.7
PL-47407	A2G	WT C-term	G(AP)10G	1.29E-07	129	3.65E-12	3.6
PL-47408	A2S	WT C-term	G(AP)10G	1.02E-07	102	3.59E-12	3.6
PL-47409	A2S/E3Q	WT C-term	G(AP)10G	1.11E-07	111	5.54E-12	5.5
PL-47410	A2G/E3D	WT C-term	G(AP)10G	1.51E-07	151	4.65E-12	4.6
PL-47411	A2S/E3D	WT C-term	G(AP)10G	3.88E-07	388	3.78E-12	3.8
PL-47412	A2G	A24E	G(AP)10G	1.62E-07	162	5.22E-12	5.2
PL-47413	A2S	A24E	G(AP)10G	6.81E-06	6810	2.99E-12	2.9
PL-47414	A2S/E3Q	A24E	G(AP)10G	1.10E-07	110	5.53E-12	5.5
PL-47415	A2G/E3D	A24E	G(AP)10G	1.53E-07	153	3.81E-12	3.8
PL-47416	A2S/E3D	A24E	G(AP)10G	2.52E-06	2520	5.52E-12	5.5
PL-47417	A2G	V27K/K28N	G(AP)10G	6.59E-08	65.9	5.52E-12	5.5
PL-47418	A2S	V27K/K28N	G(AP)10G	5.35E-08	53.5	5.17E-12	5.2
PL-47419	A2S/E3Q	V27K/K28N	G(AP)10G	7.32E-08	73.2	8.52E-12	8.5
PL-47420	A2G/E3D	V27K/K28N	G(AP)10G	8.66E-08	86.7	4.66E-12	4.7
PL-47421	A2S/E3D	V27K/K28N	G(AP)10G	1.08E-07	108	3.17E-12	3.2
PL-47422	A2G	A24E/V27K/K28N	G(AP)10G	6.55E-08	65.5	2.95E-12	2.9
PL-47423	A2S	A24E/V27K/K28N	G(AP)10G	2.52E-08	25.1	6.21E-12	6.2
PL-47424	A2S/E3Q	A24E/V27K/K28N	G(AP)10G	7.33E-08	73.3	3.77E-12	3.7
PL-47425	A2G/E3D	A24E/V27K/K28N	G(AP)10G	6.03E-08	60.3	2.52E-12	2.5
PL-47426	A2S/E3D	A24E/V27K/K28N	G(AP)10G	2.4E-07	239	3.2E-12	3.2

21/48

FIG. 17

Aggregate of Varied C-term and Linkers

Construct	GLP1 EC ₅₀ Avg (pM)	GIPR IC ₅₀ Avg (nM)
(A2G/G16E/R30G)	16 ± 4	152 ± 24
(A2G/E3D/G16E/R30G)	14 ± 3	176 ± 35
(A2S/G16E/R30G)	15 ± 3	174 ± 30
(A2S/E3D/G16E/R30G)	14 ± 3	499 ± 174
(A2S/E3Q/G16E/R30G)	15 ± 3	182 ± 42

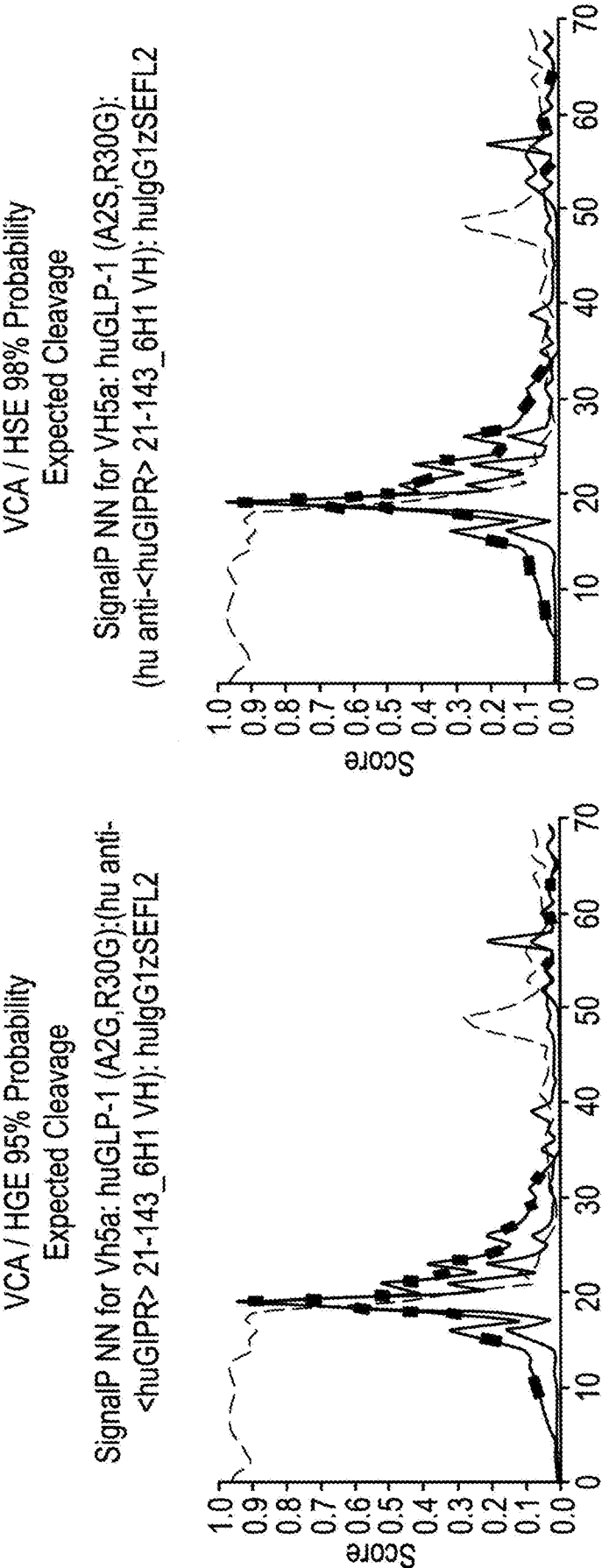
Wild type GLP1 C-term (AWLVK)

- A24E
- V27K/K28N
- A24E/V27K/K28N

Linkers

- 1Kmod {GSGSATGGSGSVASSGSGSATHL}
- (G4A)3G4
- G(AP)10G

FIG. 18



Output from the SignalP 4.0 web-server for the GLP1-GIPR sequence.
'C-score' (—) is the predicted cleavage site value, 'S-score' is the predicted
signal peptide value (---) and 'Y-score' (■■■) is a combination of C-and
S-scores.

23/48

FIG. 19

Aggregate of Varied N-term and Linkers

Construct	GLP1 EC ₅₀ Avg (pM)	GIPR IC ₅₀ Avg (nM)
WT (AWLVK)	15 ± 3	223 ± 34
A24E	10 ± 1	471 ± 150
V27K/K28N	19 ± 3	126 ± 11
A24E/V27K/K28N	15 ± 3	145 ± 16

N-termini

- A2G/G16E/R30G
- A2S/G16E/R30G
- A2S/E3Q/G16E/R30G
- A2G/ E3D/G16E/R30G
- A2S/E3D/G16E/R30G

Linkers

- 1Kmod
{GSGSATGGSGSVASSGSGSATHL}
- (G4A)3G4
- G(AP)10G

24/48

FIG. 20A

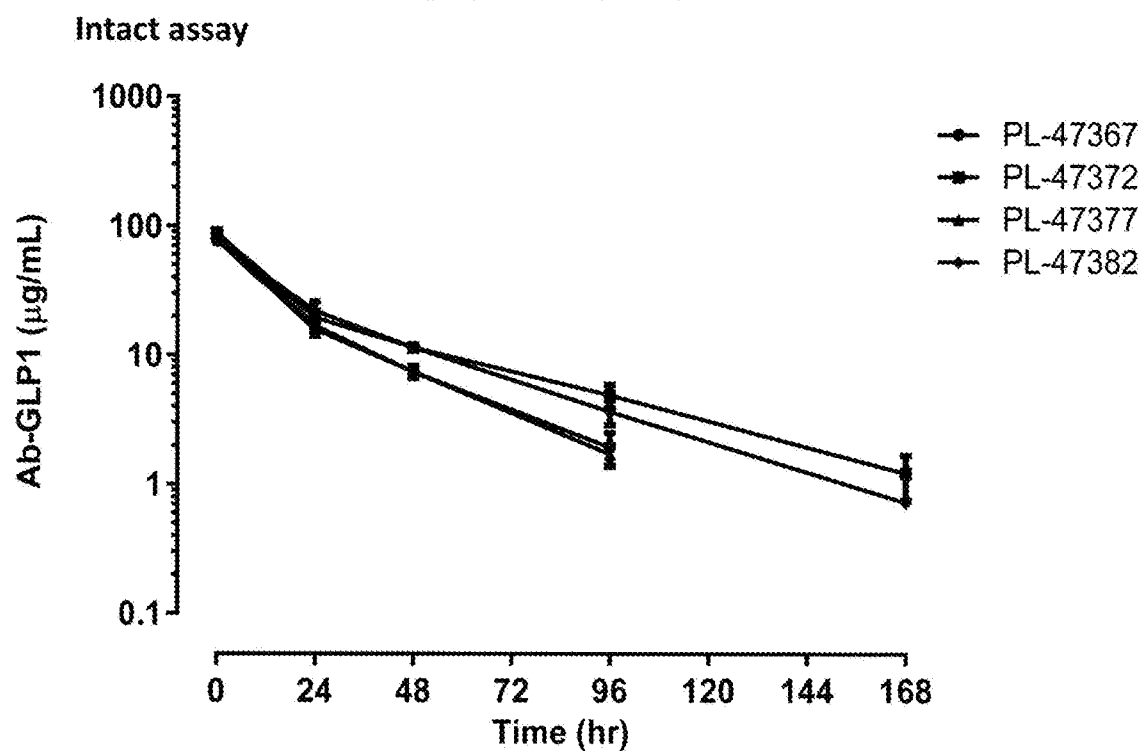


FIG. 20B

LMR	GLP1 sequence modification	C_0 ($\mu\text{g/mL}$)	$AUC_{0-\text{inf}}$ ($\text{hr} \cdot \mu\text{g/mL}$)	CL (mL/hr/kg)	$T_{1/2, \text{terminal}}$ (hr)
PL-47367	A2G/G16E/R30G	76.7	1680	2.98	23.8
PL-47372	A2G/G16E/A24E/R30G	88.2	2310	2.17	36.5
PL-47377	A2G/G16E/V27K/K28N/R30G	86.7	1800	2.78	22.0
PL-47382	A2G/G16E/A24E/V27K/K28N/R30G	75.6	2080	2.41	28.0

