

**METHOD OF TREATING OR AMELIORATING METABOLIC DISORDERS USING
GLP-1 RECEPTOR AGONISTS CONJUGATED TO ANTAGONISTS FOR GASTRIC
INHIBITORY PEPTIDE RECEPTOR (GIPR)**

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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 conjugated to an antigen binding protein specific for the gastric inhibitory peptide receptor (GIPR).

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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 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.

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[0003] GIP secretion is induced by food ingestion. GIP has a number of physiological effects in tissues, including promotion of fat storage in adipocytes and promotion of pancreatic islet β -cell function and glucose-dependent insulin secretion. GIP and glucagon like polypeptide-1 (GLP-1) are known 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).

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[0004] The GIP receptor (GIPR) is a member of the secretin-glucagon family of G-protein coupled receptors (GPCRs) having an extracellular N-terminus, seven transmembrane domains and an intracellular C-terminus. The N-terminal extracellular domains of this family of receptors are usually glycosylated and form the recognition and binding domain of the receptor. GIPR is highly expressed in a number of tissues, including the pancreas, gut, adipose tissue, heart, pituitary, adrenal cortex, and brain (Usdin et al., Endocrinology. 1993, 133:2861-2870). Human GIPR comprises 466 amino acids and is encoded by a gene located on chromosome 19q13.3 (Gremlich et al., Diabetes. 1995; 44:1202-8; Volz et al., FEBS Lett. 1995, 373:23-29). Studies have suggested that alternative mRNA splicing results in the production of GIP receptor variants of differing lengths in human, rat and mouse.

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[0005] GIPR knockout mice ($Gipr^{-/-}$) are resistant to high fat diet-induced weight gain and have improved insulin sensitivity and lipid profiles. (Yamada et al., Diabetes. 2006, 55:S86; Miyawaki et al. Nature Med. 2002, 8:738-742). In addition, a novel small molecule GIPR antagonist SKL-14959 prevents obesity and insulin resistance. (Diabetologia 2008, 51:S373, 44th EASD Annual meeting poster).

[0006] 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 insulin secretion from pancreatic β -cells (Diabetes 2004, 53:S3, 205-214). In addition to the incretin effects, GLP-1 also decreases glucagon secretion, delays gastric emptying and reduces caloric intake (Diabetes Care, 2003, 26(10): 2929-2940). GLP-1 exerts its effects by activation of the GLP-1 receptor, which belongs to a class B G-protein-coupled receptor (Endocrinology. 1993, 133(4):1907-10). The function of GLP-1 is limited by rapid degradation by the DPP-IV enzyme, resulting in a half-life of approximately 2 minutes. Recently, long-lasting GLP-1 receptor agonists (GLP-1 RAs) such as exenatide, liraglutide, dulaglutide have been developed and are now being used clinically to improve glycemic control in 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 (Bioorg. Med. Chem.Lett 2013, 23:4011-4018).

SUMMARY

[0008] In one example, the present disclosure provides a method of treating a subject with a metabolic disorder, the method comprising administering to the subject a therapeutically effective amount of a composition comprising an antigen binding protein that specifically binds to human GIPR, wherein the antigen binding protein is conjugated to a GLP-1 receptor agonist. In one example, the metabolic disorder is a disorder of glucose metabolism. In another example, the glucose metabolism disorder comprises hyperglycemia and administering the antigen binding protein reduces plasma glucose. In another example, the glucose metabolism disorder comprises hyperinsulinemia and administering the antigen binding protein reduces plasma insulin. In another example, the glucose metabolism disorder comprises glucose intolerance and administering the antigen binding protein reduces increases glucose tolerance. In another example, the glucose metabolism disorder comprises

insulin resistance and administering the antigen binding protein reduces insulin resistance. In another example, the glucose metabolism disorder comprises diabetes mellitus. In another example, the subject is obese. In another example, administering the composition reduces body weight in an obese subject. In another example, administering the composition reduces body weight gain in an obese subject. In another example, administering the composition reduces fat mass in an obese subject. In another example, the glucose metabolism disorder comprises insulin resistance and administering the composition reduces insulin resistance in an obese subject. In another example, administering the composition reduces liver steatosis in an obese subject having increased liver steatosis. In another example, administering the composition reduces liver fat content in an obese subject having increased liver fat content.

[0008a] In one aspect, the present disclosure refers to 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 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: 702, SEQ ID NO: 859, SEQ ID NO: 1016, SEQ ID NO: 1173, SEQ ID NO: 1330; and SEQ ID NO: 1487; and the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid substitution at one or more conjugation site(s) selected from the group consisting of D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455, E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612; and b) a GLP-1 receptor agonist, wherein the GLP-1 receptor agonist comprises [Aib⁸;Tyr¹⁶;Glu²²;Gly³⁶]GLP-1_(7-37) (SEQ ID NO: 3244) and is conjugated to the antibody or functional fragment thereof through the side-chain of the cysteine residue or non-canonical amino acid residue substituted at the one or more conjugation site(s).

[0008b] In another aspect, the present disclosure refers to the use of a composition comprising an antibody as defined in the claims in the manufacture of a medicament for treating a metabolic disorder, wherein the metabolic disorder is selected from the group consisting of hyperglycemia, hyperinsulinemia, glucose intolerance, insulin resistance, diabetes mellitus, Type 2 diabetes, dyslipidemia, metabolic syndrome (Syndrome X or insulin resistance syndrome), glucosuria, metabolic acidosis, diabetic neuropathy, diabetic nephropathy, diabetic retinopathy, diabetic cardiomyopathy, Type 1 diabetes and obesity.

[0009] In one example, 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, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid substitution at one or more conjugation site(s) selected from the group consisting of D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455; E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612; and a GLP-1 receptor

agonist, wherein the GLP-1 receptor agonist is conjugated to the antibody or functional fragment thereof through the side-chain of the cysteine residue or non-canonical amino acid residue substituted at the one or more conjugation site(s).

[0010] In one example, 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 example, 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 example, the antibody fragment is a Fab fragment, a Fab' fragment, or a F(ab')₂ fragment. In one example, the antibody or functional fragment thereof is of the IgG1-, IgG2- IgG3- or IgG4-type. In one example, the antibody or functional fragment thereof inhibits binding of GIP to the extracellular portion of human GIPR.

[0011] In one example, the GLP-1 receptor agonist is GLP-1(7-37) or a GLP-1(7-37) analog. In one example, the GLP-1 receptor agonist is selected from the group consisting of

exenatide, liraglutide, lixisenatide, albiglutide, dulaglutide, semaglutide, and taspoglutide. In one example, the GLP-1 receptor agonist is selected from the group consisting of GLP-1(7-37) (SEQ ID NO: 3184); GLP-1(7-36)-NH₂ (SEQ ID NO: 3185); liraglutide; albiglutide; taspoglutide; dulaglutide, semaglutide; LY2428757; 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); 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); octylGly¹⁴,Gln²⁸-exendin-4 (SEQ ID NO: 3178); Leu¹⁴,Gln²⁸,octylGly³⁴-exendin-4 (SEQ ID NO: 3179); 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); 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); GLP-1(7-36)-NH₂ (SEQ ID NO: 3185); Aib^{8,35},Arg^{26,34},Phe³¹-GLP-1(7-36)) (SEQ ID NO: 3186); 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: 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); 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); 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); 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); [N^ε-(17-carboxyheptadecanoic acid)Lys²⁰]exendin-4-NH₂ (SEQ ID NO: 3208); [N^ε-(17-carboxyhepta-decanoyl)Lys³²]exendin-4-NH₂ (SEQ ID NO: 3209); [desamino-His¹,N^ε-(17-carboxyheptadecanoyl)Lys²⁰]exendin-4-NH₂ (SEQ ID NO: 3210); [Arg^{12,27},NLe¹⁴,N^ε-(17-carboxy-heptadecanoyl)Lys³²]exendin-4-NH₂ (SEQ ID NO: 3211); [N^ε-(19-carboxy-nonadecanoylamino)Lys²⁰]exendin-4-NH₂ (SEQ ID NO: 3212); [N^ε-(15-carboxypentadecanoylamino)Lys²⁰]exendin-4-NH₂ (SEQ ID NO: 3213); [N^ε-(13-carboxytridecanoylamino)Lys²⁰]exendin-4-NH₂ (SEQ ID NO: 3214); [N^ε-(11-carboxyundecanoyl-amino)Lys²⁰]exendin-4-NH₂ (SEQ ID NO: 3215); exendin-4-Lys⁴⁰(e-MPA)-NH₂ (SEQ ID NO: 3216); exendin-4-Lys⁴⁰(e-AEEA-AEEA-MPA)-NH₂ (SEQ ID NO: 3217); exendin-4-Lys⁴⁰(e-AEEA-MPA)-NH₂ (SEQ ID NO: 3218); exendin-4-Lys⁴⁰(e-MPA)-albumin (SEQ ID NO: 3219); exendin-4-Lys⁴⁰(e-AEEA-AEEA-MPA)-albumin (SEQ ID NO: 3220); exendin-4-Lys⁴⁰(e-AEEA-MPA)-albumin (SEQ ID NO: 3221); desamino-His⁷,Arg²⁶,Lys³⁴(N^ε-(γ-Glu(N-α-hexadecanoyl)))-GLP-1(7-37) (core peptide disclosed as SEQ ID NO: 3222) (SEQ ID NO: 3222); desamino-His⁷,Arg²⁶,Lys³⁴(N^ε-octanoyl)-GLP-1(7-37) (SEQ ID NO: 3223); Arg^{26,34},Lys³⁸(N^ε-(ω-carboxypentadecanoyl)))-GLP-1(7-38) (SEQ ID NO: 3224); Arg^{26,34},Lys³⁶(N^ε-(γ-Glu(N-α-hexadecanoyl)))-GLP-1(7-36) (core peptide disclosed as SEQ ID NO: 3225) (SEQ ID NO: 3225); [Aib⁸;Lys³⁷]GLP-1_(7-37) (SEQ ID NO: 3226); [Aib⁸,Lys²⁶]GLP-1_(7-37) (SEQ ID NO: 3227); [Aib^{8,22};Lys³⁶]GLP-1(7-36)-Amide (SEQ ID NO: 3228); [Aib^{8,22};BLeu³²;Lys³⁶]GLP-1(7-36)-Amide (SEQ ID NO: 3229); [Aib^{8,22};Lys³⁷]GLP-1(7-37)-Amide (SEQ ID NO: 3230); [Aib^{8,22};BLeu³²;Lys³⁷]GLP-1(7-37)-Amide (SEQ ID NO: 3231); [Aib^{8,22};aMeLeu³²;Lys³⁷]GLP-1(7-37)-Amide (SEQ ID NO: 3232); [Aib^{8,22};AMEF¹²;Lys³⁷]GLP-1(7-37)-Amide (SEQ ID NO: 3233); [Aib^{8,22};BLeu¹⁶;Lys³⁷]GLP-1(7-37)-Amide (SEQ ID NO: 3234); [Aib^{8,22};Gly³⁶;Lys³⁷]GLP-

1(7-37)-Amide (SEQ ID NO: 3235); [Aib^{8,22};Lys^{33,37};Asn³⁴;Gly³⁶]GLP-1(7-37)-Amide (SEQ ID NO: 3236); [Aib^{8,22};Lys³³;Asn³⁴;Gly³⁶;Aeea³⁷]GLP-1(7-37)-Aeea-Lys-Amide (SEQ ID NO: 3237); [Aib^{8,22};Gly³⁶]GLP-1(7-37) (SEQ ID NO: 3238); cyclo[E²³-K²⁷][Aib⁸;Gly³⁶]GLP-1(7-37) (SEQ ID NO: 3239); cyclo[E²²-K²⁶][Aib⁸;Gly³⁶;Lys³⁷]GLP-1(7-37)-Amide (SEQ ID NO: 3240); [Aib^{8,22}]-GLP-1(7-22)-Ex4(17-39) (SEQ ID NO: 3241); [Gly^{8,36};Glu²²]GLP-1(7-37) (SEQ ID NO: 3242); [Aib⁸;Glu²²;Gly³⁶]GLP-1(7-37)-Amide (SEQ ID NO: 3243); [Aib⁸;Tyr¹⁶;Glu²²;Gly³⁶]GLP-1(7-37) (SEQ ID NO: 3244); [Aib⁸;Lys^{18,33};Glu^{22,23,30};Val²⁵;Arg²⁶;Leu²⁷;Asn³⁴;Gly³⁶]GLP-1(7-37) (SEQ ID NO: 3245); [Aib⁸;Lys^{18,33};Glu^{22,23,30};Leu²⁷;Asn³⁴;Gly³⁶]GLP-1(7-37) (SEQ ID NO: 3246); [Aib⁸;Lys¹⁸;Glu^{22,23,30};Leu²⁷;Gly³⁶]GLP-1(7-37) (SEQ ID NO: 3247); [Aib^{8,22};Ile⁹;Gly³⁶]GLP-1(7-36) (SEQ ID NO: 3248); and [Aib^{8,22};Glu¹⁵;Gly³⁶]GLP-1(7-36) (SEQ ID NO: 3249).

[0012] In one example, the GLP-1(7-37) or GLP-1(7-37) analog is conjugated to the antibody or fragment thereof at a residue that corresponds to K26, K36, K37, K39 or a C-terminal amine group of said analog.

[0013] In one example, the GLP-1 receptor agonist if conjugated to the antibody or fragment thereof via a peptide linker comprising a sequence selected from the group consisting of (Gly₃Ser)₂, (Gly₄Ser)₂, (Gly₃Ser)₃, (Gly₄Ser)₃, (Gly₃Ser)₄, (Gly₄Ser)₄, (Gly₃Ser)₅, (Gly₄Ser)₅, (Gly₃Ser)₆, and (Gly₄Ser)₆.

BRIEF DESCRIPTION OF THE DRAWINGS

[0014] FIG. 1. Reaction scheme for the generation of anti-GIPR/GLP-1 peptide conjugate

[0015] FIGS. 2A-2T. GLP-1 receptor agonist activity in CHOK1-GLP-1R H20 recombinant cells and GIPR antagonist activity in 293 HEK-GIPR #10 recombinant cells

[0016] FIGS. 3A-3C. GLP-1 agonist activity of 2G10 conjugate is more potent in cells expressing both GLP-1R and GIPR (CHOK1 hGLP-1R/hGIPR M1) compared to cells only expressing GLP-1R (CHOK1 hGLP-1R H20)

[0017] FIGS. 4A-4R. In vivo activity- glucose and body weight effects in db/db mice

[0018] FIGS. 5A-5D. GLP-1 receptor agonist and GIPR Antagonist In vivo Activity of 5G12 and 2G10 Chemical Conjugates in C57Bl6 mice (glucose tolerance test)

[0019] FIGS. 6A-6B. GLP-1 receptor agonist and GIPR Antagonist In vivo Activity of 5G12 and 2G10 Chemical Conjugates in DIO mice (plasma glucose and change in body weight)

[0020] FIG. 7. GLP-1R-GIPR bispecific conjugate 1273 reduces body weight in male spontaneously obese cynomolgus monkeys (% change from baseline)

[0021] FIG. 8. GLP-1R-GIPR bispecific conjugate 1273 reduces total energy intake in male spontaneously obese cynomolgus monkeys (% change from baseline)

5 [0022] FIG. 9. GLP-1R-GIPR bispecific conjugate 1273 reduces fasting insulin in male spontaneously obese cynomolgus monkeys (% change from baseline)

[0023] FIG. 10. GLP-1R-GIPR bispecific conjugate 1273 reduces fasting triglycerides in male spontaneously obese cynomolgus monkeys (% change from baseline)

10 [0024] FIG. 11. GLP-1R-GIPR bispecific conjugate 1273 reduces fasting total cholesterol in male spontaneously obese cynomolgus monkeys (% change from baseline)

[0025] FIG. 12. GLP-1R-GIPR bispecific conjugate 1264 reduces body weight in male spontaneously obese cynomolgus monkeys (% change from baseline)

[0026] FIG. 13. GLP-1R-GIPR bispecific conjugate 1264 reduces total energy intake in male spontaneously obese cynomolgus monkeys (% change from baseline)

- [0027] FIG. 14. GLP-1R-GIPR bispecific conjugate 1264 reduces fasting insulin in male spontaneously obese cynomolgus monkeys (% change from baseline)
- [0028] FIG. 15. GLP-1R-GIPR bispecific conjugate 1264 reduces fasting triglycerides in male spontaneously obese cynomolgus monkeys (% change from baseline)
- 5 [0029] FIG. 16. GLP-1R-GIPR bispecific conjugate 1264 reduces fasting total cholesterol in male spontaneously obese cynomolgus monkeys (% change from baseline)
- [0030] FIG. 17. GLP-1R-GIPR bispecific conjugates 1248 and 1257 reduce body weight in male spontaneously obese cynomolgus monkeys (% change from baseline)
- [0031] FIG. 18. GLP-1R-GIPR bispecific conjugates 1248 and 1257 reduce total energy
10 intake in male spontaneously obese cynomolgus monkeys (% change from baseline)
- [0032] FIG. 19. GLP-1R-GIPR bispecific conjugates 1248 and 1257 reduce fasting insulin in male spontaneously obese cynomolgus monkeys (% change from baseline)
- [0033] FIG. 20. GLP-1R-GIPR bispecific conjugates 1248 and 1257 reduce fasting triglycerides in male spontaneously obese cynomolgus monkeys (% change from baseline)
- 15 [0034] FIG. 21. GLP-1R-GIPR bispecific conjugates 1248 and 1257 reduce fasting cholesterol in male spontaneously obese cynomolgus monkeys (% change from baseline)
- [0035] FIGS. 22A-22B. Binding affinity of anti-GIPR/GLP-1R bispecific conjugates
- [0036] FIG. 23. Anti-GIPR/GLP-1R bispecific conjugate 1248 promotes strong GLP-1R and GIPR internalization in cells expressing both GLP-1R and GIPR
- 20 [0037] FIGS. 24A-24B. Time course and dose response of anti-GIPR/GLP-1R bispecific conjugates in GLP-1R internalization assay
- [0038] FIGS. 25A-25D. GLP-1R, GIPR and bispecific conjugate are co-localized upon internalization
- [0039] FIGS. 26A-26B. Inhibition of receptor internalization reduces 1248-induced cAMP
25 generation
- [0040] FIGS. 27A-27C. Bispecific conjugates show binding to GLP-1R and GIPR in FACS analysis
- [0041] FIG. 28. Anti-GIPR/GLP-1R bispecific conjugates stimulate calcium flux
- [0042] FIGS 29A-29B. Anti-GIPR/GLP-1R bispecific conjugate 1248 promotes beta-arrestin
30 recruitments through both GLP-1R and GIPR pathways
- [0043] FIG. 30. Anti-GIPR/GLP-1R bispecific conjugate 1248 stimulates insulin secretion in human pancreatic microislets

DETAILED DESCRIPTION OF THE INVENTION

[0044] 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 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 conjugated to a GLP-1 receptor agonist is administered to a subject in need thereof. Methods of administration and delivery are also provided.

[0045] Recombinant polypeptide and nucleic acid methods used herein, including in the Examples, are generally those set forth in Sambrook et al., *Molecular Cloning: A Laboratory Manual* (Cold Spring Harbor Laboratory Press, 1989) or *Current Protocols in Molecular Biology* (Ausubel et al., eds., Green Publishers Inc. and Wiley and Sons 1994), both of which are incorporated herein by reference for any purpose.

[0046] The section headings used herein are for organizational purposes only and are not to be construed as limiting the subject matter described.

[0047] 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.

[0048] Generally, nomenclatures used in connection with, and techniques of, cell and tissue culture, molecular biology, immunology, microbiology, genetics and protein and nucleic acid chemistry and hybridization described herein are those well known and commonly used in the art. The methods and techniques of the present application are generally performed according to conventional methods well known in the art and as described in various general and more specific references that are cited and discussed throughout the present specification unless otherwise indicated. See, e.g., Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 3rd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (2001), Ausubel et al., *Current Protocols in Molecular Biology*, Greene Publishing Associates (1992), and Harlow and Lane *Antibodies: A Laboratory Manual* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1990), which are incorporated herein by reference. Enzymatic reactions and purification techniques are performed according to manufacturer's

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

[0049] 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
10 not intended to limit the scope of the disclosed, which is defined solely by the claims.

[0050] Other than in the operating examples, or where otherwise indicated, all numbers expressing quantities of ingredients or reaction conditions used herein should be understood as modified in all instances by the term “about.” The term “about” when used in connection with percentages may mean $\pm 1\%$.

[0051] Following convention, as used herein “a” and “an” mean “one or more” unless
15 specifically indicated otherwise.

[0052] 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
20 amino acids that are chemically similar to the naturally occurring amino acids.

[0053] A “naturally occurring amino acid” is an amino acid that is encoded by the genetic code, as well as those amino acids that are encoded by the genetic code that are modified after synthesis, e.g., hydroxyproline, γ -carboxyglutamate, and O-phosphoserine. An amino acid analog is a compound that has the same basic chemical structure as a naturally occurring
25 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.

[0054] 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.
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[0055] A “non-naturally occurring amino acid” is a compound that has the same basic chemical structure as a naturally occurring amino acid, but is not incorporated into a growing polypeptide chain by the translation complex. “Non-naturally occurring amino acid” also includes, but is not limited to, amino acids that occur by modification (e.g., posttranslational modifications) of a naturally encoded amino acid (including but not limited to, the 20 common amino acids) but are not themselves naturally incorporated into a growing polypeptide chain by the translation complex. A non-limiting lists of examples of non-naturally occurring amino acids that can be inserted into a polypeptide sequence or substituted for a wild-type residue in polypeptide sequence include β -amino acids, homoamino acids, cyclic amino acids and amino acids with derivatized side chains. Examples include (in the L-form or D-form; abbreviated as in parentheses): citrulline (Cit), homocitrulline (hCit), N α -methylcitrulline (NMeCit), N α -methylhomocitrulline (N α -MeHoCit), ornithine (Orn), N α -Methylornithine (N α -MeOrn or NMeOrn), sarcosine (Sar), homolysine (hLys or hK), homoarginine (hArg or hR), homoglutamine (hQ), N α -methylarginine (NMeR), N α -methylleucine (N α -MeL or NMeL), N-methylhomolysine (NMeHoK), N α -methylglutamine (NMeQ), norleucine (Nle), norvaline (Nva), 1,2,3,4-tetrahydroisoquinoline (Tic), Octahydroindole-2-carboxylic acid (Oic), 3-(1-naphthyl)alanine (1-Nal), 3-(2-naphthyl)alanine (2-Nal), 1,2,3,4-tetrahydroisoquinoline (Tic), 2-indanylglycine (Igl), para-iodophenylalanine (pI-Phe), para-aminophenylalanine (4AmP or 4-Amino-Phe), 4-guanidino phenylalanine (Guf), glycyllsine (abbreviated “K(N ϵ -glycyl)” or “K(glycyl)” or “K(gly)”), nitrophenylalanine (nitrophe), aminophenylalanine (aminophe or Amino-Phe), benzylphenylalanine (benzylphe), γ -carboxyglutamic acid (γ -carboxyglu), hydroxyproline (hydroxypro), p-carboxyl-phenylalanine (Cpa), α -aminoadipic acid (Aad), N α -methyl valine (NMeVal), N- α -methyl leucine (NMeLeu), N α -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 -aminoisobutyric 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.

[0056] 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.

[0057] 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.

[0058] A composition of the present invention that includes a GLP-1 receptor agonist of the invention covalently linked, attached, or bound, either directly or indirectly through a linker moiety, to another an anti-GIPR antigen binding protein of the invention or is a “conjugate” or “conjugated” molecule, whether conjugated by chemical means (e.g., post-translationally or post-synthetically).

[0059] The term “encoding” refers to a polynucleotide sequence encoding one or more amino acids. The term does not require a start or stop codon.

[0060] 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.,
 5 (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.

[0061] 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
 10 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
 15 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
 20 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.

[0062] Recommended parameters for determining percent identity for polypeptides or nucleotide sequences using the GAP program are the following:

[0063] Algorithm: Needleman et al., 1970, J. Mol. Biol. 48:443-453;

[0064] Comparison matrix: BLOSUM 62 from Henikoff et al., 1992, supra;

[0065] Gap Penalty: 12 (but with no penalty for end gaps)

[0066] Gap Length Penalty: 4

[0067] Threshold of Similarity: 0

[0068] 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.

[0069] 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.

[0070] 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-occurring amino acid analogs and amino acid mimetics.

[0071] In various embodiments, a GIPR polypeptide comprises an amino acid sequence that is at least about 90 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 95, 96, 97, 98, or 99 percent identical 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.

[0072] The terms “GIPR activity assay” (also referred to as a “GIPR functional assay”) means an assay that can be used to measure GIP or a GIP binding protein activity in a cellular setting. In one embodiment, the “activity” (or “functional”) assay can be a cAMP assay in GIPR expressing cells, in which GIP can induce cAMP signal, and the activity of a GIP/GIPR binding protein could be measured in the presence/absence of GIP ligand, in

which IC₅₀/EC₅₀ and degree of inhibition/activation can be obtained (Biochemical and Biophysical Research Communications (2002) 290:1420–1426). In another embodiment, the “activity” (or “functional”) assay can be an insulin secretion assay in pancreatic beta cells, in which GIP can induce glucose-dependent insulin secretion, and the activity of a GIP/GIPR binding protein could be measured in the presence/absence of GIP ligand, in which IC₅₀/EC₅₀ and degree of inhibition/activation can be obtained (Biochemical and Biophysical Research Communications (2002) 290:1420–1426).

[0073] The term “GIPR binding assay” means an assay that can be used to measure binding of GIP to GIPR. In one embodiment, “GIPR binding assay” can be an assay using FMAT or FACS that measures fluorescence-labeled GIP binding to GIPR expression cells, and GIP/GIPR binding protein’s activity can be measured for displacing fluorescence-labeled GIP binding to GIPR expression cells. In another embodiment, “GIPR binding assay” can be an assay that measures radioactive-labeled GIP binding to GIPR expression cells, and GIP/GIPR binding protein’s activity can be measured for displacing radioactive labeled GIP binding to GIPR expression cells (Biochimica et Biophysica Acta (2001) 1547:143-155).

[0074] The terms “GIP”, “Gastric inhibitory polypeptide”, “glucose-dependent insulinotropic peptide” and “GIP ligand” are used interchangeably and mean a naturally-occurring wild-type polypeptide expressed in a mammal, such as a human or a mouse, and includes naturally occurring alleles (e.g., naturally occurring allelic forms of human GIP protein). For purposes of this disclosure, the term “GIP” can be used interchangeably to refer to any mature GIP polypeptide.

[0075] The 42 amino acid sequence of mature human GIP is:

[0076] YAEGTFISDY SIAMDKIHQQ DFNWLLAQK GKKNWVKHNI TQ (SEQ ID NO: 3151)

[0077] and is encoded by the DNA sequence:

[0078] tatgcggaag gcacctttat tagcgattat agcattgcga tggataaaat
tcatacagcag gattttgtga actggctgct ggcgcagaaa ggcaaaaaaa
acgattggaa acataacatt acccag (SEQ ID NO: 3152).

[0079] The 42 amino acid sequence of mature murine GIP is:

[0080] YAEGTFISDY SIAMDKIRQQ DFNWLLAQR GKKS DWKHNI TQ (SEQ ID NO: 3153)

[0081] and is encoded by the DNA sequence:

[0082] tatgcggaag gcacctttat tagcgattat agcattgcga tggataaaat
tcgccagcag gattttgtga actggctgct ggcgcagcgc ggcaaaaaaa
gcgattggaa acataacatt acccag (SEQ ID NO: 3154).

[0083] The 42 amino acid sequence of mature rat GIP is:

5 [0084] YAEGTFISDY SIAMDKIRQQ DFVNWLLAQK GKKNDWKHNL TQ (SEQ ID NO:
3155)

[0085] and is encoded by the DNA sequence:

[0086] tatgcggaag gcacctttat tagcgattat agcattgcga tggataaaat
tcgccagcag gattttgtga actggctgctg gcgcagaaaag gcaaaaaaaa
10 cgattggaaa cataacctga cccag (SEQ ID NO: 3156).

[0087] A “GIPR antagonist” refers to compounds that reduce or inhibit GIP activation of GIPR. Such antagonists include chemically synthesized small molecules and antigen binding proteins.

[0088] An “antigen binding protein” as used herein means any protein that specifically binds
15 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
20 antibodies such as nanobodies and scFvs as described further below.

[0089] 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
25 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
30 described.

[0090] “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.

5 “Framework” regions can aid in maintaining the proper conformation of the CDRs to promote binding between the antigen binding region and an antigen.

[0091] 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.

[0092] 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.

15 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.

[0093] 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.

[0094] 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.

[0095] 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.

[0096] 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.

[0097] In another embodiment, Fvs, domain antibodies and scFvs, and may be derived from an antibody of the present invention.

[0098] 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.

[0099] A “Fab fragment” is comprised of one light chain and the CH1 and variable regions of one heavy chain. The heavy chain of a Fab molecule cannot form a disulfide bond with another heavy chain molecule.

[0100] 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.

[0101] An “Fab' fragment” contains one light chain and a portion of one heavy chain that contains the VH domain and the CH1 domain and also the region between the CH1 and CH2 domains, such that an interchain disulfide bond can be formed between the two heavy chains of two Fab' fragments to form an F(ab')₂ molecule.

[0102] An “F(ab')₂ fragment” contains two light chains and two heavy chains containing a portion of the constant region between the CH1 and CH2 domains, such that an interchain disulfide bond is formed between the two heavy chains. A F(ab')₂ fragment thus is composed of two Fab' fragments that are held together by a disulfide bond between the two heavy chains.

[0103] The “Fv region” comprises the variable regions from both the heavy and light chains, but lacks the constant regions.

[0104] “Single chain antibodies” or “scFvs” are Fv molecules in which the heavy and light chain variable regions have been connected by a flexible linker to form a single polypeptide chain, which forms an antigen-binding region. scFvs are discussed in detail in International Patent Application Publication No. WO 88/01649 and United States Patent Nos. 4,946,778 and No. 5,260,203, the disclosures of which are incorporated by reference.

[0105] A “domain antibody” or “single chain immunoglobulin” is an immunologically functional immunoglobulin fragment containing only the variable region of a heavy chain or the variable region of a light chain. Examples of domain antibodies include Nanobodies®. In some instances, two or more VH regions are covalently joined with a peptide linker to create a bivalent domain antibody. The two VH regions of a bivalent domain antibody may target the same or different antigens.

[0106] 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*.

[0107] A multispecific antigen binding protein” or “multispecific antibody” is one that targets more than one antigen or epitope.

[0108] 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.

[0109] The term “compete” when used in the context of antigen binding proteins (e.g., antibodies) means competition between antigen binding proteins is determined by an assay in which the antigen binding protein (e.g., antibody or immunologically functional fragment thereof) under test prevents or inhibits specific binding of a reference antigen binding protein to a common antigen (e.g., GIPR or a fragment thereof). Numerous types of competitive binding assays can be used, for example: solid phase direct or indirect radioimmunoassay

(RIA), solid phase direct or indirect enzyme immunoassay (EIA), sandwich competition assay (see, e.g., Stahli et al., 1983, *Methods in Enzymology* 9:242-253); solid phase direct biotin-avidin EIA (see, e.g., Kirkland et al., 1986, *J. Immunol.* 137:3614-3619) solid phase direct labeled assay, solid phase direct labeled sandwich assay (see, e.g., Harlow and Lane, 1988, *Antibodies, A Laboratory Manual*, Cold Spring Harbor Press); solid phase direct label RIA using I-125 label (see, e.g., Morel et al., 1988, *Molec. Immunol.* 25:7-15); solid phase direct biotin-avidin EIA (see, e.g., Cheung, et al., 1990, *Virology* 176:546-552); and direct labeled RIA (Moldenhauer et al., 1990, *Scand. J. Immunol.* 32:77-82). Typically, such an assay involves the use of purified antigen bound to a solid surface or cells bearing either of these, an 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.

[0110] 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.

[0111] 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.

[0112] 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.

[0113] 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.

[0114] 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

5 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.

[0115] 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.

20 [0116] 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.

25 [0117] 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.

[0118] 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.

[0119] 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.”

[0120] 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.

[0121] 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.

[0122] 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.

[0123] 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.

[0124] 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.

[0125] 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.

[0126] 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.

[0127] A “variant” of a polypeptide (e.g., an antigen binding protein such as an antibody) comprises an amino acid sequence wherein one or more amino acid residues are inserted into, deleted from and/or substituted into the amino acid sequence relative to another polypeptide sequence. Variants include fusion proteins.

[0128] A “derivative” of a polypeptide is a polypeptide (e.g., an antigen binding protein such as an antibody) that has been chemically modified in some manner distinct from insertion, deletion, or substitution variants, e.g., via conjugation to another chemical moiety.

[0129] 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.

[0130] A “subject” or “patient” as used herein can be any mammal. In a typical embodiment, the subject or patient is a human.

[0131] 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.

[0132] 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.

[0133] The 466 amino acid sequence of human GIPR is (Volz et al., FEBS Lett. 373:23-29 (1995); NCBI Reference Sequence: NP_0001555):

[0134] MTTSPILQLL LRLSLCGLLL QRAETGSKGQ TAGELYQRWE RYRRECQETL
 AAAEPPSGLA CNGSFDMYVC WDYAAPNATA RASCPWYLPW HHHVAAGFVL
 5 RQCGSDGQWG LWRDHTQCEN PEKNEAFLDQ RLILERLQVM YTVGYSLSLA
 TLLLALLILS LFRRLHCTRN YIHINLFTSF MLRAAAILSR DRLLPRPGPY
 LGDQALALWN QALAACRTAQ IVTQYCVGAN YTWLLVEGVY LHSLLVLVGG
 SEEGHFRYYL LLGWGAPALF VIPWVIVRYL YENTQCWERN EVKAIWWIIR
 TPILMTILIN FLIFIRILGI LLSKLRTRQM RCRDYRLRLA RSTLTLVPLL
 10 GVHEVVFAPV TEEQARGALR FAKLGFEIFL SSFQGFLVSV LYCFINKEVQ
 SEIRRGWHHC RLRRSLGEEQ RQLPERAFRA LPSGSGPGEV PTSRGLSSGT
 LPGPGNEASR ELESYC (SEQ ID NO: 3141)

[0135] and is encoded by the DNA sequence (NCBI Reference Sequence: NM_000164):

[0136] ggcagcgggtg gcaggggctg caggagcaag tgaccaggag caggactggg
 15 gacaggcctg atcgcccctg cacgaaccag acccttcgcc gccctcacga
 tgactacctc tccgacccctg cagctgctgc tgcggctctc actgtgcggg
 ctgctgctcc agagggcgga gacaggctct aaggggcaga cggcggggga
 gctgtaccag cgctgggaac ggtaccgcag ggagtgccag gagaccttgg
 cagccgcgga accgccttca ggcctcgcct gtaacgggtc cttcgatatg
 20 tacgtctgct gggactatgc tgcacccaat gccactgccc gtgcgtcctg
 cccctggtac ctgccctggc accaccatgt ggctgcaggt ttcgtcctcc
 gccagtgtgg cagtgatggc caatggggac tttggagaga ccatacacia
 tgtgagaacc cagagaagaa tgaggccttt ctggaccaa ggctcatctt
 ggagcgggtg cagggtcatgt aactgtcgg ctactccctg tctctcgcca
 25 cactgctgct agccctgctc atcttgagtt tgttcaggcg gctacattgc
 actagaaact atatccacat caacctgttc acgtctttca tgctgcgagc
 tgcgggccatt ctgagccgag accgtctgct acctcgacct ggcccctacc
 ttggggacca ggcccttgcg ctgtggaacc aggcctcgc tgccctgccgc
 acggcccaga tcgtgacca gtactgcgtg ggtgccaact acacgtggct
 30 gctggtggag ggcgtctacc tgcacagtct cctggtgctc gtgggaggct
 ccgaggaggg ccacttccgc tactacctgc tcctcggctg gggggccccc
 gcgcttttctg tcattccctg ggtgatcgtc aggtacctgt acgagaacac
 gcagtgtggt gagcgcaacg aagtcaaggc catttggtgg attatacggg
 ccccatcct catgaccatc ttgattaatt tcctcatttt tatccgcatt
 35 cttggcattc tcctgtccaa gctgaggaca cggcaaattgc gctgccggga
 ttaccggctg aggcgtggctc gctccacgct gacgctgggtg cccctgctgg
 gtgtccacga ggtggtgttt gctcccgtga cagaggaaca ggcccggggc
 gccctgcgct tcgccaagct cggctttgag atcttcctca gtccttcca

gggcttcctg gtcagcgtcc tctactgctt catcaacaag gaggtgcagt
 cggagatccg ccgtggctgg caccactgcc gcctgcgccg cagcctgggc
 gaggagcaac gccagctccc ggagcgcgcc ttccggggccc tgccctccgg
 ctccggccccg ggcgaggtcc ccaccagccg cggcttgctc tcggggaccc
 5 tcccagggcc tgggaatgag gccagccggg agttggaaag ttactgctag
 ggggcgggat ccccggtgtc gttcagttag catggattta ttgagtgcca
 actgcgtgcc aggcccagta cggaggacgc tggggaaatg gtgaaggaaa
 cagaaaaaag gtccctgccc ttctggagat gacaactgag tggggaaaac
 agaccgtgaa cacaaaacat caagttccac acacgctatg gaatggttat
 10 gaagggaagc gagaaggggg cctaggggtg tctgggaggc gtctccaagg
 aggtgacact taagccatcc ccgaaagagg tgaaagagat cactttgggg
 agagctggag aacaggattc taggcggaag cgatagcata ggcaaaggcc
 cttgggcagg aaggcgtca gccttggtg gagtagaatt aagtcagagc
 caacaggtgg ggagagacag agaagtgggc aggggcaccc aagttgggat
 15 ttcatttcag gtgcattgga gattcttagg agtgtctctt gggggtaata
 ttttattttt taaaaaatga ggat (SEQ ID NO: 3142).

[0137] A 430 amino acid isoform of human GIPR (isoform X1), predicted by automated computational analysis, has the sequence (NCBI Reference Sequence XP_005258790):

[0138] MTTSPILQLL LRLSLCGLLL QRAETGSKGQ TAGELYQRWE RYRRECQETL
 20 AAAEPPSVAA GFVLRQCGSD GQWGLWRDHT QCENPEKNEA FLDQRLILER
 LQVMYTVGYS LSLATLLLAL LILSLFRR LH CTRNYIHINL FTSFMLRAAA
 ILSRDRLLP RGPYLGQAL ALWNQALAAC RTAQIVTQYC VGANYTWLLV
 EGVYLHSLLV LVGGSEEGHF RYLLLGWGA PALFVIPWVI VRYLYENTQC
 WERNEVKAIW WIIRTPILMT ILINFLIFIR ILGILLSKLR TRQMRCDYR
 25 LRLARSTLTL VPLLGVHEVV FAPVTEEQAR GALRFAKLGF EIFLSSFQGF
 LVSVLYCFIN KEVQSEIRRG WHHCRLRRSL GEEQRQLPER AFRALPSGSG
 PGEVPTSRGL SSGTLPGPGN EASRELESYC (SEQ ID NO: 3143)

[0139] and is encoded by the DNA sequence:

[0140] atgaccacca gcccgattct gcagctgctg ctgcgcctga gcctgtgcgg
 30 cctgctgctg cagcgcgcgg aaaccggcag caaaggccag accgcggggc
 aactgtatca gcgctgggaa cgctatcgcc gcgaatgcca ggaaaccctg
 gcggcggcg ggcagtgagg gcctgtggcg ggctttgtgc tcgcccagtg
 cggcagcgat ggccagtggg gcctgtggcg cgatcatacc cagtgcgaaa
 acccgaaaaa aaacgaagcg tttctggatc agcgcctgat tctggaacgc
 35 ctgcaggtga tgtataccgt gggctatagc ctgagcctgg cgaccctgct
 gctggcgctg ctgattctga gcctgtttcg ccgcctgcat tgcaccgcga
 actatattca tattaacctg tttaccagct ttatgctgcg cgcgggcgcg
 attctgagcc gcgacgcct gctgccgcgc ccggggcccg atctgggcga

tcaggcgctg gcgctgtgga accaggcgct ggcggcgctgc cgcaccgcgc
 agattgtgac ccagtattgc gtgggcgcga actatacctg gctgctggtg
 gaaggcgtgt atctgcatag cctgctggtg ctgggtgggcg gcagcgaaga
 aggccatttt cgctattatc tgctgctggg ctggggcgcg ccggcgctgt
 5 ttgtgattcc gtgggtgatt gtgcgctatc tgtatgaaaa caccagtgct
 tgggaacgca acgaagtga agcgatttgg tggattattc gcaccccgat
 tctgatgacc attctgatta actttctgat ttttattcgc attctgggca
 ttctgctgag caaactgcgc acccgccaga tgcgctgccg cgattatcgc
 ctgcgcctgg cgcgcagcac cctgaccctg gtgccgctgc tgggcgtgca
 10 tgaagtgggtg tttgcgccgg tgaccgaaga acaggcgcg gcgcgcgtgc
 gctttgcgaa actgggcttt gaaatttttc tgagcagctt tcagggcttt
 ctgggtgagcg tgctgtattg ctttattaac aaagaagtgc agagcgaaat
 tcgccgcggc tggcatcatt gccgcctgcg ccgcagcctg ggcaagaac
 agcggcagct gccggaacgc gcgtttcgcg cgctgccgag cggcagcggc
 15 ccgggcgaag tgccgaccag ccgcggcctg agcagcggca ccctgccggg
 cccgggcaac gaagcgagcc gcgaactgga aagctattgc (SEQ ID NO: 3144).