25/48

FIG. 20C

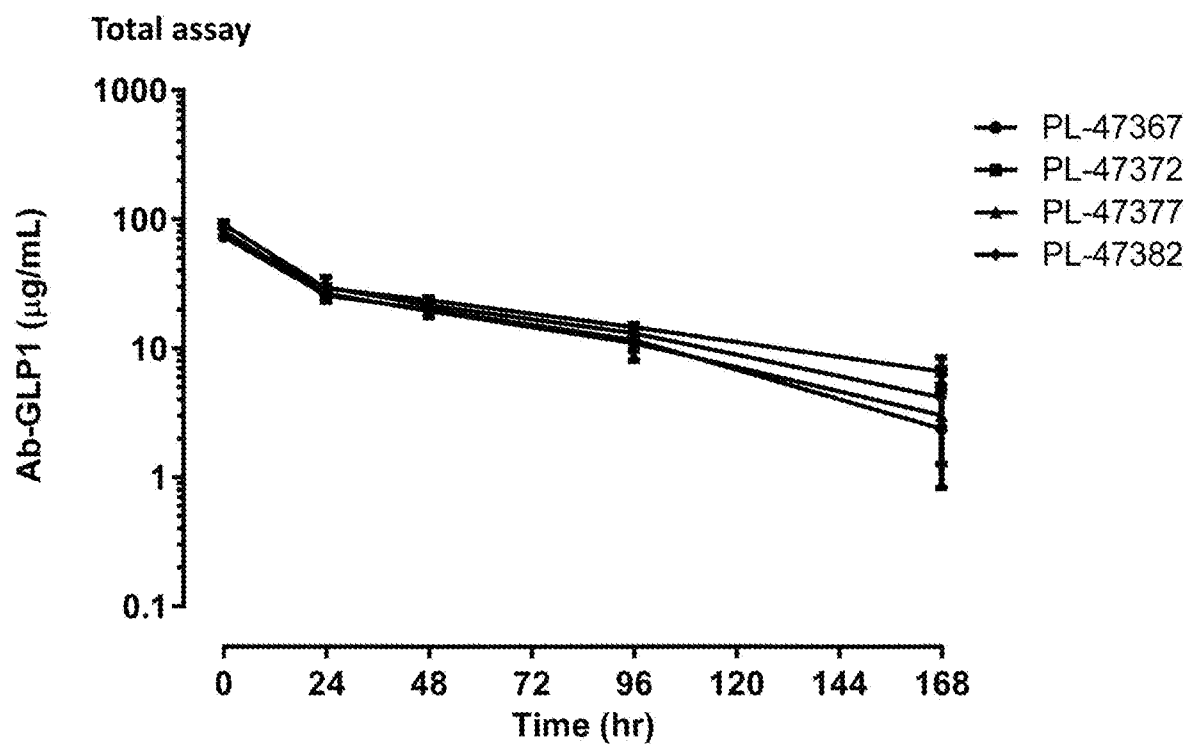


FIG. 20D

LMR	GLP1 sequence modification	C_0 ($\mu\text{g/mL}$)	$AUC_{0-\text{inf}}$ ($\text{hr} \cdot \mu\text{g/mL}$)	CL (mL/hr/kg)	$T_{1/2, \text{terminal}}$ (hr)
PL-47367	A2G/G16E/R30G	73.8	3170	1.58	41.9
PL-47372	A2G/G16E/A24E/R30G	91.4	4390	1.14	65.2
PL-47377	A2G/G16E/V27K/K28N/R30G	81.1	3300	1.52	46.1
PL-47382	A2G/G16E/A24E/V27K/K28N/R30G	74.8	3650	1.37	51.3

26/48

FIG. 21A

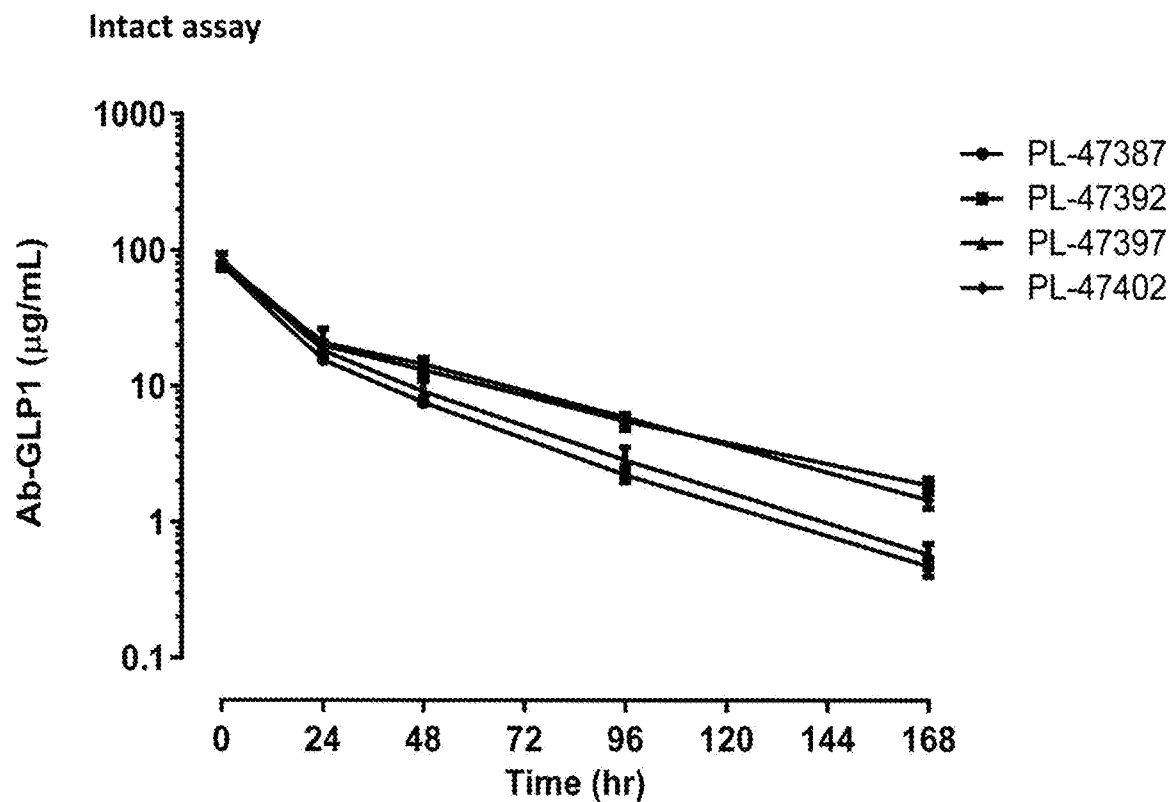


FIG. 21B

LMR	GLP1 sequence modification	C_0 ($\mu\text{g/mL}$)	$AUC_{0-\text{inf}}$ ($\text{hr} \cdot \mu\text{g/mL}$)	CL (mL/hr/kg)	$T_{1/2, \text{terminal}}$ (hr)
PL-47387	A2G/G16E/R30G	77.4	1740	2.87	30.1
PL-47392	A2G/G16E/A24E/R30G	75.5	2370	2.11	42.0
PL-47397	A2G/G16E/V27K/K28N/R30G	85.5	2010	2.49	30.3
PL-47402	A2G/G16E/A24E/V27K/K28N/R30G	83.1	2500	2.00	36.0

27/48

FIG. 21C

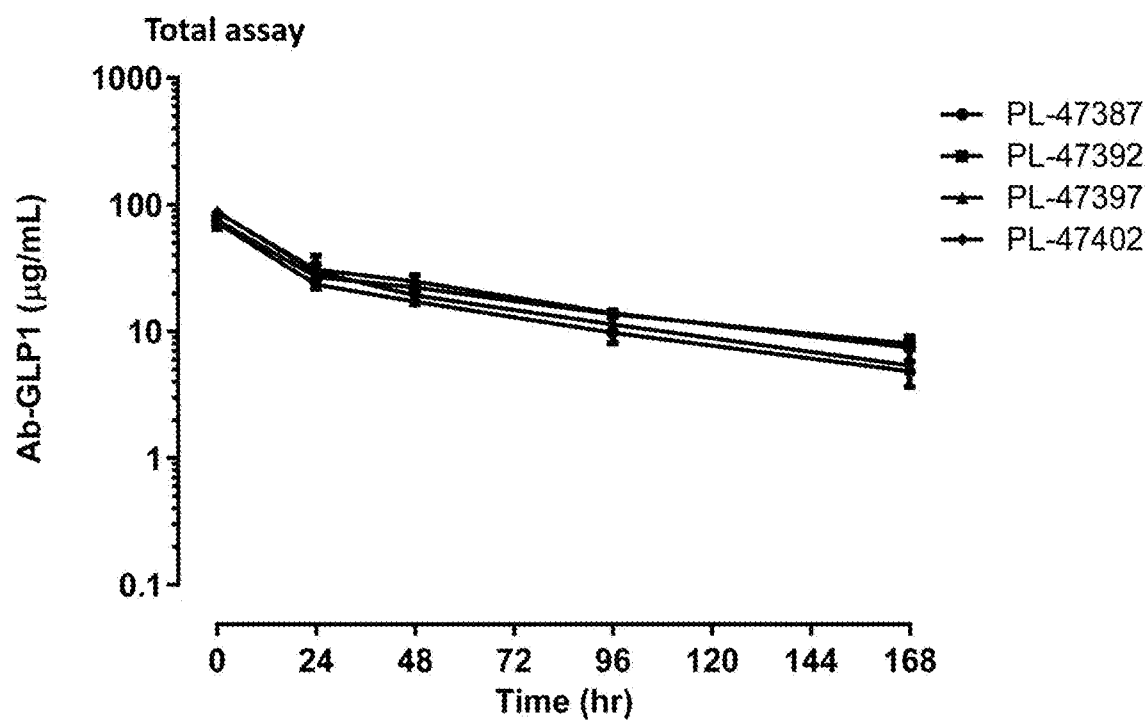


FIG. 21D

LMR	GLP1 sequence modification	C_0 ($\mu\text{g/mL}$)	$AUC_{0-\text{inf}}$ ($\text{hr} \cdot \mu\text{g/mL}$)	CL (mL/hr/kg)	$T_{1/2, \text{terminal}}$ (hr)
PL-47387	A2G/G16E/R30G	72.6	3240	1.54	63.7
PL-47392	A2G/G16E/A24E/R30G	75.8	4380	1.14	81.2
PL-47397	A2G/G16E/V27K/K28N/R30G	88.2	3840	1.30	65.4
PL-47402	A2G/G16E/A24E/V27K/K28N/R30G	87.2	4510	1.11	69.6

28/48

FIG. 22A

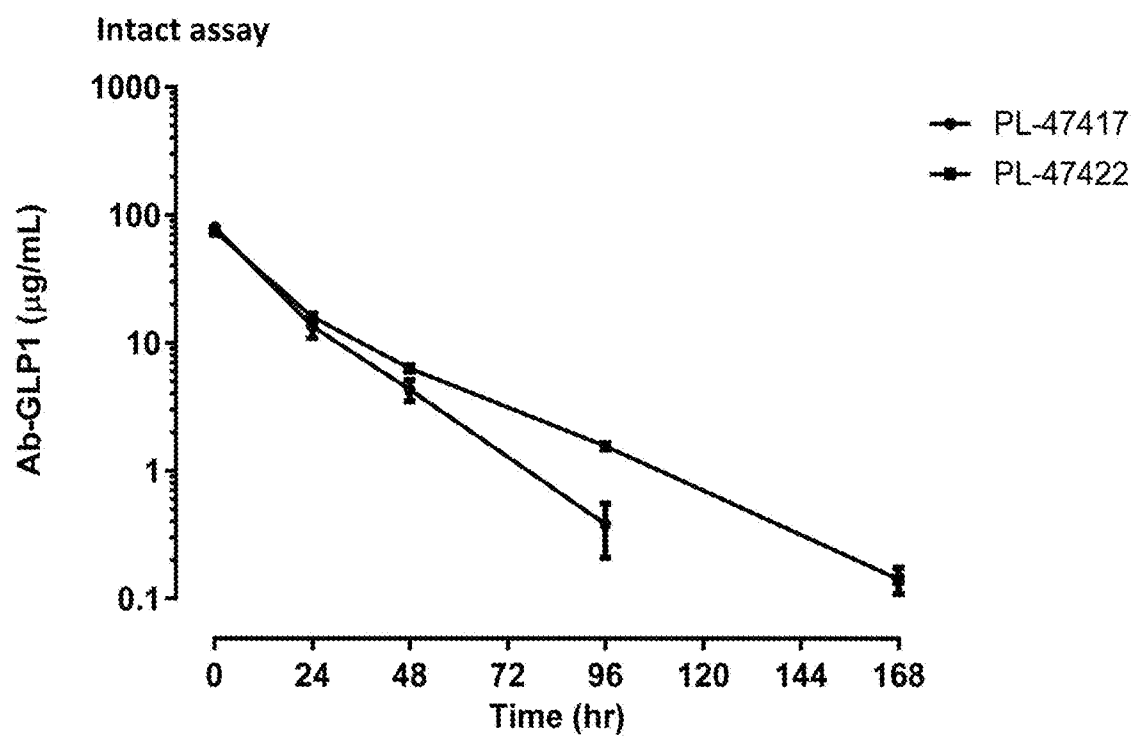


FIG. 22B

LMR	GLP1 sequence modification	C_0 ($\mu\text{g/mL}$)	$AUC_{0-\text{inf}}$ ($\text{hr} \cdot \mu\text{g/mL}$)	CL (mL/hr/kg)	$T_{1/2, \text{terminal}}$ (hr)
PL-47417	A2G/G16E/V27K/ K28N/R30G	79.4	1440	3.48	13.5
PL-47422	A2G/G16E/A24E/ V27K/K28N/R30G	74.3	1600	3.12	21.8

29/48

FIG. 22C

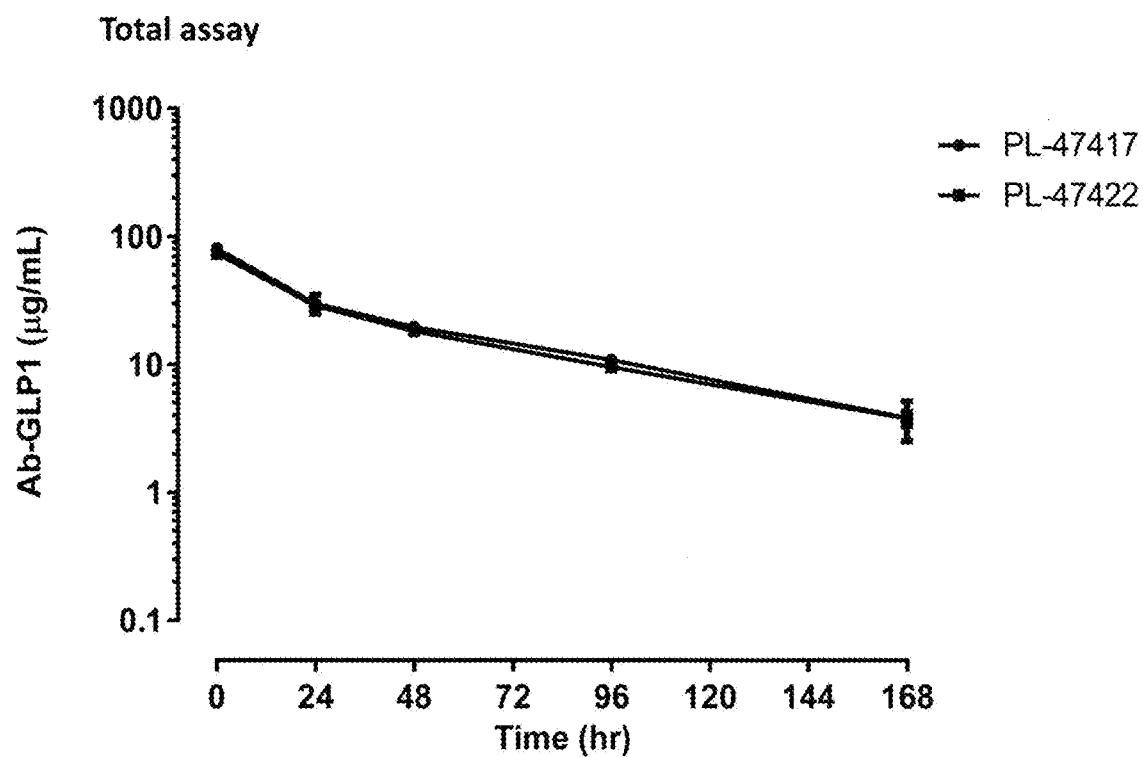


FIG. 22D

LMR	GLP1 sequence modification	C_0 ($\mu\text{g/mL}$)	$AUC_{0-\text{inf}}$ ($\text{hr} \cdot \mu\text{g/mL}$)	CL (mL/hr/kg)	$T_{1/2, \text{terminal}}$ (hr)
PL-47417	A2G/G16E/V27 K/ K28N/R30G	80.6	3450	1.45	49.5
PL-47422	A2G/G16E/A24 E/ V27K/K28N/R30G	73.8	3220	1.55	53.1

30/48

FIG. 23

Aggregate of Varied C-term and Linkers

Construct	GLP1 EC ₅₀ Avg (pM)	GIPR IC ₅₀ Avg (nM)
1Kmod	16 ± 2	309 ± 93
(G4A)3G4	24 ± 2	266 ± 53
G(AP)10G	4 ± 0	112 ± 20

N-termini

- A2G/G16E/R30G
- A2S/G16E/R30G
- A2S/E3Q/G16E/R30G
- A2G/ E3D/G16E/R30G
- A2S/E3D/G16E/R30G

Wild type GLP1 C-term (AWLVK)

- A24E
- V27K/K28N
- A24E/V27K/K28N

31/48

FIG. 24A

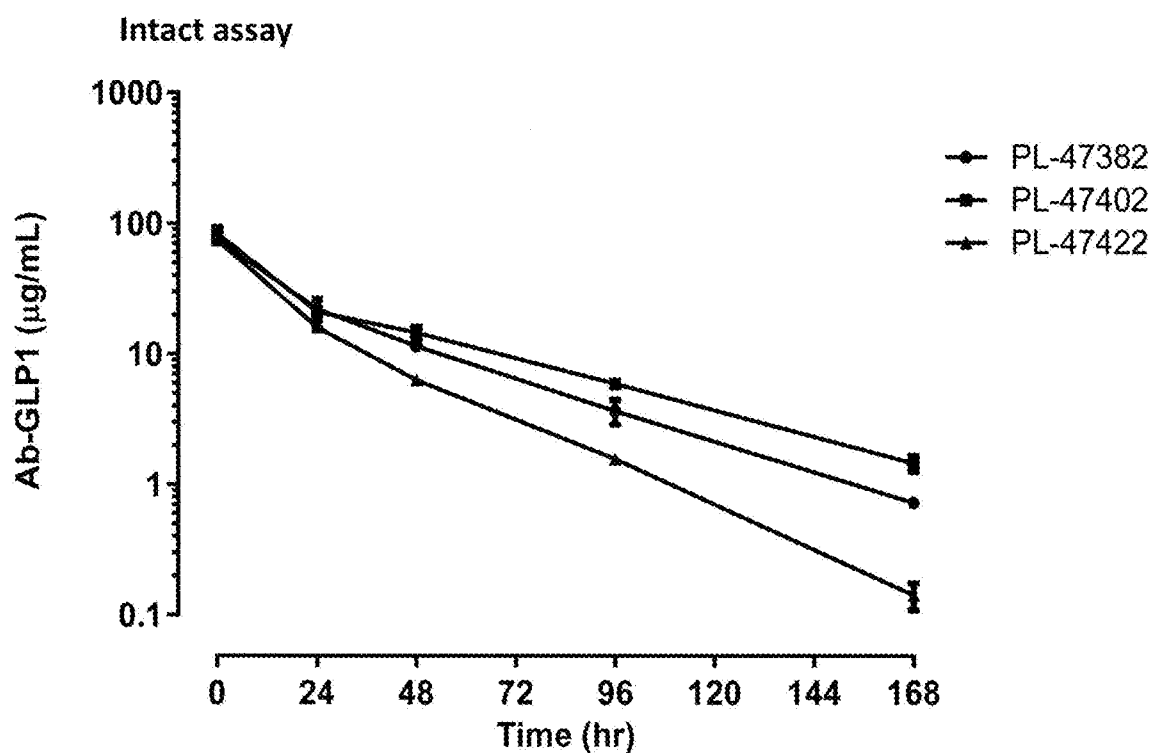


FIG. 24B

LMR	Linker	C_0 ($\mu\text{g/mL}$)	$AUC_{0-\text{inf}}$ ($\text{hr} \cdot \mu\text{g/mL}$)	CL (mL/hr/kg)	$T_{1/2, \text{terminal}}$ (hr)
PL-47382	1Kmod	75.6	2080	2.41	28.0
PL-47402	(G4A)3G4	83.1	2500	2.00	36.0
PL-47422	G(AP)10G	74.3	1600	3.12	21.8