[0141] 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):

20 **[0142]** MTTSPILQLL LRLSLCGLLL QRAETGSKGQ TAGELYQRWE RYRRECQETL
 AAAEPPSGLA CNGSFDMYVC WDYAAPNATA RASCPWYLPW HHHVAAGFVL
 RQCGSDGQWG LWRDHTQCEN PEKNEAFLDQ RLILERLQVM YTVGYSLSLA
 TLLLALLILS LFRRLHCTR N YIHINLFTSF MLRAAAILSR DRLLPRPGPY
 LGDQALALWN QALAACRTAQ IVTQYCVGAN YTWLLVEGVY LHSLLVLVGG
 25 SEEGHFRYYL LLGWGAPALF VIPWVIVRYL YENTQCWERN EVKAIWWIIR
 TPILMTILIN FLIFIRILGI LLSKLRTRQM RCRDYRLRLA RSTLTLVPLL
 GVHEVVFAPV TEEQARGALR FAKLGFEIFL SSFQGFLVSV LYCFINKEVG
 RDPAAAPALW RRRGTAPPLS AIVSQVQSEI RRGWHHCRLR RSLGEEQRQL
 PERAFRALPS GSGPGEVPTS RGLSSGTLPG PGNEASRELE SYC (SEQ ID NO: 3145)

30 **[0143]** and is encoded by the DNA sequence:

[0144] atgaccacca gcccgattct gcagctgctg ctgcgcctga gcctgtgcgg
 cctgctgctg cagcgcgcgg aaaccggcag caaaggccag accgcggggc
 aactgtatca gcgctgggaa cgctatcgcc gcgaatgcca ggaaaccctg
 gcggcggcg aaccgccgag cggcctggcg tgcaacggca gctttgatat
 35 gtatgtgtgc tgggattatg cggcgccgaa cgcgaccgcg cgcgcgagct
 gcccggtgta tctgccgtgg catcatcatg tggcggcggg ctttgtgctg
 cgccagtgcg gcagcgatgg ccagtggggc ctgtggcgcg atcatacca
 gtgcgaaaac ccggaaaaaa acgaagcggt tctggatcag cgctgattc

tggaacgcct gcaggtgatg tataccgtgg gctatagcct gagcctggcg
 accctgctgc tggcgctgct gattctgagc ctgtttcgcc gcctgcattg
 caccgcgaac tataattcata ttaacctgtt taccagcttt atgctgcgcg
 cggcgcgat tctgagccgc gatcgccctgc tggcgcgccc gggcccgtat
 5 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
 10 cccagtgctg ggaacgcaac gaagtgaag cgatttggtg gattattcgc
 accccgattc tgatgaccat tctgattaac tttctgattt ttattcgcat
 tctgggcatt ctgctgagca aactgcgcac ccgccagatg cgctgccgcg
 attatcgct gcgcctggcg cgcagcacc tgacctggt gccgctgctg
 ggcgtgcatg aagtgggtgtt tgcgccggtg accgaagaac aggcgcgcgg
 15 cgcgctgcgc tttgcgaaac tgggctttga aatttttctg agcagctttc
 agggctttct ggtgagcgtg ctgtattgct ttattaacaa agaagtgggc
 cgcgatccgg cggcggcgcc ggcgctgtgg cgccgccgcg gcaccgcgcc
 gccgctgagc gcgattgtga gccagggtgca gagcgaaatt cgccgcggct
 ggcattcattg ccgcctgcgc cgcagcctgg gcgaagaaca gcgccagctg
 20 ccggaacgcg cgtttcgcgc gctgccgagc ggcagcggcc cgggcgaagt
 gccgaccagc cgcggcctga gcagcggcac cctgccgggc ccgggcaacg
 aagcgagccg cgaactggaa agctattgct aa (SEQ ID NO: 3146)

[0145] 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,
 25 100:4903-4908.

[0146] MPLRLLLLLL WLWGLQWAET DSEGQTTTGE LYQRWEHYGQ ECQKMLETTE
 PPSGLACNGS FDMYACWNYT AANTTARVSC PWYLPWFRQV SAGFVFRQCG
 SDGQWGSWRD HTQCENPEKN GAFQDQTLIL ERLQIMYTVG YSLSLTLLLL
 ALLILSLFRR LHCTRNYIHM NLFTSFMLRA AAILTRDQLL PPLGPYTGDO
 30 APTPWNQALA ACRTAQIMTQ YCVGANYTWL LVEGVYLHHL LVIVGRSEKG
 HFRCYLLLGW GAPALFVIPW VIVRYLRENT QCWERNEVKA IWWIIRTPIL
 ITILINFLIF IRILGILVSK LRTRQMRCPD YRLRLARSTL TLVPLLGVHE
 VVFAPVTEEQ VEGSLRFAKL AFEIFLSSFQ GFLVSVLYCFINKEVQSEIRQ
 GWRHRLRLS LQEQRP RP HQ ELAPRAVPLS SACREAAVGN ALPSGMLHVP
 35 GDEVLESYC (SEQ ID NO: 3147)

[0147] and is encoded by the DNA sequence (NCBI Reference Sequence: NM_001080815):

[0148] atgccgctgc gcctgctgct gctgctgctg tggctgtggg gcctgcagtg
 ggcggaaacc gatagcgaag gccagaccac caccggcgaa ctgtatcagc

gctgggaaca ttatggccag gaatgccaga aaatgctgga aaccaccgaa
 ccgccgagcg gcctggcgtg caacggcagc tttgatatgt atgcgtgctg
 gaactatacc gcggcgaaca ccaccgcgcg cgtgagctgc ccgtggtatc
 tgccgtggtt tcgccaggtg agcgcgggct ttgtgtttcg ccagtgcggc
 5 agcgatggcc agtggggcag ctggcgcgat catacccagt gcgaaaaccc
 ggaaaaaac ggcgcgtttc aggatcagac cctgattctg gaacgcctgc
 agattatgta taccgtgggc tatagcctga gcctgaccac cctgctgctg
 gcgctgctga ttctgagcct gtttcgccgc ctgcattgca cccgcaacta
 tattcatatg aacctgttta ccagctttat gctgcgcgcg gcggcgattc
 10 tgaccgcga tcagctgctg ccgccgctgg gcccgatatac cggcgatcag
 gcgccgaccc cgtggaacca ggcgctggcg gcgtgccgca ccgcgcagat
 tatgaccagc tattgctggtg gcgcgaacta tacctggctg ctggtggaag
 gcgtgtatct gcatcatctg ctggtgattg tgggccgcag cgaaaaaggc
 cattttcgct gctatctgct gctgggctgg ggcgcgccgg cgctgtttgt
 15 gattccgtgg gtgattgtgc gctatctgcg cgaaaacacc cagtgcctgg
 aacgcaacga agtgaaagcg atttggtgga ttattcgcac cccgattctg
 attaccattc tgattaactt tctgattttt attcgcattc tgggcattct
 ggtgagcaaa ctgcgcaccc gccagatgcg ctgcccggat tatcgccctgc
 gcctggcgcg cagcaccctg accctgggtg cgctgctggg cgtgcatgaa
 20 gtggtgtttg cgccggtgac cgaagaacag gtggaaggca gcctgcgctt
 tgcgaaactg gcgtttgaaa tttttctgag cagctttcag ggctttctgg
 tgagcgtgct gtattgcttt attaacaag aagtgcagag cgaaattcgc
 cagggctggc gccatcgccg cctgcgcctg agcctgcagg aacagcgccc
 gcgccgcat caggaactgg cgccgcgcgc ggtgccgctg agcagcgctg
 25 gccgcgaagc ggcggtgggc aacgcgctgc cgagcggcat gctgcatgtg
 ccgggcgatg aagtgcctgga aagctattgc taa (SEQ ID NO: 3148)

[0149] A 230 amino acid isoform of murine GIPR, produced by alternative splicing, has the sequence (Gerhard et al., Genome Res, 14:2121-2127 (2004); NCBI Reference Sequence: AAI20674):

30 **[0150]** MPLRLLLLLL WLWGLQWAET DSEGQTTTGE LYQRWEHYGQ ECQKMLETTE
 PPSGLACNGS FDMYACWNYT AANTTARVSC PWYLPWFRQV SAGFVFRQCG
 SDGQWGSWRD HTQCENPEKN GAFQDQTLIL ERLQIMYTVG YSLSLTTLIL
 ALLILSLFRR LHCTRNYIHM NLFTSFMLRA AAILTRDQLL PPLGPYTGDD
 APTPNQVLH RLLPGGTKTF PIYFRTPPH (SEQ ID NO: 3149)

35 **[0151]** and is encoded by the DNA sequence:

[0152] atgccgctgc gcctgctgct gctgctgctg tggctgtggg gcctgcagtg
 ggcggaacc gatagcgaag gccagaccac caccggcgaa ctgtatcagc
 gctgggaaca ttatggccag gaatgccaga aaatgctgga aaccaccgaa

ccgccgagcg gcctggcgtg caacggcagc tttgatatgt atgcgtgctg
 gaactatacc gcggcgaaca ccaccgcgcg cgtgagctgc ccgtggtatc
 tgccgtggtt tcgccaggtg agcgcgggct ttgtgtttcg ccagtgcggc
 agcgaatggcc 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
 tgaccgcgca tcagctgctg ccgccgctgg gcccgataac cggcgatcag
 10 gcgccgaccc cgtggaacca ggtgctgcat cgctgctgc cgggcggcac
 caaaccttt ccgatttatt ttgcacctt tccgcatcat taa (SEQ ID NO: 3150).

[0153] 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 90% 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.

[0154] 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.

[0155] Naturally occurring residues can be divided into classes based on common side chain properties:

- [0156]** (1) hydrophobic: norleucine, Met, Ala, Val, Leu, Ile;
- [0157]** (2) neutral hydrophilic: Cys, Ser, Thr;
- [0158]** (3) acidic: Asp, Glu;
- [0159]** (4) basic: Asn, Gln, His, Lys, Arg;
- 35 **[0160]** (5) residues that influence chain orientation: Gly, Pro; and

[0161] (6) aromatic: Trp, Tyr, Phe.

[0162] Additional groups of amino acids can also be formulated using the principles described in, e.g., Creighton (1984) *PROTEINS: STRUCTURE AND MOLECULAR PROPERTIES* (2d Ed. 1993), W.H. Freeman and Company. In some instances it can be
5 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).

[0163] Conservative substitutions can involve the exchange of a member of one of these classes for another member of the same class. Non-conservative substitutions can involve the
10 exchange of a member of one of these classes for a member from another class.

[0164] Synthetic, rare, or modified amino acid residues having known similar physiochemical properties to those of an above-described grouping can be used as a “conservative” substitute for a particular amino acid residue in a sequence. For example, a D-Arg residue may serve as a substitute for a typical L-Arg residue. It also can be the case that a
15 particular substitution can be described in terms of two or more of the above described classes (e.g., a substitution with a small and hydrophobic residue means substituting one amino acid with a residue(s) that is found in both of the above-described classes or other synthetic, rare, or modified residues that are known in the art to have similar physiochemical properties to such residues meeting both definitions).

[0165] 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.

[0166] In order to express the GIPR nucleic acid sequences provided herein, the appropriate coding sequences, e.g., SEQ ID NOs: 3141, 3143 or 3145, can be cloned into a suitable
25 vector and after introduction in a suitable host, the sequence can be expressed to produce the encoded polypeptide according to standard cloning and expression techniques, which are known in the art (e.g., as described in Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual* 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989). The invention also relates to such vectors
30 comprising a nucleic acid sequence according to the invention.

[0167] A “vector” refers to a delivery vehicle that (a) promotes the expression of a polypeptide-encoding nucleic acid sequence; (b) promotes the production of the polypeptide therefrom; (c) promotes the transfection/transformation of target cells therewith; (d) promotes the replication of the nucleic acid sequence; (e) promotes stability of the nucleic acid; (f)

promotes detection of the nucleic acid and/or transformed/transfected cells; and/or (g) otherwise imparts advantageous biological and/or physiochemical function to the polypeptide-encoding nucleic acid. A vector can be any suitable vector, including chromosomal, non-chromosomal, and synthetic nucleic acid vectors (a nucleic acid sequence comprising a suitable set of expression control elements). Examples of such vectors include derivatives of SV40, bacterial plasmids, phage DNA, baculovirus, yeast plasmids, vectors derived from combinations of plasmids and phage DNA, and viral nucleic acid (RNA or DNA) vectors.

[0168] A recombinant expression vector can be designed for expression of a GIPR protein in prokaryotic (e.g., *E. coli*) or eukaryotic cells (e.g., insect cells, using baculovirus expression vectors, yeast cells, or mammalian cells). In one embodiment the host cell is a mammalian, non-human host cell. Representative host cells include those hosts typically used for cloning and expression, including *Escherichia coli* strains TOP10F', TOP10, DH10B, DH5a, HB101, W3110, BL21(DE3) and BL21 (DE3)pLysS, BLUESCRIPT (Stratagene), mammalian cell lines CHO, CHO-K1, HEK293, 293-EBNA pIN vectors (Van Heeke & Schuster, *J. Biol. Chem.* 264: 5503-5509 (1989); pET vectors (Novagen, Madison Wis.). Alternatively, the recombinant expression vector can be transcribed and translated in vitro, for example using T7 promoter regulatory sequences and T7 polymerase and an in vitro translation system. Preferably, the vector contains a promoter upstream of the cloning site containing the nucleic acid sequence encoding the polypeptide. Examples of promoters, which can be switched on and off, include the lac promoter, the T7 promoter, the trc promoter, the tac promoter and the trp promoter.

[0169] Thus, provided herein are vectors comprising a nucleic acid sequence encoding GIPR that facilitate the expression of recombinant GIPR. In various embodiments, the vectors comprise an operably linked nucleotide sequence which regulates the expression of GIPR. A vector can comprise or be associated with any suitable promoter, enhancer, and other expression-facilitating elements. Examples of such elements include strong expression promoters (e.g., a human CMV IE promoter/enhancer, an RSV promoter, SV40 promoter, SL3-3 promoter, MMTV promoter, or HIV LTR promoter, EF1alpha promoter, CAG promoter), effective poly (A) termination sequences, an origin of replication for plasmid product in *E. coli*, an antibiotic resistance gene as a selectable marker, and/or a convenient cloning site (e.g., a polylinker). Vectors also can comprise an inducible promoter as opposed to a constitutive promoter such as CMV IE. In one aspect, a nucleic acid comprising a sequence encoding a GIPR polypeptide which is operatively linked to a tissue specific

promoter which promotes expression of the sequence in a metabolically-relevant tissue, such as liver or pancreatic tissue is provided.

[0170] 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
5 nucleic acid is integrated into the host cell genome, which in other embodiments the vector or nucleic acid is extra-chromosomal.

[0171] Recombinant cells, such as yeast, bacterial (e.g., *E. coli*), and mammalian cells (e.g., immortalized mammalian cells) comprising such a nucleic acid, vector, or combinations of either or both thereof are provided. In various embodiments cells comprising a non-integrated
10 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.

[0172] A vector comprising a nucleic acid sequence encoding a GIPR polypeptide provided herein can be introduced into a host cell by transformation or by transfection. Methods of transforming a cell with an expression vector are well known.

[0173] A GIPR-encoding nucleic acid can be positioned in and/or delivered to a host cell or
15 host animal via a viral vector. Any suitable viral vector can be used in this capacity. A viral vector can comprise any number of viral polynucleotides, alone or in combination with one or more viral proteins, which facilitate delivery, replication, and/or expression of the nucleic acid of the invention in a desired host cell. The viral vector can be a polynucleotide
20 comprising all or part of a viral genome, a viral protein/nucleic acid conjugate, a virus-like particle (VLP), or an intact virus particle comprising viral nucleic acids and a GIPR polypeptide-encoding nucleic acid. A viral particle viral vector can comprise a wild-type viral particle or a modified viral particle. The viral vector can be a vector which requires the presence of another vector or wild-type virus for replication and/or expression (e.g., a viral
25 vector can be a helper-dependent virus), such as an adenoviral vector amplicon. Typically, such viral vectors consist of a wild-type viral particle, or a viral particle modified in its protein and/or nucleic acid content to increase transgene capacity or aid in transfection and/or expression of the nucleic acid (examples of such vectors include the herpes virus/AAV amplicons). Typically, a viral vector is similar to and/or derived from a virus that normally
30 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.

[0174] 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 is 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.

5 [0175] Protein purification methods that can be employed to isolate a GIPR polypeptide, as well as associated materials and reagents, are known in the art. Additional purification methods that may be useful for isolating a GIPR polypeptide can be found in references such as Bootcov MR, 1997, Proc. Natl. Acad. Sci. USA 94:11514-9, Fairlie WD, 2000, Gene 254: 67-76.

10 [0176] 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 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.

15 [0177] In one aspect the present invention is directed to a composition comprising an antibody or functional fragment thereof that specifically binds to human GIPR, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s); and a GLP-1 receptor agonist, wherein the GLP-1 receptor agonist is conjugated to the antibody or functional fragment
20 thereof through the side-chain of the cysteine residue or non-canonical amino acid residue substituted at the one or more conjugation site(s).

[0178] 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,
25 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.

[0179] The antigen binding proteins that are disclosed herein have a variety of utilities. The
30 antigen binding proteins, for instance, are useful in specific binding assays, affinity purification of GIPR, and in screening assays to identify other antagonists of GIPR activity. Other uses for the antigen binding proteins include, for example, diagnosis of GIPR-associated diseases or conditions and screening assays to determine the presence or absence of GIPR. Given that the antigen binding proteins that are provided are antagonists, the GIPR

antigen binding proteins have value in therapeutic methods in which it is useful to reduce weight gain, even while maintaining or increasing food intake, increasing % fat mass and increasing % lean mass, improving glucose tolerance, decreasing insulin levels, decreasing cholesterol and triglyceride levels. Accordingly, the antigen binding proteins have utility in the treatment and prevention of diabetes, e.g., type 2 diabetes, obesity, dyslipidemia, elevated glucose levels or elevated insulin levels.

[0180] 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.

[0181] 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.

[0182] 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.

[0183] 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.

[0184] 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:

- 5 **[0185]** (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.
- 10 **[0186]** (b) ability to decrease blood glucose;
- [0187]** (c) ability to increase glucose tolerance;
- [0188]** (d) ability to increase insulin sensitivity;
- [0189]** (e) ability to decrease body weight or reduce body weight gain;
- [0190]** (f) ability to decrease fat mass or decrease inflammation in fat tissue;
- 15 **[0191]** (g) ability to decrease fasting insulin levels;
- [0192]** (h) ability to decrease circulating cholesterol levels;
- [0193]** (i) ability to decrease circulating triglyceride levels;
- [0194]** (j) ability to decrease liver steatosis or reduce triglyceride level in liver;
- [0195]** (k) decrease AST, ALT, and/or ALP levels.
- 20 **[0196]** In one embodiment, a GIPR antigen binding protein has one or more of the following activities:
[0197] (a) binds human GIPR such that KD is ≤ 200 nM, is ≤ 150 nM, is ≤ 100 nM, is ≤ 50 nM, is ≤ 10 nM, is ≤ 5 nM, is ≤ 2 nM, or is ≤ 1 nM, e.g., as measured via a surface plasma resonance or kinetic exclusion assay technique.
- 25 **[0198]** (b) has a half-life in human serum of at least 3 days;
- [0199]** Some antigen binding proteins that are provided have an on-rate (k_a) for GIPR of at least $10^4/M \times \text{seconds}$, at least $10^5/M \times \text{seconds}$, or at least $10^6/M \times \text{seconds}$ as measured, for instance, as described below. Certain antigen binding proteins that are provided have a slow dissociation rate or off-rate. Some antigen binding proteins, for instance, have a k_d (off-rate)
- 30 of $1 \times 10^{-2} s^{-1}$, or $1 \times 10^{-3} s^{-1}$, or $1 \times 10^{-4} s^{-1}$, or $1 \times 10^{-5} s^{-1}$. In certain embodiments, the antigen binding protein has a KD (equilibrium binding affinity) of less than 25 pM, 50 pM, 100 pM, 500 pM, 1 nM, 5 nM, 10 nM, 25 nM or 50 nM.
- [0200]** 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.

[0201] 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 IgM1, 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.

[0202] 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.

[0203] 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.

[0204] 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.

[0205] 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.

[0206] 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
5 constant regions to form a complete antibody heavy and light chain, respectively.
Furthermore, each of the so generated heavy and light chain sequences may be combined to form a complete antibody structure.

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Table 1. Amino acid SEQ ID NOs.

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

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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

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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

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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

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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

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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

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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

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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

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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

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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

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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 TAAACTGGTACCAACACCTCCAGGAACGGCCC CCAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCTCCCTGCCATCAGTGGG CTCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATGACAGCCTGAATGGTCCGGTAT TCGGCGGAGGACCAAGCTGACCGTCTCTAGGT	CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCCGGATACACCTTACCGGGTACTAT ATGCATTGGTGGCAGACGGCCCTGGACAAGGG CTTGAGTGGATGGATGATCAACCTAACAGT GGTGGCACAACATATGCACAGAAGTTTCAGGGC AGGGTCAACCATGACCAAGGACACGTCCATCAGT ACAGCTACATGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGATTACTGTGCGAGAGGG GGGGATTACGTTTGGGGGACTTATCGGCCCTCAC TACTACTACGGTATGGAGCTCTGGGGCCCAAGGG ACCACGGTCACCGTCTCCTCA
			SEQ ID NO: 1571	SEQ ID NO: 1728
iPS:335914	4B1	NA	QSVLTQPPSASGTPGQRVITISCSGSSNIGSNTVNW YQHLPGTAPKLLIYTNQRPSPGVPDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDDSLNPGPVFGGGTK LTVLG	QMQVVQSGAEVKKPGASVKVSKASGYTFTGY MHWVRQAPQGQLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSLRSDDTAVYYCARG GDYVWGTYPHYYYGMDVWVGQGTITVTVSS
			SEQ ID NO: 1	SEQ ID NO: 158
iPS:335914	4B1	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGATCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAAGGAAAGCCCCA AGCGCTGATCTATGGTGCATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTACGCGGCACTGGAT CTGGGACAGAAATTCACCTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAGTGGATATCAAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTATATGGTATGATGGAA GTAATGAAAACATATGCAGACTCCGTGAAGGGCC GATTCAACCATCTCCAGAGACAATTCACAAGAATA CGCTGTATCTGCACATGAACAGCTGAGAGTCG CGGACACGGCTGTGATATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCTGGTCAACCGTCTCCTCA
			SEQ ID NO: 1572	SEQ ID NO: 1729

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		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLQSGVPSRFSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVWDGSNENYADSVKG RFTISRDN SKNTLYLHMNSLRVADTAVYYCARDG TIFGVLLGDYWGQGTLVTVSS
			SEQ ID NO: 2	SEQ ID NO: 159
		NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACAGGGAAGCCCCCTA AGCCCTGATCTATGGTGCAATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTCAAGCGCAGTGGAT CTGGGACAGAAATTCACCTCTCAAAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATATAATTAACCCCTTCACCTTCGGGCCCT GGGACCAAAAGTGGATATCAAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCACTTACAGTTACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGGAA GTAATAAATACTATGCAGACTCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCAGAGACA CGCTGTATCTGCAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTTACTGTGCGCGAGATG GGACGATTTTGGAGTGCTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
	!PS:335938	6H1	SEQ ID NO: 1573	SEQ ID NO: 1730
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLQSGVPSRFSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAIVWDGSNKYYADSVKG RFTISRDN SKNTLYLQMNLSRAEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSS
			SEQ ID NO: 3	SEQ ID NO: 160
		NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTAA ATTGGTATCAGCAGAAACAGGGAAGCCCCCTA AGCTCCTGATCTACGATGCATCCAATTTGGAA CAGGGGTCCCATCAAGGTTCAAGTGAAGTGGAT CTGGGACAGATTTAGTTTCAACCATCAGCAGCCT GCAGCCTGAAGATATTGCAACATATTACTGTCA ACAGTATGATATTCTCCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGA	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCACTTACAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGGA AGTAATAAATACTATGCAGACTCCGTGAAGGGC CGATTCAACCATCTCCAGCGACAATTCAGAGAAC ACGCTGTATCTGCAAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTTACTGTGCGAGAGAT AGGACGATTTTGGAGTGGTCTTGTGACTACTGG GGCCAGGGAACCTGGTCAACCGTCTCCTCA
	!PS:335941	2F11	SEQ ID NO: 1574	SEQ ID NO: 1731

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		AA	DIQMTQSPSSLSASVGDRTVTITCQASQDISNYLNW YQKPGKAPKLLIYDASNLETGVPSRFSGSGTD FSFTISSLQPEDIAIYYCQYDILLTFGGGKVEIKR	SEQ ID NO: 4	QVQLVESGGGVVQGRSLRLSCAASGFTFSYGM HWVRQAPGKGLEWVAIVYDGSNKYYADSVKG RFTISDINSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLDYWGQGTLVTVSS
		NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCCTCTGGCGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGTACCAAGCAG CAACCAGGACATCTCTTAAGTGTCTCATTTACT GGGCATCTACCCGGGAATCCGGGTCCCTGACC GATTCAGTGGCAGCGGTCTGGACAGATTTC CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAAAGGACCAAGGTGGA AATCAAAACGA	SEQ ID NO: 161	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCGACAGGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATCAACCTTGACAGT GGTGGCACAGACTATTACAGAGGTTTCAGGGC AGGTTCAACCATGACCAAGGACACGTCATCAGC ACAGCTACATGGAACCTGAGCAGGCTGAGATCT GACGACACGGCCGTGATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCGTCT CCTCA
	IP:335970	5C2	SEQ ID NO: 1575 DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQPGHPPKLLIYWASTRESGVPDFRSGS GSGTDFLTISSLQAEDVAVFYCQYYSTPWTFGQ GTKVEIKR	SEQ ID NO: 1732	QVPLVQSGAEVKKPGASVKVSKASGYTFTGYI HWVRQAPGQGLEWMGWINPDSSGTDYSQRFQGR FTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGTLVTVSS
	IP:335978	13H12	SEQ ID NO: 5 GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCCTCTGGCGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGTACCAAGCAG AAACCAAGGACATCTCTTAAGTGTCTCATTTACT GGGCATCTACCCGGGAATCCGGGTCCCTGACC GATTCAGTGGCAGCGGTCTGGACAGATTTC CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAAAGGACCAAGGTGGA AATCAAAACGA	SEQ ID NO: 162	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCGACAGGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATCAACCTTGACAGT GGTGGCACAGACTATTACAGAGGTTTCAGGGC AGGTTCAACCATGACCAAGGACACGTCATCAGC ACAGCTACATGGAACCTGAGCAGGCTGAGATCT GACGACACGGCCGTGATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCGTCT CCTCA
			SEQ ID NO: 1576	SEQ ID NO: 1733	

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		AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQKPGHPPKLLIYWASTRESGVPDFRSGS GSGTDFLLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR SEQ ID NO: 6	QVPLVQSGAEVKPGASVKVSKASGYTFTGYYI HWVRQAPGQGLEWMGWINPDSGGTDYSQRFQGR FTMTRDTSISTAYMELSRLSDDTAVYYCAREATI FGMLIVPFDYWGQGLVTVSS SEQ ID NO: 163
		NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAACAG AACCCAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAGTGGCAGCGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGCCAAGGGACCAAGGTGG AAATCAAAACGA SEQ ID NO: 1577	CAGGTGCCCTGGTACAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATACACTGGGTGCGTCAGGCCCTGGACAAAGG CTTGTGTGGATGGGTGGATCAGCCCTAACAGT GGTGACACAAAGCTATGCACAGAAATTTCAGGAC AGGTCACCATGACCAAGGACACGTCCATCAGC ACAGCTATATGGAGCTGAGCAGACTGAGATCT GACGACACGGCCGTGATTTCTGTACGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA SEQ ID NO: 1734
		AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRDSGVPDFRSG SGSGTDFLLTINSLQAEDVAVYYCQQYYRTPTWTF GQGTKVEIKR SEQ ID NO: 7	QVPLVQSGAEVKPGASVKVSKASGYTFTGYYI HWVRQAPGQGLVWMGWISPNSGDTSYAQKFQDR VTMTRDTSISTAYMELSRLSDDTAVYYFCTREATI FGMLIVPFDYWGQGLVTVSS SEQ ID NO: 164
		NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAGCAG AACCCAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAGTGGCAGCGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGCCAAGGGACCAAGGTGG AAATCAAAACGA SEQ ID NO: 1578	CAGGTGCCCTGGTGCAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATACACTGGGTGCGTCAGGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATAAGCCCTAACAAAT GGTGACACAAACTATGCACAGAAATTTCAGGAC AGGTCACCATGACCAAGGACACGTCCATCAGC ACAGCTATATGGAGCTGAGCAGGCTGAGATCT GACGACACGGCCGTGATTTACTGTACGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA SEQ ID NO: 1735

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		AA	DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRD SGVPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR SEQ ID NO: 8	QVPLVQSGAEVKKPGASVKVSKASGYTFTGYI HWVRQAPGQGLEWMGWISPNNGD TNYAQKFQD RVTMTDRDTSISTAYMELSRLRSDDTAVYYCTREA TIFGMILVPEFYWGQGTLVTVSS SEQ ID NO: 165
	18E3	NA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCAGACAGGTTCAAGTGGCAGTG GGTCTGGACAGACTTCACTCTCACCATCAGCA GACAGGAGCCTGATGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGTTCAACCGCTCACTTTCGG CGGAGGGACCAAGGTGGAGATCAAAACGA SEQ ID NO: 1579	CAGGTGCAGTTGCAGGAGTCCGGGCCCCAGGACTG GTGAAGCCTTCAAGACCCCTGTCCCTCACCTGC ACTGTCTCTGGTGA CTCCATCAGCAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCACCCAGGGA AGGCCCTGGAGTGGATTGGGTACATCTATTACA GTGGGAGCACCTACTACAACCCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGTCTAAGA ACCAAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGGACACGGCCGTGTATTACTGTGCGAGAGA TCGTATTACGATTTTGGAGTGGTTATGGGGGGC GGTATGGACGTCTGGGGCCAAGGGACACCGGTC ACCGTCTCCTCA SEQ ID NO: 1736
		AA	EIVLTQSPGTLSPGERATLSCRASQISYSYLAW YQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDF TLTISRQEPDDFAVYYCQQYGSSPLTFGGGTKVEI KR SEQ ID NO: 9	QVQLQESGPGLVKPSQTLSTCTVSGDSISSGGYY WSWIRQHPGKGLEWIGYIYSGSTYYNPSLKSRT ISVDTSKNQFSLKLSSVTAAADTAVYYCARDRIITFG VVMGGMDVWGQGTITVTVSS SEQ ID NO: 166
	2G10 LC1	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTG TCTGTGTCCTCCAGGGGAAAGAGCCACCCCTCTCC TGCAGGGCCAGTCAGAGTGTAGCAGCAACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACAGGGCC ACTGGTATCCAGCCAGGTCAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGCAGTCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTGGCCTCTCACTTTCGGCG GAGGGACCAAGGTGGAGATCAAAACGA SEQ ID NO: 1580	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACTTCCAGTA ACTATGCG ATGCACTGGGTCCGCCAGGCTCCAGGCGAGGGG CTGGAGTGGGTGGCAGCTATATGTTTGTATGGA AGTGATAAATACTATGCAGACTCCGTGAAGGGC CGATTCACTATCTCCAGAGACAACTCCAAGAAC ACGCTGTATCTGCAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCCCTGGTCAACCGTCTCCTCA SEQ ID NO: 1737

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	AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQKPGQAPRLLIYGAAATRAATGIPARVSGSGSGTE FTLTISLQSEDFAVYYCQQYNWPLTFGGGKVE IKR	SEQ ID NO: 10	QVQLVESGGGVVQPRSLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAIWFDGSDKYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVDPDYWGQGLVTVSS
!PS:336077	4H9.004	NA	GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACAGGGAAGCCCTA AACGCTGATCTATGGTGCATCCAGTTTGCAA GTGGGTCCCATCAAGGTTACGCGGCGAGTGAT CTGGGACAGAGTTCATCTCACAATCAGCAGCC TGCAGCCTGAAGATTTTGTAACTTAACTGTCT ACAGCATAATAGTTACCATTCACCTTCGGCCCT GGGACCAAAGTGGATGTCAAACGA	SEQ ID NO: 167
	AA	DIQMTQSPSSLSASVGDRTVTITCRASQGIRNELGW YQKPGKAPKRLIYGASLSQGVPSRFSGSGSGTE FTLTISLQPEDFVITYYCLQHNSYPFTFGPGTKVDV KR	SEQ ID NO: 1581	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCACTTCACTTCACTTGGCA TGCACTGGTCCCGCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGGAA GTAATAATACTATGCAGACTCCGTGAAGGGCC GCTTCAACCATCTCCAGAGACAATTCAGAAGACA CGCTGATCTGCAATGAACAGCTGAGAGCCG AGGACACGGCTGTATTAATCTGTGCGCGAGATG GGACGATTTTGGAGTGTCTTGGGGGACTACT GGGGCAGGGAACCTGGTCAACCTCTCCTCA
!PS:336088	6A5.004	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGACAGAGTCACCATCACTT GCCAGCGAGTCAGGACATTACCAACTATTAA ATTGGTATCAGCAGAAACAGGGAAGCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGTCCCATCAAGGTTCAAGTGAAGTGATC TGGGACAGATTTTACTTCAACATCAGCAGCCTG CAGCCTGAAGATATTGCAACATATTACTGTCAA CAGTATGATGATCTATTCACTTTCGGCCCTGGGA CCAAAGTGGATATCAAACGA	SEQ ID NO: 168
	AA	DIQMTQSPSSLSASVGDRTVTITCQASQDITNLYNW YQKPGKAPKRLIYDASNLEPGVPSRFSGSGSGTD	SEQ ID NO: 1582	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCTCTTCACTTCACTTGGCA TGCACTGGTCCCGCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGCTATATGGTATGATGGAA ATAATAATACTATGCAGACTCCGTGAAGGGCC GATTCAACCATCTCCAGAGACAGTTCCAGAAGACA CGCTGATCTGCAATGAACAGCTGAGAGCCG AGGACACGGCTGTATTAATCTGTGCGGAGAGATC GGACGATTTTGGAGTGTCTTGGGGGACTACT GCCAGGGAACCTGGTCAACCTCTCCTCA

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			FTFTISSLPEDIATYYCQYDDLFTFGPGTKVDIK R	RTFISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYLGQGTLVTVSS
			SEQ ID NO: 12	SEQ ID NO: 169
		NA	GACATCCAGATGACCCAGTCTCCATCTTCCGTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GTCGGCGAGTCAGGGTCTTATCATCTGGTTAG CCTGGTATCAGCAGAAACCGGGAAAGCCCCCTA AACTCCTGATCTATGCTGCATCCAGTTTGCAAAAG TGGGTCCCATCAAGGTTCAAGCGGCAAGTGGCTC TGGGACAGATTTCACCTCACCATCAGCAGCCT ACAGCCTGAAGATTTTGCAACTTACTATTGTCAA CAGACTAACAGTTTCCCTCCGACGTTCCGGCCAA GGGACCAAGGTGGAATCAAAACGA	CAGGTGCAGCTGCAGGAGTCGGGGCCCAAGGACTG GTGAAGCCTTCGGAGACCCCTGTCCCTCACCTGC ACTGTCTCTCAGGGCTCCATCAGTAGTTACTACT GGAGCTGGATCCGGCAGCCCGCCGGGAAGGGA CTAGAGTGGATTGGCCGTATCTATACCAAGTGGG AGCACCACCTAACACCCCTCCCTCAAGAGTCGA GTCACCATGTCAATAGACACGTCCAAAGAACCCAG TTCTCCCTGAAACTGAACCTCTGTGACCGCCCGG GACACGGCCGTGTATTACTGTGCGAGAGATGTA GCAGTGGCTGGCTTTGACTACTGGGGCCAGGGA ACCTGTGCACCGTCTCTCTCA
		AA	SEQ ID NO: 1583	SEQ ID NO: 1740
		AA	DIQMTQSPSSVSASVGDRTVTITCRASQGLIWLAW YQKPGKAPKLLIYAASSLQSGVPSRFSGSGTD FTLTISLQPEDFATYYCQQQTNSFPPTFGQGTKVEI KR	QVQLQESGPGLVKPSETLSLTCTVSQSSISSYYWS WIRQPAKGLEWIGRIYTSNSTYNPSLKSRVTMS IDTSKNQFSLKLNSTVAADTAVYYCARDVAVAGF DYWGQGTLVTVSS
		NA	SEQ ID NO: 13	SEQ ID NO: 170
		NA	GACATCCAGATGACCCAGTCTCCATCTTCCGTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GTCGGCGAGTCAGGGTCTTATCATCTGGTTAG CCTGGTATCAGCAGAAACCGGGAAAGCCCCCTA AACTCCTGATCTATGCTGCATCCAGTTTGCAAAAG TGGGTCCCATCAAGGTTCAAGCGGCAAGTGGCTC TGGGACAGATTTCACCTCACCATCAGCAGCCT ACAGCCTGAAGATTTTGCAACTTACTATTGTCAA CAGACTAACAGTTTCCCTCCGACGTTCCGGCCAA GGGACCAAGGTGGAATCAAAACGA	CAGGTGCAGCTGCAGGAGTCGGGGCCCAAGGACTG GTGAAGCCTTCGGAGACCCCTGTCCCTCACCTGC ACTGTCTCTGCGGGCTCCATCAGTAGTTACTACT GGAGCTGGATCCGGCAGCCCGCCGGGAAGGGA CTAGAGTGGATTGGCCGTATCTATACCAAGTGGG AGCACCACCTAACACCCCTCCCTCAAGAGTCGA GTCACCATGTCAATAGACACGTCCAAAGAACCCAG TTCTCCCTGAAACTGAACCTCTGTGACCGCCCGG GACACGGCCGTGTATTACTGTGCGAGAGATGTA GCAGTGGCTGGCTTTGACTACTGGGGCCAGGGA ACCTGTGCACCGTCTCTCTCA
		AA	SEQ ID NO: 1584	SEQ ID NO: 1741
		AA	DIQMTQSPSSVSASVGDRTVTITCRASQGLIWLAW YQKPGKAPKLLIYAASSLQSGVPSRFSGSGTD	QVQLQESGPGLVKPSETLSLTCTVSQSSISSYYWS WIRQPAKGLEWIGRIYTSNSTYNPSLKSRVTMS

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			FTLTISSLQPEDFATYYCQQTNSFPPTFGQGTKEI KR	IDTSKNQFSLKLSVTAADTA VYYCARDVA VAGF DYWGQGT LVT VSS
			SEQ ID NO: 14	SEQ ID NO: 171
		4H9.004.001	GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCA CCACTT GCCGGCAAGTCAGGCATTAGAAATGAGTTAG GCTGGTATCAGCAAAACAGGAAAGCCCTA AACTCCTGATCTATGTGTCATCCAGTTTGCAA GTGGGTCCCATCAAGGTTACGGCGAGTGGAT CTGGGACAGAGTTCACCTCTCAAAATCAGAGCC TGCAGCCTGAAGATTTGTAACTTATTACTGTCT ACAGCATAAATAGTTACCAATTCACCTTCGGCCA AGGGACCAAAAGTGGATGTCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGATTCACTTACAGTTACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTC AAGAACA CGCTGTATCTGCA AATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTGGAGTGCTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCA CCGTCTCCTCA
			SEQ ID NO: 1585	SEQ ID NO: 1742
		AA	DIQMTQSPSSLSASVGDRTVITCRASQGIRNELGW YQKPGKAPKLLIYGASSLQSGVPSRFSGSGTE FTLTISSLQPEDFVYYCLQHNSYPFTFGQGTKEVD VKR	QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVA VIWYDASNKY YADAVKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGT LVT VSS
			SEQ ID NO: 15	SEQ ID NO: 172
		4H9.004.002	GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCA CCACTT GCCGGCAAGTCAGGCATTAGAAATGAGTTAG GCTGGTATCAGCAAAACAGGAAAGCCCTA AACTCCTGATCTATGTGTCATCCAGTTTGCAA GTGGGTCCCATCAAGGTTACGGCGAGTGGAT CTGGGACAGAGTTCACCTCTCAAAATCAGAGCC TGCAGCCTGAAGATTTGTAACTTATTACTGTCT ACAGCATAAATAGTTACCAATTCACCTTCGGCCA AGGGACCAAAAGTGGATGTCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGATTCACTTACAGTTACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACTCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTC AAGAACA CGCTGTATCTGCA AATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTGGAGTGCTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCA CCGTCTCCTCA
			SEQ ID NO: 1586	SEQ ID NO: 1743
		AA	DIQMTQSPSSLSASVGDRTVITCRASQGIRNELGW YQKPGKAPKLLIYGASSLQSGVPSRFSGSGTE FTLTISSLQPEDFVYYCLQHNSYPFTFGQGTKEVD VKR	QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVA VIWYDASNKY YADSVKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGT LVT VSS