32/48

FIG. 24C

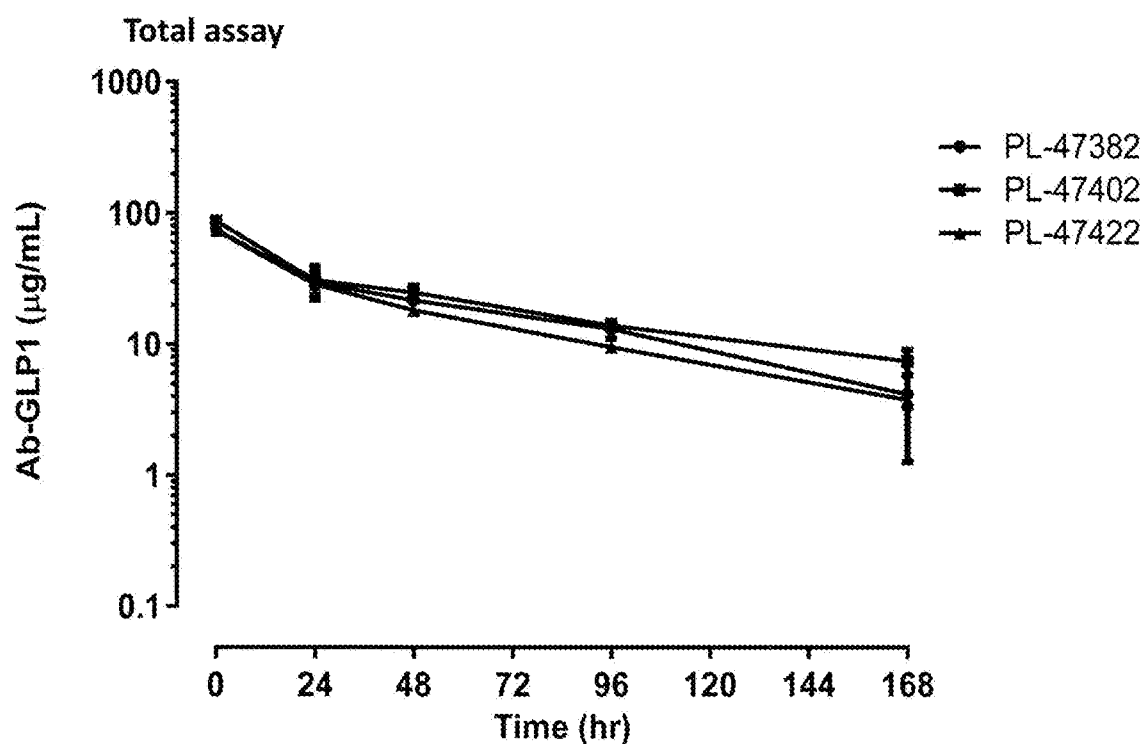


FIG. 24D

LMR	Linker	C_0 ($\mu\text{g/mL}$)	$AUC_{0-\text{inf}}$ ($\text{hr} \cdot \mu\text{g/mL}$)	CL (mL/hr/kg)	$T_{1/2, \text{terminal}}$ (hr)
PL-47382	1Kmod	74.8	3650	1.37	51.3
PL-47402	(G4A)3G4	87.2	4510	1.11	69.6
PL-47422	G(AP)10G	73.8	3220	1.55	53.1

33/48

FIG. 25

Ab: 2G10 HC & LC

Linkers: 1Kmod, (G4A)3G4 and G(AP)10G

GLP1(A2G/G16E/A24E/V27K/K28N/R30G) Triple
GLP1(7-22/A2G)Ex4(17-39) hybrid

FIG. 26

Mouse pk study

- Purpose
 - Evaluate the single dose pharmacokinetics of 4 GIPR-GLP1 recombinant fusions in mice
- Constructs
 - GLP1 analog: A2G/G16E/A24E/V27K/K28N/R30G
 - Linkers: 1Kmod or G4A
 - Fusion to heavy chain (HC) or light chain (LC) of 2G10

LMR	Description
PL-50123	GLP1(Ana)-1K- α huGIPR(2G10) HC
PL-50124	GLP1(Ana)-G4A- α huGIPR(2G10) HC
PL-50125	GLP1(Ana)-1K- α huGIPR(2G10) LC
PL-50126	GLP1(Ana)-G4A- α huGIPR(2G10) LC

- Study design
 - Each construct administered as 5 mg/kg IV bolus to CD-1 mice (n=3 per group)
 - Plasma collected at 0.083, 24, 48, 96, 168, 240, and 336 hr post-dose for PK bioanalysis by intact and total assay

34/48

FIG. 27A

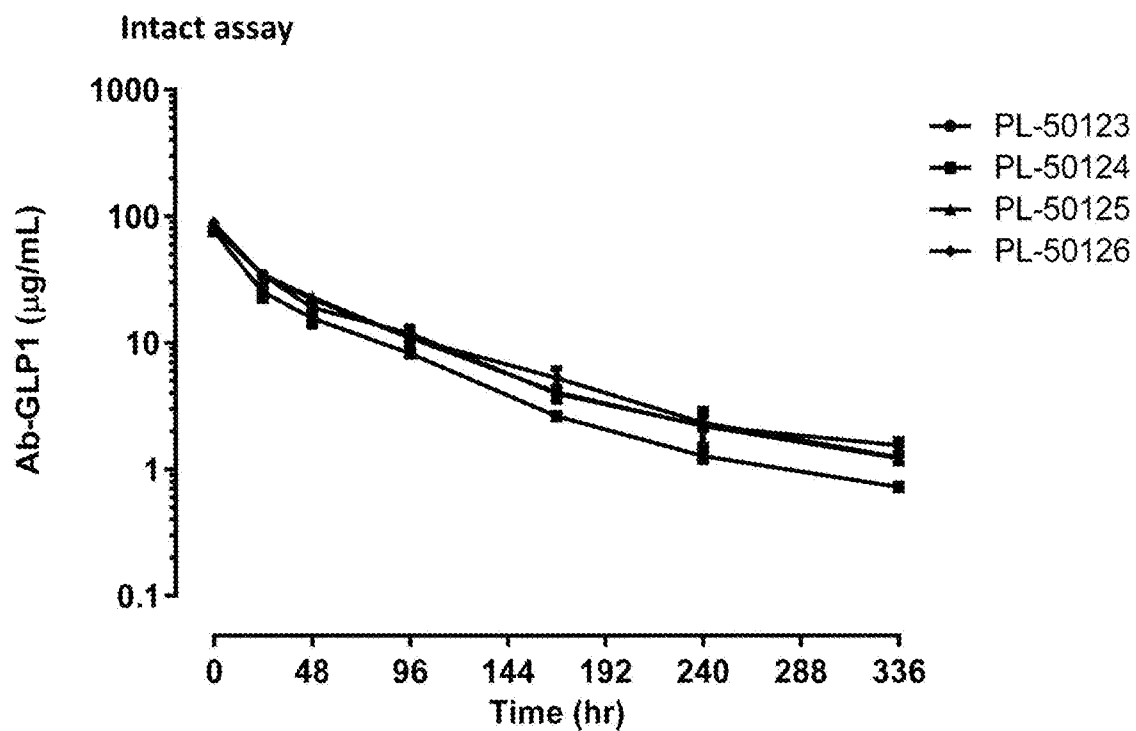


FIG. 27B

LMR	C_0 ($\mu\text{g/mL}$)	AUC_{0-t} ($\text{hr} \cdot \mu\text{g/mL}$)	CL_{0-t} (mL/hr/kg)	$T_{1/2, \text{terminal}}$ (hr)
PL-50123	80.8	3680	1.36	74.3
PL-50124	76.4	2910	1.72	69.4
PL-50125	83.6	3760	1.33	64.3
PL-50126	89.2	3980	1.26	75.4

35/48

FIG. 27C

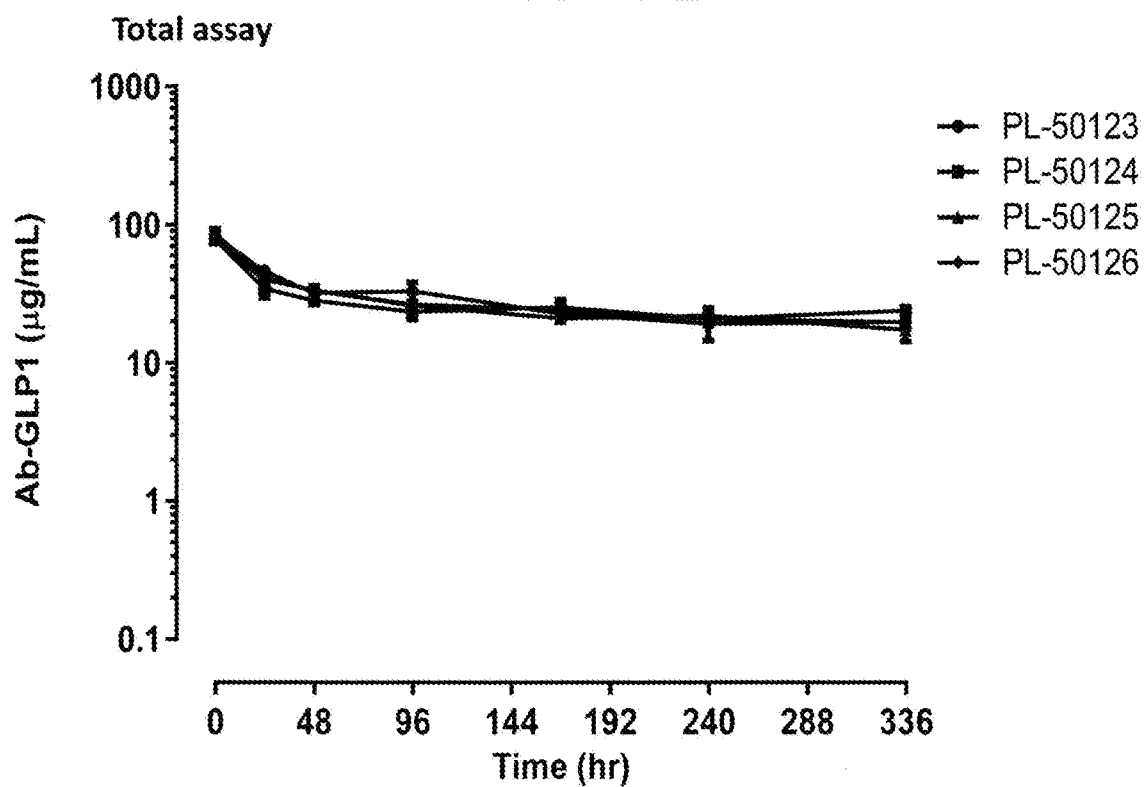


FIG. 27D

LMR	C_0 ($\mu\text{g/mL}$)	AUC_{0-t} ($\text{hr} \cdot \mu\text{g/mL}$)	CL_{0-t} (mL/hr/kg)	$T_{1/2, \text{terminal}}$ (hr)
PL-50123	83.3	9450	0.529	*n/a
PL-50124	77.9	8910	0.561	n/a
PL-50125	78.3	8860	0.564	n/a
PL-50126	85.2	9230	0.542	n/a