			SEQ ID NO: 16	SEQ ID NO: 173
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!PS:360936	4H9.004.003	NA	GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCAACCATCACTT GCCGGCAAGTCAGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACAGGGAAGCCCCCTA AACTCCTGATCTATGTCATCCAGTTTGCAA GTGGGTCCCATCAAGGTTACGCGCAGTGGAT CTGGGACAGAGTTCATCTCAATCAGCAGCC TGACGCTGAAGATTTGTAACTTATTACTGTCT ACAGCATAAAGTTACCCATTCACCTTCGGCCA AGGACCAAAAGTGGATGTCAAACGA SEQ ID NO: 1587	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGATTCACTTCCAGTTACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGGAA GTAATAAATACTATGCAGACGCCGTGAAGGCC GCTTACCATCTCCAGAGACAATTCAGAACA CGCTGATCTGCAATGAACAGCCTGAGAGCCG AGGACACGGCTGTATTACTGTGCGCGAGATG GGACGATTTTGGAGTGCTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA SEQ ID NO: 1744
		AA	DIQMTQSPSSLSASVGDRTVTITCRASQGIRNELGW YQKPGKAPKLLIYGASSLQSGVPSRFSGSGTE FTLTISLQPEDFVTYYCLQHNSYPFTFGQGTKVD VKR SEQ ID NO: 17	QVQLVESGGGVVQGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAIVYDGSNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGLVTVSS SEQ ID NO: 174
!PS:360943	4H9.004.004	NA	GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCAACCATCACTT GCCGGCAAGTCAGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACAGGGAAGCCCCCTA AACTCCTGATCTATGTCATCCAGTTTGCAA GTGGGTCCCATCAAGGTTACGCGCAGTGGAT CTGGGACAGAGTTCATCTCAATCAGCAGCC TGACGCTGAAGATTTGTAACTTATTACTGTCT ACAGCATAAAGTTACCCATTCACCTTCGGCCCT GGGACCAAAAGTGGATGTCAAACGA SEQ ID NO: 1588	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGATTCACTTCCAGTTACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGCC GCTTACCATCTCCAGAGACAATTCAGAACA CGCTGATCTGCAATGAACAGCCTGAGAGCCG AGGACACGGCTGTATTACTGTGCGCGAGATG GGACGATTTTGGAGTGCTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA SEQ ID NO: 1745
		AA	DIQMTQSPSSLSASVGDRTVTITCRASQGIRNELGW YQKPGKAPKLLIYGASSLQSGVPSRFSGSGTE FTLTISLQPEDFVTYYCLQHNSYPFTFGPGTKVDV KR SEQ ID NO: 1587	QVQLVESGGGVVQGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAIVYDASNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGLVTVSS SEQ ID NO: 1745

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!PS:360949	4H9.004.005	NA	SEQ ID NO: 18 GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACAGGAAAGCCCCCTA AACGCTGATCTATGGTGCATCCAGTTTGCAA GTGGGTCCCATCAAGGTTACGCGCAGTGGAT CTGGGACAGAGTTCATCTCACAATCAGCAGCC TGCAGCCTGAAGATTTGTAACTTATTACTGTCT ACAGCATAAATGTTACCCATTCACCTTCGGCCA AGGGACCAAAAGTGGATGTCAAACGA	SEQ ID NO: 175 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTCCAGTTACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGCC GCTTCACCATCTCCAGAGACAATTCAGAACA CGCTGATCTGCAATGAACAGCCTGAGAGCCG AGGACACGGCTGTATTACTGTGCGCGAGATG GGACGATTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCTGGTCAACCGTCTCCTCA
			SEQ ID NO: 1589 DIQMTQSPSSLSASVGDRTVTITCRASQGIRNELGW YQKPGKAPKRLIYGASSLQSGVPSRFSGSGSTE FTLTISLQPEDFVTYYCLQHNSYPFTFGQGTKVD VKR	SEQ ID NO: 1746 QVQLVESGGGVVQGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAIVWYDASNKYADAVKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGLVTVSS
!PS:359761	4H9.004.006	NA	SEQ ID NO: 19 GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACAGGAAAGCCCCCTA AACTCCTGATCTATGTGTCATCCAGTTTGCAA GTGGGTCCCATCAAGGTTACGCGCAGTGGAT CTGGGACAGAGTTCATCTCACAATCAGCAGCC TGCAGCCTGAAGATTTGTAACTTATTACTGTCT ACAGCATAAATGTTACCCATTCACCTTCGGCCA AGGGACCAAAAGTGGATGTCAAACGA	SEQ ID NO: 176 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTCCAGTTACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGCC GCTTCACCATCTCCAGAGACAATTCAGAACA CGCTGATCTGCAATGAACAGCCTGAGAGCCG AGGACACGGCTGTATTACTGTGCGCGAGATA GGACGATTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCTGGTCAACCGTCTCCTCA
			SEQ ID NO: 1590 DIQMTQSPSSLSASVGDRTVTITCRASQGIRNELGW YQKPGKAPKRLIYGASSLQSGVPSRFSGSGSTE FTLTISLQPEDFVTYYCLQHNSYPFTFGQGTKVD VKR	SEQ ID NO: 1747 QVQLVESGGGVVQGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAIVWYDASNKYADAVKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLLGDYWGQGLVTVSS

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!PS:360955	4B1.010	SEQ ID NO: 20	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTTAG GCTGTATCAGCAGAAACCAAGGAAAGCCCCA AGCTCCTGATCTATGGTGCATCCAGTTTGCAA GTGGGTCCCTTCAAAGTTCAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAAAACGA	SEQ ID NO: 1591	SEQ ID NO: 177	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGCAGACGCCGTGAAGGGCC GATTACCATCTCCAGAGACAATTCCAAGAATA CGCTGTATCTGCAAAATGAACAGCCTGAGAGTCG CGGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCTCTGGTCAACCGTCTCCTCA
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK R	SEQ ID NO: 1748	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDNSKNTLYLQMNSLRVADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSS	
!PS:360962	4B1.011	SEQ ID NO: 21	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTTAG GCTGTATCAGCAGAAACCAAGGAAAGCCCCA AGCGCTGATCTATGGTGCATCCAGTTTGCAA GTGGGTCCCTTCAAAGTTCAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAAAACGA	SEQ ID NO: 1592	SEQ ID NO: 178	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGCAGACGCCGTGAAGGGCC GATTACCATCTCCAGAGACAATTCCAAGAATA CGCTGTATCTGCAAAATGAACAGCCTGAGAGTCG CGGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCTCTGGTCAACCGTCTCCTCA
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK R	SEQ ID NO: 1749	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDNSKNTLYLQMNSLRVADTAVYYCARDG TIFGVVLGDYWGQGLVTVSS	

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		SEQ ID NO: 22	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTTAG GCTGTATCAGCAGAAACCAAGGAAAGCCCCA AGCTCCTGATCTATGGTGCATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTCAAGCGGCAGTGGAT CTGGACAGAAATTCACCTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAAACGA	SEQ ID NO: 1593	SEQ ID NO: 179	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGATTCACTTTCAGTAACCTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACTCCGTGAAGGGCC GATTACCATCTCCAGAGACAATTCACAAGAATA CGCTGTATCTGCAATGAACAGCCTGAGAGTCG CGGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA
IPS:360968	4B1.012	NA				
		SEQ ID NO: 23	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	SEQ ID NO: 180	SEQ ID NO: 1750	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKVG RFTISRDN SKNTLYLQMNSLRVADTAVYYCARDG TIFGVVLGDYWGQGLTVTVSS
		SEQ ID NO: 23	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTTAG GCTGTATCAGCAGAAACCAAGGAAAGCCCCA AGCTCCTGATCTATGGTGCATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTCAAGCGGCAGTGGAT CTGGACAGAAATTCACCTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAAAACGA	SEQ ID NO: 180	SEQ ID NO: 1751	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGATTCACTTTCAGTAACCTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACTCCGTGAAGGGCC GATTACCATCTCCAGAGACAATTCACAAGAATA CGCTGTATCTGCACATGAACAGCCTGAGAGTCG CGGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA
IPS:360974	4B1.013	NA				
		SEQ ID NO: 1594	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSTEFT LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK R	SEQ ID NO: 180	SEQ ID NO: 1751	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADSVKVG RFTISRDN SKNTLYLHMNSLRVADTAVYYCARDG TIFGVVLGDYWGQGLTVTVSS
		AA				

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!PS:360978	4B1.014	SEQ ID NO: 24	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACAGGGAAGCCCCCTA AGCTCTGATCTATGTCATCCAGTTTGCAA GTGGGTCCCTTCAAAGTTACGCGGCACTGGAT CTGGGACAGAAATTCATCTCAATCAGCAGCC TGCAGCCTGAAGATTTCGCACTTACTGTCT ACAGCATATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAAAACGA	SEQ ID NO: 181	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCACTTTCAGTAACCTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGGAA GTAATGAAAACATATGACAGCCCGTGAAGGCC GATTACCATCTCCAGAGACAATTCACAAGAATA CGCTGTATCTGCACATGAACAGCCTGAGAGTCG CGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCTGGTCAACCGTCTCCTCA
		SEQ ID NO: 1595	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK R	SEQ ID NO: 1752	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVWYDGSNENYADAVKG RFTISRDN SKNTLYLHMNSLRVADTAVYYCARDG TIFGVVLGDYWGQGLVTVSS
!PS:359785	4B1.015	SEQ ID NO: 25	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACAGGGAAGCCCCCTA AGCTCTGATCTATGTCATCCAGTTTGCAA GTGGGTCCCTTCAAAGTTCAAGCGGCACTGGAT CTGGGACAGAAATTCATCTCAATCAGCAGCC TGCAGCCTGAAGATTTCGCACTTACTGTCT ACAGCATATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAAAACGA	SEQ ID NO: 182	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCACTTTCAGTAACCTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGACAGCCCGTGAAGGCC GATTACCATCTCCAGAGACAATTCACAAGAATA CGCTGTATCTGCAAATGAACAGCCTGAGAGTCG AGGACACGGCTGTGTATTATTGTGCGCGAGATA GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCTGGTCAACCGTCTCCTCA
		SEQ ID NO: 1596	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK R	SEQ ID NO: 1753	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVWYDASNENYADAVKG RFTISRDN SKNTLYLQMNLSLRVEDTAVYYCARDR TIFGVVLGDYWGQGLVTVSS

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		SEQ ID NO: 26	SEQ ID NO: 183
IP:360982	4B1.016	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTAG GCTGTATCAGCAGAAACAGGGAAGCCCCTA AGCTCCTGATCTATGTCATCCAGTTTGCAA GTGGGTCCCTTCAAAGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAAAACGA
			SEQ ID NO: 1754 QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDN SKNTLYLQMNSLRVEDTAVYYCARDG TIFGVVLGDYWGQGTLVTVSS
		SEQ ID NO: 27	SEQ ID NO: 184
IP:335922	18F2	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACCTTAGAAATTATTAG GCTGTATCACCAGAAACAGGGAAGCCCCTA AGCGCTGATCTATGTCATCCAGTTTGCAA GTGGGTCCCTTCAAAGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAAACGA
			SEQ ID NO: 1755 QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDGSNENYADSVKG RFTISRDN SKNTLYLHMNSLRADTAVYYCARDG TIFGVVLGDYWGQGLVTVSS
		SEQ ID NO: 1597	SEQ ID NO: 1754
IP:360982	4B1.016	AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSTEFT LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK R
			SEQ ID NO: 1755 QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDGSNENYADSVKG RFTISRDN SKNTLYLHMNSLRADTAVYYCARDG TIFGVVLGDYWGQGLVTVSS
		SEQ ID NO: 1598	SEQ ID NO: 1755
		DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YHQKPGKAPKRLIYGASSLQSGVPSRFSGSGSTE FTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDGSNENYADSVKG RFTISRDN SKNTLYLHMNSLRADTAVYYCARDG TIFGVVLGDYWGQGLVTVSS

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!PS:360986	18F2.002	NA	SEQ ID NO: 28 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACCTTAGAAATTTAG GCTGGTATCAACAGAAACAGGGAAGCCCCCTA AGCTCCTGATCTATGTTGATCCAGTTTGCAA GTGGGTCCTTCAAGTTACGCGGAGTGGAT CTGGGACAGAAATTCATCTCACAATCAGCAGCC TGACGCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAGTGGATATCAAAACGA	SEQ ID NO: 185 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCACTTTCAGTAACCTTTGGCA TGCACTGGTCCGCCAGGCCCAAGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGCAGACGCCGTGAAGGCC GATTACCATCTCCAGAGACAATTCACAAGACA CGCTGATCTGCAATGACAGCCTGAGAGCCG CGACACGGCTGTGTAATTAATGCGGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
			SEQ ID NO: 1599 DIQMTQSPSSLSASIGDRVTITCRASQDLRNVLGW YQKPGKAPKLLIYGASSLQSGVPSRFSGSGTE FTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR	SEQ ID NO: 1756 QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVWYDASNENYADAVKG RFTISRDN SKNTLYLQMNSLRAADTA VYYCARDG TIFGVVLGDYWGQGLVTVSS
!PS:360995	18F2.003	NA	SEQ ID NO: 29 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACCTTAGAAATTTAG GCTGGTATCAACAGAAACAGGGAAGCCCCCTA AGCTCCTGATCTATGTTGATCCAGTTTGCAA GTGGGTCCTTCAAGTTACGCGGAGTGGAT CTGGGACAGAAATTCATCTCACAATCAGCAGCC TGACGCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAGTGGATATCAAAACGA	SEQ ID NO: 186 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCACTTTCAGTAACCTTTGGCA TGCACTGGTCCGCCAGGCCCAAGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGCAGACGCCGTGAAGGCC GATTACCATCTCCAGAGACAATTCACAAGACA CGCTGATCTGCAATGACAGCCTGAGAGCCG CGACACGGCTGTGTAATTAATGCGGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
			SEQ ID NO: 1600 DIQMTQSPSSLSASIGDRVTITCRASQDLRNVLGW YQKPGKAPKLLIYGASSLQSGVPSRFSGSGTE FTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR	SEQ ID NO: 1757 QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVWYDASNENYADAVKG RFTISRDN SKNTLYLHMNSLRAADTA VYYCARDG TIFGVVLGDYWGQGLVTVSS

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!PS:360999	18F2.004	NA	SEQ ID NO: 30 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACCTTAGAAATTTAG GCTGGTATCACCAAGAACACAGGAAAGCCCCCTA AGCTCCTGATCTATGTCATCCAGTTTGCAA GTGGGTCCTTCAAGTTACGCGGAGTGGAT CTGGGACAGAAATTCATCTCACAATCAGCAGCC TGACGCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAGTGGATATCAAAACGA	SEQ ID NO: 187 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGATTCACTTTCAGTAACCTTTGGCA TGCACTGGTCCGCCAGGCCCAAGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGCAGACGCCGTGAAGGCC GATTACCATCTCCAGAGACAATTCACAAGACA CGCTATCTGCAATGAACAGCCTGAGAGCCG CGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
			SEQ ID NO: 1601 DIQMTQSPSSLSASIGDRVTITCRASQDLRNLYLW YHQPGRKAPKLLIYGASSLQSGVPSRFSGSGTE FTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR	SEQ ID NO: 1758 QVQLVESGGGVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVWYDASNENYADAVKG RFTISRDN SKNTLYLQMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGLVTVSS
!PS:361005	18F2.005	NA	SEQ ID NO: 31 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACCTTAGAAATTTAG GCTGGTATCAACAGAAACACAGGAAAGCCCCCTA AGCGCTGATCTATGTCATCCAGTTTGCAA GTGGGTCCTTCAAGTTCAAGCGGCAAGTGGAT CTGGGACAGAAATTCATCTCACAATCAGCAGCC TGACGCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAGTGGATATCAAAACGA	SEQ ID NO: 188 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGATTCACTTTCAGTAACCTTTGGCA TGCACTGGTCCGCCAGGCCCAAGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGCAGACGCCGTGAAGGCC GATTACCATCTCCAGAGACAATTCACAAGACA CGCTATCTGCAATGAACAGCCTGAGAGCCG CGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
			SEQ ID NO: 1602 DIQMTQSPSSLSASIGDRVTITCRASQDLRNLYLW YHQPGRKAPKLLIYGASSLQSGVPSRFSGSGTE FTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR	SEQ ID NO: 1759 QVQLVESGGGVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVWYDASNENYADAVKG RFTISRDN SKNTLYLQMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGLVTVSS

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		SEQ ID NO: 32	SEQ ID NO: 189
		GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTATAGGAGACAGAGTCACCATCACTTGCCGGCAAGTCAGGACCTTAGAAATTTAGGCTGTATCAACAGAAACAGGAAAGCCCTAAGCCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGTCCCTTCAAGGTTCAAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACAAATCAGCAGCCTGCAGCCTGAAGATTTGCAACTTATTACTGTCTACAGCATAATAATTACCCCTTCACTTTCGGCCCTGGACCAAAAGTGGATATCAAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGGTGTCCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACTTTCAGTAACTTTGGCATGCACTGGGTCCGCCAGGCCCAAGCAAGGGGTGGAGTGGGTGGCAGTTATATGGTATGATGCAAGTAATGAAAACTATGCAGACGCCGTGAAGGGCCGATTCAACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCACATGAACAGCCTGAGAGCCGCGGACACGGCTGTGTATTACTGTGCGGAGAGATGGACGATCTTTGGAGTGGTCTTGGGGGACTACTGGGCCAGGGAACCTGGTCAACCGTCTCCTCA
18F2.006	!PS:361009	NA	NA
		SEQ ID NO: 1603	SEQ ID NO: 1760
		DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGWYQKPGKAPKRLIYGASSLQSGVPSRFSGSGTEFTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAIVWYDASNENYADAVKGRFTISRDNSKNTLYLHMNSLRAADTAVYYCARDGTIFGVVLGDYWGQGTLVTVSS
		SEQ ID NO: 33	SEQ ID NO: 190
		GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTATAGGAGACAGAGTCACCATCACTTGCCGGCAAGTCAGGACCTTAGAAATTTAGGCTGTATCAACAGAAACAGGAAAGCCCTAAGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGTCCCTTCAAGGTTCAAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACAAATCAGCAGCCTGCAGCCTGAAGATTTGCAACTTATTACTGTCTACAGCATAATAATTACCCCTTCACTTTCGGCCCTGGACCAAAAGTGGATATCAAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGGTGTCCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACTTTCAGTAACTTTGGCATGCACTGGGTCCGCCAGGCCCAAGCAAGGGGTGGAGTGGGTGGCAGTTATATGGTATGATGCAAGTAATGAAAACTATGCAGACGCCGTGAAGGGCCGATTCAACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCACATGAACAGCCTGAGAGCCGCGGACACGGCTGTGTATTACTGTGCGGAGAGATGGACGATCTTTGGAGTGGTCTTGGGGGACTACTGGGCCAGGGAACCTGGTCAACCGTCTCCTCA
18F2.007	!PS:361013	NA	NA
		SEQ ID NO: 1604	SEQ ID NO: 1761
		DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGWYHQKPGKAPKLLIYGASSLQSGVPSRFSGSGTEFTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAIVWYDASNENYADAVKGRFTISRDNSKNTLYLHMNSLRAADTAVYYCARDGTIFGVVLGDYWGQGLVTVSS
		AA	AA

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	!PS:361017	18F2.008	NA	SEQ ID NO: 34 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACCTTAGAAATTTAG GCTGGTATCACCAAGAACAGGGAAGCCCCCTA AGCCCTGATCTATGGTGCAATCCAGTTTGCAA GTGGGTCCTTCAAGGTTACGCGGCAAGTGAT CTGGGACAGAAATTCATCTCTCAATCAGCAGCC TGACGCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAGTGGATATCAAAACGA	SEQ ID NO: 191 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCACTTTCAGTAACCTTTGGCA TGCACTGGTCCGCCAGGCCCAAGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGCAGACGCCGTGAAGGCC GATTACCATCTCCAGAGACAATTCACAAGACA CGCTATCTGCAATGAACAGCCTGAGAGCCG CGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
				SEQ ID NO: 1605 DIQMTQSPSSLSASIGDRVTITCRASQDLRNLYLW YHQPQKAPKRLIYGASSLQSGVPSRFSGSGTE FTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR	SEQ ID NO: 1762 QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVWYDASNENYADAVKG RFTISRDN SKNTLYLQMNSLR AADTA VYYCARDG TIFGVVLGDYWGQGLVTVSS
	!PS:361021	18F2.009	NA	SEQ ID NO: 35 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACCTTAGAAATTTAG GCTGGTATCAACAGAAACAGGGAAGCCCCCTA AGCTCCTGATCTATGTGCATCCAGTTTGCAA GTGGGTCCTTCAAGGTTCAAGCGGCAAGTGAT CTGGGACAGAAATTCATCTCTCAATCAGCAGCC TGACGCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAGTGGATATCAAAACGA	SEQ ID NO: 192 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCACTTTCAGTAACCTTTGGCA TGCACTGGTCCGCCAGGCCCAAGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGAA GTAATGAAAACATATGCAGACGCCGTGAAGGCC GATTACCATCTCCAGAGACAATTCACAAGACA CGCTGTATCTGCAATGAACAGCCTGAGAGCCG CGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
				SEQ ID NO: 1606 DIQMTQSPSSLSASIGDRVTITCRASQDLRNLYLW YQKQPGKAPKLLIYGASSLQSGVPSRFSGSGTE FTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR	SEQ ID NO: 1763 QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVWYDASNENYADAVKG RFTISRDN SKNTLYLQMNSLR AADTA VYYCARDG TIFGVVLGDYWGQGLVTVSS

		SEQ ID NO: 36	GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTATAGGAGACAGAGTCACCATCACTTGCCGGCAAGTCAGGACCTTAGAAATTTATTAGGCTGTATCAACAGAAACCAAGGAAAGCCCTAAGCTCCTGATCTATGTGTCATCCAGTTTGCAAAGTGGGTCCCTTCAAGGTTCAAGCGGCAGTGGATCTGGACAGAAATTCATCTCACAATCAGCAGCCTGCAGCCTGAAGATTTGCAACTTATTACTGTCTACAGCATAATAATTACCCCTTCACTTTCGGCCCTGGACCAAAAGTGGATATCAAAACGA	SEQ ID NO: 193	CAGTGCAGCTGGTGGAGTCTGGGGAGGCGGTGTCCAGCCTGGAGGTCCTTGAGACTCTCCCTGTGCAGGCTCTGGATTCACTTTCAGTAACCTTTGGCATGCACTGGGTCCGCCAGGCCCAAGCAAGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGCAAATAATGAAAACCTATGCAGACTCCGTGAAGGGCCGATTCAACCATCTCCAGAGACAAATTCCAAGAACAACGCTGTATCTGCAAAATGAACAGCCTGAGAGCCGCGGACACGGCTGTGTATTACTGTGCGGAGAGATGGACGATCTTTGGAGTGGTCTTTGGGGGACTACTGGGCCAGGGAACCTGGTCAACCGTCTCTCTCA	
18F2.010	IP:361028	NA	SEQ ID NO: 1607	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGWYQKPGKAPKLLIYGASSLSQGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	SEQ ID NO: 1764	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAWIWYDASNENYADSVKGRFTISRDNSKNTLYLQMNSLRAADTAVYYCARDGTIFGVVLGDYWGQGTLVTVSS
		AA	SEQ ID NO: 37	GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTATAGGAGACAGAGTCACCATCACTTGCCGGCAAGTCAGGACCTTAGAAATTTATTAGGCTGTATCAACAGAAACCAAGGAAAGCCCTAAGCTCCTGATCTATGTGTCATCCAGTTTGCAAAGTGGGTCCCTTCAAGGTTCAAGCGGCAGTGGATCTGGACAGAAATTCATCTCACAATCAGCAGCCTGCAGCCTGAAGATTTGCAACTTATTACTGTCTACAGCATAATAATTACCCCTTCACTTTCGGCCAAAGGACCAAAAGTGGATATCAAAACGA	SEQ ID NO: 194	CAGTGCAGCTGGTGGAGTCTGGGGAGGCGGTGTCCAGCCTGGAGGTCCTTGAGACTCTCCCTGTGCAGGCTCTGGATTCACTTTCAGTAACCTTTGGCATGCACTGGGTCCGCCAGGCCCAAGCAAGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGCAAATAATGAAAACCTATGCAGACGCCGTGAAGGGCCGATTCAACCATCTCCAGAGACAAATTCCAAGAACAACGCTGTATCTGCAAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGGAGAGATAGGACGATCTTTGGAGTGGTCTTTGGGGGACTACTGGGCCAGGGAACCTGGTCAACCGTCTCTCTCA
18F2.011	IP:360535	NA	SEQ ID NO: 1608	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGWYQKPGKAPKLLIYGASSLSQGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIKR	SEQ ID NO: 1765	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAWIWYDASNENYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVIGDYWGQGTIVTVSS
		AA				

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!PS:361035	18F2.012	NA	SEQ ID NO: 38 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACCTTAGAAATTATTAG GCTGGTATCAACAGAAACACAGGAAAGCCCCA AGCTCCTGATCTATGTCATCCAGTTTGCAA GTGGGTCCTTCAAGGTTACGCGGAGTGGAT CTGGGACAGAAATTCATCTCTCAATCAGCAGCC TGACGCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAAACGA	SEQ ID NO: 195 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTTCAGTAACCTTTGGCA TGCACTGGTCCGCCAGGCCCAAGCAAGGGGC TGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGACAGCCCGTGAAGGCC GATTACCATCTCCAGAGACAATTCCAAGAACAA CGCTGATCTGCAATGAACAGCCTGAGAGCCG AGGACACGGCTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
			SEQ ID NO: 1609 DIQMTQSPSSLSASIGDRVTITCRASQDLRNLYLGW YQKPGKAPKLLIYGASSLQSGVPSRFSGSGTE FTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR	SEQ ID NO: 1766 QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVWYDASNENYADAVKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDG TIFGVVLGDYWGQGLVTVSS
!PS:359940	2F11.002	NA	SEQ ID NO: 39 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTAA ATTGGTATCAGCAGAAACACAGGAAAGCCCCA AGCTCCTGATCTACGATGCATCCAAATTTGAAA CAGGGTCCCATCAAGGTTCAAGTGAAGTGGAT CTGGGACAGATTTTAGTCTCAACATCAGCAGCC TGCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATATTCTCCTCACTTTCGGCGGAGG GACCAAAGGTGGAGATCAAGCGA	SEQ ID NO: 196 CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGACAGCCCGTGAAGGGC CGATTCAACCATCTCCAGGACAAATTCCAAGAAC ACGCTGTATCTGCAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTGGAGTGGTCTTGAAGTCTGG GGCCAGGGAACCTGGTCAACCGTCTCCTCA
			SEQ ID NO: 1610 DIQMTQSPSSLSASVGDRTITCAASQDISNYLNW YQKPGKAPKLLIYDASNLETGVPSRFSGSGTD FSLTISLQPEDFATYYCQYDILLTFGGGKVEIK R	SEQ ID NO: 1767 QVQLVESGGGVVQPRSLRLSCAASGFTFSYGM HWVRQAPGKGLEWVAIVWYDASNKYADAVKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLGDYWGQGLVTVSS

A-2124-WO-PCT

!PS:361039	2F11.003	NA	SEQ ID NO: 40 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGCGAGTCAGGACATTAGCAACTATTAA ATTGGTATCAGCAGAAACAGGAAAGCCCCCTA AGCTCCTGATCTACGATGCATCCAATTTGGAA CAGGGTCCCATCAAGGTTCAAGTGGAAAGTGAT CTGGGACAGATTTAGTCTCACCATCAGCAGCC TGCAGCCTGAAGATTTTGCACATATTACTGTCA ACAGTATGATATTCCTCCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGA	SEQ ID NO: 197 CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTCCAGTAGCTATGGC ATGCAGTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGCAGACGCCGTGAAGGC CGATTCAACCATCTCCAGCGACAATTCCAAAGAAC ACGCTGTATCTGCAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTGGAGTGGTCTTGACTACTGG GGCCAGGGAACCCGTGTCACCGTCTCCTCA
		AA	SEQ ID NO: 1611 DIQMTQSPSSLSASVGDRTVTITCQASQDISNYLNW YQKPGKAPKLLIYDASNLETGVPSRFSGSGTD FSLTISLQPEDFATYYCQYDILLTFGGGKVEIK R	SEQ ID NO: 1768 QVQLVESGGGVVQPRSLRLSCAASGFTFSYGM HWVRQAPGKGLEWVAIVWYDASNKYADAVKG RFTISDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLDYWGQGLVTVSS
!PS:361043	2F11.004	NA	SEQ ID NO: 41 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGCGAGTCAGGACATTAGCAACTATTAA ATTGGTATCAGCAGAAACAGGAAAGCCCCCTA AGCTCCTGATCTACGATGCATCCAATTTGGAA CAGGGTCCCATCAAGGTTCAAGTGGAAAGTGAT CTGGGACAGATTTAGTCTCACCATCAGCAGCC TGCAGCCTGAAGATATTGCAACATATTACTGTC AACAGTATGATATTCTCCTCACTTTCGGCGGAG GGACCAAGGTGGAGATCAAGCGA	SEQ ID NO: 198 CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTCCAGTAGCTATGGC ATGCAGTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGCAGACGCCGTGAAGGC CGATTCAACCATCTCCAGGGAACAATCCAAAGAAC ACGCTGTATCTGCAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTGGAGTGGTCTTGACTACTGG GGCCAGGGAACCCGTGTCACCGTCTCCTCA
		AA	SEQ ID NO: 1612 DIQMTQSPSSLSASVGDRTVTITCQASQDISNYLNW YQKPGKAPKLLIYDASNLETGVPSRFSGSGTD FSLTISLQPEDFATYYCQYDILLTFGGGKVEIKR	SEQ ID NO: 1769 QVQLVESGGGVVQPRSLRLSCAASGFTFSYGM HWVRQAPGKGLEWVAIVWYDASNKYADAVKG RFTISDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLDYWGQGLVTVSS

IPs:361049	2F11.005	NA	<p>SEQ ID NO: 42</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCGAGTCAGGACATTAGCAACTATTTAAATTGGTATCAGCAGAAACCAGGGAAGCCCCTAAGCTCTGATCTACGATGCATCCAATTTGGAAA</p> <p>CAGGGGTCCCATCAAGGTTTCAGTGGAAGTGGATCTGGACAGATTTTAGTTTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACATATTACTGTCAACAGTATGATATTCTCTCACTTTCGGCGGAGG</p> <p>GACCAAGGTGGAGATCAAGCGA</p> <p>SEQ ID NO: 1613</p>	<p>SEQ ID NO: 199</p> <p>CAGGTGCAACTGGTGGAGTCTGGGGAGGCGGTGTCCAGCCTGGAGGTCCTTGAGACTCTCCCTGTGCAGCGTCTGATTACACTTCAGTAGCTATGGCATGCACTGGTCCGCAAGCTCCAGGCAAGGGCTGGAGTGGTGCGAGTTATATGTTATGATGCAAGTAATAAATACTATGCAGACGCCGTGAAGGCGGATTCACCATCTCCAGGGACAAATTCAGAAACACGCTGATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTTACTGTGCGAGAGATAGGACGATTTTGGAGTGGTCTTGACTACTGGGCCAGGGAACCCCTGGTCACCGTCTCCTCA</p> <p>SEQ ID NO: 1770</p>
		AA	<p>DIQMTQSPSSLSASVGDRTVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGGTD</p> <p>FSFTISLQPEDFATYYCQQYDILLTFGGGTVKVEIKR</p> <p>SEQ ID NO: 43</p>	<p>SEQ ID NO: 200</p> <p>CAGGTGCAACTGGTGGAGTCTGGGGAGGCGGTGTCCAGCCTGGAGGTCCTTGAGACTCTCCCTGTGCAGCGTCTGATTACACTTCAGTAGCTATGGCATGCACTGGTCCGCAAGCTCCAGGCAAGGGCTGGAGTGGTGCGAGTTATATGTTATGATGCAAGTAATAAATACTATGCAGACGCCGTGAAGGCGGATTCACCATCTCCAGGGACAAATTCAGAAACACGCTGATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTTACTGTGCGAGAGATAGGACGATTTTGGAGTGGTCTTGACTACTGGGCCAGGGAACCCCTGGTCACCGTCTCCTCA</p> <p>SEQ ID NO: 1771</p>
IPs:361055	2F11.006	NA	<p>SEQ ID NO: 42</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCGAGTCAGGACATTAGCAACTATTTAAATTGGTATCAGCAGAAACCAGGGAAGCCCCTAAGCTCTGATCTACGATGCATCCAATTTGGAAA</p> <p>CAGGGGTCCCATCAAGGTTTCAGTGGAAGTGGATCTGGACAGATTTTAGTTTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACATATTACTGTCAACAGTATGATATTCTCTCACTTTCGGCGGAGG</p> <p>GACCAAGGTGGAGATCAAGCGA</p> <p>SEQ ID NO: 1614</p>	<p>SEQ ID NO: 200</p> <p>CAGGTGCAACTGGTGGAGTCTGGGGAGGCGGTGTCCAGCCTGGAGGTCCTTGAGACTCTCCCTGTGCAGCGTCTGATTACACTTCAGTAGCTATGGCATGCACTGGTCCGCAAGCTCCAGGCAAGGGCTGGAGTGGTGCGAGTTATATGTTATGATGCAAGTAATAAATACTATGCAGACGCCGTGAAGGCGGATTCACCATCTCCAGGGACAAATTCAGAAACACGCTGATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTTACTGTGCGAGAGATAGGACGATTTTGGAGTGGTCTTGACTACTGGGCCAGGGAACCCCTGGTCACCGTCTCCTCA</p> <p>SEQ ID NO: 1771</p>
		AA	<p>DIQMTQSPSSLSASVGDRTVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGGTD</p> <p>FSLTISLQPEDATYYCQQYDILLTFGGGTVKVEIKR</p> <p>SEQ ID NO: 43</p>	<p>SEQ ID NO: 200</p> <p>CAGGTGCAACTGGTGGAGTCTGGGGAGGCGGTGTCCAGCCTGGAGGTCCTTGAGACTCTCCCTGTGCAGCGTCTGATTACACTTCAGTAGCTATGGCATGCACTGGTCCGCAAGCTCCAGGCAAGGGCTGGAGTGGTGCGAGTTATATGTTATGATGCAAGTAATAAATACTATGCAGACGCCGTGAAGGCGGATTCACCATCTCCAGGGACAAATTCAGAAACACGCTGATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTTACTGTGCGAGAGATAGGACGATTTTGGAGTGGTCTTGACTACTGGGCCAGGGAACCCCTGGTCACCGTCTCCTCA</p> <p>SEQ ID NO: 1771</p>

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!PS:361059	2F11.007	NA	SEQ ID NO: 44	SEQ ID NO: 201
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGCGAGTCAGGACATTAGCAACTATTAAATTGGTATCAGCAGAAACAGGGAAGCCCCCTAAGCTCTGATCTACGATGCATCCCAATTGGAAAACAGGGTCCCATCAAGGTTTCAGTGGAAAGTGATCTGGGACAGATTTAGTTTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACATATTACTGTCAACAGTATGATATTCCTCTCACTTTCGGCGGAGG	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTGTCCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGGCTCTGGATTCACTTCCAGTAGCTATGGCATGCACTGGTCCGCCAGGCTCCAGGCAAGGGCTGGAGTGGTGGCAGTTATATGGTATGATGCAAGTAATAAATACTATGCAGACGCCGTGAAGGCGCATTCACCATCTCCAGGACAATTCCAAAGAACACGCTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGGAGAGATAGGACGATTTTGGAGTGGTTCTTGACTACTGGGCCAGGGAACCCCTGGTCACCGTCTCCTCA
!PS:361063	2F11.008	NA	SEQ ID NO: 1615	SEQ ID NO: 1772
			DIQMTQSPSSLSASVGDRTVTITCQASQDISNYLNWYQKPGKAPKLLIYDASNLETGVPSRFSGSGGTD	QVQLVESGGGVVQPRSLRLSCAASGFTFSYGMHWVRQAPGKGLEWVAIVWYDASNKYADAVKGRFTISDINSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVLDYWGQGLVTVSS
!PS:361063	2F11.008	NA	SEQ ID NO: 45	SEQ ID NO: 202
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGCGAGTCAGGACATTAGCAACTATTAAATTGGTATCAGCAGAAACAGGGAAGCCCCCTAAGCTCTGATCTACGATGCATCCCAATTGGAAAACAGGGTCCCATCAAGGTTTCAGTGGAAAGTGATCTGGGACAGATTTAGTTTCACCATCAGCAGCCTGCAGCCTGAAGATATTGCAACATATTACTGTCAACAGTATGATATTCCTCTCACTTTCGGCGGAGG	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTGTCCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGGCTCTGGATTCACTTCCAGTAGCTATGGCATGCACTGGTCCGCCAGGCTCCAGGCAAGGGCTGGAGTGGTGGCAGTTATATGGTATGATGCAAGTAATAAATACTATGCAGACGCCGTGAAGGCGCATTCACCATCTCCAGGACAATTCCAAAGAACACGCTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGGAGAGATAGGACGATTTTGGAGTGGTTCTTGACTACTGGGCCAGGGAACCCCTGGTCACCGTCTCCTCA
!PS:361063	2F11.008	AA	SEQ ID NO: 1616	SEQ ID NO: 1773
			DIQMTQSPSSLSASVGDRTVTITCQASQDISNYLNWYQKPGKAPKLLIYDASNLETGVPSRFSGSGGTD	QVQLVESGGGVVQPRSLRLSCAASGFTFSYGMHWVRQAPGKGLEWVAIVWYDASNKYADAVKGRFTISDINSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVLDYWGQGLVTVSS

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!PS:359949	2F11.009	NA	SEQ ID NO: 46	SEQ ID NO: 203
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCGAGTCAGGACATTAGCAACTATTAAATTGGTATCAGCAGAAACAGGGAAGCCCCCTAAGCTCCTGATCTACGATGCATCCAAATTGGAAA	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTGTCCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGGCTCTGGATTCACTTCCAGTAGCTATGGCATGCACTGGTCCGCCAGGCTCCAGGCAAGGGCTGGAGTGGTGGCAGTTATATGGTATGATGCAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTCAACCATCTCCAGGACAAATCCCAAGAACACGCTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATAGGACGATTTTGGAGTGGTTCTTGACTACTGGGCCAGGGAACCCCTGGTCACCGTCTCCTCA
!PS:359956	2F11.010	NA	SEQ ID NO: 1617	SEQ ID NO: 1774
			DIQMTQSPSSLSASVGDRTVTITCQASQDISNYLNWYQKPGKAPKLLIYDASNLETGVPSRFSGSGTD	QVQLVESGGGVVQPRSLRLSCAASGFTFSYGMHWVRQAPGKGLEWVAIVWYDASNKYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLDYWGQGLVTVSS
!PS:359956	2F11.010	NA	SEQ ID NO: 47	SEQ ID NO: 204
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCGAGTCAGGACATTAGCAACTATTAAATTGGTATCAGCAGAAACAGGGAAGCCCCCTAAGCTCCTGATCTACGATGCATCCAAATTGGAAA	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTGTCCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGGCTCTGGATTCACTTCCAGTAGCTATGGCATGCACTGGTCCGCCAGGCTCCAGGCAAGGGCTGGAGTGGTGGCAGTTATATGGTATGATGGAAGTAATAAATACTATGCAGACGCCGTGAAGGGCCGATTCAACCATCTCCAGGACAAATCCCAAGAACACGCTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATAGGACGATTTTGGAGTGGTTCTTGACTACTGGGCCAGGGAACCCCTGGTCACCGTCTCCTCA
!PS:359956	2F11.010	AA	SEQ ID NO: 1618	SEQ ID NO: 1775
			DIQMTQSPSSLSASVGDRTVTITCQASQDISNYLNWYQKPGKAPKLLIYDASNLETGVPSRFSGSGTD	QVQLVESGGGVVQPRSLRLSCAASGFTFSYGMHWVRQAPGKGLEWVAIVWYDASNKYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLDYWGQGLVTVSS

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!PS:359865	6H1.002	NA	SEQ ID NO: 48 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTAG GCTGTATCAGCAGAAACCAGGAAAGCCCCTA AGCGCTGATCTATGGTGCATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTTCAGCGGCAGTGGAT CTGGGACAGAAATTCACCTCTCACAATCAGCAGCC TGACGCCTGAAGATTTGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTTCGGCCCT GGGACCAAAGTGGATATCAAAACGA	SEQ ID NO: 1619 DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLQSGVPSRFSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	SEQ ID NO: 1776 QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAIVIWDASNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSS
		AA	SEQ ID NO: 49 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTAG GCTGTATCAGCAGAAACCAGGAAAGCCCCTA AGCGCTGATCTATGGTGCATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTTCAGCGGCAGTGGAT CTGGGACAGAAATTCACCTCTCACAATCAGCAGCC TGACGCCTGAAGATTTGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTTCGGCCCT GGGACCAAAGTGGATATCAAAACGA	SEQ ID NO: 1620 DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLQSGVPSRFSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	SEQ ID NO: 206 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGATTCACTTCACTTCACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATA GGACGATTTTGGAGTGTCTTTGGGGGACTACT GGGGCCAGGGAACCTGGTCAACCGTCTCCTCA
!PS:359869	6H1.003	NA	SEQ ID NO: 1620 DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLQSGVPSRFSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	SEQ ID NO: 1777 QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAIVIWDASNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLLGDYWGQGLVTVSS	
		AA	SEQ ID NO: 1778 QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAIVIWDASNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLLGDYWGQGLVTVSS		

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IP:359873	6H1.004	NA	SEQ ID NO: 50	SEQ ID NO: 207
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTATAGGAGACAGAGTCACCATCACTTGCCGGCAAGTCAGGACATTAGAGATTATTAGGCTGGTATCAGCAGAAACCAGGAAAGCCCTAAGCTCTGATCTATGGTGCATCCAGTTTGCAAAGTGGGTCCCTCAAGGTTACGCGGAGTGGATCTGGGACAGAAATTCATCTCACAAATCAGCAGCCTGCAGCCTGAAGATTTCGCAACTTATTACTGTCTACAGCATAAATAATTACCCCTTCACCTTCGGCCAAAGGACCAAAGTGGATATCAAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGGCTGGATTCACTTCCAGTTACTTTGGCATGCACTGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGTGGCAGTTATATGGTATGATGCAAATAATAACTATGCAGACGCCGTGAAGGGCCGCTTCAACATCTCCAGAGACAATTCGAAGACAACGCTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTTACTGTGCGCGAGATGGACGATTTTGGAGTGCTCTTGGGGGACTACTGGGCCAGGGAACCTGGTCAACCGTCTCCTCA
IP:359877	6H1.005	NA	SEQ ID NO: 1621	SEQ ID NO: 1778
			DIQMTQSPSSLSASIGDRVITITCRASQDIRDYLGWYQQKPGKAPKLLIYGASLQSGVPSRFSGSGTEFTLTISLQPEDFATYYCLQHNNYPFTFGQGTKVDIKR	QVQLVESGGGVVQGRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAWIWYDASNKYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGTIFGVLLGDYWGQGLVTVSS
IP:359877	6H1.005	NA	SEQ ID NO: 51	SEQ ID NO: 208
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTATAGGAGACAGAGTCACCATCACTTGCCGGCAAGTCAGGACATTAGAGATTATTAGGCTGGTATCAGCAGAAACCAGGAAAGCCCTAAGCTCTGATCTATGGTGCATCCAGTTTGCAAAGTGGGTCCCTTCAAGTTACGCGGAGTGGATCTGGGACAGAAATTCATCTCACAAATCAGCAGCCTGCAGCCTGAAGATTTCGCAACTTATTACTGTCTACAGCATAAATAATTACCCCTTCACCTTCGGCCAAAGGACCAAAGTGGATATCAAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGGCTGGATTCACTTCCAGTTACTTTGGCATGCACTGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGTGGCAGTTATATGGTATGATGCAAATAATAACTATGCAGACGCCGTGAAGGGCCGCTTCAACATCTCCAGAGACAATTCGAAGACAACGCTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTTACTGTGCGCGAGATAAGACGATTTTGGAGTGCTCTTGGGGGACTACTGGGCCAGGGAACCTGGTCAACCGTCTCCTCA
IP:359877	6H1.005	AA	SEQ ID NO: 1622	SEQ ID NO: 1779
			DIQMTQSPSSLSASIGDRVITITCRASQDIRDYLGWYQQKPGKAPKLLIYGASLQSGVPSRFSGSGTEFTLTISLQPEDFATYYCLQHNNYPFTFGQGTKVDIKR	QVQLVESGGGVVQGRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAWIWYDASNKYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVLLGDYWGQGLVTVSS

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!PS:361067	6H1.006	NA	SEQ ID NO: 52	SEQ ID NO: 209
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTATAGGAGACAGAGTCACCATCACTTGCCGGCAAGTCAGGACATTAGAGATTATTAGGCTGGTATCAGCAGAAACCAGGAAAGCCCCAAGCTCTGATCTATGGTGCATCCAGTTTGCAAAGTGGGTCCCTTCAAGGTTACGCGCAGTGGATCTGGGACAGAAATTCATCTCAATCAGCAGCCTGACGCTGAAGATTTCGCAACTTATTACTGTACAGCATAAATAATTACCCCTTCACTTTCGGCCCTGGGACCAAAGTGGATATCAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGGCTCTGATTCACTTACAGTTACTTTGGCATGCACTGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGTGGCAGTTATATGGTATGATGGAAATAATAACTATGCAGACTCCGTGAAGGGCCGCTTCAACATCTCCAGAGACAATTCAGAACAACGCTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTATTACTGTGCGCGAGATGGACGATTTTGGAGTGTCTTGGGGGACTACTGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA
!PS:361071	6H1.007	NA	SEQ ID NO: 1623	SEQ ID NO: 1780
			DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKLLIYGASSLQSGVPSRFSGSGTEFTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	QVQLVESGGGVVQPGSRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAWIWDGSKNYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGTIFGVLLGDYWGQGLVTVSS
!PS:361071	6H1.007	NA	SEQ ID NO: 53	SEQ ID NO: 210
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTATAGGAGACAGAGTCACCATCACTTGCCGGCAAGTCAGGACATTAGAGATTATTAGGCTGGTATCAGCAGAAACCAGGAAAGCCCCAAGCTCTGATCTATGGTGCATCCAGTTTGCAAAGTGGGTCCCTTCAAGGTTACGCGCAGTGGATCTGGGACAGAAATTCATCTCAATCAGCAGCCTGACGCTGAAGATTTCGCAACTTATTACTGTACAGCATAAATAATTACCCCTTCACTTTCGGCCCTGGGACCAAAGTGGATATCAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGGCTCTGATTCACTTACAGTTACTTTGGCATGCACTGGTCCGCCAGGCTCCAGGCAAGGGCTGGAGTGGTGGCAGTTATATGGTATGATGCAAATAATAACTATGCAGACTCCGTGAAGGGCCGCTTCAACATCTCCAGAGACAATTCAGAACAACGCTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTATTACTGTGCGCGAGATGGACGATTTTGGAGTGTCTTGGGGGACTACTGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA
!PS:361071	6H1.007	AA	SEQ ID NO: 1624	SEQ ID NO: 1781
			DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKLLIYGASSLQSGVPSRFSGSGTEFTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	QVQLVESGGGVVQPGSRSLRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAWIWDGSKNYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGTIFGVLLGDYWGQGLVTVSS
!PS:361071	6H1.007	AA	SEQ ID NO: 54	SEQ ID NO: 211

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IPs:361075	6H1.008	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACCAGGGAAGCCCCTA AGTCCTGATCTATGGTGCAATCCAGTTTGCAA GTGGGTCCCTTCAAGTTTCAGCGGCAAGTGGAT CTGGGACAGAAATTCATCTCACAATCAGCAGCC TGACGCCTGAAGATTTTCGCAACTTATTACTGTCT ACAGCATAAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAAACGA	SEQ ID NO: 1625	SEQ ID NO: 1782	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTCAAGTTACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGGAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCAACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTGGAGTGCTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	SEQ ID NO: 55	SEQ ID NO: 212	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAIVWYDGSNKYYADA VKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGGLVTVSS
IPs:361079	6A5.004.001	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTAA ATTGGTATCAGCAGAAACCAGGGAAGCCCCTA AACTCCTGATCTACGATGCTTCCAAATTTGGAGCC AGGGGTCCCATCAAGGTTTCAGTGGAAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATGATCTATTACCTTTCGGCCCTGGG ACCAAAGTGGATATCAAAACGA	SEQ ID NO: 1626	SEQ ID NO: 1783	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAAGTAGCTATGGCA TGCACTGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGTGGCAGCTATATGGTATGATGCAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGATTCCAGAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGGAGAGATC GGACGATTTTGGAGTGCTCTTGAAGTACTGGG GCCAGGGAACCTGGTCAACCGTCTCCTCA
		AA	DIQMTQSPSSLSASVGDRTVTITCAASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGGTD FTLTISSLQPEDFATYYCQQYDDLFTFGPGTKVDIK R	SEQ ID NO: 55	SEQ ID NO: 212	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDANNKYYADA VKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGOGTLVTVSS

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!PS:361085	6A5.004.002	NA	SEQ ID NO: 56	SEQ ID NO: 213
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGACAGAGTCACCATCACTT GCCAGCGAGTCAGGACATTACCACTATTAA ATTGGTATCAGCAGAAACAGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGAGCC AGGGTCCCATCAAGGTTCAAGTGGAAGTGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATATTGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAAGTGGATATCAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCTGTGATTCTCTTCAGTAGCTATGGCA TGCACCTGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGTGGCAGCTATATGATGATGCAA ATAATAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTGGAGTGGTCTTGAAGTACTGGG GCCAGGGAACCTGGTCAACCGTCTCCTCA
!PS:361091	6A5.004.003	NA	SEQ ID NO: 1627	SEQ ID NO: 1784
			DIQMTQSPSSLSASVGDRTTITCQASQDITNLYNW YQKPGKAPKLLIYDASNLEPGVPSRFSGSGTD FTLTISSLQPEDIATYYCQYDDLFTFGPGTKVDIK R	QVQLVESGGGVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAIIWYDANNKYADAVKG RFTISRDSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGQGLVTVSS
!PS:361091	6A5.004.003	NA	SEQ ID NO: 57	SEQ ID NO: 214
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGACAGAGTCACCATCACTT GCCAGCGAGTCAGGACATTACCACTATTAA ATTGGTATCAGCAGAAACAGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGAGCC AGGGTCCCATCAAGGTTCAAGTGGAAGTGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAAGTGGATATCAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCTGTGATTCTCTTCAGTAGCTATGGCA TGCACCTGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGTGGCAGCTATATGATGATGCAA ATAATAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTGGAGTGGTCTTGAAGTACTCG GCCAGGGAACCTGGTCAACCGTCTCCTCA
!PS:361091	6A5.004.003	AA	SEQ ID NO: 1628	SEQ ID NO: 1785
			DIQMTQSPSSLSASVGDRTTITCQASQDITNLYNW YQKPGKAPKLLIYDASNLEPGVPSRFSGSGTD FTLTISSLQPEDFATYYCQYDDLFTFGPGTKVDIK R	QVQLVESGGGVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAIIWYDANNKYADAVKG RFTISRDSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYLGGQGLVTVSS

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!PS:361095	6A5.004.004	NA	SEQ ID NO: 58	SEQ ID NO: 215
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGACAGAGTCACCATCACTT GCCAGCGAGTCAGGACATTACCACTATTAA ATTGGTATCAGCAGAAACAGGAAAGCCCCA AACTCTGATCTACGATGCTTCCAAATTGGAGCC AGGGTCCCATCAAGGTTCACTGGAAGTGGATC TGGGACAGATTTTACTTTCCCATCAGCAGCCTG CAGCCTGAAGATTTTGCAACATATTACTGTCAA CAGTATGATGATCTATTCACTTTCGGCCCTGGGA CCAAAGTGGATATCAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGTCTGGATTCTCTTCACTAGTATGGCA TGCACTGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGTGGCAGCTATATGATATGATGCAA ATAATAATACTATGACAGACCCCTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCACAAGACA CGCTGATCTGCAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGATTACTGTGCGAGAGATC GGACGATTTTGGAGTGGTCTTGAAGTACTGGG GCCAGGGAACCCCTGGTCAACCTCTCCTCA
!PS:361101	6A5.004.005	NA	SEQ ID NO: 59	SEQ ID NO: 216
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGACAGAGTCACCATCACTT GCCAGCGAGTCAGGACATTACCACTATTAA ATTGGTATCAGCAGAAACAGGAAAGCCCCA AACTCTGATCTACGATGCTTCCAAATTGGAGCC AGGGTCCCATCAAGGTTCACTGGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATATTGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAAGTGGATATCAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGTCTGGATTCTCTTCACTAGTATGGCA TGCACTGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGTGGCAGCTATATGATATGATGCAA ATAATAATACTATGACAGACCCCTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCACAAGACA CGCTGATCTGCAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGATTACTGTGCGAGAGATC GGACGATTTTGGAGTGGTCTTGAAGTACTGGG GCCAGGGAACCCCTGGTCAACCTCTCCTCA
		AA	SEQ ID NO: 1629	SEQ ID NO: 1786
			DIQMTQSPSSLSASVGDRTVTITCQASQDITNLYNW YQKPGKAPKLLIYDASNLEPGVPSRFSGSGTD FTFTISSLQPEDFATYYCQYDDLFITFGPGTKVDIK R	QVQLVESGGGVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAIWYDANNKYADAVKG RFTISRDSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGQGLVTVSS
		AA	SEQ ID NO: 1630	SEQ ID NO: 1787
			DIQMTQSPSSLSASVGDRTVTITCQASQDITNLYNW YQKPGKAPKLLIYDASNLEPGVPSRFSGSGTD FTLTISSLQPEDIATYYCQYDDLFITFGPGTKVDIK R	QVQLVESGGGVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAIWYDANNKYADAVKG RFTISRDSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGQGLVTVSS

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	IP:361105	6A5.004.006	NA	SEQ ID NO: 60	SEQ ID NO: 217
				GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTGGGGACAGAGTCACCATCACTTGCCAGCGAGTCAGGACATTACCACTATTAAATTGGTATCAGCAGAAACAGGAAAGCCCCTA AACTCTGATCTACGATGCTTCCAATTGGAGCCAGGGTCCCATCAAGGTTCAAGTGAAGTGATCTGAGGACAGATTTACTTTACCATCAGCAGCCTG CAGCCTGAAGATTTGCAACATATTACTGTCAA CAGTATGATGATCTATTCACTTTCGGCCCTGGGA CCAAAGTGGATATCAAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCTCTTCAGTAGCTATGGCA TGCACCTGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGTGGCAGCTATATGATGATGCAA ATAATAATACTATGCAGACGCCGTGAAGGGCC GATTACCATCTCCAGAGACAGTTCCAAAGACA CGCTGATCTGCAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGATTACTGTGCGAGAGATC GGACGATTTTGGAGTGGTCTTGAGTACCTCG GCCAGGGAACCTGGTCAACCGTCTCCTCA
	AA			SEQ ID NO: 1631	SEQ ID NO: 1788
				DIQMTQSPSSLSASVGDRTVTITCQASQDITNLYNW YQKPGKAPKLLIYDASNLEPGVPSRFSGSGTD FTFTISLQPEDFATYYCQYDDLFTFPGTKVDIK R	QVQLVESGGGVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAIWYDANNKYADAVKGRFTISRDSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLEYLGQGTLVTVSS
	IP:361109	6A5.004.007	NA	SEQ ID NO: 61	SEQ ID NO: 218
				GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTGGGGACAGAGTCACCATCACTTGCCAGCGAGTCAGGACATTACCACTATTAAATTGGTATCAGCAGAAACAGGAAAGCCCCTA AACTCTGATCTACGATGCTTCCAATTGGAGCCAGGGTCCCATCAAGGTTCAAGTGAAGTGATCTGAGGACAGATTTACTTTACCATCAGCAGCCTG CAGCCTGAAGATATTGCAACATATTACTGTCAA CAGTATGATGATCTATTCACTTTCGGCCCTGGGA CCAAAGTGGATATCAAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCTCTTCAGTAGCTATGGCA TGCACCTGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGTGGCAGCTATATGATGATGCAA ATAATAATACTATGCAGACGCCGTGAAGGGCC GATTACCATCTCCAGAGACAGTTCCAAAGACA CGCTGATCTGCAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGATTACTGTGCGAGAGATC GGACGATTTTGGAGTGGTCTTGAGTACTGGG GCCAGGGAACCTGGTCAACCGTCTCCTCA
	AA			SEQ ID NO: 1632	SEQ ID NO: 1789
				DIQMTQSPSSLSASVGDRTVTITCQASQDITNLYNW YQKPGKAPKLLIYDASNLEPGVPSRFSGSGTD FTFTISLQPEDIATYYCQYDDLFTFPGTKVDIK R	QVQLVESGGGVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAIWYDANNKYADAVKGRFTISRDSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLEYWGQGTLVTVSS

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!PS:361113	6A5.004.008	NA	SEQ ID NO: 62	SEQ ID NO: 219
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGACAGAGTCACCATCACTT GCCAGCGAGTCAGGACATTACCAACTATTAA ATTGGTATCAGCAGAAACAGGAAAGCCCCA AACTCCTGATCTACGATGCTTCCAAATTGGAGCC AGGGTCCCATCAAGGTTTCAGTGGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAAGTGGATATCAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTGTGATTCTCTTCACTAGTATGGCA TGCACTGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGTGGCAGCTATATGATATGATGGAA ATAATAATACTATGACAGACCCCTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCACAAGACA CGCTGATCTGCAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGATTACTGTGCGAGAGATC GGACGATTTTGGAGTGGTCTTGAAGTACTGGG GCCAGGGAACCCCTGGTCAACCTCTCCTCA
!PS:361120	6A5.004.009	NA	SEQ ID NO: 63	SEQ ID NO: 220
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGACAGAGTCACCATCACTT GCCAGCGAGTCAGGACATTACCAACTATTAA ATTGGTATCAGCAGAAACAGGAAAGCCCCA AACTCCTGATCTACGATGCTTCCAAATTGGAGCC AGGGTCCCATCAAGGTTTCAGTGGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAAGTGGATATCAACGA	QVQLVESGGGVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLWVAIWYDGNKKYYADAVKG RFTISRDSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGQGLVTVSS
AA	6A5.004.009	AA	SEQ ID NO: 1633	SEQ ID NO: 1790
			DIQMTQSPSSLSASVGDRTITCQASQDITNLYNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGTD FTLTISLQPEDFATYYCQQYDDLFTFGPGTKVDIK R	QVQLVESGGGVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLWVAIWYDGNKKYYADAVKG RFTISRDSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGQGLVTVSS
AA	6A5.004.009	AA	SEQ ID NO: 1634	SEQ ID NO: 1791
			DIQMTQSPSSLSASVGDRTITCQASQDITNLYNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGTD FTLTISLQPEDFATYYCQQYDDLFTFGPGTKVDIK R	QVQLVESGGGVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLWVAIWYDANNKYYADSVKG RFTISRDSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGQGLVTVSS

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IP:359890	6A5.004.011	NA	SEQ ID NO: 64	SEQ ID NO: 221
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTGGGGACAGAGTCACCATCACTTGCCAGCGAGTCAGGACATTACCACTATTAAATTGGTATCAGCAGAAACAGGAAAGCCCCATAACTCTGATCTACGATGCTTCCAATTGGAGCCAGGGTCCCATCAAGGTTCAAGTGAAGTGATCTGGGACAGATTTACTCTACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACATATTACTGTCAACAGTATGATGATCTATTCACTTTCGGCCAAAGGACCAAAGTGGATATCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCTCTGATTCTCTTCAGTAGCTATGGCATGCAGTGGTCCGCCAGCCTCCAGGCAAGGGGCTGGAGTGGTGGCAGCTATATGATGATGCAATAAATAACTATATGACAGCCGTGAAGGGCGATTACCATCTCCAGAGACAGTTCACAAGAACACGCTGATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTATTACTGTGCGAGAGATCGGACGATTTTGGAGTGGTCTTGAGTACTGGGCCAGGGAACCTGGTCAACCGTCTCCTCA
IP:359890	6A5.004.011	NA	SEQ ID NO: 1635	SEQ ID NO: 1792
			DIQMTQSPSSLSASVGDRVVTITCQASQDITNLYNWYQKPGKAPKLLIYDASNLEPGVPSRFSGSGTDFTLTISLQPEDFATYYCQYDDLFITFGQGTKVDIKR	QVQLVESGGGVQPGRSLRLSCAASGFSFSSYGMHWVRQPPGKGLEWVAIWYDANNKYADAVKGRFTISRDSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLEYWGQGLVTVSS
IP:359890	6A5.004.011	NA	SEQ ID NO: 65	SEQ ID NO: 222
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTGGGGACAGAGTCACCATCACTTGCCAGCGAGTCAGGACATTACCACTATTAAATTGGTATCAGCAGAAACAGGAAAGCCCCATAACTCTGATCTACGATGCTTCCAATTGGAGCCAGGGTCCCATCAAGTTCAGTGAAGTGATCTGGGACAGATTTACTCTACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACATATTACTGTCAACAGTATGATGATCTATTCACTTTCGGCCAAAGGACCAAAGTGGATATCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCTCTGATTCTCTTCAGTAGCTATGGCATGCAGTGGTCCGCCAGCCTCCAGGCAAGGGGCTGGAGTGGTGGCAGCTATATGATGATGCAATAAATAACTATGACAGCCGTGAAGGGCGATTACCATCTCCAGAGACAGTTCACAAGAACACGCTGATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTATTACTGTGCGAGAGATCGGACGATTTTGGAGTGGTCTTGAGTACTCGGCCAGGGAACCTGGTCAACCGTCTCCTCA
IP:359890	6A5.004.011	AA	SEQ ID NO: 1636	SEQ ID NO: 1793
			DIQMTQSPSSLSASVGDRVVTITCQASQDITNLYNWYQKPGKAPKLLIYDASNLEPGVPSRFSGSGTDFTLTISLQPEDFATYYCQYDDLFITFGQGTKVDIKR	QVQLVESGGGVQPGRSLRLSCAASGFSFSSYGMHWVRQPPGKGLEWVAIWYDANNKYADAVKGRFTISRDSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLEYLGGQGLVTVSS

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IP:359567	2A11.002	NA	SEQ ID NO: 66	SEQ ID NO: 223
			GAAATTGTGTTGACGCAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCT GCAGGCCAGTCAGATTTTACCAGCACCTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCAGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCAGACAGGTTCACTGTCAGTGGCAGTG GGTCTGGACAGACTTCACTCTCACCATCAGCA GATTGGAGCCTGAAGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGCTCACCTCGCTTCGGCC AAGGGACACGACTGGAGATTAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTTCAGTAGCTATGGC ATGCATGGGTCCGCCAGGCTCCAGGCAAGGGA CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGAAGACGCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAAATCCAAAGAAC ACGCTGTTTCTGCAAGTGAACAGCCTGAGAGCC GAGGACACGGCTGTGATTACTGTGCGAGAGGG ATTACGATTTTGGTGCATGGGTTTGAATATTGGG GCCAGGGAACCCCTGGTCAACCGTCTCCTCA
IP:335965	2A11.003	NA	SEQ ID NO: 67	SEQ ID NO: 224
			GAAATTGTGTTGACGCAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCT GCAGGCCAGTCAGATTTTACCAGCACCTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCAGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCAGACAGGTTCACTGTCAGTGGCAGTG GGTCTGGACAGACTTCACTCTCACCATCAGCA GATTGGAGCCTGAAGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGCTCACCTCGCTTCGGCC AAGGGACACGACTGGAGATTAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTTCAGTAGCTATGGC ATGCATGGGTCCGCCAGGCTCCAGGCAAGGGA CTGGAGTGGTGGCAGTTATATGGTATGATGGA AGTAATAAATACTATGAAGACTCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAAATCCAAAGAAC ACGCTGTTTCTGCAAGTGAACAGCCTGAGAGCC GAGGACACGGCTGTGATTACTGTGCGAGAGGG ATTACGATTTTGGTGCATGGGTTTGAATATTGGG GCCAGGGAACCCCTGGTCAACCGTCTCCTCA
		AA	SEQ ID NO: 1637	SEQ ID NO: 1794
			EIVLTQSPGTLSPGERATLSCRASQIFTSTYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDF TLTISRLEPEDFAVYYCQQYGSSPRFGQGRLEIKR	QVQLVESGGGVVQGRSLRLSCAASGFSFSSYGM HWVRQAPGKGLEWVAIVWYDASNKYIEDAVKGG RFTISRDN SKNTLFLQVNSLRAEDTAVYYCARGITI FGHGFYWGQGLVTVSS
		AA	SEQ ID NO: 1638	SEQ ID NO: 1795
			EIVLTQSPGTLSPGERATLSCRASQIFTSTYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDF TLTISRLEPEDFAVYYCQQYGSSPRFGQGRLEIKR	QVQLVESGGGVVQGRSLRLSCAASGFSFSSYGM HWVRQAPGKGLEWVAIVWYDGSNKYYEDSVKGG RFTISRDN SKNTLFLQVNSLRAEDTAVYYCARGITI FGHGFYWGQGLVTVSS

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!PS:361158	2A11.004	NA	SEQ ID NO: 68	SEQ ID NO: 225
			GAAATTGTTGACGCAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGAAAGAGCCACCCCTCTCCT GCAGGCCAGTCAGATTTTACCAGCACCTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCAGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCAGACAGAGTTTCAAGTGGCAGTG GGTCTGGACAGACTTCACTCTCACCATCAGCA GATTGGAGCCTGAAGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGCTCACCTCGCTTCGGCC AAGGGACACGACTGGAGATTAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGATTCAAGTTTCAGTAGCTATGGC ATGCACTGGTCCGCCAGGCTCCAGGCAAGGGA CTGGAGTGGTGGCAGTTATATGGTATGATGGA AGTAATAAATACTATGAAGACGCCGTGAAGGCG CGATTCAACCATCTCCAGAGACAAATTCCAAGAAC ACGCTGTTTCTGCAAGTGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGGG ATTACGATTTTGGTCAATGGGTTTGAATATTGGG GCCAGGGAACCCCTGGTCAACCGTCTCCTCA
!PS:361165	2A11.005	NA	SEQ ID NO: 1639	SEQ ID NO: 1796
			EIVLTQSPGTLSPGERATLSCRASQIFTSTYLAW YQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDF TLTISRLEPEDFAVYYCQQYGSSPRFQGQTRLEIKR	QVQLVESGGGVQPGRSLRLSCAASGFSFSSYGM HWVRQAPGKGLEWVAIVWYDGSNKYYEDAVKG RFTISRDN SKNTLFLQVNSLRAEDTAVYYCARGITI FGHGFYWGQGLVTVSS
!PS:361165	2A11.005	NA	SEQ ID NO: 69	SEQ ID NO: 226
			GAAATTGTTGACGCAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGAAAGAGCCACCCCTCTCCT GCAGGCCAGTCAGATTTTACCAGCACCTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCAGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCAGACAGAGTTTCAAGTGGCAGTG GGTCTGGACAGACTTCACTCTCACCATCAGCA GATTGGAGCCTGAAGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGCTCACCTCGCTTCGGCC AAGGGACACGACTGGAGATTAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGATTCAAGTTTCAGTAGCTATGGC ATGCACTGGTCCGCCAGGCTCCAGGCAAGGGA CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGAAGACTCCGTGAAGGCG CGATTCAACCATCTCCAGAGACAAATTCCAAGAAC ACGCTGTTTCTGCAAGTGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGGG ATTACGATTTTGGTCAATGGGTTTGAATATTGGG GCCAGGGAACCCCTGGTCAACCGTCTCCTCA
!PS:361165	2A11.005	AA	SEQ ID NO: 1640	SEQ ID NO: 1797
			EIVLTQSPGTLSPGERATLSCRASQIFTSTYLAW YQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDF TLTISRLEPEDFAVYYCQQYGSSPRFQGQTRLEIKR	QVQLVESGGGVQPGRSLRLSCAASGFSFSSYGM HWVRQAPGKGLEWVAIVWYDASNKYYEDSVKG RFTISRDN SKNTLFLQVNSLRAEDTAVYYCARGITI FGHGFYWGQGLVTVSS

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!PS:361172	2G10_LC1.003	NA	SEQ ID NO: 70 GAAATAGTGATGACGCAGTCTCCAGCCACCCTG TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTTAGCAACCTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAAGCCACAGGGCC ACTGGTATCCCAAGCAGGTTCAAGTGCCAGTGGG TCTGGGACAGAGTTCACCTCCACCATCAGCAGC CTGCAGTCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTGGCCTCTCACTTTCGGCG GAGGGACCAAGGTGGAGATCAAACGA	SEQ ID NO: 227 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACTTCCAGTAAGTATGGC ATGCAGTGGTCCGCCAGGCTCCAGGCGAGGGG CTGGAGTGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAACTCCAAAGAAC ACGCTGTATCTGCAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTAATTACTGTGCGAGAGAT CAGCGGATTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCTGGTCAACCGTCTCCTCA
			SEQ ID NO: 1641 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQKPGQAPRLLIYGAAATRATGIPARFSGSGSTE FTLTISLQSEDFAVYYCQQYNWPLTFGGGKVE IKR	SEQ ID NO: 1798 QVQLVESGGGVVQPRSLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAIWFDASDKYYADA VKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGLTVTVSS
!PS:361178	2G10_LC1.004	NA	SEQ ID NO: 71 GAAATAGTGATGACGCAGTCTCCAGCCACCCTG TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTTAGCAACCTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAAGCCACAGGGCC ACTGGTATCCCAAGCAGGTTCAAGTGCCAGTGGG TCTGGGACAGAGTTCACCTCCACCATCAGCAGC CTGCAGTCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTGGCCTCTCACTTTCGGCG GAGGGACCAAGGTGGAGATCAAACGA	SEQ ID NO: 228 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACTTCCAGTAAGTATGGC ATGCAGTGGTCCGCCAGGCTCCAGGCGAGGGG CTGGAGTGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACTCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAACTCCAAAGAAC ACGCTGTATCTGCAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTAATTACTGTGCGAGAGAT CAGCGGATTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCTGGTCAACCGTCTCCTCA
			SEQ ID NO: 1642 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQKPGQAPRLLIYGAAATRATGIPARFSGSGSTE FTLTISLQSEDFAVYYCQQYNWPLTFGGGKVE IKR	SEQ ID NO: 1799 QVQLVESGGGVVQPRSLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAIWFDASDKYYADSVKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGLTVTVSS

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!PS:361185	2G10_LC1.005	NA	SEQ ID NO: 72	SEQ ID NO: 229
			GAAATAGTGATGACGCAGTCTCCAGCCACCCTG TCTGTCTCCAGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTAGCAGCACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGACGCCACCAGGGCC ACTGGTATCCAGCCAGGTTCAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGCAGTCTGAAGATTTTGCACTTATTACTGTC AGCAGTATAATAACTGGCTCTCACCTTTCGGCG GAGGGACCAAGGTGGAGATCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAATACTATGGC ATGCACCTGGTCCGCCAGGCTCCAGCGAGGGG CTGGAGTGGTGGCAGCTATATGGTTTGATGGA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAACTCCAAAGAAC ACGCTGTATCTGCAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCTGTGTACCGTCTCCTCA
!PS:361192	2G10_LC1.006	NA	SEQ ID NO: 1643	SEQ ID NO: 1800
			EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAAATRAATGIPARFSGSGTE FTLTISLQSEDFAVYYCQQYNWPLTFGGGKVE IKR	QVQLVESGGGVVQPRSLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAIWFDGSDKYADAVKG RFTISRDNKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGLVTVSS
!PS:361192	2G10_LC1.006	NA	SEQ ID NO: 73	SEQ ID NO: 230
			GAAATAGTGATGACGCAGTCTCCAGCCACCCTG TCTGTCTCTCCAGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTAGCAGCACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGACGCCACCAGGGCC ACTGGTATCCAGCCAGGTTCAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGCAGTCTGAAGATTTTGCACTTATTACTGTC AGCAGTATAATAACTGGCTCTCACCTTTCGGCG GAGGGACCAAGGTGGAGATCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAATACTATGGC ATGCACCTGGTCCGCCAGGCTCCAGCGAGGGG CTGGAGTGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAACTCCAAAGAAC ACGCTGTATCTGCAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCTGTGTACCGTCTCCTCA
!PS:361192	2G10_LC1.006	AA	SEQ ID NO: 1644	SEQ ID NO: 1801
			EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAAATRAATGIPARVSGSGTE FTLTISLQSEDFAVYYCQQYNWPLTFGGGKVE IKR	QVQLVESGGGVVQPRSLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAIWFDGSDKYADAVKG RFTISRDNKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGLVTVSS

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IP:359609	2G10 LC1.007	NA	SEQ ID NO: 74	SEQ ID NO: 231
			GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTAGCAGCACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGACGCCACCAGGGCC ACTGGTATCCAGCCAGGTTCAAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGGAGCCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTTCCCTCTCACTTTCCGGCGG AGGGACCAAGGTGGAGATCAAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTA ACTATGGC ATGCAC TGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAACTCCAAAGAAC AGCTGTATCTGCAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCTGTGTACCGTCTCCTCA
IP:359615	2G10 LC1.008	NA	SEQ ID NO: 1645	SEQ ID NO: 1802
			EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAAATRATGIPARFSGSGTE FTLTISSLEPEDFAVYYCQQYNPNPLTFGGGGTKVEI KR	QVQLVESGGGVQPGRSLRLSCAASGFTFSNYGM HWVRQAPGKGLEWVAIWFDASDKYYADAVKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGLVTVSS
IP:359615	2G10 LC1.008	NA	SEQ ID NO: 75	SEQ ID NO: 232
			GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTAGCAGCACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGACGCCACCAGGGCC ACTGGTATCCAGCCAGGTTCAAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGGAGCCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTATCCTCTCACTTTCCGGCGG AGGGACCAAGGTGGAGATCAAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTA ACTATGGC ATGCAC TGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAACTCCAAAGAAC AGCTGTATCTGCAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCTGTGTACCGTCTCCTCA
IP:359615	2G10 LC1.008	AA	SEQ ID NO: 1646	SEQ ID NO: 1803
			EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAAATRATGIPARFSGSGTE FTLTISSLEPEDFAVYYCQQYNPNPLTFGGGGTKVEI KR	QVQLVESGGGVQPGRSLRLSCAASGFTFSNYGM HWVRQAPGKGLEWVAIWFDASDKYYADAVKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGLVTVSS

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!PS:361196	2G10 LC1.009	NA	SEQ ID NO: 76	SEQ ID NO: 233
			GAAATAGTGATGACGAGTCTCCAGCCACCCTG TCTGTCTCCAGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTAGCAGCACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGACGCCACCAGGGCC ACTGGTATCCAGCCAGGTTCACTGAGGAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGGAGCCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTGGCTCTCACTTTCGGGG GAGGGACCAAGGTGGAGATCAAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAAGTATGGC ATGCACTGGTCCGCCAGGCTCCAGCGAGGGG CTGGAGTGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAACTCCAAAGAAC ACGCTGTATCTGCAAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCTGTGTACCGTCTCCTCA
!PS:361202	2G10 LC1.010	NA	SEQ ID NO: 1647	SEQ ID NO: 1804
			EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAAATRATGIPARFSGSGTE FTLTISSELPEDFAVYYCQQYNWPLTFGGGTKVE IKR	QVQLVESGGGVQPGRSLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAIWFDASDKYYADA VKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGLTVTVSS
!PS:361202	2G10 LC1.010	NA	SEQ ID NO: 77	SEQ ID NO: 234
			GAAATAGTGATGACGAGTCTCCAGCCACCCTG TCTGTCTCTCCAGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTAGCAGCACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGACGCCACCAGGGCC ACTGGTATCCAGCCAGGTTCACTGAGGAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGGAGCCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTGGCTCTCACTTTCGGGG GAGGGACCAAGGTGGAGATCAAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAAGTATGGC ATGCACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAACTCCAAAGAAC ACGCTGTATCTGCAAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCTGTGTACCGTCTCCTCA
!PS:361202	2G10 LC1.010	AA	SEQ ID NO: 1648	SEQ ID NO: 1805
			EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAAATRATGIPARFSGSGTE FTLTISSELPEDFAVYYCQQYNWPLTFGGGTKVE IKR	QVQLVESGGGVQPGRSLRLSCAASGFTFSNYGM HWVRQAPGKGLEWVAIWFDASDKYYADA VKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGLTVTVSS

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!PS:359644	18E3.002	NA	SEQ ID NO: 78	SEQ ID NO: 235
			GAAATTGTTGACGCAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCAGACAGGTTCACTGGCAGTG GGTCTGGACAGACTTCACTCTCACCATCAGCA GACTGGAGCCTGATGATTTGTCAGTGTATTACTG TCAGCAGTATGGTAGTTCAACCGCTCACTTTCGGC GGAGGGACCAAGGTGGAGATCAAAACGA	CAGGTGCAGTTGCAGGAGTCGGGGCCAGGACTG GTGAAGCCTTCAGAGACCCCTGTCCCTCACCTGC ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCCCCAGGGA AGGGCTGGAGTGGATTGGGTACATCTATTACA GTGGGAGCACCTACTACAACCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGTCTAAGA ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGGACACGGCCGTGTATTACTGTGCGAGAGA TCGTATTACGATTTTGGAGTGGTTATGGGGGGC GGTATGGACGTCTGGGGCCAAAGGGACACCGGTC ACCGTCTCCTCA
!PS:361206	18E3.003	NA	SEQ ID NO: 1649	SEQ ID NO: 1806
			EIVLTQSPGTLSPGERATLSCRASQISYSYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDF TLTISRLEPDDFAVYYCQQYGSSPLTFGGGKVEIK R	QVQLQESGPGLVKPSETLSLTCTVSGDSISSGGYY WSWIRQPPGKGLEWIGYIYSGSTYYNPSLKSRT ISVDTSKNQFSLKLSSTVAADTAVYYCARDRTITFG VVMGGMDVWVGQGTITVTVSS
!PS:361206	18E3.003	NA	SEQ ID NO: 79	SEQ ID NO: 236
			GAAATTGTTGACGCAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCAGACAGGTTCACTGGCAGTG GGTCTGGACAGACTTCACTCTCACCATCAGCA GACAGGAGCCTGATGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGTTCAACCGCTCACTTTCGG CGGAGGGACCAAGGTGGAGATCAAAACGA	CAGGTGCAGTTGCAGGAGTCGGGGCCAGGACTG GTGAAGCCTTCAGAGACCCCTGTCCCTCACCTGC ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCCCCAGGGA AGGGCTGGAGTGGATTGGGTACATCTATTACA GTGGGAGCACCTACTACAACCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGTCTAAGA ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGGACACGGCCGTGTATTACTGTGCGAGAGA TCGTATTACGATTTTGGAGTGGTTATGGGGGGC GGTATGGACGTCTGGGGCCAAAGGGACACCGGTC ACCGTCTCCTCA
!PS:361206	18E3.003	AA	SEQ ID NO: 1650	SEQ ID NO: 1807
			EIVLTQSPGTLSPGERATLSCRASQISYSYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDF TLTISRQEPDDFAVYYCQQYGSSPLTFGGGKVEI KR	QVQLQESGPGLVKPSETLSLTCTVSGDSISSGGYY WSWIRQPPGKGLEWIGYIYSGSTYYNPSLKSRT ISVDTSKNQFSLKLSSTVAADTAVYYCARDRTITFG VVMGGMDVWVGQGTITVTVSS