*Terminal slope insufficient for accurate half-life determination

36/48

FIG. 28

Ab: 2G10 HC & LC

Linkers: 1Kmod & (G4A)3G4

GLP1(A2G/G16E/A24E/V27K/K28N/R30G) Triple (Ana)

GLP1(A2G/G16E/A24E/R30G) Single (Ana1)

FIG. 29

Construct	PL	GIPR IC ₅₀ (nM)	GLP1 EC ₅₀ (pM)	GLP1 EC ₅₀ (pM)	Avg GLP1 (pM)
Triple-1K-HC	51747	73.6	17.2	9.9	13.6
Triple-G4A-HC	51748	73.6	15.9	18.0	17.0
Triple-1K-LC	51749	60.8	12.3	10.8	11.6
Triple-G4A-LC	51750	44.9	8.9	14.5	11.7
Single-1K-HC	51752	50.7	11.2	15.3	13.3
Single-G4A-HC	51751	49.2	12.1	19.7	15.9
Single-1K-LC	51754	65.4	15.7	13.5	14.6
Single-G4A-LC	51757	30.6	9.8	9.7	9.8

37/48

FIG. 30

Mouse pk study

- Purpose
 - Evaluate the single dose pharmacokinetics of 4 GIPR-GLP1 recombinant fusions in mice
- Constructs
 - GLP1 analog: A2G/G16E/A24E/R30G
 - Linkers: 1Kmod or G4A
 - Fusion to heavy chain (HC) or light chain (LC) of 2G10

LMR	Description
PL-51409	GLP1(Ana)-1K- α huGIPR(2G10) HC
PL-51408	GLP1(Ana)-G4A- α huGIPR(2G10) HC
PL-51406	GLP1(Ana)-1K- α huGIPR(2G10) LC
PL-51407	GLP1(Ana)-G4A- α huGIPR(2G10) LC

- Study design
 - Each construct administered as 5 mg/kg IV bolus to CD-1 mice (n=3 per group)
 - Plasma collected at 0.083, 24, 48, 96, 168, 240, and 336 hr post-dose for PK bioanalysis by intact and total assay

38/48

FIG. 31A

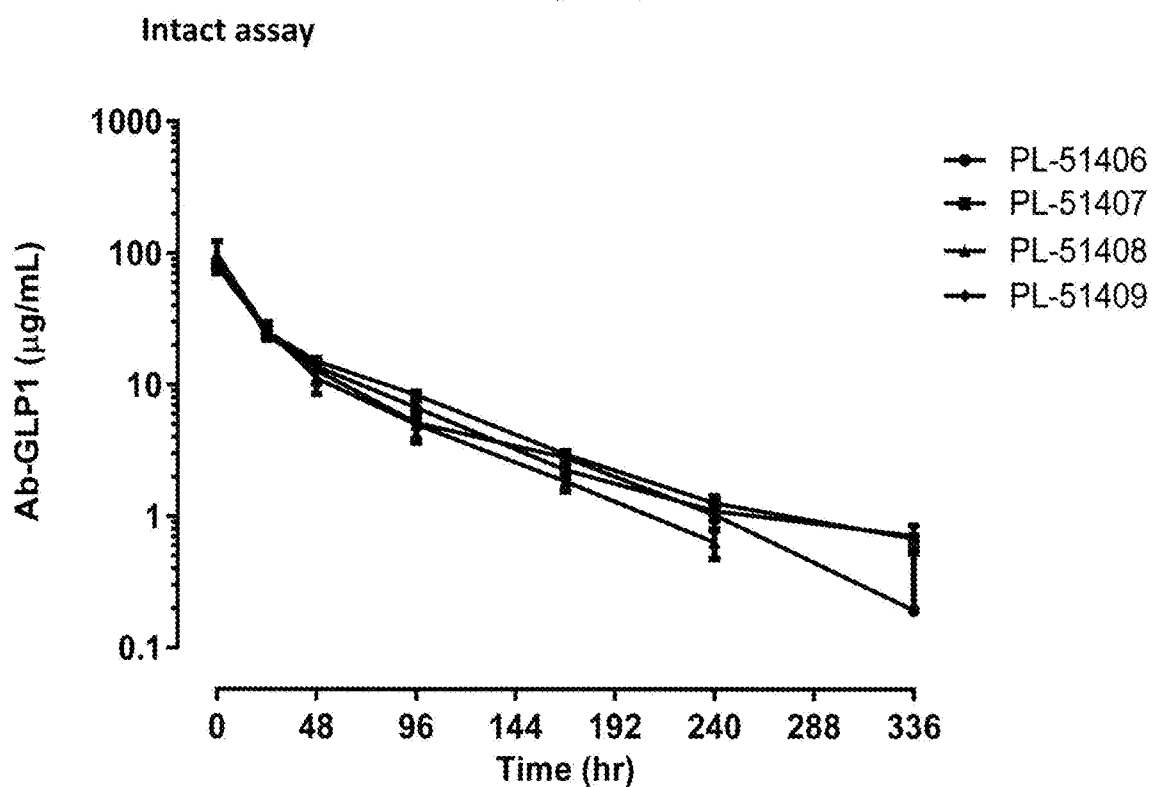


FIG. 31B

LMR	C_0 ($\mu\text{g/mL}$)	AUC_{0-t} ($\text{hr} \cdot \mu\text{g/mL}$)	CL_{0-t} (mL/hr/kg)	$T_{1/2, \text{terminal}}$ (hr)
PL-51409	91.6	2860	1.75	70.0
PL-51408	98.3	2660	1.88	47.7
PL-51406	78.7	2600	1.92	57.9
PL-51407	81.1	2980	1.68	68.8