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	!PS:359628	18E3.004	NA	SEQ ID NO: 80	SEQ ID NO: 237
				GAAATTGTTGACGCGAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCT GCAGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCAGACAGGTTCAAGTGGCAGTG GGTCTGGACAGACTTCACTCTCACCATCAGCA GACTGGAGCCTGATGATTTTGCAGTGTATTACTG TCAGCAGTATGGTAGTTCAACCGCTCACTTTCGGC GGAGGGACCAAGGTGGAGATCAAAACGA	CAGGTGCAGTTGCAGGAGTCTGGGGCCAGGACTG GTGAAGCCTTACAGACCCCTGTCCCTCACCTGC ACTGTCTCTGGTACTCCATCAGCAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCCCCAGGGA AGGGCTGGAGTGGATTGGGTACATCTATTACA GTGGGAGCACCTACTACAACCCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGTCTAAGA ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGACACGGCCGTGTATTACTGTGCGAGAGA TCGTATTACGATTTTGGAGTGGTTATGGGGGGC GGTATGGACGTCTGGGGCCAAGGGACACCGGTC ACCGTCTCCTCA
	!PS:359637	18E3.005	NA	SEQ ID NO: 1651	SEQ ID NO: 1808
				EIVLTQSPGTLSPGERATLSCRASQISYSYLAW YQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDF TLTISRLEPDDFAVYYCQYGSSPLTFGGGTVKVEIK R	QVQLQESGPGLVKPSQTLSTCTVSGDSISSGGYY WSWIRQHPGKLEWIGYIYSGSTYYNPSLKSRT ISVDTSKNQFSLKLSSTVAADTAVYYCARDRTITFG VVMGGMDVWVGQTTVTVSS
	!PS:359637	18E3.005	NA	SEQ ID NO: 81	SEQ ID NO: 238
				GAAATTGTTGACGCGAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCT GCAGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCAGACAGGTTCAAGTGGCAGTG GGTCTGGACAGACTTCACTCTCACCATCAGCA GACTGGAGCCTGATGATTTTGCAGTGTATTACTG TCAGCAGTATGGTAGTTCAACCGCTCACTTTCGGC GGAGGGACCAAGGTGGAGATCAAAACGA	CAGGTGCAGTTGCAGGAGTCTGGGGCCAGGACTG GTGAAGCCTTACAGACCCCTGTCCCTCACCTGC ACTGTCTCTGGTACTCCATCAGCAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCACCCAGGGA AGGGCTGGAGTGGATTGGGTACATCTATTACA GTGGGAGCACCTACTACAACCCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGTCTAAGA ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGACACGGCCGTGTATTACTGTGCGAGAGA TCGTATTACGATTTTGGAGTGGTTATGGGGGGC GGTATGGACGTCTGGGGCCAAGGGACACCGGTC ACCGTCTCCTCA
	!PS:359637	18E3.005	AA	SEQ ID NO: 1652	SEQ ID NO: 1809
				EIVLTQSPGTLSPGERATLSCRASQISYSYLAW YQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDF TLTISRLEPDDFAVYYCQYGSSPLTFGGGTVKVEIK R	QVQLQESGPGLVKPSETLSLTCTVSGDSISSGGYY WSWIRQHPGKLEWIGYIYSGSTYYNPSLKSRT ISVDTSKNQFSLKLSSTVAADTAVYYCARDRTITFG VVMGGMDVWVGQTTVTVSS

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	!PS:361210	18E3.006	NA	SEQ ID NO: 82 GAAATTGTTGTTGACGCAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCT GCAGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCAGACAGGTTCAAGTGGCAGTG GGTCTGGACAGACTTCACTCTCACCATCAGCA GACTGGAGCCTGATGATTTTGCAGTGTATTACTG TCAGCAGTATGGTAGTTCAACCGCTCACTTTCGGC GGAGGGACCAAGGTGGAGATCAAAACGA	SEQ ID NO: 239 CAGGTGCAGTTGCAGGAGTCTGGGGCCAGGACTG GTGAAGCCTTACAGACCCCTGTCCCTCACCTGC ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCACCAGGGA AGGGCTGGAGTGGATTGGGTACATCTATTACA GTGGGAGCACCTACTACAACCCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGTCTAAGA ACCACTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGACACGGCCGTGTATTACTGTGCGAGAGA TCGTATTACGATTTTGGAGTGGTTATGGGGGGC GGTATGGACGTCTGGGGCCAAGGGACCACGGTC ACCGTCTCCTCA
				SEQ ID NO: 1653 EIVLTQSPGTLSPGERATLSCRASQISYSYLAW YQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDF TLTISRLEPDDFAVYYCQYQYSSPLTFGGGKVEIK R	SEQ ID NO: 1810 QVQLQESGPGLVKPSQTLSTCTVSGDSISSGGYY WSWIRQHPGKGLEWIGYIYSGSTYINPSLKSRT ISVDTSKNQFSLKLSSTVAADTAVYYCARDRTITFG VVMGGMDVWVGQTTVTVSS
	!PS:361214	18E3.007	NA	SEQ ID NO: 83 GAAATTGTTGTTGACGCAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCT GCAGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCAGACAGGTTCAAGTGGCAGTG GACTGGAGCCTGATGATTTTGCAGTGTATTACT GACAGGAGCCTGATGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGTTCAACCGCTCACTTTCGG CGGAGGGACCAAGGTGGAGATCAAAACGA	SEQ ID NO: 240 CAGGTGCAGTTGCAGGAGTCTGGGGCCAGGACTG GTGAAGCCTTACAGACCCCTGTCCCTCACCTGC ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCACCAGGGA AGGGCTGGAGTGGATTGGGTACATCTATTACA GTGGGAGCACCTACTACAACCCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGTCTAAGA ACCACTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGACACGGCCGTGTATTACTGTGCGAGAGA TCGTATTACGATTTTGGAGTGGTTATGGGGGGC GGTATGGACGTCTGGGGCCAAGGGACCACGGTC ACCGTCTCCTCA
				SEQ ID NO: 1654 EIVLTQSPGTLSPGERATLSCRASQISYSYLAW YQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDF TLTISRLEPDDFAVYYCQYQYSSPLTFGGGKVEI KR	SEQ ID NO: 1811 QVQLQESGPGLVKPSQTLSTCTVSGDSISSGGYY WSWIRQHPGKGLEWIGYIYSGSTYINPSLKSRT ISVDTSKNQFSLKLSSTVAADTAVYYCARDRTITFG VVMGGMDVWVGQTTVTVSS

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!PS:361218	18E3.008	NA	SEQ ID NO: 84	SEQ ID NO: 241
			GAAATTGTTGACGCGAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCT GCAGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCAGACAGAGTTCAAGTGGCAGTG GGTCTGGACAGACTTCACTCTCACCATCAGCA GACAGAGCCTGATGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGTTCAACCGCTCACTTTCCGG CGGAGGGACCAAGGTGGAGATCAAAACGA	CAGGTGCAGTTGCAGGAGTCGGGGCCAGGACTG GTGAAGCCTTACAGACCCTGTCCCTCACCTGC ACTGTCTCTGGTGAAGTCCATCAGCAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCCCCAGGGA AGGCTGGAGTGGATTGGGTACATCTATTACA GTGGGAGCACCTACTACAACCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGTCTAAGA ACCAAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGGACACGGCCGTGTATTACTGTGCGAGAGA TCGTATTACGATTTTGGAGTGGTTATGGGGGGC GGTATGGACGTCTGGGGCCAAAGGGACCACGGTC ACCGTCTCCTCA
!PS:361222	5C2.006	NA	SEQ ID NO: 1655	SEQ ID NO: 1812
			EIVLTQSPGTLSPGERATLSCRASQISYSYLAW YQKPGQAPRLIYGASSRATGIPDRFSGSGGTDF TLTISRQEPDDFAVYYCQYQYSSPLTFGGGKVEI KR	QVQLQESGPGLVKPSQTLSTCTVSGDSISSGGYY WSWIRQPPGKGLEWIGYIYSGSTYYPNPSLKSRT ISVDTSKNQFSLKLSSTVAADTAVYYCARDRIITFG VVMGGMDVWVGQTTVTVSS
!PS:361222	5C2.006	NA	SEQ ID NO: 85	SEQ ID NO: 242
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTATTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG CAACCAGGACATCCTCCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGTCCCTGACC GATTCAGTGGCAGCGGTCTGGGACAGATTICA CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTTCGGCCAAAGGGACCAAGGTGGA AATCAAAACGA	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCGACAGGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATCAACCTGAAAGT GGTGGCACAGACTATTACAGAGGTTTCAGGGC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCTACATGGAACCTGAACAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCGTCT CCTCA
		AA	SEQ ID NO: 1656	SEQ ID NO: 1813
			DIVMTQSPDSLAVSLGERATINCKSSQVLSNNK NYIAWYQQQPGHPPKLLIYWASTRESGVDPFRFSGS GSGTDFLTISSLQAEDVAVFYCQQYYPWPWTFGQ GTKVEIKR	QVQLVQSGAEVKKPGASVKVSKASGYTFTGYI HWVRQAPGQGLEWMGWINPESGGTDYSQRFQGR VTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGLVTVSS

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!PS:361229	SC2.007	NA	SEQ ID NO: 86	SEQ ID NO: 243
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAAGCAG CAACAGGACATCCTCCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGGTCCCTGACC GATTCAGTGGCAGCGGGTCTGGGACAGATTTC CTCTCACCATCAGCAGCCTGCAGGCTGAAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAAAGGGACCAAGGTGGA AATCAAAACGA	CAGTGCCCGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCAGACAGGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATCAACCTGAAAGT GGTGGCACAGACTATTCACAGAGGTTTCAGGGC AGGTTCAACCATGACCAAGGACACGTCATCAGC ACAGCCTACATGGAACCTGAACAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCGTCT CCTCA
!PS:361236	SC2.008	AA	SEQ ID NO: 1657	SEQ ID NO: 1814
			DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQPGHPPKLLIYWASTRESGVPDFRFGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR	QVPLVQSGAEVKKPGASVKVCKASGYTFTGYI HWVRAPQGQGLEWMGWINPESGGTDYSQRFQGR FTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI FGMVIVPFDYWQQGTLVTVSS
!PS:361236	SC2.008	NA	SEQ ID NO: 87	SEQ ID NO: 244
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAAGCAG CAACCAGGACATCCTCCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGGTCCCTGACC GATTCAGTGGCAGCGGGTCTGGGACAGATTTC CTCTCACCATCAGCAGCCTGCAGGCTGAAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAAAGGGACCAAGGTGGA AATCAAAACGA	CAGGTGCAGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCAGACAGGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATCAACCCCTGACGCT GGTGGCACAGACTATTCACAGAGGTTTCAGGGC AGGTTCAACCATGACCAAGGACACGTCATCAGC ACAGCCTACATGGAACCTGAACAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCGTCT CCTCA
!PS:361236	SC2.008	AA	SEQ ID NO: 1658	SEQ ID NO: 1815
			DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQPGHPPKLLIYWASTRESGVPDFRFGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR	QVQLVQSGAEVKKPGASVKVCKASGYTFTGYI HWVRAPQGQGLEWMGWINPDAGGTDYSQRFQGR RVTMTRDTSISTAYMELNRLRSDDTAVYYCAREA TIFGMVIVPFDYWQQGTLVTVSS

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!PS:359685	SC2.009	NA	SEQ ID NO: 88	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAAGCAG CAACAGGACATCCTCCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGGTCCCTGACC GATTCAGTGGCAGCGGGTCTGGGACAGATTTC CTCTACCATCAGCAGCCTGCAGGCTGAAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAAAGGGACCAAGGTGGA AATCAAAACGA	SEQ ID NO: 245	CAGTGCCGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCAGACAGGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATCAACCTGTACGGCT GGTGGCACAGACTATTCACAGAGGTTTCAAGGC AGGTTCAACCATGACCAAGGACACGTCATCAGC ACAGCCTACATGGAACCTGAACAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCGTCT CCTCA
			SEQ ID NO: 1659	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQPGHPPKLLIYWASTRESGVPDFRFGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR	SEQ ID NO: 1816	QVPLVQSGAEVKKPGASVKVCKASGYTFTGYI HWVRAPQGQGLEWMGWINPDAGGTDYSQRFQ RFTMTRDTSISTAYMELNRLRSDDTAVYYCAREA TIFGMVIVPFDYWGGQTLVTVSS
!PS:361240	SC2.010	NA	SEQ ID NO: 89	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAAGCAG CAACAGGACATCCTCCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGGTCCCTGACC GATTCAGTGGCAGCGGGTCTGGGACAGATTTC CTCTACCATCAGCAGCCTGCAGGCTGAAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAAAGGGACCAAGGTGGA AATCAAAACGA	SEQ ID NO: 246	CAGTGCGAGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCAGACAGGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATCAACCCGTGACAGT GGTGGCACAGACTATTCACAGAGGTTTCAAGGC AGGTTCAACCATGACCAAGGACACGTCATCAGC ACAGCCTACATGGAACCTGAACAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCGTCT CCTCA
			SEQ ID NO: 1660	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQPGHPPKLLIYWASTRESGVPDFRFGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR	SEQ ID NO: 1817	QVQLVQSGAEVKKPGASVKVCKASGYTFTGYI HWVRAPQGQGLEWMGWINPDGSGTDYSQRFQGR VTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI FGMVIVPFDYWGGQTLVTVSS

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!PS:361247	SC2.011	NA	SEQ ID NO: 90	SEQ ID NO: 247
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG CAACAGGACATCCTCCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGGTCCCTGACC GATTCAGTGGCAGCGGCTCTGGGACAGATTTC CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAAAGGGACCAAGGTGGA AATCAAAACGA	CAGGTGCAGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATCAACCTTGACAGT GGTGGCACAGACTATTCACAGAGGTTTCAAGGGC AGGTTCAACCATGACCAAGGACACGTCATCAGC ACAGCCTACATGGAACCTGAACAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCGTCT CCTCA
!PS:361254	SC2.012	NA	SEQ ID NO: 1661	SEQ ID NO: 1818
			DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQPGHPPKLLIYWASTRESGVPDFRFGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR	QVQLVQSGAEVKKPGASVKVSKASGYTFTGYI HWVRAPGQGLEWMGWINPDSGGTDYSQRFQGR FTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGLVTVSS
!PS:361254	SC2.012	NA	SEQ ID NO: 91	SEQ ID NO: 248
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG CAACCAGGACATCCTCCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGGTCCCTGACC GATTCAGTGGCAGCGGCTCTGGGACAGATTTC CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAAAGGGACCAAGGTGGA AATCAAAACGA	CAGGTGCCCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATCAACCCCTGACAGT GGTGGCACAGACTATTCACAGAGGTTTCAAGGGC AGGTTCAACCATGACCAAGGACACGTCATCAGC ACAGCCTACATGGAACCTGAACAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCGTCT CCTCA
!PS:361254	SC2.012	AA	SEQ ID NO: 1662	SEQ ID NO: 1819
			DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQPGHPPKLLIYWASTRESGVPDFRFGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR	QVPLVQSGAEVKKPGASVKVSKASGYTFTGYI HWVRAPGQGLEWMGWINPDSGGTDYSQRFQGR VTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGLVTVSS

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!PS:361261	SC2.013	NA	SEQ ID NO: 92	SEQ ID NO: 249
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAAGCAG CAACAGGACATCCTCCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGGTCCCTGACC GATTCAGTGGCAGCGGGTCTGGGACAGATTTC CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAAAGGGACCAAGGTGGA AATCAAAACGA	CAGGTGCAGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATCAACCTTGACGCT GGTGGCACAGACTATTCACAGAGGTTTCAAGGGC AGGTTCAACCATGACCAAGGACACGTCATCAGC ACAGCCTACATGGAACCTGAACAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCGTCT CCTCA
!PS:361268	SC2.014	NA	SEQ ID NO: 1663	SEQ ID NO: 1820
			DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQPGHPPKLLIYWASTRESGVPDFRFGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR	QVQLVQSGAEVKKPGASVKVSKASGYTFTGYI HWVRAPQGQGLEWMGWINPDAGGTDYSQRFQ RFTMTRDTSISTAYMELNRLRSDDTAVYYCAREA TIFGMVIVPFDYWGQGLVTVSS
!PS:361268	SC2.014	NA	SEQ ID NO: 93	SEQ ID NO: 250
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAAGCAG CAACCAGGACATCCTCCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGGTCCCTGACC GATTCAGTGGCAGCGGGTCTGGGACAGATTTC CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAAAGGGACCAAGGTGGA AATCAAAACGA	CAGGTGCCGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATCAACCCCTGACGCT GGTGGCACAGACTATTCACAGAGGTTTCAAGGGC AGGTTCAACCATGACCAAGGACACGTCATCAGC ACAGCCTACATGGAACCTGAACAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCGTCT CCTCA
!PS:361268	SC2.014	AA	SEQ ID NO: 1664	SEQ ID NO: 1821
			DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQPGHPPKLLIYWASTRESGVPDFRFGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR	QVPLVQSGAEVKKPGASVKVSKASGYTFTGYI HWVRAPQGQGLEWMGWINPDAGGTDYSQRFQ RVTMTRDTSISTAYMELNRLRSDDTAVYYCAREA TIFGMVIVPFDYWGQGLVTVSS

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!PS:359669	SC2.015	NA	SEQ ID NO: 94	SEQ ID NO: 251
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAAGCAG AACCAAGGACAACCTCCTAAGCTGCTCATTTAC TGGGCATCTACCCGGGAATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAAGCAGCTGCGAGGCTGAAGAT GTGGCAGTTTTTTACTGTCAACAATATTATAGTA CTCCGTGGACGTTCTGGCCAAAGGGACCAAGGTGG AAATCAAAACGA	CAGGTGCAGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATCAACCTGTACGGCT GGTGGCACAGACTATTCACAGAGGTTTCAAGGGC AGGGTCAACCATGACCAAGGGACACGTCCATCAGC ACAGCCTACATGGAACCTGAACAGCCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCAACCGTCT CCTCA
!PS:359678	SC2.016	NA	SEQ ID NO: 1665	SEQ ID NO: 1822
			DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQKPGQPPKLLIYWASTRESGVPDFRFGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR	QVQLVQSGAEVKKPGASVKVSKASGYTFTGYI HWVRAPQGQGLEWMGWINPDAGGTDYSQRFQ RVMTTRDTSISTAYMELNSLRSDDTAVYYCAREA TIFGMVIVPFDYWGQGLVTVSS
!PS:359678	SC2.016	NA	SEQ ID NO: 95	SEQ ID NO: 252
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAAGCAG AAACCAGGACAACCTCCTAAGCTGCTCATTTAC TGGGCATCTACCCGGGAATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAAGCAGCTGCGAGGCTGAAGAT GTGGCAGTTTTTTACTGTCAACAATATTATAGTA CTCCGTGGACGTTCTGGCCAAAGGGACCAAGGTGG AAATCAAAACGA	CAGGTGCAGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATCAACCTGAAAGT GGTGGCACAGACTATTCACAGAGGTTTCAAGGGC AGGGTCAACCATGACCAAGGGACACGTCCATCAGC ACAGCCTACATGGAACCTGAACAGCCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCAACCGTCT CCTCA
!PS:359678	SC2.016	AA	SEQ ID NO: 1666	SEQ ID NO: 1823
			DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQKPGQPPKLLIYWASTRESGVPDFRFGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR	QVQLVQSGAEVKKPGASVKVSKASGYTFTGYI HWVRAPQGQGLEWMGWINPESGGTDYSQRFQGR VTMTRDTSISTAYMELNSLRSDDTAVYYCAREATI FGMVIVPFDYWGQGLVTVSS

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	!PS:361275	11C1.002	NA	SEQ ID NO: 96 GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAACAG AACCAAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTGGCCAAAGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 96 CAGTGCCGCTGGTACAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCGTCAGGCCCTTGGACAAGGG CTTGTGTGATGGGTGGATCAGCCCTAACAGT GGTGAACAAAGCTATGCACAGAAGTTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGACTGAGATCT GACGACACGGCCGTGATTTCTGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA	SEQ ID NO: 253
				SEQ ID NO: 1667 DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRESGVDPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1824 QVPLVQSGAEVKKPGASVKVCKASGYTFTGYI HWVRQAPGQGLVWMGWISPNSETSYAQKFQDR VTMTRDTSISTAYMELSRRLSDDTAVYFCAREATI FGMLIVPFDYWGQGLVTVSS	SEQ ID NO: 254
	!PS:361282	11C1.003	NA	SEQ ID NO: 97 GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAACAG AACCAAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTGGCCAAAGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 97 CAGTGCCGCTGGTACAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCGTCAGGCCCTTGGACAAGGG CTTGTGTGATGGGTGGATCAGCCCTAACAGT GGTGACACAAAGCTATGCACAGAAGTTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGACTGAGATCT GACGACACGGCCGTGATTTCTGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA	SEQ ID NO: 1825
				SEQ ID NO: 1668 DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRESGVDPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1825 QVPLVQSGAEVKKPGASVKVCKASGYTFTGYI HWVRQAPGQGLVWMGWISPNSETSYAQKFQDR VTMTRDTSISTAYMELSRRLSDDTAVYFCAREATI FGMLIVPFDYWGQGLVTVSS	

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	!PS:361289	11C1.004	NA	SEQ ID NO: 98	SEQ ID NO: 255
				GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAACAG AACCAAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGCCAAGGGACCAAGGTGG AAATCAAAACGA	CAGTGCCGCTGGTACAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCGTCAGGCCCTTGGACAAGGG CTTGTGTGATGGGTGGATCAGCCCTAACAGT GGTGAACAAAGCTATGCACAGAAGTTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGACTGAGATCT GACGACACGGCCGTGATTTCTGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
AA				SEQ ID NO: 1669	SEQ ID NO: 1826
				DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRDSGVPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	QVPLVQSGAEVKKPGASVKVCKASGYTFTGYI HWVRQAPGQGLVWMGWISPNSETSYAQKFQDR VTMTRDTSISTAYMELSRLRSDDTAVYFCAREATI FGMLIVPFDYWGQGLVTVSS
	!PS:359712	11C1.005	NA	SEQ ID NO: 99	SEQ ID NO: 256
				GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAACAG AAACCAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGAAATCCGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGCCAAGGGACCAAGGTGG AAATCAAAACGA	CAGTGCCGCTGGTACAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCGTCAGGCCCTTGGACAAGGG CTTGTGTGATGGGTGGATCAGCCCTAACAGT GGTGAACAAAGCTATGCACAGAAGTTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGACTGAGATCT GACGACACGGCCGTGATTTCTGTACGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
AA				SEQ ID NO: 1670	SEQ ID NO: 1827
				DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRDSGVPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	QVPLVQSGAEVKKPGASVKVCKASGYTFTGYI HWVRQAPGQGLVWMGWISPNSETSYAQKFQDR VTMTRDTSISTAYMELSRLRSDDTAVYFCAREATI FGMLIVPFDYWGQGLVTVSS

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!PS:361293	11C1.006	NA	SEQ ID NO: 100 GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAACAG AACCAAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 257 CAGGTGCCGCTGGTACAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCGTCAGGCCCTTGGACAAGGG CTTGTGTGGATGGGTGGATCAGCCCTAACAGT GGTGACACAAGCTATGCACAGAAGTTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGACTGAGATCT GACGACACGGCCGTGATTTCTGTACGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
			SEQ ID NO: 1671 DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRESGVDPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1828 QVPLVQSGAEVKKPGASVKVCKASGYTFTGYI HWVRQAPGQGLVWMGWISPNSGDTSYAQKFQDR VTMTRDTSISTAYMELSRRLSDDTAVYFCTREATI FGMLIVPFDYWGQGLVTVSS
!PS:361297	11C1.007	NA	SEQ ID NO: 101 GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAACAG AAACCAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 258 CAGGTGCCGCTGGTACAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCGTCAGGCCCTTGGACAAGGG CTTGTGTGGATGGGTGGATCAGCCCTAACAGT GGTGAAACAAGCTATGCACAGAAGTTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGACTGAGATCT GACGACACGGCCGTGATTTCTGTACGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
			SEQ ID NO: 1672 DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRDSGVDPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1829 QVPLVQSGAEVKKPGASVKVCKASGYTFTGYI HWVRQAPGQGLVWMGWISPNSGDTSYAQKFQDR VTMTRDTSISTAYMELSRRLSDDTAVYFCTREATI FGMLIVPFDYWGQGLVTVSS

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!PS:361301	11C1.008	NA	SEQ ID NO: 102 GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAACAG AACCAAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 259 CAGGTGCCGCTGGTACAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCGTCAGGCCCTTGGACAAGGG CTTGTGTGATGGGTGGATCAGCCCTAACAGT GGTGACACAAGCTATGCACAGAAGTTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGACTGAGATCT GACGACACGGCCGTGATTTCTGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCAACCGTCT CCTCA
			SEQ ID NO: 1673 DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRDSGVPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1830 QVPLVQSGAEVKKPGASVKVCKASGYTFTGYI HWVRAPGQGLVWMGWISPNSGDTSYAQKFQDR VTMTRDTSISTAYMELSRLSRDDTAVYFCAREATI FGMLIVPFDYWGQGLVTVSS
!PS:359703	11C1.009	NA	SEQ ID NO: 103 GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAACAG AAACCAGGACAGCCTCCTAAACTGCTCATTTAC TGGACTTCTACCCGAGAAATCCGGGTCCCTGAC CGATTTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 260 CAGGTGCAGCTGGTACAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCGTCAGGCCCTTGGACAAGGG CTTGAGTGGATGGGTGGATCAGCCCTAACAGT GGTGAAACAAGCTATGCACAGAAGTTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGCCTGAGATCT GACGACACGGCCGTGATTTCTGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCAACCGTCT CCTCA
			SEQ ID NO: 1674 DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRDSGVPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1831 QVQLVQSGAEVKKPGASVKVCKASGYTFTGYI HWVRAPGQGLEWMGWISPNSETSYAQKFQDR VTMTRDTSISTAYMELSSLRSDDTAVYFCAREATI FGMLIVPFDYWGQGLVTVSS

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!PS:361305	11C1.010	NA	SEQ ID NO: 104 GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCCTGGGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACTTAGCTTGGTACCAACAG AACCAAGGACAGCTCTAACCTGCTCATTTAC TGGACTTCTACCCGAGAAATCCGGGGTCCCTGAC CGATTCAAGTGGACGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGGACCAAGGTGG AATCAAAACGA	SEQ ID NO: 261 CAGGTGCAGCTGGTACAGTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCGTCAGGCCCTTGGACAAGGG CTTGAGTGGATGGGTGGATCAGCCCTAACAGT GGTGAACAAAGCTATGCACAGAAGTTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGACTGAGATCT GACGACACGGCCGTGATTTCTGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
			SEQ ID NO: 1675 DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRESGVPDFRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1832 QVQLVQSGAEVKKPGASVKVSKASGYTFTGYI HWVRAPGQGLEWMGWISPNSETSYAQKFQDR VTMTRDTSISTA YMELSR LRSDDTAVYFCAREATI FGMLIVPDFYWGQGLVTVSS
!PS:361312	13H12.002	NA	SEQ ID NO: 105 GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCCTGGGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAAGCAG AAACCAGGACATCCTCCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGTCCCTGACC GATTCAGTGGCAGCGGTCTGGGACAGATTTC CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAAAGGGACCAAGGTGGA AATCAAAACGA	SEQ ID NO: 262 CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCGACAGGCCCTTGGACAAGGA CTTGAGTGGATGGGTGGATCAACCCCTGAAAGT GGTGGCACAGACTATTACAGAGGTTTCAGGGC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTACATGGAACCTGAGCAGGCTGAGATCT GACGACACGGCCGTGTTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGTTATTGTACCCGTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
			SEQ ID NO: 1676 DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGHPPKLLIYWASTRESGVPDFRFSG SGSGTDFLTISSLQAEDVAVFYCQQYYSTPWFQ GQGTKVEIKR	SEQ ID NO: 1833 QVPLVQSGAEVKKPGASVKVSKASGYTFTGYI HWVRAPGQGLEWMGWISPNSETSYAQKFQDR VTMTRDTSISTA YMELSR LRSDDTAVYFCAREATI FGMVIVPDFYWGQGLVTVSS

A-2124-WO-PCT

	!PS:359744	13H12.003	NA	SEQ ID NO: 106 GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAAGCAG AACCAAGGACATCCCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGGTCCCTGACC GATTCAGTGGCAGCGGCTCTGGGACAGATTTC CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAAAGGGACCAAGGTGGA AATCAAAACGA	SEQ ID NO: 263 CAGGTGCCGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCACAGGCCCTGGACAAAGGA CTTGAGTGGATGGGTGGATCAACCTGAAAGT GGTGGCACAGACTATTCACAGAGGTTTCAGGGC AGGTTCAACCATGACCAAGGACACGTCATCAGC ACAGCCTACATGGAACCTGACAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
				SEQ ID NO: 1677 DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQKPGHPPKLLIYWASTRESGVPDFRFGS GSGTDFLTITSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR	SEQ ID NO: 1834 QVPLVQSGAEVKKPGASVKVCKASGYTFTGYYI HWVRAPGQGLEWMGWINPESGGTDYSQRFQGR FTMTRDTSISTAYMELSRISDDTAVYYCAREATI FGMVIVPFDYWGQGLVTVSS
	!PS:361319	13H12.004	NA	SEQ ID NO: 107 GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAAGCAG AAACCAGGACATCCCTCCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGGTCCCTGACC GATTCAGTGGCAGCGGCTCTGGGACAGATTTC CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAAAGGGACCAAGGTGGA AATCAAAACGA	SEQ ID NO: 264 CAGGTGCCGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCACAGGCCCTGGACAAAGGA CTTGAGTGGATGGGTGGATCAACCCTGACAGT GGTGGCACAGACTATTCACAGAGGTTTCAGGGC AGGTTCAACCATGACCAAGGACACGTCATCAGC ACAGCCTACATGGAACCTGACAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
				SEQ ID NO: 1678 DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQKPGHPPKLLIYWASTRESGVPDFRFGS GSGTDFLTITSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR	SEQ ID NO: 1835 QVPLVQSGAEVKKPGASVKVCKASGYTFTGYYI HWVRAPGQGLEWMGWINPDSGGTDYSQRFQGR VTMTRDTSISTAYMELSRISDDTAVYYCAREATI FGMVIVPFDYWGQGLVTVSS

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	!PS:359737	13H12.005	NA	SEQ ID NO: 108	SEQ ID NO: 265
				GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAAGCAG AACCAAGGACAACCTCCTAAGCTGCTCATTTAC TGGGCATCTACCCGGGAATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAAGCAGCTGCGAGGCTGAAGAT GTGGCAGTTTTTTACTGTCAACAATATTATAGTA CTCCGTGGACGTTCTGGCCAAAGGGACCAAGGTGG AAATCAAAACGA	CAGGTGCAGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCAGACAGGCCCTGGACAAGGA CTTGAGTGGATGGGTGGATCAACCTGAAAGT GGTGGCACAGACTATTACAGAGGTTTCAGGGC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCTACATGGAACCTGAGCAGCCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
AA				SEQ ID NO: 1679	SEQ ID NO: 1836
				DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQKPGQPPKLLIYWASTRESGVPDFRFGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR	QVQLVQSGAEVKKPGASVKVSKASGYTFTGYI HWVRAPGQGLEWMGWINPESGGTDYSQRFQGR VTMTRDTSISTAYMELSSLRSDDTAVYYCAREATI FGMVIVPFDYWGQGLVTVSS
NA	!PS:361326	13H12.006		SEQ ID NO: 109	SEQ ID NO: 266
				GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAAGCAG AACCAAGGACAACCTCCTAAGCTGCTCATTTAC TGGGCATCTACCCGGGAATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAAGCAGCTGCGAGGCTGAAGAT GTGGCAGTTTTTTACTGTCAACAATATTATAGTA CTCCGTGGACGTTCTGGCCAAAGGGACCAAGGTGG AAATCAAAACGA	CAGGTGCCGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCAGACAGGCCCTGGACAAGGA CTTGAGTGGATGGGTGGATCAACCCTGAAAGT GGTGGCACAGACTATTACAGAGGTTTCAGGGC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCTACATGGAACCTGAGCAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
AA				SEQ ID NO: 1680	SEQ ID NO: 1837
				DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQKPGQPPKLLIYWASTRESGVPDFRFGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR	QVPLVQSGAEVKKPGASVKVSKASGYTFTGYI HWVRAPGQGLEWMGWINPESGGTDYSQRFQGR VTMTRDTSISTAYMELSSLRSDDTAVYYCAREATI FGMVIVPFDYWGQGLVTVSS

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!PS:361330	12H11.002	NA	SEQ ID NO: 110 GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAGCAG AACCAAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 267 CAGGTGCCGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCGTCAGGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATAAGCCCTAACCAA GGTGAAACAAACTATGCACAGAAATTTACAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT GACGACACGGCCGTGTTACTGTGCGGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCGTCT CCTCA
		AA	SEQ ID NO: 1681 DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRDSGVPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1838 QVPLVQSGAEVKKPGASVKVCKASGYTFTGYYI HWVRAPQGQGLEWMGWISPNQGETNYAQKFQD RVTMTDRDTSISTAYMELSLRSDDTAVYYCAREA TIFGMLIVPFDYWGQGLTVTVSS
!PS:361337	12H11.003	NA	SEQ ID NO: 111 GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAGCAG AAACCAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 268 CAGGTGCCGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCGTCAGGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATAAGCCCTAACCAA GGTGACACAAACTATGCACAGAAATTTACAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT GACGACACGGCCGTGTTACTGTGCGGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCGTCT CCTCA
		AA	SEQ ID NO: 1682 DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRDSGVPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1839 QVPLVQSGAEVKKPGASVKVCKASGYTFTGYYI HWVRAPQGQGLEWMGWISPNQGETNYAQKFQD RVTMTDRDTSISTAYMELSLRSDDTAVYYCAREA TIFGMLIVPFDYWGQGLTVTVSS

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	!PS:361344	12H11.004	NA	SEQ ID NO: 112 GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAGCAG AACCAAGGACAGCTCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 269 CAGGTGCCGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCGTCAGGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATAAGCCCTAACCAA GGTGAAACAAACTATGCACAGAAATTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT GACGACACGGCCGTGTTACTGTACGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCGTCT CCTCA
				SEQ ID NO: 1683 DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRD SGVPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1840 QVPLVQSGAEVKKPGASVKVCKASGYTFTGYYI HWVRAPQGQGLEWMGWISPNQGETNYAQKFQD RVTMTDRDTSISTAYMELSLRSDDTAVYYCTREA TIFGMLIVPFDYWGQGLTVTVSS
	!PS:361351	12H11.005	NA	SEQ ID NO: 113 GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAGCAG AAACCAGGACAGCTCTTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 270 CAGGTGCCGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCGTCAGGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATAAGCCCTAACCAAT GGTGAAACAAACTATGCACAGAAATTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT GACGACACGGCCGTGTTACTGTGCGGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCGTCT CCTCA
				SEQ ID NO: 1684 DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRD SGVPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1841 QVPLVQSGAEVKKPGASVKVCKASGYTFTGYYI HWVRAPQGQGLEWMGWISPNQGETNYAQKFQD RVTMTDRDTSISTAYMELSLRSDDTAVYYCAREA TIFGMLIVPFDYWGQGLTVTVSS

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	!PS:361358	12H11.006	NA	SEQ ID NO: 114 GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAGCAG AACCAAGGACAGCTCTTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCAAGGTGG AAATCAAACGA	SEQ ID NO: 271 CAGGTGCCGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCGTCAGGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATAAGCCCTAACAAAT GGTGACACAAACTATGCACAGAAATTTACAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT GACGACACGGCCGTGTTACTGTGCGGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCGTCT CCTCA
				SEQ ID NO: 1685 DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRD SGVPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1842 QVPLVQSGAEVKKPGASVKVCKASGYTFTGYYI HWVRAPQGQLEWMGWISPNNGDTNYAQKFQD RVTMTDRDTSISTAYMELSLRSDDTAVYYCAREA TIFGMLIVPFDYWGQGLTVTVSS
	!PS:361365	12H11.007	NA	SEQ ID NO: 115 GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAGCAG AAACCAGGACAGCTCTTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCAAGGTGG AAATCAAACGA	SEQ ID NO: 272 CAGGTGCCGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCGTCAGGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATAAGCCCTAACCAA GGTGACACAAACTATGCACAGAAATTTACAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT GACGACACGGCCGTGTTACTGTACGAGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCGTCT CCTCA
				SEQ ID NO: 1686 DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRD SGVPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1843 QVPLVQSGAEVKKPGASVKVCKASGYTFTGYYI HWVRAPQGQLEWMGWISPNNGDTNYAQKFQD RVTMTDRDTSISTAYMELSLRSDDTAVYYCTREA TIFGMLIVPFDYWGQGLTVTVSS

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	!PS:361372	12H11.008	NA	SEQ ID NO: 116 GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAGCAG AACCAAGGACAGCTCTTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 116 CAGTGCCGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGTGCGTCAGGCCCTTGGACAAGGG CTTGAGTGGATGGGTGGATAAGCCCTAACAAAT GGTGAACAAACTATGCACAGAAATTTACAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT GACGACACGGCCGTGTTACTGTACGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCAACCGTCT CCTCA	SEQ ID NO: 273
				SEQ ID NO: 1687 DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRDSGVPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1844 QVPLVQSGAEVKKPGASVKVCKASGYTFTGYYI HWVRAPQGQGLEWMGWISPNNGETNYAQKFQD RVMTMTRDTSISTAYMELSLRSDDTAVYYCTREA TIFGMLIVPFDYWGQGLTVTVSS	
	!PS:361379	12H11.009	NA	SEQ ID NO: 117 GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAGCAG AAACCAGGACAGCTCTTAACCTGCTCATTTAC TGGACTTCTACCCGAGAAATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 274 CAGTGCCGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGTGCGTCAGGCCCTTGGACAAGGG CTTGAGTGGATGGGTGGATAAGCCCTAACCAA GGTGAACAAACTATGCACAGAAATTTACAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT GACGACACGGCCGTGTTACTGTGCGGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCAACCGTCT CCTCA	
				SEQ ID NO: 1688 DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRDSGVPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1845 QVPLVQSGAEVKKPGASVKVCKASGYTFTGYYI HWVRAPQGQGLEWMGWISPNNGETNYAQKFQD RVMTMTRDTSISTAYMELSLRSDDTAVYYCAREA TIFGMLIVPFDYWGQGLTVTVSS	

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!PS:361383	12H11.010	NA	SEQ ID NO: 118 GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAGCAG AACCAAGGACAGCCTCTAACCTGCTCATTTAC TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCTGGCCAAAGGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 275 CAGGTGCCGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCGTCAGGCCCTTGGACAAGGG CTTGAGTGGATGGGTGGATAAGCCCTAACAAAT GGTGACACAAACTATGCACAGAAATTTTACAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT GACGACACGGCCGTGTTACTGTGCGGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCAACCGTCT CCTCA
		AA	SEQ ID NO: 1689 DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSSTRESGVPDFRFG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1846 QVPLVQSGAEVKKPGASVKVCKASGYTFTGYYI HWVRAPQGQLEWMGWISPNNGDTNYAQKFQD RVTMTDRDTSISTAYMELSLRSDDTAVYYCAREA TIFGMLIVPFDYWGQGLTVTVSS
!PS:361387	12H11.011	NA	SEQ ID NO: 119 GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAGCAG AAACCAGGACAGCCTCTAACCTGCTCATTTAC TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCTGGCCAAAGGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 276 CAGGTGCCGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCGTCAGGCCCTTGGACAAGGG CTTGAGTGGATGGGTGGATAAGCCCTAACCAA GGTGACACAAACTATGCACAGAAATTTTACAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT GACGACACGGCCGTGTTACTGTGCGGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCAACCGTCT CCTCA
		AA	SEQ ID NO: 1690 DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSSTRESGVPDFRFG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1847 QVPLVQSGAEVKKPGASVKVCKASGYTFTGYYI HWVRAPQGQLEWMGWISPNNGDTNYAQKFQD RVTMTDRDTSISTAYMELSLRSDDTAVYYCAREA TIFGMLIVPFDYWGQGLTVTVSS

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!PS:361391	12H11.012	NA	SEQ ID NO: 120 GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCCTGGGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACTTAGCTTGGTACCAGCAG AACCAAGGACAGCTCTTAACCTGCTCATTTAC TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 1277 CAGGTGCCGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCGTCAGGCCCTTGGACAAGGG CTTGAGTGGATGGGTGGATAAGCCCTAACAAAT GGTGAACAAACTATGCACAGAAGTTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT GACGACACGGCCGTGTTACTGTGCGGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCAACCGTCT CCTCA
			SEQ ID NO: 1691 DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRESGVDPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1848 QVPLVQSGAEVKKPGASVKVCKASGYTFTGYYI HWVRAPQGQGLEWMGWISPNNGETNYAQKFQD RVTMTDRDTSISTAYMELSLRSDDTAVYYCAREA TIFGMLIVPFDYWGQGLTVTVSS
!PS:361395	12H11.013	NA	SEQ ID NO: 121 GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCCTGGGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACTTAGCTTGGTACCAGCAG AAACCAGGACAGCTCCTAAACTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 278 CAGGTGCAGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCGTCAGGCCCTTGGACAAGGG CTTGAGTGGATGGGTGGATAAGCCCTAACCAA GGTGAACAAACTATGCACAGAAGTTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGCCTGAGATCT GACGACACGGCCGTGTTACTGTGCGGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCAACCGTCT CCTCA
			SEQ ID NO: 1692 DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRDSGVDPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1849 QVQLVQSGAEVKKPGASVKVCKASGYTFTGYYI HWVRAPQGQGLEWMGWISPNNGETNYAQKFQD RVTMTDRDTSISTAYMELSLRSDDTAVYYCAREA TIFGMLIVPFDYWGQGLTVTVSS

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	!PS:361402	12H11.014	NA	SEQ ID NO: 122	SEQ ID NO: 279
				GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACTTAGCTTGGTACCAGCAG AACCAAGGACAGCTCTAAACTGCTCATTTAC TGGACTTCTACCCGAGAAATCCGGGTCCTGAC CGATTCAAGTGGCAGCGGCTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTGGCCAAAGGGACCAAGGTGG AAATCAAAACGA	CAGGTGCAGCTGGTGCAAGTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGTGCCTCAGGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATAAGCCCTAACCAA GGTGAACAAACTATGCACAGAAATTTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGCCTGAGATCT GACGACACGGCCGTGTTACTGTGCGGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
	!PS:361406	2C2.005.001	NA	SEQ ID NO: 1693	SEQ ID NO: 1850
				DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPKLLIYWTSRESGVPDFRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPTWTF GQGTKVEIKR	QVQLVQSGAEVKKPGASVKVSKASGYTFTGYVI HWVRAPQGLEWMGWISPNQGETNYAQKFQD RVMTMTRDTSISTAYMELSSLRSDDTAVYYCAREA TIFGMLIVPFDYWGQGLVTVSS
	!PS:361406	2C2.005.001	NA	SEQ ID NO: 123	SEQ ID NO: 280
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	AA		AA	SEQ ID NO: 1694	SEQ ID NO: 1851
				QSVLTQPPSASGTPGQQRVTISCGSSSNIQSQTWNW YQHLPGTAPKLLIYTNNQRPSPGVPDFRFSKSGTS ASLAISGLQSEDEADYFCATFDESLSGPVFGGK LTVLG	QMQVVQSGAEVKKPGASVKVSKASGYTFTGYI MHWVRQAPQGLEWMGWINPNSSGNTYAQKFQ GRVTMTRDTSISTAYMELSLRLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWVGQGLTVTVSS

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	!PS:361412	2C2.005.002	NA	SEQ ID NO: 124 CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGTCACCATCTCTTGT CTGGAAGTAGCTCCAACATCGGAAGTCAAACTG TAACTGGTACAGCACCTCCAGGAACGGCCC CCAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATGAAGCCTGCAAGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCTCCTAGGT	SEQ ID NO: 281 CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGCTTCCGGATACACCTTCAACCGGCTACTAT ATGCATTGGTGGCAGACAGCCCCCTGGACAAGGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGGCAAACTATGCACAGAAGTTTCAGGGC AGGGTCAACCATGACCAAGGACACGTCCATCAGT ACAGCTACATGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGGATTACGTTTGGGGGACTTATCGGCCCTCAC TACTACTACGGTATGGACGTCTGGGGCCAAGGG ACCACGGTCACCGTCTCCTCA
				SEQ ID NO: 1695 QSVLTQPPSASGTPGQRVTISCSGSSNIGSQTVNW YQHLPGTAPKLLIYTNNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDES LQGPVFGGGTK LTVLG	SEQ ID NO: 1852 QMQVVQSGAEVKKPGASVKVSKASGYTFTGYY MHWVVRQAPQGQLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSLRSDDTAVYYCARG GDYVVGTYRPHYYYGMDVVGQGTITVTVSS
	!PS:361418	2C2.005.003	NA	SEQ ID NO: 125 CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGTCACCATCTCTTGT CTGGAAGTAGCTCCAACATCGGAAGTAAATATG TAACTGGTACCAAGCACCTCCAGGAACGGCCC CCAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATGAAGCCTGAGTGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCTCCTAGGT	SEQ ID NO: 282 CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGCTTCCGGATACACCTTCAACCGGCTACTAT ATGCATTGGTGGCAGACAGCCCCCTGGACAAGGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGGCAAACTATGCACAGAAGTTTCAGGGC AGGGTCAACCATGACCAAGGACACGTCCATCAGT ACAGCTACATGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGGATTACGTTTGGGGGACTTATCGGCCCTCAC TACTACTACGGTATGGACGTCTGGGGCCAAGGG ACCACGGTCACCGTCTCCTCA
				SEQ ID NO: 1696 QSVLTQPPSASGTPGQRVTISCSGSSNIGSNYVNW YQHLPGTAPKLLIYTNNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDES LSGPVFGGGTK LTVLG	SEQ ID NO: 1853 QMQVVQSGAEVKKPGASVKVSKASGYTFTGYY MHWVVRQAPQGQLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSLRSDDTAVYYCARG GDYVVGTYRPHYYYGMDVVGQGTITVTVSS

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	!PS:361424	2C2.005.004	NA	SEQ ID NO: 126 CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGTCACCATCTCTTGT CTGGAAGTAGCTCCAACATCGGAAGTAATTATG TAACTGGTACAGCACCTCCAGGAACGGCCC CCAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATGAAGCCTGCAAGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCTCCTAGGT	SEQ ID NO: 123 CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGCTTCCGGATACACCTTCAACCGGCTACTAT ATGCATTGGTGGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGGCAACAACATATGCACAGAAGTTTCAGGGC AGGGTCAACCATGACCAAGGACACGTCCATCAGT ACAGCTACATGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGGGAATTACGTTTGGGGGACTTATCGGCCCTCAC TACTACTACGGTATGGACGTCTGGGGCCCAAGGG ACCACGGTCACCGTCTCCTCA
				SEQ ID NO: 1697 QSVLTQPPSASGTPGQRVTISCSGSSNIGSNYVNW YQHLPGTAPKLLIYTNNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDES LQGPVFGGGTK LTVLG	SEQ ID NO: 1854 QMQVVQSGAEVKKPGASVKVSKASGYTFTGYY MHWVVRQAPQGQLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSLRSDDTAVYYCARG GDYVVGTYRPHYYYGMDVWVGQGTITVTVSS
	!PS:361430	2C2.005.005	NA	SEQ ID NO: 127 CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGTCACCATCTCTTGT CTGGAAGTAGCTCCAACATCGGAAGTCAAACTG TAACTGGTACCAAGCACCTCCAGGAACGGCCC CCAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATGACAGCCTGAATGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCTCCTAGGT	SEQ ID NO: 284 CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGCTTCCGGATACACCTTCAACCGGCTACTAT ATGCATTGGTGGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGGCAACAACATATGCACAGAAGTTTCAGGGC AGGGTCAACCATGACCAAGGACACGTCCATCAGT ACAGCTACATGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGGGAATTACGTTTGGGGGACTTATCGGCCCTCAC TACTACTACGGTATGGACGTCTGGGGCCCAAGGG ACCACGGTCACCGTCTCCTCA
				SEQ ID NO: 1698 QSVLTQPPSASGTPGQRVTISCSGSSNIGSQTVNW YQHLPGTAPKLLIYTNNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDDSLNGLPVGGGTK LTVLG	SEQ ID NO: 1855 QMQVVQSGAEVKKPGASVKVSKASGYTFTGYY MHWVVRQAPQGQLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSLRSDDTAVYYCARG GDYVVGTYRPHYYYGMDVWVGQGTITVTVSS

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	!PS:361436	2C2.005.006	NA	SEQ ID NO: 128 CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG GGACCCCGGGCAGAGGTCACCATCTCTTGT CTGGAAGTAGCTCCAACATCGGAAGTAATTATG TAACTGGTACAGCACCTCCAGGAACGGCCC CCAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATGACAGCTGAATGGTCCGGTAT TCGGCGGAGGACCAAGCTGACCGTCTCCTAGGT	SEQ ID NO: 1285 CAGATGCAGGTGGTGCACTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGCTTCCGGATACACCTTCACCCGGCTACTAT ATGCATTGGTGGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGGCAAACTATGCACAGAAGTTTCAGGGC AGGGTCAACCATGACCAAGGACACGTCCATCAGT ACAGCTACATGAGCTGAGCAGGCTGAGGTCT GACGACAGGCCGTGTATTACTGTGCGAGAGGG GGGATTACGTTTGGGGGACTTATCGGCCCTCAC TACTACTACGGTATGGACGTCTGGGGCCAAGGG ACCACGGTCACCGTCTCCTCA
				SEQ ID NO: 1699 QSVLTQPPSASGTPGQRVTISCSGSSNIGSNYVNW YQHLPGTAPKLLIYTNNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDDSLNPGPVFGGGTK LTVLG	SEQ ID NO: 1856 QMQVVQSGAEVKKPGASVKVSKASGYTFTGYY MHWVRAQPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWVGQGTITVTVSS
	!PS:361442	2C2.005.007	NA	SEQ ID NO: 129 CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG GGACCCCGGGCAGAGGTCACCATCTCTTGT CTGGAAGTAGCTCCAACATCGGAAGTAATACTG TAACTGGTACCAAGCACCTCCAGGAACGGCCC CCAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATGAAGCTGAATGGTCCGGTAT TCGGCGGAGGACCAAGCTGACCGTCTCCTAGGT	SEQ ID NO: 286 CAGATGCAGGTGGTGCACTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGCTTCCGGATACACCTTCACCCGGCTACTAT ATGCATTGGTGGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGGCAAACTATGCACAGAAGTTTCAGGGC AGGGTCAACCATGACCAAGGACACGTCCATCAGT ACAGCTACATGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGGATTACGTTTGGGGGACTTATCGGCCCTCAC TACTACTACGGTATGGACGTCTGGGGCCAAGGG ACCACGGTCACCGTCTCCTCA
				SEQ ID NO: 1700 QSVLTQPPSASGTPGQRVTISCSGSSNIGSNYVNW YQHLPGTAPKLLIYTNNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDESINPGPVFGGGTK LTVLG	SEQ ID NO: 1857 QMQVVQSGAEVKKPGASVKVSKASGYTFTGYY MHWVRAQPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWVGQGTITVTVSS

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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 ATGCATTGGTGGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGGCAAACTATGCACAGAAGTTTCAGGGC AGGGTCAACCATGACCAAGGACACGTCCATCAGT ACAGCTACATGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGGATTACGTTTGGGGGACTTATCGGCCCTCAC TACTACTACGGTATGGACGTCTGGGGCCAAAGGG ACCACGGTCACCGTCTCCTCA
				SEQ ID NO: 1701 QSVLTQPPSASGTPGQRVTISCSGSSNIGSNTVNW YQHLPGTAPKLLIYTNNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDDSLQGPVFGGGTK LTVLG	SEQ ID NO: 1858 QMQVVQSGAEVKKPGASVKVSKASGYTFTGY MHWVVRQAPQGQLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSLRSDDTAVYYCARG GDYVVGTYRPHYYYGMDVWVGQGTTVTVSS
	!PS:361454	2C2.005.009	NA	SEQ ID NO: 131 CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGTCACCATCTCTTGT CTGGAAGTAGCTCCAACATCGGAAGTAATACTG TAACTGGTACCAAGCACCTCCAGGAACGGCCC CCAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATGACAGCTGAGTGGTCCGGTAT TCGGCGGAGGACCAAGCTGACCGTCTCCTAGGT	SEQ ID NO: 288 CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGTCTCCTGC AAGCTTCCGGATACACCTTCAACCGGCTACTAT ATGCATTGGTGGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGGCAAACTATGCACAGAAGTTTCAGGGC AGGGTCAACCATGACCAAGGACACGTCCATCAGT ACAGCTACATGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGGATTACGTTTGGGGGACTTATCGGCCCTCAC TACTACTACGGTATGGACGTCTGGGGCCAAAGGG ACCACGGTCACCGTCTCCTCA
				SEQ ID NO: 1702 QSVLTQPPSASGTPGQRVTISCSGSSNIGSNTVNW YQHLPGTAPKLLIYTNNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDDSLQGPVFGGGTK LTVLG	SEQ ID NO: 1859 QMQVVQSGAEVKKPGASVKVSKASGYTFTGY MHWVVRQAPQGQLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSLRSDDTAVYYCARG GDYVVGTYRPHYYYGMDVWVGQGTTVTVSS

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!PS:361460	2C2.005.010	NA	SEQ ID NO: 132 CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGTCACCATCTCTTGT CTGGAAGTAGCTCCAACATCGGAAGTAATACTG TAACTGGTACAGCACCTCCAGGAACGGCCC CCAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATGACAGCCTGAATGCTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCTCCTAGGT	SEQ ID NO: 132 CAGTGTGCTGCTGAGTGTGCGAGTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGCTTCCGGATACACCTTCAACCGGCTACTAT ATGCATTGGTGGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGGCAAACTATGCACAGAAGTTTCAGGGC AGGGTCAACCATGACCAAGGACACGTCCATCAGT ACAGCTACATGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGGATTACGTTTGGGGGACTTATCGGCCCTCAC TACTACTACGGTATGGACGTCTGGGGCCAAAGGG ACCACGGTCACCGTCTCCTCA	SEQ ID NO: 289
			SEQ ID NO: 1703 QSVLTQPPSASGTPGQRVTISCSGSSNIGSNTVNW YQHLPGTAPKLLIYTNNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDDSLNAPVFGGGTK LTVLG	SEQ ID NO: 1860 QMQVVQSGAEVKKPGASVKVSKASGYTFTGYY MHWVVRQAPQGQLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWVGQGTITVTVSS	SEQ ID NO: 1860
!PS:361466	2C2.005.011	NA	SEQ ID NO: 133 CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGTCACCATCTCTTGT CTGGAAGTAGCTCCAACATCGGAAGTAATACTG TAACTGGTACCAACCTCCAGGAACGGCCC CCAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATGACAGCCTGAATGCTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCTCCTAGGT	SEQ ID NO: 133 CAGTGTGCTGCTGAGTGTGCGAGTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGCTTCCGGATACACCTTCAACCGGCTACTAT ATGCATTGGTGGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGGCAAACTATGCACAGAAGTTTCAGGGC AGGGTCAACCATGACCAAGGACACGTCCATCAGT ACAGCTACATGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGGATTACGTTTGGGGGACTTATCGGCCCTCAC TACTACTACGGTATGGACGTCTGGGGCCAAAGGG ACCACGGTCACCGTCTCCTCA	SEQ ID NO: 290
			SEQ ID NO: 1704 QSVLTQPPSASGTPGQRVTISCSGSSNIGSNTVNW YQHLPGTAPKLLIYTNNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDDSLNAPVFGGGTK LTVLG	SEQ ID NO: 1861 QMQVVQSGAEVKKPGASVKVSKASGYTFTGYY MHWVVRQAPQGQLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWVGQGTITVTVSS	SEQ ID NO: 1861

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	!PS:361472	2C2.005.012	NA	SEQ ID NO: 134 CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGGTCACCATCTCTTGT CTGGAAGTAGCTCCAACATCGGAAGTAATTATG TAACTGGTACAGCACCTCCAGGAACGGCCC CCAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATAGCAGCTGAATGCTCCGGTAT TCGGCGGAGGACCAAGCTGACCGTCTCCTAGGT	SEQ ID NO: 134 CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGCTTCCGGATACACCTTCAACCGGCTACTAT ATGCATTGGTGGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGGCAAACTATGCACAGAAGTTTCAGGGC AGGGTCAACCATGACCAAGGACACGTCCATCAGT ACAGCTACATGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGTAATTACTGTGCGAGAGGG GGGGAATTACGTTTGGGGGACTTATCGGCCCTCAC TACTACTACGGTATGGACGTCTGGGGCCAAGGG ACCACGGTCACCGTCTCCTCA	SEQ ID NO: 291
				SEQ ID NO: 1705 QSVLTQPPSASGTPGQRVTISCSGSSNIGSNYVNW YQHLPGTAPKLLIYTNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDSSLNAPVFGGGTK LTVLG	SEQ ID NO: 1862 QMQVVQSGAEVKKPGASVKVCKASGYTFTGYY MHWVRAQPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSLRSDDTAVYYCARG GDYVVGTYRPHYYYGMDVWVGQGTITVTVSS	
	!PS:361478	2C2.005.013	NA	SEQ ID NO: 135 CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGGTCACCATCTCTTGT CTGGAAGTAGCTCCAACATCGGAAGTAATTATG TAACTGGTACCAAGCACCTCCAGGAACGGCCC CCAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATAGCAGCTGAATGCTCCGGTAT TCGGCGGAGGACCAAGCTGACCGTCTCCTAGGT	SEQ ID NO: 292 CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGCTTCCGGATACACCTTCAACCGGCTACTAT ATGCATTGGTGGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGGCAAACTATGCACAGAAGTTTCAGGGC AGGGTCAACCATGACCAAGGACACGTCCATCAGT ACAGCTACATGAGCTGAGCAGCCTGAGGTCT GACGACACGGCCGTGTAATTACTGTGCGAGAGGG GGGGAATTACGTTTTCGGGACTTATCGGCCCTCACT ACTACTACGGTATGGACGTCTGGGGCCAAGGGA CCACGGTCACCGTCTCCTCA	SEQ ID NO: 292
				SEQ ID NO: 1706 QSVLTQPPSASGTPGQRVTISCSGSSNIGSNYVNW YQHLPGTAPKLLIYTNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDSSLNAPVFGGGTK LTVLG	SEQ ID NO: 1863 QMQVVQSGAEVKKPGASVKVCKASGYTFTGYY MHWVRAQPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSLRSDDTAVYYCARG GDYVVGTYRPHYYYGMDVWVGQGTITVTVSS	

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!PS:361485	2C2.005.014	NA	SEQ ID NO: 136	CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGTCACCATCTCTTGT CTGGAAGTAGCTCCAACATCGGAAGTCAAACTG TAAACTGGTACAGCACCTCCAGGAACGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATGAAGCCTGAGTGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCTCCTAGGT	SEQ ID NO: 1707	QSVLTQPPSASGTPGQRVTISCGSSSNIQSQTWNW YQHLPGTAPKLLIYTNNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDESLSGPVFGGK LTVLG	SEQ ID NO: 1864	QMQVVQSGAEVKKPGASVKVSKASGYTFTGY MHWVRQAPQGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTTRDTSISTAYMELSLRLSDDTAVYYCARG GDYVFGTYRPHYYYGMDVWVGQGTITVTVSS
			SEQ ID NO: 293	CAGATGCAGGTGGTGACGTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCCGGATACACCTTCACCGGCTACTAT ATGCATTGGGTGCACAGGCCCTGGACAAGGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGGACAAACTATGCACAGAAAGTTTCAGGGC AGGGTACCATGACCAAGGACACGTCCATCAGT ACAGCTACATGGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGGGATTACGTTTTTCGGGACTTATCGGCCTCACT ACTACTACGGTATGGACGTCTGGGGCCAAAGGA CCACGGTACCGTCTCCTCA				
		SEQ ID NO: 137	GACATCCAGATGACCCAGTCTCCATCCTCCTCTGT CTGCATCTATAGGAGACAGAGTCAACCATCACTT GCCGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCAACAGAAACCAAGGAAAGCCCCTA AGCGCTGATCTATGGTGCATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTCAAGCGGCAGTGGAT CTGGGACAGAAATTCAC'TCTCACAATCAGCAGCC TGCAGCCTGAAAGATTTGCGAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTTCGGCCAA GGGACCAAAAGTGGATATCAAAACGA	SEQ ID NO: 1708	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YQQKPGKAPKRLIY'GASSLQSGVPSRFSGSGSTE FTLTISLQPEDFATYYCLQHNNYPFTFGQGTKVDI KR	SEQ ID NO: 1865	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGK'GLEWVAIVYDASNENYADAVK G RFTISRDNKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLGDYWGQGTI'VTVSS	
!PS:361845	18F2.013	NA	SEQ ID NO: 137	GACATCCAGATGACCCAGTCTCCATCCTCCTCTGT CTGCATCTATAGGAGACAGAGTCAACCATCACTT GCCGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCAACAGAAACCAAGGAAAGCCCCTA AGCGCTGATCTATGGTGCATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTCAAGCGGCAGTGGAT CTGGGACAGAAATTCAC'TCTCACAATCAGCAGCC TGCAGCCTGAAAGATTTGCGAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTTCGGCCAA GGGACCAAAAGTGGATATCAAAACGA	SEQ ID NO: 137	GACATCCAGATGACCCAGTCTCCATCCTCCTCTGT CTGCATCTATAGGAGACAGAGTCAACCATCACTT GCCGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCAACAGAAACCAAGGAAAGCCCCTA AGCGCTGATCTATGGTGCATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTCAAGCGGCAGTGGAT CTGGGACAGAAATTCAC'TCTCACAATCAGCAGCC TGCAGCCTGAAAGATTTGCGAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTTCGGCCAA GGGACCAAAAGTGGATATCAAAACGA	SEQ ID NO: 294	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCAC'TGGTCCGCCAGGCCCAAGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCAACCATCTCCAGAGACAATTCOAAGAAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATA GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA
			SEQ ID NO: 1865	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGK'GLEWVAIVYDASNENYADAVK G RFTISRDNKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLGDYWGQGTI'VTVSS				

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IP:361851	6H1.009	NA	SEQ ID NO: 138	SEQ ID NO: 295
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGAAAGCCCTA AGCGCTGATCTATGGTGCATCCAGTTTGCAA GTGGGTCCCTCAAGGTTACGGCGAGTGGAT CTGGGACAGAAATTCATCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACCTTCAGTTACTTTGGCA TGCATGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATAATACTATGACAGCGCTGAAGGGCC GCTTCAACATCTCCAGAGACAATTCAGAACA CGCTGATCTGCAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTTACTGTGCGCGAGATA GGACGATTTTGGAGTGTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
IP:361855	2C2.005.015	NA	SEQ ID NO: 1709	SEQ ID NO: 1866
			DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLQSGVPSRFSGSGTEFT LTISLQPEDFATYYCLQHNNYPFTFGQGTKVDIK R	QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIWYDASNKYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLLGDYWVGQGLVTVSS
IP:361855	2C2.005.015	NA	SEQ ID NO: 139	SEQ ID NO: 296
			CAGTCTGTGCTGACTCAGCCACCTCAGCGTCTG GGACCCCGGGCAGAGGTCACCATCTCTTGT CTGGAAGTAGCTCCAAACATCGGAAGTAATACTG TAACTGGTACCAACAACATCCCAAGGAACGGCCC CCAAACCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATAGCAGCTGAGTGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCTCCTAGGT	CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCCTCTGC AAGCTTCCGGATACACCTTCAACCGGCTACTAT ATGCATTGGGTGCGACAGGCCCCCTGGACAAGGG CTTGAGTGGATGGGATGGATCAACCTTAACAGT GGTGGCAACAACATATGCACAGAAGTTTCAGGGC AGGTCACCATGACCAAGGACACGTCCATCAGT ACAGCTACATGAGCTGAGCAGGCTGAGGTCT GACGACACGGCGTGTATTACTGTGCGGAGAGGG GGGGATTACGTTTGGGGGACTTATCGGCCCTCAC TACTACTACGGTATGGACGTCTGGGGCCAAAGGG ACCACGTCACCGTCTCCTCA
IP:361855	2C2.005.015	AA	SEQ ID NO: 1710	SEQ ID NO: 1867
			QSVLTQPPSASGTPGQRVTISCGSSSNGSNTVNW YQQLPGTAPKLLIYTNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDSSLSPVPVFGGTK LTVLG	QMQVVSQGAEVKKPGASVKVSKASGYTFTGYY MHWVRQAPQGQLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSLRSDDTAVYYCARG GDYVWGTYPHYYYGMDVDVWVGQGTTVTVSS

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IP:336067	SG12.006	NA	SEQ ID NO: 140	SEQ ID NO: 297
			GACATCCAGCTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGGCAAGTCAGACCATTAGCAGGTTTAAATTGGTATCAGCAGAAACCTGGGAAAGCCCCTG AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG TGGGTCCCATCAAGATTCAAGTGGCAGTGGTTC TGGGACAGATTTCACTCTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGATCAGTTTGGCCA GGGGACCAAGCTGGAGATCACACGA	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT ACAGGCTCTGGATTCACCTTCAGTAGCTATGGC ATACACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAAGTGGTGGCAGTTATATGGTATGATGGA AGTAATAAGTTCCATGCAGACTCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAAATCCAAAGAAC ACCTGTATCTGCAAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC TGGGGCCAAAGGACAAAGGTCACCGTCTCTTCA
IP:336169	17B11.002	NA	SEQ ID NO: 1711	SEQ ID NO: 1868
			DIQLTQSPSSLASVGDRTVTITCRASQTISRFLNWX QKPKGAPELLIYVASSLQSGVPSRFSGSGTDFT LTISLQPEDFATYYCQQSYSTLISFGQGTKLEITR	QVQLVESGGGVVQPRSLRLSCTASGFTFSYGIH WVRQAPGKGLEWVAIVWYDGSNKFHADSVKGRF TISRDNSKNTLYLQMNSLRAEDSAMFYFCARGKVA GMPEAFEIWIWQGQTKVTVSS
IP:336169	17B11.002	NA	SEQ ID NO: 141	SEQ ID NO: 298
			CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG CGCCCCAGGACAGAAAGTCAACATCTCCTGTCTG CTGGAAGCAGCTCCAAACAATTGGAAATAATTATG TATCCTGGTATGAGCAGTTCCTCCAGGAACAGCCC CCAAACTCCTCATTTATGACAAATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTCAGCCACCTGGGCATCACCGG ACTCCAGACTGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGTGTGGT ATTGGCGGAGGGACCAAACTGACCGTCTCTAGG T	CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAAGTTATGAT ATCAACTGGGTGCGACAGGCCACTGGACAAAGG CTTGAGTGGATGGATGGATGAACCTAACAGT GGTAACACAGGCTATGCACAGAAAGTTCCAGGC AGAGTCACCATGACCAAGGACACCTCCATAAGC ACAGCTACATGGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGTTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCAAAG GGACCACGGTCACCGTCTCCTCA
IP:336169	17B11.002	AA	SEQ ID NO: 1712	SEQ ID NO: 1869
			QSVLTQPPSVSAAPGQKVTISCGSSNIGNNYVS WYEQFPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTS ATLGITGLQTGDEADYYCGTWDSSLSAVVFGGTT KLTVLG	QMQLVQSGAEVKKPGASVKVSKKASGYTFTSYDI NWVRQATGQGLEWMGMWNPNSGNTGYAQKFQ GRVTMTRDTSISTAYMELSSLSRSDTAVYYCARG GDYVWGSYRPYYYYGMDVWVGQGTITVTVSS

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	!PS:361127	5G12.006.001	NA	SEQ ID NO: 142	SEQ ID NO: 299
				GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGCAAGTCAGACCATTAGCAGGTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCTG AGTCTGTATCTATGTTGCATCCAGTTTGCAAAG TGGGTCCCATCAAGATTCAAGTGGCAGTGGTTC TGGACAGATTTCACTCTCAACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGATCAGTTTGGCCA GGGGACCAAGCTGGAGATCAAAACGA	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGTCTGGATTCACTTCACTAGTATGGC ATACATGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAAATCCAAAGAC ACGCTGTATCTGCAAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC TGGGGCCAAAGGGACAAAGGTCACCGTCTCTTCA
			AA	SEQ ID NO: 1713	SEQ ID NO: 1870
				DIQLTQSPSSLASVGDRTVTITCRASQTISRFLNWY QQKPGKAPELLIYVASSLQSGVPSRFSGSGTDFT LTISSLQPEDFATYYCQQSYSTLISFGGQGTKLEIKR	QVQLVESGGGVVQPRSLRLSCAASGFTFSSYGIH WVRQAPGKGLEWVAIVWYDASNKFHADA VKGR FTISRDNSKNTLYLQMNSLRAEDSAMFYFCARGKV AGMPEAFEIWGQGTKVTVSS
	!PS:361136	5G12.006.002	NA	SEQ ID NO: 143	SEQ ID NO: 300
				GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGCAAGTCAGACCATTAGCAGGTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCTG AGTCTGTATCTATGTTGCATCCAGTTTGCAAAG TGGGTCCCATCAAGATTCAAGTGGCAGTGGTTC TGGACAGATTTCACTCTCAACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGATCAGTTTGGCCA GGGGACCAAGCTGGAGATCAAAACGA	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT ACAGGTCTGGATTCACTTCACTAGTATGGC ATACATGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAAATCCAAAGAC ACGCTGTATCTGCAAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC TGGGGCCAAAGGGACAAAGGTCACCGTCTCTTCA
			AA	SEQ ID NO: 1714	SEQ ID NO: 1871
				DIQLTQSPSSLASVGDRTVTITCRASQTISRFLNWY QQKPGKAPELLIYVASSLQSGVPSRFSGSGTDFT LTISSLQPEDFATYYCQQSYSTLISFGGQGTKLEIKR	QVQLVESGGGVVQPRSLRLSCTASGFTFSSYGIH WVRQAPGKGLEWVAIVWYDASNKFHADA VKGR FTISRDNSKNTLYLQMNSLRAEDSAMFYFCARGKV AGMPEAFEIWGQGTKVTVSS

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!PS:361140	5G12.006.003	NA	SEQ ID NO: 144	SEQ ID NO: 301
			GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGCAAGTCAGACCAATTAGCAGGTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCTG AGTCTGTATCTATGTTGCATCCAGTTTGCAAAG TGGGTCCCATCAAGATTCAAGTGGCAGTGGTTC TGGGACAGATTTCACTCTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGATCAGTTTGGCCA GGGGACCAAGCTGGAGATCACACGA	CAGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACCTTCAGTAGCTATGGC ATACACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAAATTCCAAAGAC ACGCTGTATCTGCAAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCGTGAAGCTTTTGAAATC TGGGGCCAAAGGGACAAAGGTCACCGTCTCTTCA
!PS:359919	5G12.006.004	NA	SEQ ID NO: 145	SEQ ID NO: 302
			GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGCAAGTCAGACCAATTAGCAGGTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCTA AGTCTGTATCTATGTTGCATCCAGTTTGCAAAG TGGGTCCCATCAAGATTCAAGTGGCAGTGGTTC TGGGACAGATTTCACTCTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGATCAGTTTGGCCA GGGGACCAAGCTGGAGATCAACGA	CAGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACCTTCAGTAGCTATGGC ATACACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAAATTCCAAAGAC ACGCTGTATCTGCAAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCGTGAAGCTTTTGAAATC TGGGGCCAAAGGGACAAAGGTCACCGTCTCTTCA
		AA	SEQ ID NO: 1715	SEQ ID NO: 1872
			DIQLTQSPSSLASVGDRTVTITCRASQTISRFLNWX QQKPGKAPELLIYVASSLQSGVPSRFSGSGTDFT LTISSLQPEDFATYYCQQSYSTLISFGQGTCKLEIR	QVQLVESGGGVVQPRSLRLSCAASGFTFSYGIH WVRQAPGKGLEWVAIVWYDASNKFHADA VKGR FTISRDNSKNTLYLQMNSLRAEDSAMFYFCARGKV AGMPEAFEIWGQGTKVTVSS
		AA	SEQ ID NO: 1716	SEQ ID NO: 1873
			DIQLTQSPSSLASVGDRTVTITCRASQTISRFLNWX QQKPGKAPKLLIYVASSLQSGVPSRFSGSGTDF LTISSLQPEDFATYYCQQSYSTLISFGQGTCKLEIKR	QVQLVESGGGVVQPRSLRLSCAASGFTFSYGIH WVRQAPGKGLEWVAIVWYDASNKFHADA VKGR FTISRDNSKNTLYLQMNSLRAEDSAMFYFCARGKV AGMPEAFEIWGQGTKVTVSS

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	IP:361144	SG12.006.005	NA	SEQ ID NO: 146	SEQ ID NO: 303
				GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGCAAGTCAGACCATTAGCAGGTTTAA ATTGGTATCAGCAGAAACCTGGAAAGCCCCCTG AGTCTGTATCTATGTTGCATCCAGTTTGCAAAG TGGGTCCCATCAAGATTCAAGTGGCAGTGGTTC TGGACAGATTTCACTCTCAACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGATCAGTTTGGCCA GGGGACCAAGCTGGAGATCAAAACGA	CAGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACCTTCAGTAGCTATGGC ATACACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAGTTCCATGCAGACTCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAAATCCAAAGAAC ACGCTGTATCTGCAAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC TGGGGCCAAAGGGACAAAGGTCACCGTCTCTTCA
	AA			SEQ ID NO: 1717	SEQ ID NO: 1874
				DIQLTQSPSSLASVGDRTVTITCRASQTISRFLNWY QQKPGKAPELLIYVASSLQSGVPSRFSGSGTDFT LTISSLQPEDFATYYCQQSYSTLISFGGQGTKLEIKR	QVQLVESGGGVVQPRSLRLSCAASGFTFSYGIH WVRQAPGKGLEWVAIVWYDASNKFHADSVKGRF TISRDN SKNTLYLQMNSLRAEDSAM YFCARGKVA GMPEAFEIWGQGTKVTVSS
	IP:361151	SG12.006.006	NA	SEQ ID NO: 147	SEQ ID NO: 304
				GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGCAAGTCAGACCATTAGCAGGTTTAA ATTGGTATCAGCAGAAACCTGGAAAGCCCCCTG AGTCTGTATCTATGTTGCATCCAGTTTGCAAAG TGGGTCCCATCAAGATTCAAGTGGCAGTGGTTC TGGACAGATTTCACTCTCAACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGATCAGTTTGGCCA GGGGACCAAGCTGGAGATCAAAACGA	CAGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACCTTCAGTAGCTATGGC ATACACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGGA AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAAATCCAAAGAAC ACGCTGTATCTGCAAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC TGGGGCCAAAGGGACAAAGGTCACCGTCTCTTCA
	AA			SEQ ID NO: 1718	SEQ ID NO: 1875
				DIQLTQSPSSLASVGDRTVTITCRASQTISRFLNWY QQKPGKAPELLIYVASSLQSGVPSRFSGSGTDFT LTISSLQPEDFATYYCQQSYSTLISFGGQGTKLEIKR	QVQLVESGGGVVQPRSLRLSCAASGFTFSYGIH WVRQAPGKGLEWVAIVWYDGSNKFHADAVKGR FTISRDN SKNTLYLQMNSLRAEDSAM YFCARGKV AGMPEAFEIWGQGTKVTVSS

		SEQ ID NO: 148	CAGTCTGTGTGACGCAGCGCCCTCAGTGTCTG CGGCCACGACAGAAGGTACCATCTCCTGCT CTGGAAGCAGCTCCAAACATTGGAATAATTATG TATCCTGGTATCAGCAGCTCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGAATTCCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTACGCCACCTGGGCATCACCGG ACTCCAGACTGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGTGTGGT ATTCTGGCGGAGGGACCAAACTGACCCGTCTAGG T	SEQ ID NO: 1719	SEQ ID NO: 1876	SEQ ID NO: 305
	17B11.002.001	IPs:361491	NA	QSVLTQPPSVSAAPGQKVTISCSGSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLGTGLQTGDEADYYCGTWDSSL SAVVFGGG TKLTVLG	QMLVQSGAEVKKPGASVKVSKKASGYTFTSYDI NWVRQATGQGLEWMGWMNPNNSGDTGYAQKFQ GRVTMTRDTSISTAYMELSSRLSQDTAVYYCARG GDYVWGSYRPPYYYYGMDVWVGQTTVTVSS	CAAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAAGTTATGAT ATCAAATGCTGGTGCAGACAGGCCACTGGACAAGGG CTTGAGTGGATGGATGGATGAACCCCTAACAGT GGTGGCACAGGCTATGCACAGAAAGTTCCAGGGC AGAGTACCAATGACCAAGGACACCTCCATAAGC ACAGCTACATGGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCAAAG GGACCACGGTCACCGTCTCTCTCA
			AA	QSVLTQPPSVSAAPGQKVTISCSGSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLGTGLQTGDEADYYCGTWDSSL SAVVFGGG TKLTVLG	QMLVQSGAEVKKPGASVKVSKKASGYTFTSYDI NWVRQATGQGLEWMGWMNPNNSGDTGYAQKFQ GRVTMTRDTSISTAYMELSSRLSQDTAVYYCARG GDYVWGSYRPPYYYYGMDVWVGQTTVTVSS	CAAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAAGTTATGAT ATCAAATGCTGGTGCAGACAGGCCACTGGACAAGGG CTTGAGTGGATGGATGGATGAACCCCTAACAGT GGTAACACAGGCTATGCACAGAAAGTTCCAGGGC AGAGTACCATGACCAAGGACACCTCCATAAGC ACAGCTACATGGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCAAAG GGACCACGGTCACCGTCTCTCTCA
	17B11.002.002	IPs:361499	NA	QSVLTQPPSVSAAPGQKVTISCSGSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLGTGLQTGDEADYYCGTWDSSL SAVVFGGG TKLTVLG	QMLVQSGAEVKKPGASVKVSKKASGYTFTSYDI NWVRQATGQGLEWMGWMNPNNSGDTGYAQKFQ GRVTMTRDTSISTAYMELSSRLSQDTAVYYCARG GDYVWGSYRPPYYYYGMDVWVGQTTVTVSS	CAAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAAGTTATGAT ATCAAATGCTGGTGCAGACAGGCCACTGGACAAGGG CTTGAGTGGATGGATGGATGAACCCCTAACAGT GGTAACACAGGCTATGCACAGAAAGTTCCAGGGC AGAGTACCATGACCAAGGACACCTCCATAAGC ACAGCTACATGGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCAAAG GGACCACGGTCACCGTCTCTCTCA
			AA	QSVLTQPPSVSAAPGQKVTISCSGSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLGTGLQTGDEADYYCGTWDSSL SAVVFGGG TKLTVLG	QMLVQSGAEVKKPGASVKVSKKASGYTFTSYDI NWVRQATGQGLEWMGWMNPNNSGDTGYAQKFQ GRVTMTRDTSISTAYMELSSRLSQDTAVYYCARG GDYVWGSYRPPYYYYGMDVWVGQTTVTVSS	CAAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAAGTTATGAT ATCAAATGCTGGTGCAGACAGGCCACTGGACAAGGG CTTGAGTGGATGGATGGATGAACCCCTAACAGT GGTAACACAGGCTATGCACAGAAAGTTCCAGGGC AGAGTACCATGACCAAGGACACCTCCATAAGC ACAGCTACATGGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCAAAG GGACCACGGTCACCGTCTCTCTCA

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	!PS:361503	17B11.002.003	NA	SEQ ID NO: 150 CAGTCTGTGTTGACGCGAGCGCCCTCAGTGTCTG CGCCCCAGGACAGAAAGGTACCATCTCCTGCT CTGGAAGCAGCTCCAACAATTGGAATAATTATG TATCCTGGTATGAGCAGTTCACAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCAGTCAGCCACCTGGGCATCACCGG ACTCCAGACTGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGTGTGGT ATTCCGGCGAGGACCAAACTGACCGTCTCTAGG T	SEQ ID NO: 307 CAAATGCAGCTGGTGCAAGTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCAAGTTATGAT ATCAACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGATGGATGAACCTAACAGT GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCAACATGACCAAGGACACCTCCATAAGC ACAGCCTACATGGAGCTGACAGCCTGAGATCT CAGGACACGGCCGTGTTACTGTGCGAGAGGG GGTGATTACGTTTGGGGGAGTTATCGTCCCTACT ACTACTACGGTATGGACGTCTGGGGGCCAAG GGACCACGGTCAACCGTCTCCTCA
				SEQ ID NO: 1721 QSVLTQPPSVSAAPGQKVITISCSGSSNIGNNYVS WYEQPFGTAPKLLIYDNNKRPSGIPDRFSGSKSGTS ATLGITGLQTGDEADYYCGTWDSSLSAVVFGGGT KLTVLG	SEQ ID NO: 1878 QMQLVQSGAEVKKPGASVKVSKASGYTFTSYDI NWVRQATGQGLEWMGMNPNSSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDTA VYYCARG GDYVWGSYRPYYYYGMDVWVGQGTITVTVSS
	!PS:361507	17B11.002.004	NA	SEQ ID NO: 151 CAGTCTGTGTTGACGCGAGCGCCCTCAGTGTCTG CGCCCCAGGACAGAAAGGTACCATCTCCTGCT CTGGAAGCAGCTCCAACAATTGGAATAATTATG TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCAGTCAGCCACCTGGCCATCACCGG ACTCCAGACTGGGACGAGGCCGATTATTACTG CGGAACATTCGAAAGCAGCCTGAGTGTGTGGT ATTCCGGCGAGGACCAAACTGACCGTCTCTAGG T	SEQ ID NO: 308 CAAATGCAGCTGGTGCAAGTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCAAGTTATGAT ATCAACTGGGTGCGACAGGCCCTGGACAAGGG CTTGAGTGGATGGATGGATGAACCTAACAGT GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCAACATGACCAAGGACACCTCCATAAGC ACAGCCTACATGGAGCTGACAGCCTGAGATCT GACGACACGGCCGTGTTACTGTGCGAGAGGG GGTGATTACGTTTGGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGGCCAAG GGACCACGGTCAACCGTCTCCTCA
				SEQ ID NO: 1722 QSVLTQPPSVSAAPGQKVITISCSGSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLAITGLQTGDEADYYCGTFESSLSAVVFGGGT KLTVLG	SEQ ID NO: 1879 QMQLVQSGAEVKKPGASVKVSKASGYTFTSYDI NWVRQAPGQGLEWMGMNPNSSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDTA VYYCARG GDYVWGSYRPYYYYGMDVWVGQGTITVTVSS