39/48

FIG. 31C

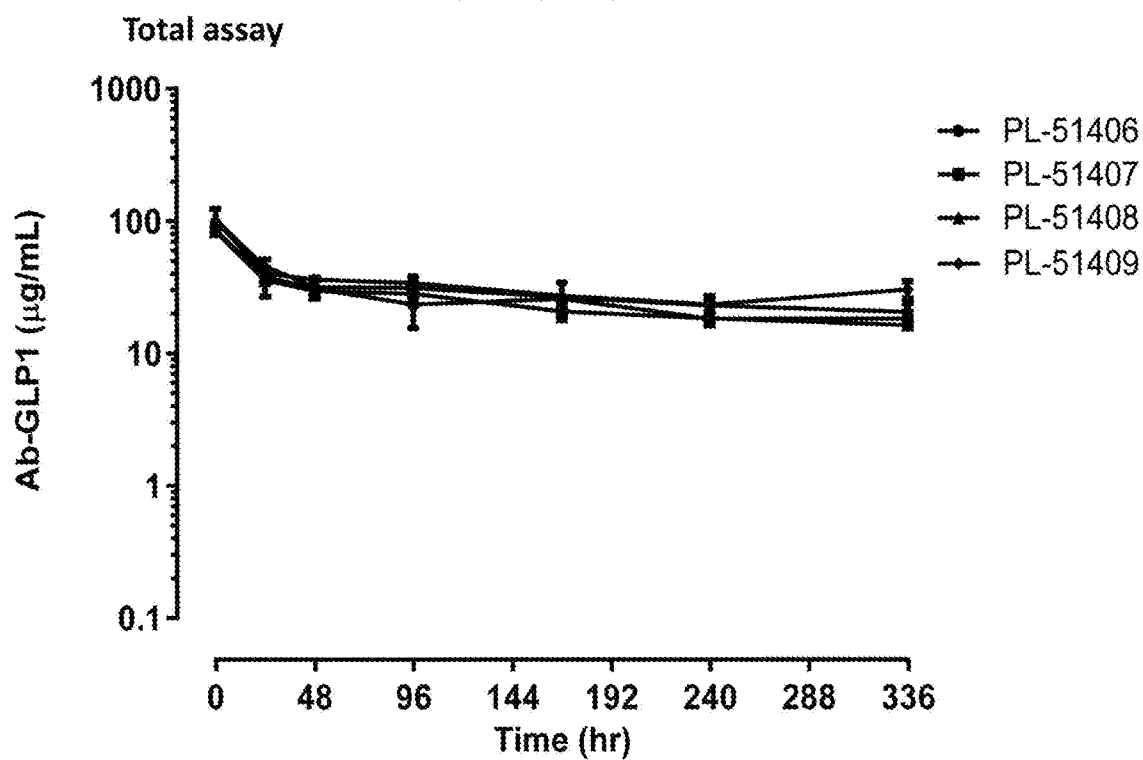


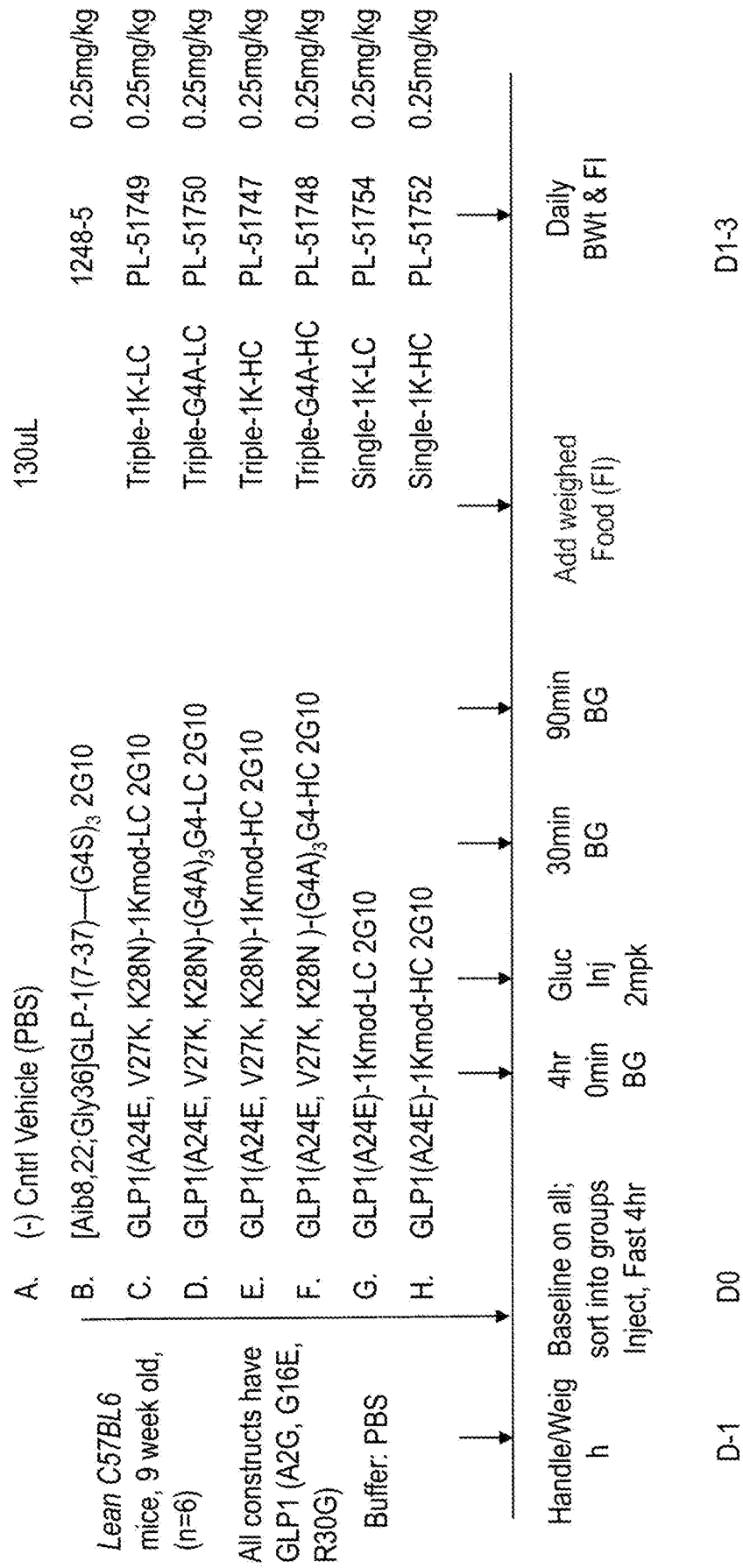
FIG. 31D

LMR	C_0 ($\mu\text{g/mL}$)	AUC_{0-t} ($\text{hr} \cdot \mu\text{g/mL}$)	CL_{0-t} (mL/hr/kg)	$T_{1/2, \text{terminal}}$ (hr)
PL-51409	100	10900	0.459	*n/a
PL-51408	104	10200	0.490	n/a
PL-51406	85.5	8740	0.572	n/a
PL-51407	83.5	8450	0.592	n/a

*Terminal slope insufficient for accurate half-life determination

40/48

FIG. 32



41/48

FIG. 33A

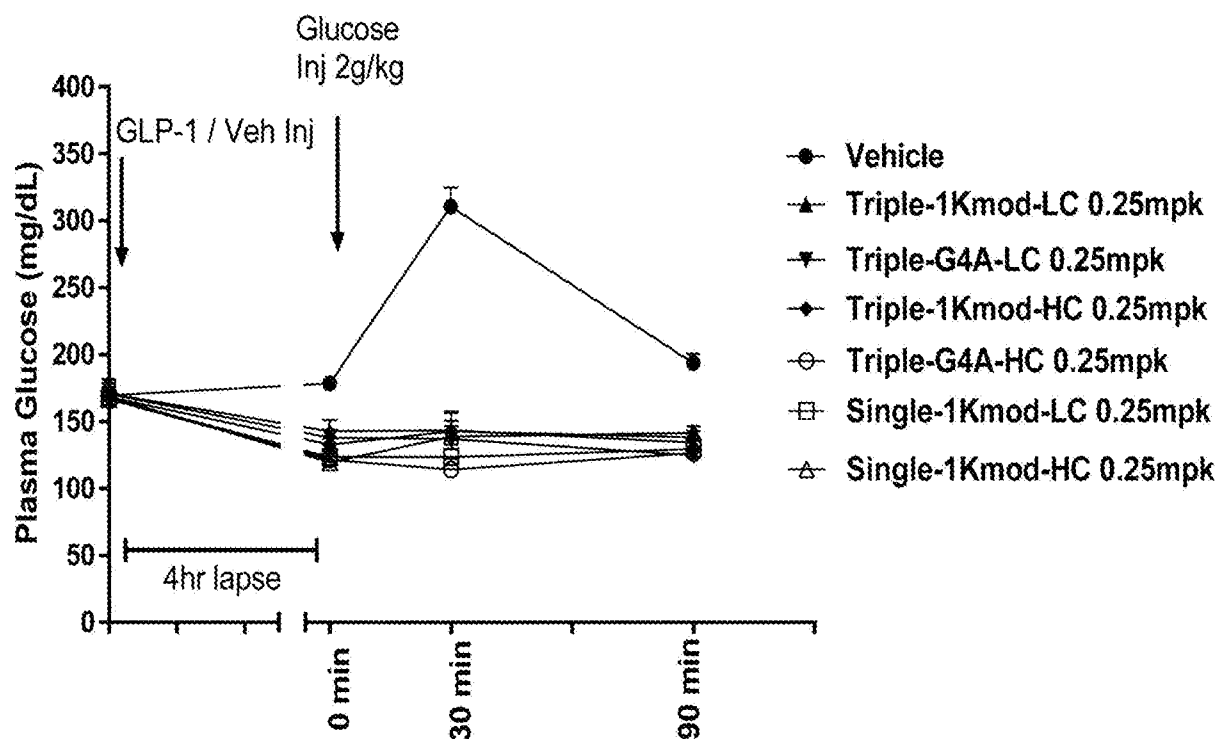


FIG. 33B

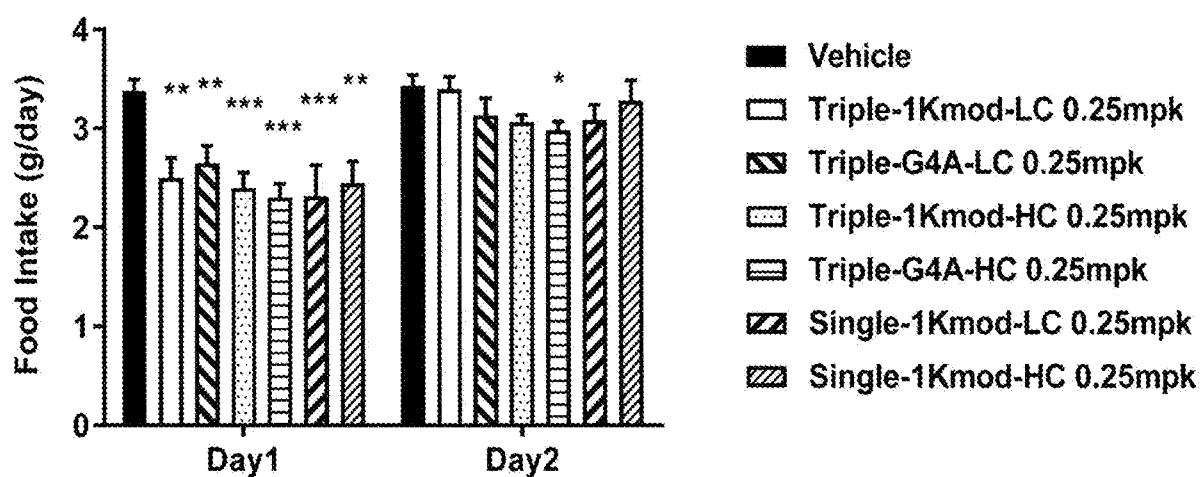


FIG. 33C

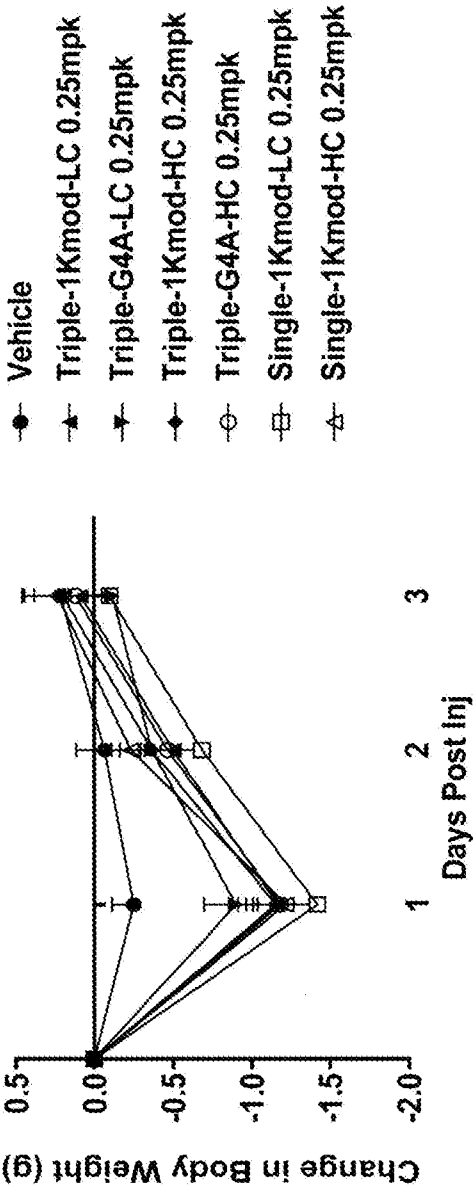
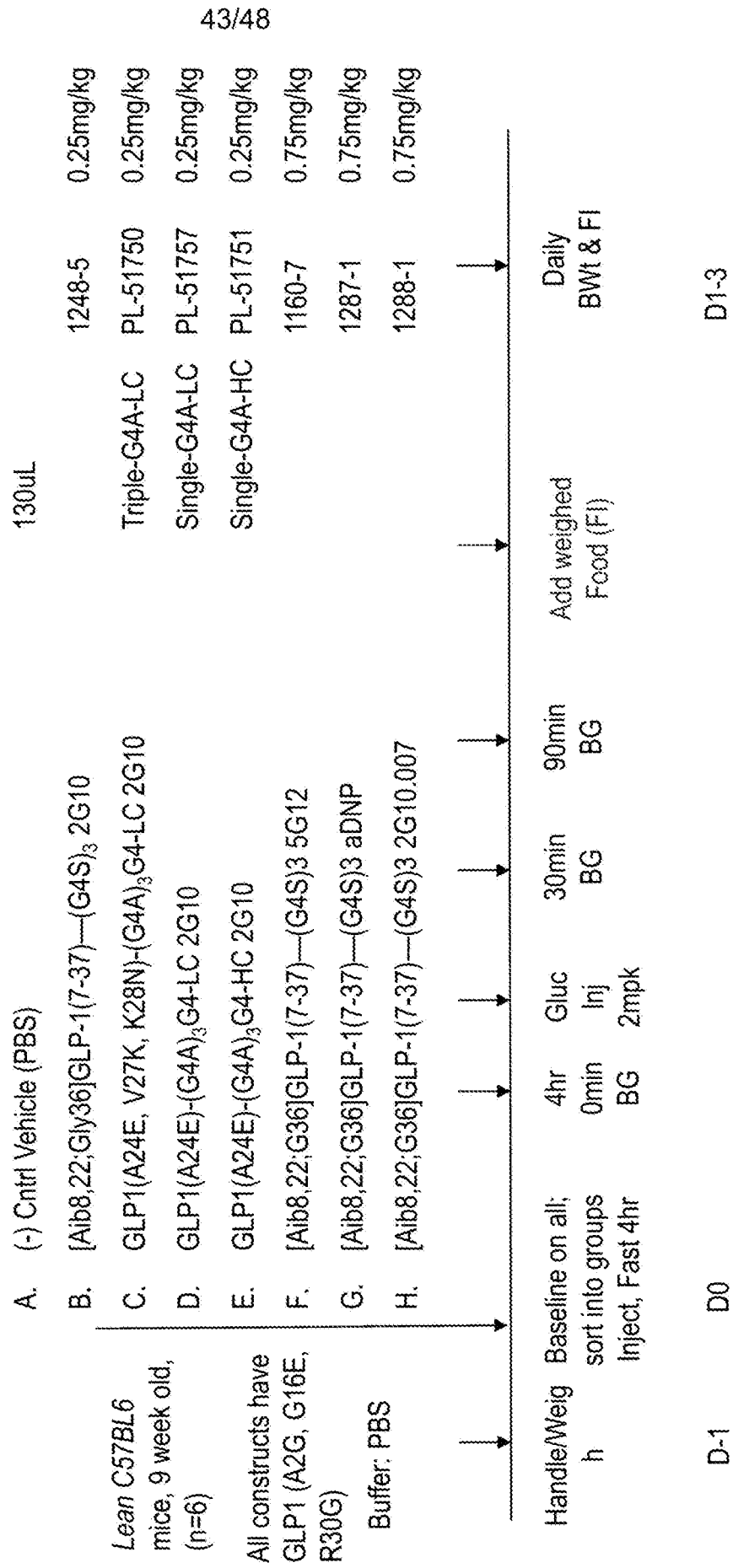