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	!PS:361514	17B11.002.005	NA	SEQ ID NO: 152 CAGTCTGTGTTGACGCGAGCGGCCCTCAGTGTCTG CGCCCCAGGACAGAAAGGTACCATCTCCTGCT CTGGAAGCAGCTCCAAACATTGGAATAATTATG TATCCTGGTATCAGCAGCTCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCAGTCAGCCACCTGGCCATCACCGG ACTCCAGACTGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGTGTGGT ATTCCGGCGGAGGACCAAACTGACCGTCTCTAGG T	SEQ ID NO: 309 CAAATGCAGCTGGTGCAAGTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCAAGTTATGAT ATCAACTGGGTGCGACAGGCCACTGGACAAGG CTTGAGTGGATGGATGGATGAACCTAACAGT GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCAACATGACCAAGGACACCTCCATAAGC ACAGCTACATGGAGCTGACAGCCTGAGATCT CAGGACACGGCCGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGAGTTATCGTCCCTACT ACTACTACGGTATGGACGTCTGGGGCCCAAG GGACCACGGTCAACCGTCTCCTCA
				SEQ ID NO: 1723 QSVLTQPPSVSAAPGQKVTISCSGSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLAITGLQTGDEADYYCGTWDSSL SAVVFGGG TKLTVLG	SEQ ID NO: 1880 QMQLVQSGAEVKKPGASVKVSKASGYTFTSYDI NWVRQATGQGLEWMGMNPNSSGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDTA VYYCARG GDYVWGSYRPYYYYGMDVWVGQTTVTVSS
	!PS:360582	17B11.002.006	NA	SEQ ID NO: 153 CAGTCTGTGTTGACGCGAGCGGCCCTCAGTGTCTG CGCCCCAGGACAGAAAGGTACCATCTCCTGCT CTGGAAGCAGCTCCAAACATTGGAATAATTATG TATCCTGGTATCAGCAGCTCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCAGTCAGCCACCTGGCCATCACCGG ACTCCAGACTGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGTGTGGT ATTCCGGCGGAGGACCAAACTGACCGTCTCTAGG T	SEQ ID NO: 310 CAAATGCAGCTGGTGCAAGTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCAAGTTATGAT ATCAACTGGGTGCGACAGGCCCTGGACAAGGG CTTGAGTGGATGGATGGATGAACCTAACAGT GGTAACACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCAACATGACCAAGGACACCTCCATAAGC ACAGCTACATGGAGCTGACAGCCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCCAAG GGACCACGGTCAACCGTCTCCTCA
				SEQ ID NO: 1724 QSVLTQPPSVSAAPGQKVTISCSGSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLAITGLQTGDEADYYCGTWDSSL SAVVFGGG TKLTVLG	SEQ ID NO: 1881 QMQLVQSGAEVKKPGASVKVSKASGYTFTSYDI NWVRQAPGQGLEWMGMNPNSSGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDTA VYYCARG GDYVWGSYRPYYYYGMDVWVGQTTVTVSS

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	!PS:361518	17B11.002.007	NA	SEQ ID NO: 154 CAGTCTGTGTTGACGCGAGCGCCCTCAGTGTCTG CGCCCCAGGACAGAAAGGTACCATCTCCTGCT CTGGAAGCAGCTCCAAACATTGGAATAATTATG TATCCTGGTATCAGCAGCTCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCAGTCAGCCACCTGGGCATCACCGG ACTCCAGACTGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGTGTGGT ATTCCGGCGGAGGACCAAACTGACCGTCTCTAGG T	SEQ ID NO: 311 CAAATGCAGCTGGTGCACTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCAAGTTATGAT ATCAACTGGGTGCGACAGGCCACTGGACAAGG CTTGAGTGGATGGATGGATGAACCTAACAGT GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCAACATGACCAAGGACACCTCCATAAGC ACAGCTACATGGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGTTACTGTGCGAGAGGG GGTGATTACGTTTTCGGGAGTTATCGTCCCTACT ACTACTACGCTATGGACGCTCTGGGGCCCAAG GGACCACGGTCAACCGTCTCCTCA
				SEQ ID NO: 1725 QSVLTQPPSVSAAPGQKVTISCSGSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLGITGLQTGDEADYYCGTWDSSL SAVVFGGG TKLTVLG	SEQ ID NO: 1882 QMQLVQSGAEVKKPGASVKVSKASGYTFTSYDI NWVRQATGQGLEWMGMNPNSSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDTA VYYCARG GDYVFGSYRPPY YYYGMDVWVGQGT TVTVSS
	!PS:360570	17B11.002.008	NA	SEQ ID NO: 155 CAGTCTGTGTTGACGCGAGCGCCCTCAGTGTCTG CGCCCCAGGACAGAAAGGTACCATCTCCTGCT CTGGAAGCAGCTCCAAACATTGGAATAATTATG TATCCTGGTATCAGCAGCTCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCAGTCAGCCACCTGGCCATCACCGG ACTCCAGACTGGGACGAGGCCGATTATTACTG CGGAACATTCGAAAGCAGCCTGAGTGTGTGGT ATTCCGGCGGAGGACCAAACTGACCGTCTCTAGG T	SEQ ID NO: 312 CAAATGCAGCTGGTGCACTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCAAGTTATGAT ATCAACTGGGTGCGACAGGCCCTGGACAAGGG CTTGAGTGGATGGATGGATGAACCTAACAGT GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCAACATGACCAAGGACACCTCCATAAGC ACAGCTACATGGAGCTGAGCAGCCTGAGATCT GACGACACGGCCGTGTTACTGTGCGAGAGGG GGTGATTACGTTTTCGGGAGTTATCGTCCCTACT ACTACTACGCTATGGACGCTCTGGGGCCCAAG GGACCACGGTCAACCGTCTCCTCA
				SEQ ID NO: 1726 QSVLTQPPSVSAAPGQKVTISCSGSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLAITGLQTGDEADYYCGTFESSLSAVVFGGGT KLTVLG	SEQ ID NO: 1883 QMQLVQSGAEVKKPGASVKVSKASGYTFTSYDI NWVRQAPGQGLEWMGMNPNSSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDDTA VYYCARG GDYVFGSYRPPY YYYGMDVWVGQGT TVTVSS

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		SEQ ID NO: 156	SEQ ID NO: 313
!PS:362051	5G12.005.001	NA	GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGCAAGTCAGACCATTAGCAGGTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCTA AGCTCCTGATCTATGTTGCATCCAGTTGCAAG TGGGTCCCATCAAGATTCAAGTGGCAGTGGTTC TGGGACAGATTTCACCTCAACCATCAGCAGTCT GCAACCTGAAGATTTTGAACCTTACTACTGTCA ACAGAGTTACAGTACCTGCTCAGTTTGGCCA GGGACCAAGCTGGAGATCAACGA
			CAGTGCAGTTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCACTTCCAGTAGCTATGGC ATACACTGGTCCGCCAGGCTCCAGCAAGGGG CTGGAGTGGTGGCAGTTATATGTTATGATGCA AGTAATAAGTTCATGCAGACGCCGTGAAGGC CGATTCAACCATCTCCAGAGACAATTCACAAGAC ACGCTGTATCTGCAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGTGGTATGCTGAAGCTTTTGAATC TGGGCCCAAGGACATTGGTCAACCGTCTCTTCA
		SEQ ID NO: 1727	SEQ ID NO: 1884
AA		AA	QVQLVESGGGVQPGRSLRLSCAASGFTFSSYGIH WVRQAPGKGLEWVAIVWYDASNKPHADAVKGR FTISRDNSKNTLYLQMNSLRAEDSAMYPFCARGKV R
			SEQ ID NO: 157

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	CDR1	CDR2	CDR3
!PS:336175	2C2.005	NA	TCTGGAAGTAGCTCCAAACATCG GAAGTAATACTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGACAGCCTG AATGGTCCGGTA
			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	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2200	SEQ ID NO: 2357	SEQ ID NO: 2514
			RASQDIRDYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 630	SEQ ID NO: 787	SEQ ID NO: 944

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!PS:335938	6H1	NA	CGGGCAAGTCAGGACATTAGAG ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2201 RASQDIRDYL G	SEQ ID NO: 2358 GASSLQS	SEQ ID NO: 2515 LQHNNYPFT
		AA	SEQ ID NO: 631	SEQ ID NO: 788	SEQ ID NO: 945
!PS:335941	2F11	NA	CAGGCGAGTCAGGACATTAGCA ACTATTTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCCTCA CT
		AA	SEQ ID NO: 2202 QASQDISNYLN	SEQ ID NO: 2359 DASNLET	SEQ ID NO: 2516 QQYDILLT
		AA	SEQ ID NO: 632	SEQ ID NO: 789	SEQ ID NO: 946
!PS:335970	5C2	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
		AA	SEQ ID NO: 2203 KSSQSVLSSNNKNYIA	SEQ ID NO: 2360 WASTRES	SEQ ID NO: 2517 QQYSTPWT
		AA	SEQ ID NO: 633	SEQ ID NO: 790	SEQ ID NO: 947
!PS:335978	13H12	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
		AA	SEQ ID NO: 2204 KSSQSVLSSNNKNYIA	SEQ ID NO: 2361 WASTRES	SEQ ID NO: 2518 QQYSTPWT
		AA	SEQ ID NO: 634	SEQ ID NO: 791	SEQ ID NO: 948
!PS:335986	11C1	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC	CAGCAATATTATCGTACTCCGT GGACG
		AA	SEQ ID NO: 2205 KSSQSVLSSNNKNYLA	SEQ ID NO: 2362 WTSTRDS	SEQ ID NO: 2519 QQYRTPWT
		AA	SEQ ID NO: 635	SEQ ID NO: 792	SEQ ID NO: 949
!PS:335994	12H11	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC	CAGCAATATTATCGTACTCCGT GGACG
		AA	SEQ ID NO: 2206	SEQ ID NO: 2363	SEQ ID NO: 2520

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		AA	KSSQSVLSSNNKNYLA SEQ ID NO: 636	WTSTRDS SEQ ID NO: 793	QYYRTPWT SEQ ID NO: 950
!PS:336024	18E3	NA	AGGCCAGTCAGAGTATTAGTT ACAGTTACTTAGCC	GGTGCATCCAGCAGGGGCCACT	CAGCAGTATGGTAGTTCACCCGC TCACT
		AA	SEQ ID NO: 2207 RASQISYSYLA	SEQ ID NO: 2364 GASSRAT	SEQ ID NO: 2521 QQYSSPLT
!PS:336041	2G10_LC1	NA	SEQ ID NO: 637 AGGCCAGTCAGAGTGTTAGCA 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 GGTGCATCCAGTTTGC AAAAGT	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 GATGCTTCCAATTGGAGCCA	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 CGGCGAGTCAGGGTCTTATCA TCTGGTTAGCC	SEQ ID NO: 797 GCTGCATCCAGTTTGC AAAAGT	SEQ ID NO: 954 CAACAGACTAACAGTTTCCCTC CGACG
		AA	SEQ ID NO: 2211 RASQGLIWL A	SEQ ID NO: 2368 AASSLQS	SEQ ID NO: 2525 QQTNSFPPT
			SEQ ID NO: 641	SEQ ID NO: 798	SEQ ID NO: 955

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!PS:359621	17H11.004.00	NA	CGGGCAGTCAGGGTCTTATCA TCTGGTTAGCC	GCTGCATCCAGTTTGCAAAAGT	CAACAGACTAACAGTTTCCCTC CGACG
			SEQ ID NO: 2212	SEQ ID NO: 2369	SEQ ID NO: 2526
			RASQGLIWL	AASSLQS	QQTNSFPPT
!PS:359781	4H9.004.001	NA	SEQ ID NO: 642	SEQ ID NO: 799	SEQ ID NO: 956
			CGGGCAAGTCAGGGCATTAGAA ATGAGTTAGGC	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATAATAGTTACCCAT TCACT
			SEQ ID NO: 2213	SEQ ID NO: 2370	SEQ ID NO: 2527
!PS:360929	4H9.004.002	AA	RASQGIRNELG	GASSLQS	LQHNSYPFT
			SEQ ID NO: 643	SEQ ID NO: 800	SEQ ID NO: 957
			CGGGCAAGTCAGGGCATTAGAA ATGAGTTAGGC	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATAATAGTTACCCAT TCACT
!PS:360936	4H9.004.003	NA	SEQ ID NO: 2214	SEQ ID NO: 2371	SEQ ID NO: 2528
			RASQGIRNELG	GASSLQS	LQHNSYPFT
			SEQ ID NO: 644	SEQ ID NO: 801	SEQ ID NO: 958
!PS:360943	4H9.004.004	AA	CGGGCAAGTCAGGGCATTAGAA ATGAGTTAGGC	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATAATAGTTACCCAT TCACT
			SEQ ID NO: 2215	SEQ ID NO: 2372	SEQ ID NO: 2529
			RASQGIRNELG	GASSLQS	LQHNSYPFT
!PS:360949	4H9.004.005	NA	SEQ ID NO: 645	SEQ ID NO: 802	SEQ ID NO: 959
			CGGGCAAGTCAGGGCATTAGAA ATGAGTTAGGC	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATAATAGTTACCCAT TCACT
			SEQ ID NO: 2216	SEQ ID NO: 2373	SEQ ID NO: 2530
!PS:360949	4H9.004.005	AA	RASQGIRNELG	GASSLQS	LQHNSYPFT
			SEQ ID NO: 646	SEQ ID NO: 803	SEQ ID NO: 960
			CGGGCAAGTCAGGGCATTAGAA ATGAGTTAGGC	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATAATAGTTACCCAT TCACT
!PS:360949	4H9.004.005	NA	SEQ ID NO: 2217	SEQ ID NO: 2374	SEQ ID NO: 2531
			RASQGIRNELG	GASSLQS	LQHNSYPFT
			SEQ ID NO: 647	SEQ ID NO: 804	SEQ ID NO: 961

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!PS:359761	4B1.004.006	NA	CGGGCAAGTCAGGCATTAGAA ATGAGTTAGGC	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATAATAGTTACCCCAT TCACT
		AA	SEQ ID NO: 2218 RASQDIRNELG	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	CGGGCAAGTCAGGACATTAGAG ATTATTAGGC	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2219 RASQDIRDYL	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	CGGGCAAGTCAGGACATTAGAG ATTATTAGGC	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2220 RASQDIRDYL	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	CGGGCAAGTCAGGACATTAGAG ATTATTAGGC	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2221 RASQDIRDYL	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	CGGGCAAGTCAGGACATTAGAG ATTATTAGGC	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2222 RASQDIRDYL	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	CGGGCAAGTCAGGACATTAGAG ATTATTAGGC	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2223 RASQDIRDYL	SEQ ID NO: 2380 GASSLQS	SEQ ID NO: 2537 LQHNNYPFT
		AA	SEQ ID NO: 653	SEQ ID NO: 810	SEQ ID NO: 967

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!PS:359785	4B1.015	NA	CGGGCAAGTCAGGACATTAGAG ATTATTAGGC	GGTGCATCCAGTTTGCAAAAGT	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	GGTGCATCCAGTTTGCAAAAGT	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	GGTGCATCCAGTTTGCAAAAGT	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	GGTGCATCCAGTTTGCAAAAGT	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	GGTGCATCCAGTTTGCAAAAGT	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	GGTGCATCCAGTTTGCAAAAGT	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

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!PS:361005	18F2.005	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTAGGC	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2230	SEQ ID NO: 2387	SEQ ID NO: 2544
			RASQDLRNYLG	GASSLQS	LQHNNYPFT
!PS:361009	18F2.006	NA	SEQ ID NO: 660	SEQ ID NO: 817	SEQ ID NO: 974
			CGGGCAAGTCAGGACCTTAGAA ATTATTAGGC	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2231	SEQ ID NO: 2388	SEQ ID NO: 2545
!PS:361013	18F2.007	AA	RASQDLRNYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 661	SEQ ID NO: 818	SEQ ID NO: 975
		NA	CGGGCAAGTCAGGACCTTAGAA ATTATTAGGC	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATAATAATTACCCCT TCACT
!PS:361017	18F2.008	AA	SEQ ID NO: 2232	SEQ ID NO: 2389	SEQ ID NO: 2546
			RASQDLRNYLG	GASSLQS	LQHNNYPFT
		NA	SEQ ID NO: 662	SEQ ID NO: 819	SEQ ID NO: 976
!PS:361021	18F2.009	AA	CGGGCAAGTCAGGACCTTAGAA ATTATTAGGC	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2233	SEQ ID NO: 2390	SEQ ID NO: 2547
		NA	RASQDLRNYLG	GASSLQS	LQHNNYPFT
!PS:361028	18F2.010	AA	SEQ ID NO: 663	SEQ ID NO: 820	SEQ ID NO: 977
			CGGGCAAGTCAGGACCTTAGAA ATTATTAGGC	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATAATAATTACCCCT TCACT
		NA	SEQ ID NO: 2234	SEQ ID NO: 2391	SEQ ID NO: 2548
!PS:361028	18F2.010	AA	RASQDLRNYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 664	SEQ ID NO: 821	SEQ ID NO: 978
		NA	CGGGCAAGTCAGGACCTTAGAA ATTATTAGGC	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATAATAATTACCCCT TCACT
!PS:361028	18F2.010	AA	SEQ ID NO: 2235	SEQ ID NO: 2392	SEQ ID NO: 2549
			RASQDLRNYLG	GASSLQS	LQHNNYPFT
		NA	SEQ ID NO: 665	SEQ ID NO: 822	SEQ ID NO: 979

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!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
		NA	QASQDISNYLN	DASNLET	QQYDILLT
		AA	SEQ ID NO: 670	SEQ ID NO: 827	SEQ ID NO: 984
			CAGGCGAGTCAGGACATTAGCA ACTATTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCCTCA CT
		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

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!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

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!PS:359869	6H1.003	NA	CGGGCAAGTCAGGACATTAGAG ATTATTAGGC	GGTGCATCCAGTTTGCAAAAGT	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	GGTGCATCCAGTTTGCAAAAGT	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	GGTGCATCCAGTTTGCAAAAGT	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	GGTGCATCCAGTTTGCAAAAGT	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	GGTGCATCCAGTTTGCAAAAGT	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	GGTGCATCCAGTTTGCAAAAGT	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

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!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	SEQ ID NO: 684	SEQ ID NO: 841	SEQ ID NO: 998
			CAGCGAGTCAGGACATTACCA ACTATTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
		AA	SEQ ID NO: 2255	SEQ ID NO: 2412	SEQ ID NO: 2569
!PS:361091	6A5.004.003	AA	QASQDITNYLN	DASNLEP	QQYDDLFT
			SEQ ID NO: 685	SEQ ID NO: 842	SEQ ID NO: 999
		NA	CAGCGAGTCAGGACATTACCA ACTATTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
!PS:361095	6A5.004.004	AA	SEQ ID NO: 2256	SEQ ID NO: 2413	SEQ ID NO: 2570
			QASQDITNYLN	DASNLEP	QQYDDLFT
		NA	SEQ ID NO: 686	SEQ ID NO: 843	SEQ ID NO: 1000
!PS:361101	6A5.004.005	AA	CAGCGAGTCAGGACATTACCA ACTATTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
			SEQ ID NO: 2257	SEQ ID NO: 2414	SEQ ID NO: 2571
		NA	QASQDITNYLN	DASNLEP	QQYDDLFT
!PS:361105	6A5.004.006	AA	SEQ ID NO: 687	SEQ ID NO: 844	SEQ ID NO: 1001
			CAGCGAGTCAGGACATTACCA ACTATTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
		NA	SEQ ID NO: 2258	SEQ ID NO: 2415	SEQ ID NO: 2572
!PS:361105	6A5.004.006	AA	QASQDITNYLN	DASNLEP	QQYDDLFT
			SEQ ID NO: 688	SEQ ID NO: 845	SEQ ID NO: 1002
		NA	CAGCGAGTCAGGACATTACCA ACTATTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
!PS:361105	6A5.004.006	AA	SEQ ID NO: 2259	SEQ ID NO: 2416	SEQ ID NO: 2573
			QASQDITNYLN	DASNLEP	QQYDDLFT
		NA	SEQ ID NO: 689	SEQ ID NO: 846	SEQ ID NO: 1003

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!PS:361109	6A5.004.007	NA	CAGCGAGTCAGGACATTACCA ACTATTTAAAT	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 ACTATTTAAAT	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 ACTATTTAAAT	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 ACTATTTAAAT	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 ACTATTTAAAT	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

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!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	SEQ ID NO: 696	SEQ ID NO: 853	SEQ ID NO: 1010
			AGGGCCAGTCAGATTTTACCA GCACCTACTTAGCC	GGTGCATCCAGCAGGGGCCACT	CAGCAGTATGGTAGCTCACCTC GC
		AA	SEQ ID NO: 2267	SEQ ID NO: 2424	SEQ ID NO: 2581
!PS:361165	2A11.005	NA	RASQIFTSTYLA	GASSRAT	QQYGSSPR
			SEQ ID NO: 697	SEQ ID NO: 854	SEQ ID NO: 1011
		AA	AGGGCCAGTCAGATTTTACCA GCACCTACTTAGCC	GGTGCATCCAGCAGGGGCCACT	CAGCAGTATGGTAGCTCACCTC GC
!PS:361172	2G10_LC1.00 ³	NA	SEQ ID NO: 2268	SEQ ID NO: 2425	SEQ ID NO: 2582
			RASQIFTSTYLA	GASSRAT	QQYGSSPR
		AA	SEQ ID NO: 698	SEQ ID NO: 855	SEQ ID NO: 1012
!PS:361178	2G10_LC1.00 ⁴	NA	AGGGCCAGTCAGAGTGTAGCA GCAACTTAGCC	GGTGCAGCCACCAGGGGCCACT	CAGCAGTATAATAAAGTGGCCTC TCACT
			SEQ ID NO: 2269	SEQ ID NO: 2426	SEQ ID NO: 2583
		AA	RASQSVSSNLA	GAATRAT	QQYNNWPLT
!PS:361185	2G10_LC1.00 ⁵	NA	SEQ ID NO: 699	SEQ ID NO: 856	SEQ ID NO: 1013
			AGGGCCAGTCAGAGTGTAGCA GCAACTTAGCC	GGTGCAGCCACCAGGGGCCACT	CAGCAGTATAATAAAGTGGCCTC TCACT
		AA	SEQ ID NO: 2270	SEQ ID NO: 2427	SEQ ID NO: 2584
!PS:361185	2G10_LC1.00 ⁵	NA	RASQSVSSNLA	GAATRAT	QQYNNWPLT
			SEQ ID NO: 700	SEQ ID NO: 857	SEQ ID NO: 1014
		AA	AGGGCCAGTCAGAGTGTAGCA GCAACTTAGCC	GGTGCAGCCACCAGGGGCCACT	CAGCAGTATAATAAAGTGGCCTC TCACT
!PS:361185	2G10_LC1.00 ⁵	NA	SEQ ID NO: 2271	SEQ ID NO: 2428	SEQ ID NO: 2585
			RASQSVSSNLA	GAATRAT	QQYNNWPLT
		AA	SEQ ID NO: 701	SEQ ID NO: 858	SEQ ID NO: 1015

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!PS:361192	2G10_LC1.00 6	NA	AGGGCCAGTCAGAGTGTTAGCA GCAACTTAGCC	GGTGAGCCACCAGGGCCACT	CAGCAGTATAATAACTGGCCTC TCACT
		AA	SEQ ID NO: 2272	SEQ ID NO: 2429	SEQ ID NO: 2586
			RASQSVSSNLA	GAATRAT	QQYNNWPLT
!PS:359609	2G10_LC1.00 7	NA	AGGGCCAGTCAGAGTGTTAGCA GCAACTTAGCC	GGTGAGCCACCAGGGCCACT	CAGCAGTATAATAACTTCCCTC TCACT
		AA	SEQ ID NO: 2273	SEQ ID NO: 2430	SEQ ID NO: 2587
			RASQSVSSNLA	GAATRAT	QQYNNFPLT
!PS:359615	2G10_LC1.00 8	NA	AGGGCCAGTCAGAGTGTTAGCA GCAACTTAGCC	GGTGAGCCACCAGGGCCACT	CAGCAGTATAATAACTATCCTC TCACT
		AA	SEQ ID NO: 2274	SEQ ID NO: 2431	SEQ ID NO: 2588
			RASQSVSSNLA	GAATRAT	QQYNNYPLT
!PS:361196	2G10_LC1.00 9	NA	AGGGCCAGTCAGAGTGTTAGCA GCAACTTAGCC	GGTGAGCCACCAGGGCCACT	CAGCAGTATAATAACTGGCCTC TCACT
		AA	SEQ ID NO: 2275	SEQ ID NO: 2432	SEQ ID NO: 2589
			RASQSVSSNLA	GAATRAT	QQYNNWPLT
!PS:361202	2G10_LC1.01 0	NA	AGGGCCAGTCAGAGTGTTAGCA GCAACTTAGCC	GGTGAGCCACCAGGGCCACT	CAGCAGTATAATAACTGGCCTC TCACT
		AA	SEQ ID NO: 2276	SEQ ID NO: 2433	SEQ ID NO: 2590
			RASQSVSSNLA	GAATRAT	QQYNNWPLT
!PS:359644	18E3.002	NA	AGGGCCAGTCAGAGTATTAGTT ACAGTTACTTAGCC	GGTGATCCAGCAGGGCCACT	CAGCAGTATGGTAGTTCACCGC TCACT
		AA	SEQ ID NO: 2277	SEQ ID NO: 2434	SEQ ID NO: 2591
			RASQSVSSNLA	GASSRAT	QQYSSPLT
			SEQ ID NO: 707	SEQ ID NO: 864	SEQ ID NO: 1021

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!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

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

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!PS:361247	5C2.011	NA	AAGTCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
		AA	SEQ ID NO: 2289	SEQ ID NO: 2446	SEQ ID NO: 2603
			KSSQSVLSSNNKNYIA	WASTRES	QQYYSTPWT
!PS:361254	5C2.012	NA	AAGTCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
		AA	SEQ ID NO: 2290	SEQ ID NO: 2447	SEQ ID NO: 2604
			KSSQSVLSSNNKNYIA	WASTRES	QQYYSTPWT
!PS:361261	5C2.013	NA	AAGTCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
		AA	SEQ ID NO: 2291	SEQ ID NO: 2448	SEQ ID NO: 2605
			KSSQSVLSSNNKNYIA	WASTRES	QQYYSTPWT
!PS:361268	5C2.014	NA	AAGTCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
		AA	SEQ ID NO: 2292	SEQ ID NO: 2449	SEQ ID NO: 2606
			KSSQSVLSSNNKNYIA	WASTRES	QQYYSTPWT
!PS:359669	5C2.015	NA	AAGTCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
		AA	SEQ ID NO: 2293	SEQ ID NO: 2450	SEQ ID NO: 2607
			KSSQSVLSSNNKNYIA	WASTRES	QQYYSTPWT
			SEQ ID NO: 723	SEQ ID NO: 880	SEQ ID NO: 1037

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

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!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 QQYYRTPWT 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 QQYYRTPWT 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 QQYYRTPWT 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 QQYYRTPWT 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 QQYYRTPWT SEQ ID NO: 1047

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

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

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

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

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2C2.005.003	!PS:361418	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATTATGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGAAAGCCTG AGTGGTCCGGTA
		AA	SEQ ID NO: 2324 SGSSNIGSNYVN	SEQ ID NO: 2481 TNNQRPS	SEQ ID NO: 2638 ATFDESLQGPV
		AA	SEQ ID NO: 754	SEQ ID NO: 911	SEQ ID NO: 1068
2C2.005.004	!PS:361424	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATTATGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGAAAGCCTG CAAGTCCGGTA
		AA	SEQ ID NO: 2325 SGSSNIGSNYVN	SEQ ID NO: 2482 TNNQRPS	SEQ ID NO: 2639 ATFDESLQGPV
		AA	SEQ ID NO: 755	SEQ ID NO: 912	SEQ ID NO: 1069
2C2.005.005	!PS:361430	NA	TCTGGAAGTAGCTCCAACATCG GAAGTCAAACTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGACAGCCTG AATGGTCCGGTA
		AA	SEQ ID NO: 2326 SGSSNIGSQTVN	SEQ ID NO: 2483 TNNQRPS	SEQ ID NO: 2640 ATFDDSLNQPV
		AA	SEQ ID NO: 756	SEQ ID NO: 913	SEQ ID NO: 1070
2C2.005.006	!PS:361436	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATTATGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGACAGCCTG AATGGTCCGGTA
		AA	SEQ ID NO: 2327 SGSSNIGSNYVN	SEQ ID NO: 2484 TNNQRPS	SEQ ID NO: 2641 ATFDDSLNQPV
		AA	SEQ ID NO: 757	SEQ ID NO: 914	SEQ ID NO: 1071
2C2.005.007	!PS:361442	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATACTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGAAAGCCTG AATGGTCCGGTA
		AA	SEQ ID NO: 2328 SGSSNIGSNYVN	SEQ ID NO: 2485 TNNQRPS	SEQ ID NO: 2642 ATFDESLNQPV
		AA	SEQ ID NO: 758	SEQ ID NO: 915	SEQ ID NO: 1072
2C2.005.008	!PS:361448	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATACTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGACAGCCTG 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

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!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 GAAGTCAAACTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGAAAGCCTG AGTGGTCCGGTA
		AA	SEQ ID NO: 2335 SGSSNIGSNTVN	SEQ ID NO: 2492 TNNQRPS	SEQ ID NO: 2649 ATFDESLSGPV
		AA	SEQ ID NO: 765	SEQ ID NO: 922	SEQ ID NO: 1079

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!PS:361845	18F2.013	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTAGGC	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 ATTATTAGGC	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	SGSSNIGSNTVN	TNNQRPS	ATFDSSLSPV
			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	SGSSNIGNNYVS	DNNKRPS	GTWDSSL SAVV
		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

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!PS:361136	5G12.006.002	NA	CGGGCAAGTCAGACCATTAGCA GGTTTTTAAAT	GTTGCATCCAGTTTGC AAAAGT	CAACAGAGTTACAGTACCCTG ATCAGT
		AA	SEQ ID NO: 2342	SEQ ID NO: 2499	SEQ ID NO: 2656
			RASQTISRFLN	VASSLQS	QQSYSTLIS
!PS:361140	5G12.006.003	NA	CGGGCAAGTCAGACCATTAGCA GGTTTTTAAAT	GTTGCATCCAGTTTGC AAAAGT	CAACAGAGTTACAGTACCCTG ATCAGT
		AA	SEQ ID NO: 2343	SEQ ID NO: 2500	SEQ ID NO: 2657
			RASQTISRFLN	VASSLQS	QQSYSTLIS
!PS:359919	5G12.006.004	NA	CGGGCAAGTCAGACCATTAGCA GGTTTTTAAAT	GTTGCATCCAGTTTGC AAAAGT	CAACAGAGTTACAGTACCCTG ATCAGT
		AA	SEQ ID NO: 2344	SEQ ID NO: 2501	SEQ ID NO: 2658
			RASQTISRFLN	VASSLQS	QQSYSTLIS
!PS:361144	5G12.006.005	NA	CGGGCAAGTCAGACCATTAGCA GGTTTTTAAAT	GTTGCATCCAGTTTGC AAAAGT	CAACAGAGTTACAGTACCCTG ATCAGT
		AA	SEQ ID NO: 2345	SEQ ID NO: 2502	SEQ ID NO: 2659
			RASQTISRFLN	VASSLQS	QQSYSTLIS
!PS:361151	5G12.006.006	NA	CGGGCAAGTCAGACCATTAGCA GGTTTTTAAAT	GTTGCATCCAGTTTGC AAAAGT	CAACAGAGTTACAGTACCCTG ATCAGT
		AA	SEQ ID NO: 2346	SEQ ID NO: 2503	SEQ ID NO: 2660
			RASQTISRFLN	VASSLQS	QQSYSTLIS
!PS:361491	17B11.002.001	NA	TCTGGAAGCAGCTCCAACATTG GAAATAATTATGTATCC	GACAATAATAAGCGACCCCTCA	GGAACATGGGATAGCAGCCTG AGTGCTGTGGTA
		AA	SEQ ID NO: 2347	SEQ ID NO: 2504	SEQ ID NO: 2661
			SGSSSNIGNNYVS	DNNKRPS	GTWDSLSAVV
			SEQ ID NO: 777	SEQ ID NO: 934	SEQ ID NO: 1091

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

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IPS:360570	17B11.002.008	NA	TCTGGAAGCAGCTCCAACATTG GAAATAATTATGTATCC	GACAATAATAAGCGACCCCTCA	GGAACATTTCGAAAGCAGCCTG AGTGCTGTGGTA
		AA	SEQ ID NO: 2354	SEQ ID NO: 2511	SEQ ID NO: 2668
			SGSSSNIGNNYVS	DNNKRPS	GTFESSLSAVV
IPS:362051	5G12.005.001	NA	SEQ ID NO: 784	SEQ ID NO: 941	SEQ ID NO: 1098
			CGGCAAGTCAGACCATTAGCA GGTTTTTAAAT	GTTGCATCCAGTTTGCAAAGT	CAACAGAGTTACAGTACCCCTGC TCAGT
		AA	SEQ ID NO: 2355	SEQ ID NO: 2512	SEQ ID NO: 2669
			RASQTISRFLN	VASSLQS	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
IPS:336175	2C2.005	NA	GGCTACTATATGCAT	TGGATCAACCCCTAACAGTGGTG GCACAAACTATGCACAGAAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCTCACTACTACT ACGGTATGGACGTC
			SEQ ID NO: 2670	SEQ ID NO: 2827	SEQ ID NO: 2984
		AA	GYVMH	WINPNSGGTNYAQKFQG	GGDYVWGTYPHYYYGMDV
IPS:335914	4B1	NA	SEQ ID NO: 1100	SEQ ID NO: 1257	SEQ ID NO: 1414
			AAC TT TGGCATGCAC	GTTATATGGTATGATGGAAGTA ATGAAAACCTATGCAGACTCCGT GAAGGC	GATGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
		AA	SEQ ID NO: 2671	SEQ ID NO: 2828	SEQ ID NO: 2985
			NFGMH	VIWYDGSNENYADSVKG	DGTIFGVVLGDY
			SEQ ID NO: 1101	SEQ ID NO: 1258	SEQ ID NO: 1415

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!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	NA	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 TCAGGGC	GAGGCCACGATTTTGGGAATGG TTATTGTACCGTTTGACTAC
!PS:335978	13H12	NA	SEQ ID NO: 2674	SEQ ID NO: 2831	SEQ ID NO: 2988
			GYIYH	WINPDSGGTDYSQRFQG	EATIFGMVIVPFDY
			SEQ ID NO: 1104	SEQ ID NO: 1261	SEQ ID NO: 1418
!PS:335986	11C1	AA	GGCTACTATATCCAC	TGGATCAACCCCTGACAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGGCCACGATTTTGGGAATGG TTATTGTACCGTTTGACTAC
			SEQ ID NO: 2675	SEQ ID NO: 2832	SEQ ID NO: 2989
			GYIYH	WINPDSGGTDYSQRFQG	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

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

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!PS:336099	17H11.004	NA	AGTTACTACTGGAGC	CGTATCTATACCAGTGGGAGCA CCAACACTACAACCCCTCCCTCAA GAGT	GATGTAGCAGTGGCTGGCTTTG ACTAC
			SEQ ID NO: 2682	SEQ ID NO: 2839	SEQ ID NO: 2996
			SYWWS	RIYTSNSTYNPSLKS	DVAVAGFDY
!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	SYWWS	RIYTSNSTYNPSLKS	DVAVAGFDY
			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	AA	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	NA	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

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!PS:360943	4H9.004.004	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC	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 GAAGGGC	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 GAAGGGC	GATGGGACGATTTTGGAGTGC TCTTGGGGGACTAC
!PS:360955	4B1.010	AA	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	NA	AACCTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACCTATGCAGACGCCG TGAAGGGC	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2690	SEQ ID NO: 2847	SEQ ID NO: 3004
			NFGMH	VIWYDASNENYADAVKG	DGTIFGVVLLGDY
!PS:360962	4B1.011	AA	SEQ ID NO: 1120	SEQ ID NO: 1277	SEQ ID NO: 1434
			AACCTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACCTATGCAGACGCCG TGAAGGGC	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

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

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

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18F2.006	!PS:361009	NA	AACCTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGC	GATGGGACGATCTTTGGAGTGG TCCTTGGGGGACTAC
			SEQ ID NO: 2702	SEQ ID NO: 2859	SEQ ID NO: 3016
			NFGMH	VIWYDASNENYADAVKG	DGTIFGVVLGDY
18F2.007	!PS:361013	AA	SEQ ID NO: 1132	SEQ ID NO: 1289	SEQ ID NO: 1446
			AACCTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGC	GATGGGACGATCTTTGGAGTGG TCCTTGGGGGACTAC
			SEQ ID NO: 2703	SEQ ID NO: 2860	SEQ ID NO: 3017
18F2.008	!PS:361017	AA	NFGMH	VIWYDASNENYADAVKG	DGTIFGVVLGDY
			SEQ ID NO: 1133	SEQ ID NO: 1290	SEQ ID NO: 1447
			AACCTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGC	GATGGGACGATCTTTGGAGTGG TCCTTGGGGGACTAC
18F2.009	!PS:361021	NA	SEQ ID NO: 2704	SEQ ID NO: 2861	SEQ ID NO: 3018
			NFGMH	VIWYDASNENYADAVKG	DGTIFGVVLGDY
			SEQ ID NO: 1134	SEQ ID NO: 1291	SEQ ID NO: 1448
18F2.010	!PS:361028	AA	AACCTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGC	GATGGGACGATCTTTGGAGTGG TCCTTGGGGGACTAC
			SEQ ID NO: 2705	SEQ ID NO: 2862	SEQ ID NO: 3019
			NFGMH	VIWYDASNENYADAVKG	DGTIFGVVLGDY
18F2.011	!PS:361032	NA	SEQ ID NO: 1135	SEQ ID NO: 1292	SEQ ID NO: 1449
			AACCTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACTCCGT GAAGGC	GATGGGACGATCTTTGGAGTGG TCCTTGGGGGACTAC
			SEQ ID NO: 2706	SEQ ID NO: 2863	SEQ ID NO: 3020
18F2.012	!PS:361036	AA	NFGMH	VIWYDASNENYADSVKG	DGTIFGVVLGDY
			SEQ ID NO: 1136	SEQ ID NO: 1293	SEQ ID NO: 1450