FIG. 33D

Biologic Lot or Reg #	REQ	Description	Linker / Ab Site
PL-51747	54630	GLP1(A2G, G16E, A24E, V27K, K28N, R30G)-1Kmod-HC 2G10	1Kmod - 2G10-HC
PL-51748	54630	GLP1(A2G, G16E, A24E, V27K, K28N, R30G)-(G4A)3G4-HC 2G10	(G4A)3G4 - 2G10-HC
PL-51749	54630	GLP1(A2G, G16E, A24E, V27K, K28N, R30G)-1Kmod-LC 2G10	1Kmod - 2G10-LC
PL-51752	54630	GLP1(A2G, G16E, A24E, R30G)-1Kmod-HC 2G10	1Kmod - 2G10-HC
PL-51754	54322	GLP1(A2G, G16E, A24E, R30G)-1Kmod-LC 2G10	1Kmod - 2G10-LC
PL-51750	54630	GLP1(A2G, G16E, A24E, V27K, K28N, R30G)-(G4A)3G4-LC 2G10	(G4A)3G4 - 2G10-LC

FIG. 34



44/48

FIG. 35A

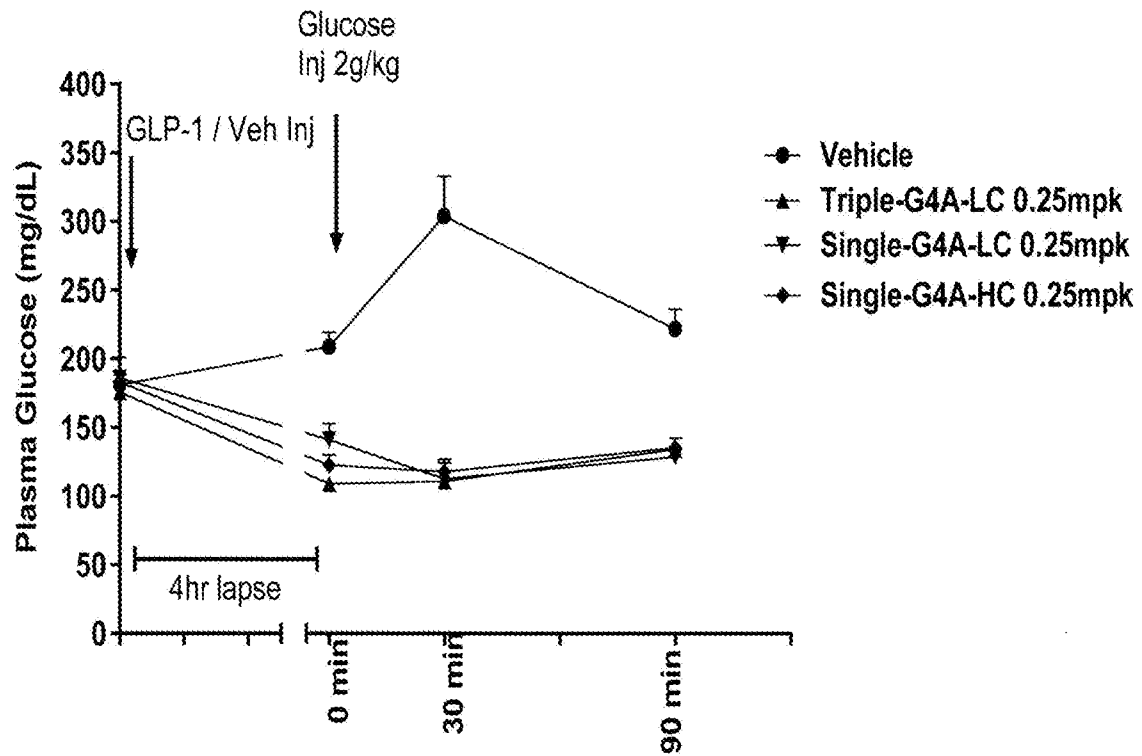


FIG. 35B

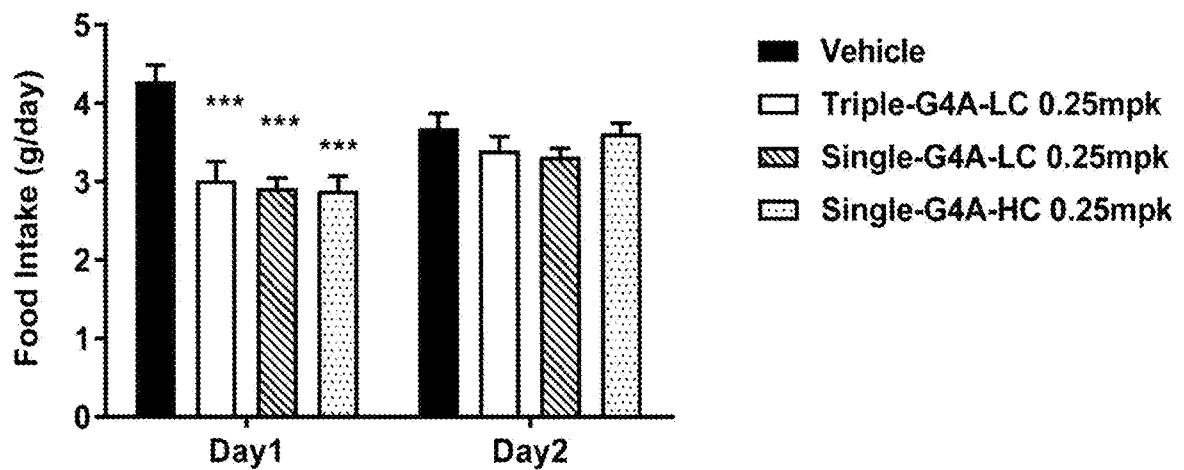


FIG. 35C

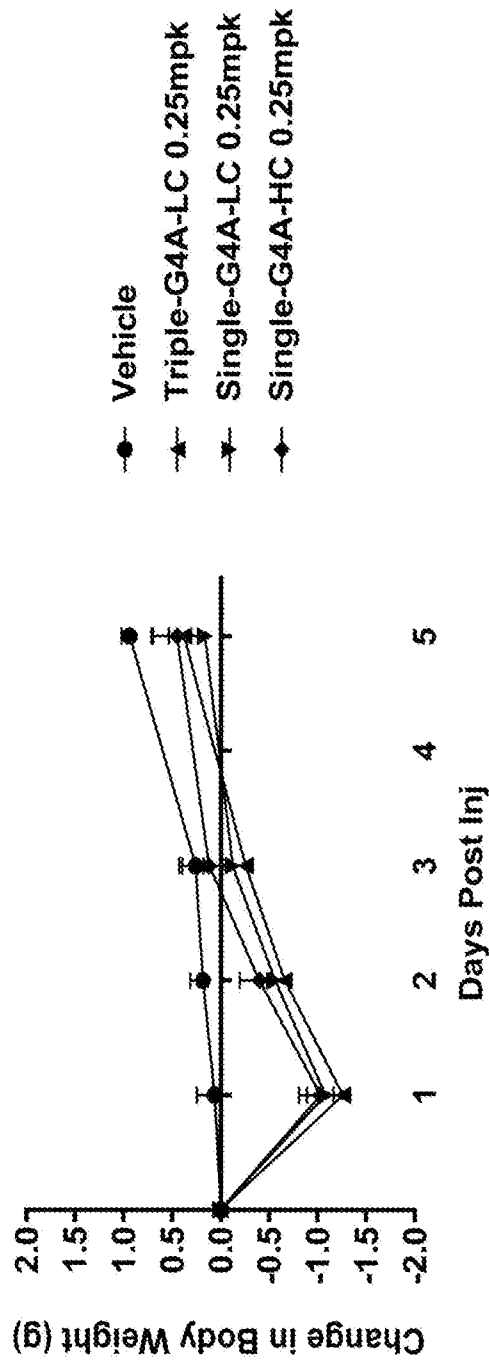


FIG. 35D

Biologic Lot or Reg #	REQ	Description	Linker / Ab Site
PL-51750	54630	GLP1(A2G, G16E, A24E, V27K, K28N, R30G)-(G4A)3G4-LC 2G10	(G4A)3G4 - 2G10-LC
PL-51751	54630	GLP1(A2G, G16E, A24E, R30G)-(G4A)3G4-HC 2G10	(G4A)3G4 - 2G10-HC
PL-51757	54322	GLP1(A2G, G16E, A24E, R30G)-(G4A)3G4-LC 2G10	(G4A)3G4 - 2G10-LC

FIG. 36A

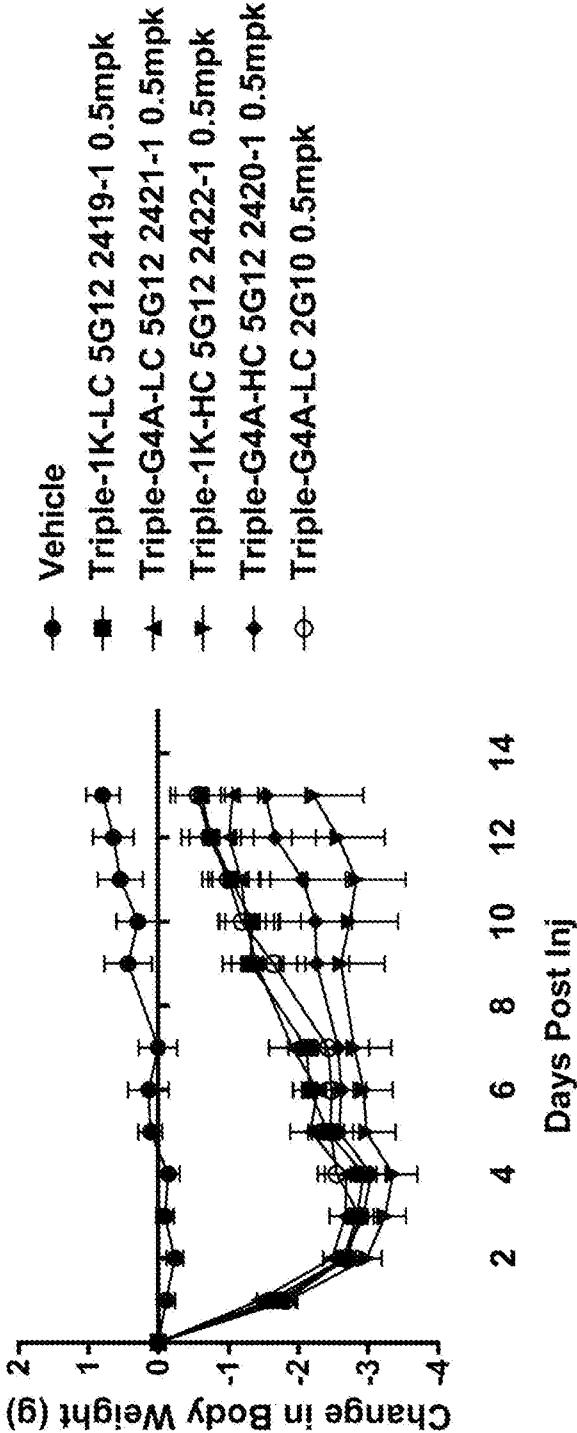


FIG. 36B

Biologic Lot or Reg #	REQ	Description	Linker / Ab Site
2419-1		GLP1(A2G, G18E, A24E, V27K, K28N, R30G)- 1Kmod-LC 5G12	1Kmod - 5G12-LC
2420-1		GLP1(A2G, G18E, A24E, V27K, K28N, R30G)- (G4A)3G4-HC 5G12	(G4A)3G4 - 5G12-HC
2421-1		GLP1(A2G, G18E, A24E, V27K, K28N, R30G)- (G4A)3G4-LC 5G12	(G4A)3G4 - 5G12-LC
2422-1		GLP1(A2G, G18E, A24E, V27K, K28N, R30G)- 1Kmod-HC 5G12	1Kmod - 5G12-HC
PL-51750		GLP1(A2G, G18E, A24E, V27K, K28N, R30G)- (G4A)3G4-LC 2G10	(G4A)3G4 - 2G10-LC

47/48

FIG. 37A

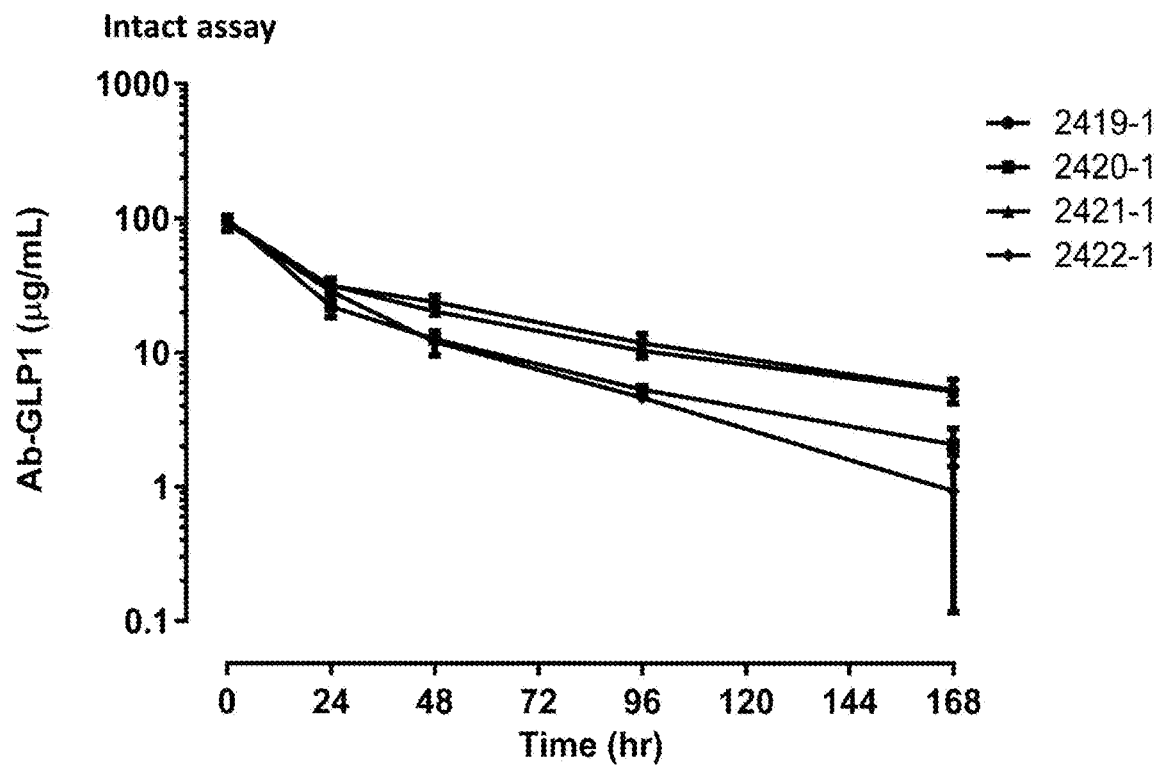


FIG. 37B

BioReg	C_0 ($\mu\text{g/mL}$)	AUC_{0-t} ($\text{hr} \cdot \mu\text{g/mL}$)	CL_{0-t} (mL/hr/kg)	$T_{1/2, \text{terminal}}$ (hr)
2419-1	95.6	3660	1.37	55.9
2420-1	99.0	2560	1.95	46.4
2421-1	90.6	3380	1.48	58.0
2422-1	93.4	2490	2.01	37.2

48/48

FIG. 37C

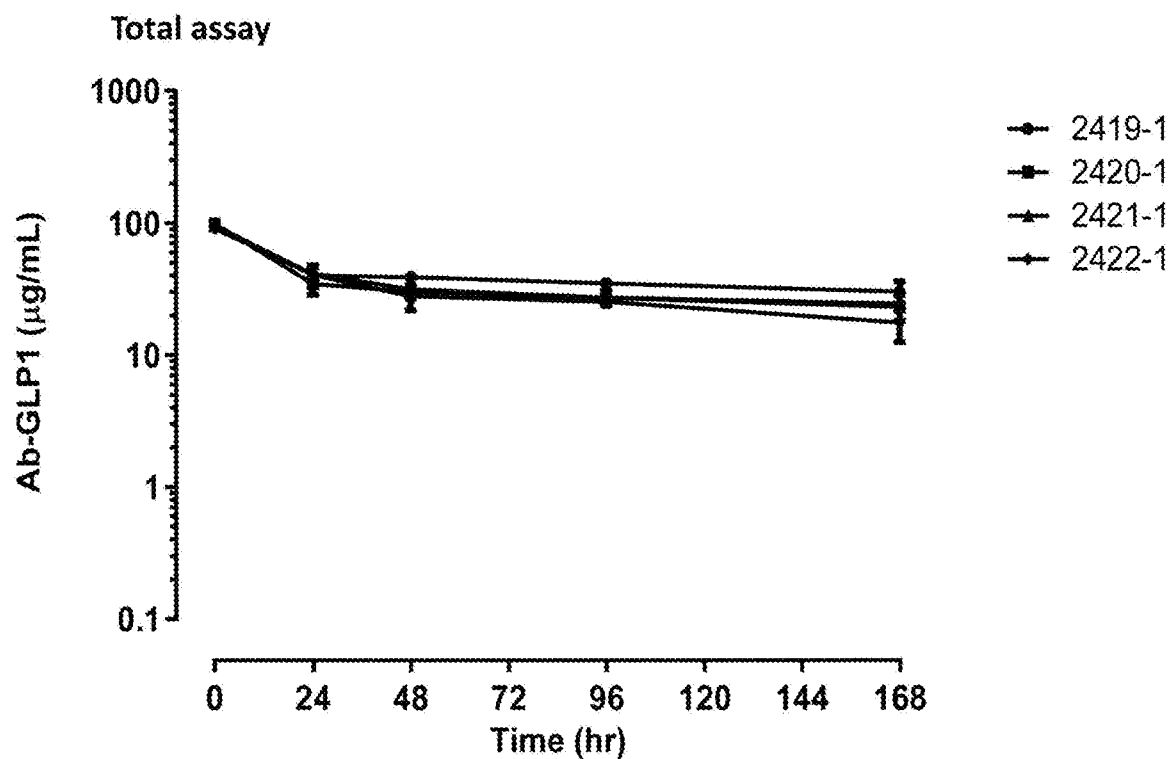


FIG. 37D

BioReg	C_0 ($\mu\text{g/mL}$)	AUC_{0-t} ($\text{hr} \cdot \mu\text{g/mL}$)	CL_{0-t} (mL/hr/kg)	$T_{1/2, \text{terminal}}$ (hr)
2419-1	97.2	6710	0.745	*n/a
2420-1	98.8	5570	0.898	n/a
2421-1	95.3	5790	0.864	n/a
2422-1	91.1	5230	0.956	n/a

*Terminal slope insufficient for accurate half-life determination

FIG. 3

Ab: 6H1 HC

Linker: 1Kmod

GLP1: (A2G/E3H/R30G), (A2V/E3H/R30G), (A2S/E3H/R30G), (A2G/E3D/R30G), (A2V/E3D/R30G), (A2S/E3D/R30G), (0A/A2G/R30G), (A2V/R30G), (A2S/R30G), (A2G/E3Q/R30G), (A2V/E3Q/R30G), (A2S/E3Q/R30G)