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!PS:360535	18F2.011	NA	AAC TTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAAC TATGCAGACGCCG TGAAGGC	GATAGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
		AA	SEQ ID NO: 2707 NFGMH	SEQ ID NO: 2864 VIWYDASNENYADAVKG	SEQ ID NO: 3021 DRTIFGVVLGDY
			SEQ ID NO: 1137	SEQ ID NO: 1294	SEQ ID NO: 1451
!PS:361035	18F2.012	NA	AAC TTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAAC TATGCAGACGCCG TGAAGGC	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
		AA	SEQ ID NO: 2708 NFGMH	SEQ ID NO: 2865 VIWYDASNENYADAVKG	SEQ ID NO: 3022 DGTFGVVLGDY
			SEQ ID NO: 1138	SEQ ID NO: 1295	SEQ ID NO: 1452
!PS:359940	2F11.002	NA	AGCTATGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGC	GATAGGACGATTTTGGAGTGG TTCTTGACTAC
		AA	SEQ ID NO: 2709 SYGMH	SEQ ID NO: 2866 VIWYDASNKYYADAVKG	SEQ ID NO: 3023 DRTIFGVVLDY
			SEQ ID NO: 1139	SEQ ID NO: 1296	SEQ ID NO: 1453
!PS:361039	2F11.003	NA	AGCTATGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGC	GATAGGACGATTTTGGAGTGG TTCTTGACTAC
		AA	SEQ ID NO: 2710 SYGMH	SEQ ID NO: 2867 VIWYDASNKYYADAVKG	SEQ ID NO: 3024 DRTIFGVVLDY
			SEQ ID NO: 1140	SEQ ID NO: 1297	SEQ ID NO: 1454
!PS:361043	2F11.004	NA	AGCTATGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGC	GATAGGACGATTTTGGAGTGG TTCTTGACTAC
		AA	SEQ ID NO: 2711 SYGMH	SEQ ID NO: 2868 VIWYDASNKYYADAVKG	SEQ ID NO: 3025 DRTIFGVVLDY
			SEQ ID NO: 1141	SEQ ID NO: 1298	SEQ ID NO: 1455

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!PS:361049	2F11.005	NA	AGCTATGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC	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 GAAGGGC	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 GAAGGGC	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 GAAGGGC	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 GAAGGGC	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

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!PS:35956	2F11.010	NA	AGCTATGGCATGCAC	GTTATATGGTATGATGGAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC	GATAGGACGATTTTGGAGTGG TTCTTGACTAC
			SEQ ID NO: 2717	SEQ ID NO: 2874	SEQ ID NO: 3031
		AA	SYGMH	VIWYDASNKYYADAVKG	DRTIFGVLLDY
!PS:35985	6H1.002		SEQ ID NO: 1147	SEQ ID NO: 1304	SEQ ID NO: 1461
		NA	TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC	GATGGACGATTTTGGAGTGC TCCTGGGGGACTAC
			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 GAAGGGC	GATAGGACGATTTTGGAGTGC TCCTGGGGGACTAC
!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 GAAGGGC	GATGGACGATTTTGGAGTGC TCCTGGGGGACTAC
			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 GAAGGGC	GATAGGACGATTTTGGAGTGC TCCTGGGGGACTAC
			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

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!PS:361067	6H1.006	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGGAAGTA ATAAATACTATGCAGACTCCGT GAAGGC	GATGGGACGATTTTGGAGTGC TCCTGGGGGACTAC
			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	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACTCCGT GAAGGC	GATGGGACGATTTTGGAGTGC TCCTGGGGGACTAC
			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 TCCTGGGGGACTAC
!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	GCTATATGGTATGATGCAAAATA 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	GCTATATGGTATGATGCAAAATA 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

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!PS:361091	6A5.004.003	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAAATA ATAAATACTATGCAGACGCCGT GAAGGGC	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 GAAGGGC	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 GAAGGGC	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 GAAGGGC	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 GAAGGGC	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

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!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	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAATA ATAAATACTATGCAGACTCCGT GAAGGC	GATCGGACGATTTTGGAGTGG TCCTTGAGTAC
			SEQ ID NO: 2733	SEQ ID NO: 2890	SEQ ID NO: 3047
			SYGMH	AIWYDANNKYYADSVKG	DRTIFGVVLEY
!PS:359896	6A5.004.010	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAATA ATAAATACTATGCAGACGCCGT GAAGGC	GATCGGACGATTTTGGAGTGG TCCTTGAGTAC
			SEQ ID NO: 1163	SEQ ID NO: 1320	SEQ ID NO: 1477
			SYGMH	AIWYDANNKYYADSVKG	DRTIFGVVLEY
!PS:359890	6A5.004.011	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAATA ATAAATACTATGCAGACGCCGT GAAGGC	GATCGGACGATTTTGGAGTGG TCCTTGAGTAC
			SEQ ID NO: 2734	SEQ ID NO: 2891	SEQ ID NO: 3048
			SYGMH	AIWYDANNKYYADAVKG	DRTIFGVVLEY
!PS:359567	2A11.002	AA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAATA ATAAATACTATGCAGACGCCGT GAAGGC	GATCGGACGATTTTGGAGTGG TCCTTGAGTAC
			SEQ ID NO: 1164	SEQ ID NO: 1321	SEQ ID NO: 1478
			SYGMH	AIWYDANNKYYADSVKG	DRTIFGVVLEY
!PS:359567	2A11.002	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAATA ATAAATACTATGCAGACGCCGT GAAGGC	GATCGGACGATTTTGGAGTGG TCCTTGAGTAC
			SEQ ID NO: 2735	SEQ ID NO: 2892	SEQ ID NO: 3049
			SYGMH	AIWYDANNKYYADAVKG	DRTIFGVVLEY
!PS:359567	2A11.002	AA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAATA ATAAATACTATGCAGACGCCGT GAAGGC	GATCGGACGATTTTGGAGTGG TCCTTGAGTAC
			SEQ ID NO: 1165	SEQ ID NO: 1322	SEQ ID NO: 1479
			SYGMH	AIWYDANNKYYADSVKG	DRTIFGVVLEY
!PS:359567	2A11.002	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAATA ATAAATACTATGCAGACGCCGT GAAGGC	GATCGGACGATTTTGGAGTGG TCCTTGAGTAC
			SEQ ID NO: 2736	SEQ ID NO: 2893	SEQ ID NO: 3050
			SYGMH	VIWYDASNKYYEDAVKG	GITIFGHGFEY
!PS:359567	2A11.002	AA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAATA ATAAATACTATGCAGACGCCGT GAAGGC	GATCGGACGATTTTGGAGTGG TCCTTGAGTAC
			SEQ ID NO: 1166	SEQ ID NO: 1323	SEQ ID NO: 1480
			SYGMH	VIWYDASNKYYEDAVKG	GITIFGHGFEY

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!PS:335965	2A11.003	NA	AGCTATGGCATGCAC	GTTATATGGTATGATGGAAGTA ATAAATACTATGAAGACTCCGT GAAGGGC	GGGATTACGATTTTGGTTCATG 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	GTTATATGGTATGATGGAAGTA ATAAATACTATGAAGACTCCGT GAAGGGC	GGGATTACGATTTTGGTTCATG 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	GTTATATGGTATGATGGAAGTA ATAAATACTATGAAGACTCCGT GAAGGGC	GGGATTACGATTTTGGTTCATG GGTTTGAATAT
!PS:361172	2A11.005		SEQ ID NO: 2739	SEQ ID NO: 2896	SEQ ID NO: 3053
		AA	SYGMH	VIWYDGSNKYYEDSVKG	GITIFGHGEY
			SEQ ID NO: 1169	SEQ ID NO: 1326	SEQ ID NO: 1483
!PS:361178	2G10_LC1.003	NA	AACATATGGCATGCAC	GCTATATGGTTTGTGCAAGTG ATAAATACTATGCAGACGCCGT GAAGGGC	GATCAGGCGATTTTGGAGTGG 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	AACATATGGCATGCAC	GCTATATGGTTTGTGCAAGTG ATAAATACTATGCAGACTCCGT GAAGGGC	GATCAGGCGATTTTGGAGTGG 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

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!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: 1329	SEQ ID NO: 1486
		NA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTG ATAAATACTATGCAGACGCCGT GAAGGC	GATCAGCGGATTTTGGAGTGG TCCCCGACTAC
		SEQ ID NO: 2743		SEQ ID NO: 2900	SEQ ID NO: 3057
!PS:359609	2G10_LC1.007	AA	NYGMH	AIWFDASDKYYADAVKG	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: 2901	SEQ ID NO: 3058
		AA	NYGMH	AIWFDASDKYYADAVKG	DQAIFGVVPDY
		SEQ ID NO: 1174		SEQ ID NO: 1331	SEQ ID NO: 1488
!PS:359615	2G10_LC1.008	NA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTG ATAAATACTATGCAGACGCCGT GAAGGC	GATCAGCGGATTTTGGAGTGG TCCCCGACTAC
		AA	SEQ ID NO: 2745	SEQ ID NO: 2902	SEQ ID NO: 3059
		NYGMH		AIWFDASDKYYADAVKG	DQAIFGVVPDY
!PS:361196	2G10_LC1.009	AA	SEQ ID NO: 1175	SEQ ID NO: 1332	SEQ ID NO: 1489
		NA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTG ATAAATACTATGCAGACGCCGT GAAGGC	GATCAGCGGATTTTGGAGTGG TCCCCGACTAC
		SEQ ID NO: 2746		SEQ ID NO: 2903	SEQ ID NO: 3060
!PS:361196	2G10_LC1.009	AA	NYGMH	AIWFDASDKYYADAVKG	DQAIFGVVPDY
		SEQ ID NO: 1176		SEQ ID NO: 1333	SEQ ID NO: 1490

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!PS:361202	2G10_LC1.010	NA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTG ATAAATACTATGCAGACGCCGT GAAGGC	GATCAGCGGATTTTGGAGTGG TCCCCGACTAC
			SEQ ID NO: 2747	SEQ ID NO: 2904	SEQ ID NO: 3061
		AA	NYGMH	AIWFDASDKYYADAVKG	DQAIFGVVPDY
!PS:359644	18E3.002		SEQ ID NO: 1177	SEQ ID NO: 1334	SEQ ID NO: 1491
		NA	AGTGGTGGTTACTACTGGAGC	TACATCTATTACAGTGGGAGCA CCTACTACAACCCGTCCTCAA GAGT	GATCGTATTACGATTTTGGAG TGGTTATGGGGGCGGTATGG ACGTC
		AA	SEQ ID NO: 2748 SGGYYS	SEQ ID NO: 2905 YIYSGSTYYNPSLKS	SEQ ID NO: 3062 DRITIFGVVMGGGMDV
!PS:361206	18E3.003		SEQ ID NO: 1178	SEQ ID NO: 1335	SEQ ID NO: 1492
		NA	AGTGGTGGTTACTACTGGAGC	TACATCTATTACAGTGGGAGCA CCTACTACAACCCGTCCTCAA GAGT	GATCGTATTACGATTTTGGAG TGGTTATGGGGGCGGTATGG ACGTC
		AA	SEQ ID NO: 2749 SGGYYS	SEQ ID NO: 2906 YIYSGSTYYNPSLKS	SEQ ID NO: 3063 DRITIFGVVMGGGMDV
!PS:359628	18E3.004		SEQ ID NO: 1179	SEQ ID NO: 1336	SEQ ID NO: 1493
		NA	AGTGGTGGTTACTACTGGAGC	TACATCTATTACAGTGGGAGCA CCTACTACAACCCGTCCTCAA GAGT	GATCGTATTACGATTTTGGAG TGGTTATGGGGGCGGTATGG ACGTC
		AA	SEQ ID NO: 2750 SGGYYS	SEQ ID NO: 2907 YIYSGSTYYNPSLKS	SEQ ID NO: 3064 DRITIFGVVMGGGMDV
!PS:359637	18E3.005		SEQ ID NO: 1180	SEQ ID NO: 1337	SEQ ID NO: 1494
		NA	AGTGGTGGTTACTACTGGAGC	TACATCTATTACAGTGGGAGCA CCTACTACAACCCGTCCTCAA GAGT	GATCGTATTACGATTTTGGAG TGGTTATGGGGGCGGTATGG ACGTC
		AA	SEQ ID NO: 2751 SGGYYS	SEQ ID NO: 2908 YIYSGSTYYNPSLKS	SEQ ID NO: 3065 DRITIFGVVMGGGMDV
			SEQ ID NO: 1181	SEQ ID NO: 1338	SEQ ID NO: 1495

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

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!PS:361236	5C2.008	NA	GGCTACTATATCCAC	TGGATCAACCCCTGACGCTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGCCACGATTTTGGAAATGG TTATTGTACCGTTTGACTAC
		AA	SEQ ID NO: 2757	SEQ ID NO: 2914	SEQ ID NO: 3071
			GYIYH	WINPDAGGTDYSQRFQG	EATIFGMVIVPFDY
!PS:359685	5C2.009	NA	GGCTACTATATCCAC	TGGATCAACCCCTGACGCTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGCCACGATTTTGGAAATGG TTATTGTACCGTTTGACTAC
		AA	SEQ ID NO: 2758	SEQ ID NO: 2915	SEQ ID NO: 3072
			GYIYH	WINPDAGGTDYSQRFQG	EATIFGMVIVPFDY
!PS:361240	5C2.010	NA	GGCTACTATATCCAC	TGGATCAACCCCTGACAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGCCACGATTTTGGAAATGG TTATTGTACCGTTTGACTAC
		AA	SEQ ID NO: 2759	SEQ ID NO: 2916	SEQ ID NO: 3073
			GYIYH	WINPDSGGTDYSQRFQG	EATIFGMVIVPFDY
!PS:361247	5C2.011	NA	GGCTACTATATCCAC	TGGATCAACCCCTGACAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGCCACGATTTTGGAAATGG TTATTGTACCGTTTGACTAC
		AA	SEQ ID NO: 1189	SEQ ID NO: 1346	SEQ ID NO: 1503
			GYIYH	WINPDSGGTDYSQRFQG	EATIFGMVIVPFDY
!PS:361254	5C2.012	NA	GGCTACTATATCCAC	TGGATCAACCCCTGACAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGCCACGATTTTGGAAATGG TTATTGTACCGTTTGACTAC
		AA	SEQ ID NO: 2760	SEQ ID NO: 2917	SEQ ID NO: 3074
			GYIYH	WINPDSGGTDYSQRFQG	EATIFGMVIVPFDY
!PS:361254	5C2.012	NA	GGCTACTATATCCAC	TGGATCAACCCCTGACAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGCCACGATTTTGGAAATGG TTATTGTACCGTTTGACTAC
		AA	SEQ ID NO: 2761	SEQ ID NO: 2918	SEQ ID NO: 3075
			GYIYH	WINPDSGGTDYSQRFQG	EATIFGMVIVPFDY

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!PS:361261	5C2.013	NA	GGCTACTATATCCAC	TGGATCAACCCCTGACGCTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGCCACGATTTTGGAAATGG 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	GAGCCACGATTTTGGAAATGG 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	GAGCCACGATTTTGGAAATGG 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	GAGCCACGATTTTGGAAATGG 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	GAGCCACGATTTTGGAAATGC TTATTGTACCAATTGACTAC
		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

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!PS:361282	11C1.003	NA	GGCTACTATATACAC	TGATCAGCCCTAACAGTGGTG 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	TGATCAGCCCTAACAGTGGTG 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	TGATCAGCCCTAACAGTGGTG 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	TGATCAGCCCTAACAGTGGTG 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	TGATCAGCCCTAACAGTGGTG 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

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!PS:361301	11C1.008	NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG ACACAAGCTATGCACAGAAGT TTCAGGAC	GAGGCCACGATTTTGGAAATGC TTATTGTACCATTTGACTAC
		AA	SEQ ID NO: 2772	SEQ ID NO: 2929	SEQ ID NO: 3086
			GYIYH	WISPSGDTSYAQKFQD	EATIFGMLIVPFDY
!PS:359703	11C1.009	NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG AAACAAGCTATGCACAGAAGT TTCAGGAC	GAGGCCACGATTTTGGAAATGC TTATTGTACCATTTGACTAC
		AA	SEQ ID NO: 2773	SEQ ID NO: 2930	SEQ ID NO: 3087
			GYIYH	WISPSGETSYAQKFQD	EATIFGMLIVPFDY
!PS:361305	11C1.010	NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG AAACAAGCTATGCACAGAAGT TTCAGGAC	GAGGCCACGATTTTGGAAATGC TTATTGTACCATTTGACTAC
		AA	SEQ ID NO: 2774	SEQ ID NO: 2931	SEQ ID NO: 3088
			GYIYH	WISPSGETSYAQKFQD	EATIFGMLIVPFDY
!PS:361312	13H12.002	NA	GGCTACTATATCCAC	TGGATCAACCCCTGAAAGTGGTG GCACAGACTATTACAGAGGTT TCAGGGC	GAGGCCACGATTTTGGAAATGG TTATTGTACCGTTTGACTAC
		AA	SEQ ID NO: 2775	SEQ ID NO: 2932	SEQ ID NO: 3089
			GYIYH	WINPESGGTDYSQRFQG	EATIFGMVIVPFDY
!PS:359744	13H12.003	NA	GGCTACTATATCCAC	TGGATCAACCCCTGAAAGTGGTG GCACAGACTATTACAGAGGTT TCAGGGC	GAGGCCACGATTTTGGAAATGG TTATTGTACCGTTTGACTAC
		AA	SEQ ID NO: 2776	SEQ ID NO: 2933	SEQ ID NO: 3090
			GYIYH	WINPESGGTDYSQRFQG	EATIFGMVIVPFDY
		AA	SEQ ID NO: 1206	SEQ ID NO: 1363	SEQ ID NO: 1520

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

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

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!PS:361379	12H11.009	NA	GGCTACTATATACAC	TGGATAAGCCCTAACCAAGGT GAAACAAACTATGCACAGAAG TTCAGGAC	GAGCCACGATTTTGGAAATGC TTATTGTACCATTTGACTAC
		AA	SEQ ID NO: 2787	SEQ ID NO: 2944	SEQ ID NO: 3101
			GYIYH	WISPNQGETNYAQKFQD	EATIFGMLIVPFDY
!PS:361383	12H11.010	NA	GGCTACTATATACAC	TGGATAAGCCCTAACCAATGGTG ACACAAACTATGCACAGAAGT TTCAGGAC	GAGCCACGATTTTGGAAATGC TTATTGTACCATTTGACTAC
		AA	SEQ ID NO: 2788	SEQ ID NO: 2945	SEQ ID NO: 3102
			GYIYH	WISPNNGDTNYAQKFQD	EATIFGMLIVPFDY
!PS:361387	12H11.011	NA	GGCTACTATATACAC	TGGATAAGCCCTAACCAAGGT GACACAAACTATGCACAGAAG TTCAGGAC	GAGCCACGATTTTGGAAATGC TTATTGTACCATTTGACTAC
		AA	SEQ ID NO: 2789	SEQ ID NO: 2946	SEQ ID NO: 3103
			GYIYH	WISPNQDNTNYAQKFQD	EATIFGMLIVPFDY
!PS:361391	12H11.012	NA	GGCTACTATATACAC	TGGATAAGCCCTAACCAATGGTG AAACAAACTATGCACAGAAGT TTCAGGAC	GAGCCACGATTTTGGAAATGC TTATTGTACCATTTGACTAC
		AA	SEQ ID NO: 2790	SEQ ID NO: 2947	SEQ ID NO: 3104
			GYIYH	WISPNNGETNYAQKFQD	EATIFGMLIVPFDY
!PS:361395	12H11.013	NA	GGCTACTATATACAC	TGGATAAGCCCTAACCAAGGT GAAACAAACTATGCACAGAAG TTCAGGAC	GAGCCACGATTTTGGAAATGC TTATTGTACCATTTGACTAC
		AA	SEQ ID NO: 2791	SEQ ID NO: 2948	SEQ ID NO: 3105
			GYIYH	WISPNQGETNYAQKFQD	EATIFGMLIVPFDY
!PS:361395	12H11.013	AA	SEQ ID NO: 1221	SEQ ID NO: 1378	SEQ ID NO: 1535

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!PS:361402	12H11.014	NA	GGCTACTATATACAC	TGGATAAGCCCTAACCAAGGT GAAACAAACTATGCACAGAAG TTTCAGGAC	GAGGCCACGATTTTGGAAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2792	SEQ ID NO: 2949	SEQ ID NO: 3106
		AA	GYMH	WISPNQGETNYAQKFQD	EATIFGMLIVPFDY
!PS:361406	2C2.005.001		SEQ ID NO: 1222	SEQ ID NO: 1379	SEQ ID NO: 1536
		NA	GGCTACTATATGCAT	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACAGAAGT TTCAGGGC	GGGGGGATTACGTTTGGGGG ACTTATCGGCTCCTACTACT ACGGTATGGACGTC
		AA	GYMH	WINPNSGGTNYAQKFQG	GGDYVWGTYPHYYYGMDV
!PS:361412	2C2.005.002		SEQ ID NO: 2793	SEQ ID NO: 2950	SEQ ID NO: 3107
			SEQ ID NO: 1223	SEQ ID NO: 1380	SEQ ID NO: 1537
		NA	GGCTACTATATGCAT	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACAGAAGT TTCAGGGC	GGGGGGATTACGTTTGGGGG ACTTATCGGCTCCTACTACT ACGGTATGGACGTC
!PS:361418	2C2.005.003		SEQ ID NO: 2794	SEQ ID NO: 2951	SEQ ID NO: 3108
		AA	GYMH	WINPNSGGTNYAQKFQG	GGDYVWGTYPHYYYGMDV
			SEQ ID NO: 1224	SEQ ID NO: 1381	SEQ ID NO: 1538
!PS:361418	2C2.005.003	NA	GGCTACTATATGCAT	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACAGAAGT TTCAGGGC	GGGGGGATTACGTTTGGGGG ACTTATCGGCTCCTACTACT ACGGTATGGACGTC
			SEQ ID NO: 2795	SEQ ID NO: 2952	SEQ ID NO: 3109
		AA	GYMH	WINPNSGGTNYAQKFQG	GGDYVWGTYPHYYYGMDV
!PS:361424	2C2.005.004		SEQ ID NO: 1225	SEQ ID NO: 1382	SEQ ID NO: 1539
		NA	GGCTACTATATGCAT	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACAGAAGT TTCAGGGC	GGGGGGATTACGTTTGGGGG ACTTATCGGCTCCTACTACT ACGGTATGGACGTC
			SEQ ID NO: 2796	SEQ ID NO: 2953	SEQ ID NO: 3110
!PS:361424	2C2.005.004	AA	GYMH	WINPNSGGTNYAQKFQG	GGDYVWGTYPHYYYGMDV
			SEQ ID NO: 1226	SEQ ID NO: 1383	SEQ ID NO: 1540

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

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IPS:361460	2C2.005.010	NA	GGCTACTATATGCAT	TGGATCAACCCCTAACAGTGGTG GCACAAACTATGCACAGAAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACTACT ACGGTATGGACGTC
		AA	SEQ ID NO: 2802 GYMH	SEQ ID NO: 2959 WINPNSGGTNYAQKFQG	SEQ ID NO: 3116 GGDYVWGTYPHYYYGMDV
		NA	GGCTACTATATGCAT	TGGATCAACCCCTAACAGTGGTG GCACAAACTATGCACAGAAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACTACT ACGGTATGGACGTC
IPS:361466	2C2.005.011	AA	SEQ ID NO: 2803 GYMH	SEQ ID NO: 2960 WINPNSGGTNYAQKFQG	SEQ ID NO: 3117 GGDYVWGTYPHYYYGMDV
		NA	GGCTACTATATGCAT	TGGATCAACCCCTAACAGTGGTG GCACAAACTATGCACAGAAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACTACT ACGGTATGGACGTC
		AA	SEQ ID NO: 2804 GYMH	SEQ ID NO: 2961 WINPNSGGTNYAQKFQG	SEQ ID NO: 3118 GGDYVWGTYPHYYYGMDV
IPS:361472	2C2.005.012	AA	SEQ ID NO: 1234	SEQ ID NO: 1391	SEQ ID NO: 1548
		NA	GGCTACTATATGCAT	TGGATCAACCCCTAACAGTGGTG GCACAAACTATGCACAGAAAGT TTCAGGGC	GGGGGGGATTACGTTTTCGGGA CTTATCGGCCTCACTACTACTA CGGTATGGACGTC
		AA	SEQ ID NO: 2805 GYMH	SEQ ID NO: 2962 WINPNSGGTNYAQKFQG	SEQ ID NO: 3119 GGDYVWGTYPHYYYGMDV
IPS:361478	2C2.005.013	AA	SEQ ID NO: 1235	SEQ ID NO: 1392	SEQ ID NO: 1549
		NA	GGCTACTATATGCAT	TGGATCAACCCCTAACAGTGGTG GCACAAACTATGCACAGAAAGT TTCAGGGC	GGGGGGGATTACGTTTTCGGGA CTTATCGGCCTCACTACTACTA CGGTATGGACGTC
		AA	SEQ ID NO: 2806 GYMH	SEQ ID NO: 2963 WINPNSGGTNYAQKFQG	SEQ ID NO: 3120 GGDYVWGTYPHYYYGMDV
IPS:361485	2C2.005.014	AA	SEQ ID NO: 1236	SEQ ID NO: 1393	SEQ ID NO: 1550
		NA	GGCTACTATATGCAT	TGGATCAACCCCTAACAGTGGTG GCACAAACTATGCACAGAAAGT TTCAGGGC	GGGGGGGATTACGTTTTCGGGA CTTATCGGCCTCACTACTACTA CGGTATGGACGTC
		AA	SEQ ID NO: 2806 GYMH	SEQ ID NO: 2963 WINPNSGGTNYAQKFQG	SEQ ID NO: 3120 GGDYVWGTYPHYYYGMDV

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!PS:361845	18F2.013	NA	AACCTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGC	GATAGGACGATCTTTGGAGTGG TCCTGGGGGACTAC
			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	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGC	GATAGGACGATTTTGGAGTGC TCCTGGGGGACTAC
			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 ACTTATCGGCCTCACTACTACT ACGGTATGGACGTC
!PS:361855	2C2.005.015	NA	SEQ ID NO: 2809	SEQ ID NO: 2966	SEQ ID NO: 3123
			GYYMH	WINPNSGGTNYAQKFQG	GGDYVWGTYPHYYYGMDV
			SEQ ID NO: 1239	SEQ ID NO: 1396	SEQ ID NO: 1553
!PS:336067	5G12.006	NA	AGCTATGGCATAAC	GTTATATGGTATGATGGAAGTA ATAAGTTCCATGCAGACTCCGT GAAGGC	GGAAAAGTGGCTGGTATGCCT GAAAGCTTTTGAAATC
			SEQ ID NO: 2810	SEQ ID NO: 2967	SEQ ID NO: 3124
			SYGIH	VIWYDGSNKFHADSVKG	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	WMNPNSGNTGYAQKFQG	GGDYVWGSYRPPYYYYGMDV
			SEQ ID NO: 1241	SEQ ID NO: 1398	SEQ ID NO: 1555

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!PS:361127	5G12.006.001	NA	AGCTATGGCATAAC	GTTATATGGTATGATGCAAGTA ATAAGTTCCATGCAGACGCCGT GAAGGGC	GGAAAAAGTGGTGGTATGCCT GAAAGCTTTTGAAATC
			SEQ ID NO: 2812	SEQ ID NO: 2969	SEQ ID NO: 3126
			SYGIH	VIWYDASNKFHADAVKG	GKVAGMPEAFEI
!PS:361136	5G12.006.002	AA	SEQ ID NO: 1242	SEQ ID NO: 1399	SEQ ID NO: 1556
			AGCTATGGCATAAC	GTTATATGGTATGATGCAAGTA ATAAGTTCCATGCAGACGCCGT GAAGGGC	GGAAAAAGTGGTGGTATGCCT GAAAGCTTTTGAAATC
			SEQ ID NO: 2813	SEQ ID NO: 2970	SEQ ID NO: 3127
!PS:361140	5G12.006.003	AA	SYGIH	VIWYDASNKFHADAVKG	GKVAGMPEAFEI
			SEQ ID NO: 1243	SEQ ID NO: 1400	SEQ ID NO: 1557
			AGCTATGGCATAAC	GTTATATGGTATGATGCAAGTA ATAAGTTCCATGCAGACGCCGT GAAGGGC	GGAAAAAGTGGTGGTATGCCT GAAAGCTTTTGAAATC
!PS:35919	5G12.006.004	NA	SEQ ID NO: 2814	SEQ ID NO: 2971	SEQ ID NO: 3128
			SYGIH	VIWYDASNKFHADAVKG	GKVAGMPEAFEI
			SEQ ID NO: 1244	SEQ ID NO: 1401	SEQ ID NO: 1558
!PS:361144	5G12.006.005	AA	AGCTATGGCATAAC	GTTATATGGTATGATGCAAGTA ATAAGTTCCATGCAGACGCCGT GAAGGGC	GGAAAAAGTGGTGGTATGCCT GAAAGCTTTTGAAATC
			SEQ ID NO: 2815	SEQ ID NO: 2972	SEQ ID NO: 3129
			SYGIH	VIWYDASNKFHADAVKG	GKVAGMPEAFEI
!PS:361144	5G12.006.005	NA	SEQ ID NO: 1245	SEQ ID NO: 1402	SEQ ID NO: 1559
			AGCTATGGCATAAC	GTTATATGGTATGATGCAAGTA ATAAGTTCCATGCAGACTCCGT GAAGGGC	GGAAAAAGTGGTGGTATGCCT GAAAGCTTTTGAAATC
			SEQ ID NO: 2816	SEQ ID NO: 2973	SEQ ID NO: 3130
!PS:361144	5G12.006.005	AA	SYGIH	VIWYDASNKFHADSVKG	GKVAGMPEAFEI
			SEQ ID NO: 1246	SEQ ID NO: 1403	SEQ ID NO: 1560

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!PS:361151	5G12.006.006	NA	AGCTATGGCATAAC	GTTATATGGTATGATGGAAGTA ATAAGTTCCATGCAGACGCCGT GAAGGGC	GGAAAAAGTGGTGGTATGCCT GAAAGCTTTTGAAATC
			SEQ ID NO: 2817	SEQ ID NO: 2974	SEQ ID NO: 3131
			SYGIH	VIWYDGSNKFHADAVKG	GKVAGMPEAFEI
!PS:361491	17B11.002.001	AA	SEQ ID NO: 1247	SEQ ID NO: 1404	SEQ ID NO: 1561
			AGTTATGATATCAAC	TGGATGAACCCCTAACAGTGGTG GCACAGGCTATGCACAGAAAGT TCCAGGGC	GGGGTGATTACGTTTGGGGG AGTTATCGTCCCTACTACTACT ACTACGGTATGGACGTC
			SEQ ID NO: 2818	SEQ ID NO: 2975	SEQ ID NO: 3132
!PS:361499	17B11.002.002	AA	SYDIN	WMNPNSGGTGYAQKFQG	GGDYVWGSYRPPYYYYGMDV
			SEQ ID NO: 1248	SEQ ID NO: 1405	SEQ ID NO: 1562
			AGTTATGATATCAAC	TGGATGAACCCCTAACAGTGGTA ACACAGGCTATGCACAGAAAGT TCCAGGGC	GGGGTGATTACGTTTGGGGG AGTTATCGTCCCTACTACTACT ACTACGGTATGGACGTC
!PS:361503	17B11.002.003	NA	SEQ ID NO: 2819	SEQ ID NO: 2976	SEQ ID NO: 3133
			SYDIN	WMNPNSGNTGYAQKFQG	GGDYVWGSYRPPYYYYGMDV
			SEQ ID NO: 1249	SEQ ID NO: 1406	SEQ ID NO: 1563
!PS:361507	17B11.002.004	AA	AGTTATGATATCAAC	TGGATGAACCCCTAACAGTGGTG GCACAGGCTATGCACAGAAAGT TCCAGGGC	GGGGTGATTACGTTTGGGGG AGTTATCGTCCCTACTACTACT ACTACGGTATGGACGTC
			SEQ ID NO: 2820	SEQ ID NO: 2977	SEQ ID NO: 3134
			SYDIN	WMNPNSGGTGYAQKFQG	GGDYVWGSYRPPYYYYGMDV
!PS:361507	17B11.002.004	NA	SEQ ID NO: 1250	SEQ ID NO: 1407	SEQ ID NO: 1564
			AGTTATGATATCAAC	TGGATGAACCCCTAACAGTGGTG GCACAGGCTATGCACAGAAAGT TCCAGGGC	GGGGTGATTACGTTTGGGGG AGTTATCGTCCCTACTACTACT ACTACGGTATGGACGTC
			SEQ ID NO: 2821	SEQ ID NO: 2978	SEQ ID NO: 3135
!PS:361507	17B11.002.004	AA	SYDIN	WMNPNSGGTGYAQKFQG	GGDYVWGSYRPPYYYYGMDV
			SEQ ID NO: 1251	SEQ ID NO: 1408	SEQ ID NO: 1565

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!PS:361514	17B11.002.005	NA	AGTTATGATATCAAC	TGGATGAACCCCTAACAGTGGTG GCACAGGCTATGCACAGAAAGT TCCAGGGC	GGGGGTGATTACGTTTGGGGG AGTTATCGTCCCTACTACT ACTACGGTATGGACGTC
			SEQ ID NO: 2822	SEQ ID NO: 2979	SEQ ID NO: 3136
			SYDIN	WMNPNSGGTGYAQKFQG	GGDYVWGSYRPPYYYGMDV
!PS:360582	17B11.002.006	NA	AGTTATGATATCAAC	TGGATGAACCCCTAACAGTGGTA ACACAGGCTATGCACAGAAAGT TCCAGGGC	GGGGGTGATTACGTTTGGGGG AGTTATCGTCCCTACTACT ACTACGGTATGGACGTC
			SEQ ID NO: 2823	SEQ ID NO: 1409	SEQ ID NO: 1566
			SYDIN	WMNPNSGNTGYAQKFQG	GGDYVWGSYRPPYYYGMDV
!PS:361518	17B11.002.007	NA	AGTTATGATATCAAC	TGGATGAACCCCTAACAGTGGTG GCACAGGCTATGCACAGAAAGT TCCAGGGC	GGGGGTGATTACGTTTTCGGGA GTTATCGTCCCTACTACTA CTACGGTATGGACGTC
			SEQ ID NO: 2824	SEQ ID NO: 1410	SEQ ID NO: 1567
			SYDIN	WMNPNSGGTGYAQKFQG	GGDYVWGSYRPPYYYGMDV
!PS:360570	17B11.002.008	NA	AGTTATGATATCAAC	TGGATGAACCCCTAACAGTGGTG GCACAGGCTATGCACAGAAAGT TCCAGGGC	GGGGGTGATTACGTTTTCGGGA GTTATCGTCCCTACTACTA CTACGGTATGGACGTC
			SEQ ID NO: 2825	SEQ ID NO: 1411	SEQ ID NO: 1568
			SYDIN	WMNPNSGGTGYAQKFQG	GGDYVWGSYRPPYYYGMDV
!PS:362051	5G12.005.001	NA	AGCTATGGCATAAC	TGGATGAACCCCTAACAGTGGTG GCACAGGCTATGCACAGAAAGT GAAGGGC	GGAAAGTGGCTGGTATGCCT GAAGCTTTTGAATC
			SEQ ID NO: 2826	SEQ ID NO: 1412	SEQ ID NO: 1569
			SYGIH	VIWYDASNKFHADAVKG	GKVAGMPEAFEI
			SEQ ID NO: 1256	SEQ ID NO: 1413	SEQ ID NO: 1570

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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 GGACCCCGGGCAGAGGGTCACCATCTCTGT CTGGAAGTAGCTCCAAACATCGGAAGTAATACTG TAAACTGGTACCAGCACCTCCCAGGAACGGCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTCTGTG CAACATTTCGATGACAGCCTGAATGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCCTAGGTC AGCCCAAGGTGCCCCCTCGGTCACTCTGTTCCT GCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGC CACACTGGTGTGTCTCATAAGTGACTTCTACCCG GGAGCCGTGACAGTGGCTGGAAGGCAGATAG CAGCCCCGTC AAGCGGGAGTGGAACCAACCAC ACCTTCCAAACAAAGCAACAACAAGTACGCGGC CAGCAGCTATCTGAGCCTGACGCTGAGCAGTG GAAGTCCCACAGAAAGCTACAGCTGCCAGGTCAC GCATGAAGGGAGCACCCGTGGAGAAAGACAGTGG CCCCACAGAAATGTTCA	CAGATGCAGGTGGTGCAGCTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCCGGATACACCTTACCCGGCTACTAT ATGCATTGGGTGCACAGGCCCCTGACAAAGGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGGCACAACTATGCACAGAAATTTTCAGGGC AGGTCACCATGACAGGACACGTCATCAGT ACAGCTACATGGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGGGATTACGTTTGGGGGACTTATCGGCCCTCAC TACTACTACGGTATGGACGTCTGGGGCCAAGGG ACCAAGGTCAACCTCTCCCTCAGCCTCCACCAAG GGCCCATCGGTCTTCCCCCTGGCACCTCCTCCA AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA CGGTGTGCTGGAACCTCAGGGGCCCTGACCAGCG GCGTGACACCTTCCCGGTGTCTACAGTCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT CTGCAACGTGAATCACAAGCCCAGCAACACCAA GGTGACAAAGAAAGTTGAGCCCCAATCTTGTGA CAAACCTCACACATGCCACCCGTGCCAGCACCC TGAACTCCTGGGGGACCGTCAGTCTTCTCTTC CCCCCAAACCCAAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTCAATGCGTGGTGGTGAC GTGAGCCACGAAGACCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCC AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG CACGTACCGTTGTGTACGCGTCTCACCGTCTG CACCAGGACTGGTGAATGGCAAGGAGTACAA GTGCAAGGTCTCCAAACAAAGCCCTCCAGCCCC CATCGAGAAACCACATCTCCAAAGCCAAAGGGCA

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			<p> GCCCCGAGAACACAGGTGTACACCCCTGCCCCC ATCCCGGAGGAGATGACCAAGAACCCAGGTCA GCTTGACCTGCCCTGGTCAAAGGCTTCTATCCCA GCGACATCGCCGTGGAGTGGGAGAGCAATGGG CAGCCGAGAACAACTACAAAGACCACGCCCTCCC GTGCTGGACTCCGACGGCTCCTTCTTCTCTATA GCAAGCTCACCGTGGACAAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAAACCACTACACGCAGAAAGAGC CTCTCCCTGTCTCCGGGTAAA </p>
			<p> SEQ ID NO: 1885 QSVLTQPPSASGTPGQQRVTISCSGSSNIGSNTVNW YQHLPGTAPKLLIYTNNQRPSPGVDRFSGSKSGTS ASLAISGLOSEDEADYFCATFDDSLNGPVFGGGTK LTVLGGPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGA VTVAWKADSSPVKAGVETTTTPSKQSNKKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS </p>
	AA		<p> SEQ ID NO: 2042 QMQVVQSGAEVKKPGASVKVSKASGYTFTGY MHWVRQAPGQGLEWMGWNPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLSDDTA VYYCARG GDYVWGTYPHYYYGMDVWVGQGTTVTVSSAST KGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LSDSGSFELYSKLTVDKSRWQQGNVVFSCVMHEA LHNHYTQKLSLSLSPGK </p>
IPS:335914	4B1	NA	<p> SEQ ID NO: 315 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCCTT GCCGGGCAAGTCAGGACATTAGAGATTATTAG GCTGTATCAGCAGAAACCAAGGAAAGCCCTA AGCGCTGATCTATGGTGATCCAGTTTGCAAA GTGGGTCCCTTCAAGGTTTCAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAACGAAACGGTGGCT </p>
			<p> SEQ ID NO: 472 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACCTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGGAA GTAATGAAAACTATGCAGACTCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAAGAATA CGCTGTATCTGCACATGAACAGCCTGAGAGTCG CGGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTTGGGGGACTACT </p>

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	<p>GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACCTGCCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCCGAAATCAGCCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT</p>	<p>GGGGCCAGGGAACCCCTGGTCACCCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGCTGCCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGC CCTGACCAAGCGGCGTGCAACCTTCCCGGTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAAACCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCAATAAGCCAAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCATCCCGGAGGAGATGACCA AGAACCAAGGTACGCTGACCTGCCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGAGCCGGAGACAACATACAAG ACACGCTTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
	<p>SEQ ID NO: 1886</p>	<p>SEQ ID NO: 2043</p>
AA	<p>DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTEFT LTISLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA</p>	<p>QVQLVESGGGVVQPGSRSLRSLSCAASGFTFSNFGM HWVRQAPGKGLEWVAWIYDGSNENYADSVKIG RFTISRDNSKNTLYLHMNSLRVADTA VYYCARDG TIFGVVLGDYWGQGTLLVTVSSASTKGPSVFLAPS</p>

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			<p>KVQWKVDNALQSGNSQESVTEQDSKDSYSTLSST LTLKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC</p>		<p>SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVLEFPPKPKDITLMISRTPETVTVVVDVSHED PEVKFNWYVDGVEVHNAAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK</p>
			<p>SEQ ID NO: 316</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAACCAAGGGAAGCCCTA AGCCCTGATCTATGGTGATCCAGTTTGC AAA GTGGGTCCCTTCAAGGTTCAAGGCGAGTGGAT CTGGGACAGAAATCACTCTCACAAATCAGCAGCC TGACGCCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAACGAACGGTGGCT GCACCATCTGTCTTCACTTCCCGCCATCTGATG AGCAGTTGAATACTGGAACCTGCCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCAAAAGAGCTTCAACA GGGGAGAGTGT</p>	6H1	<p>SEQ ID NO: 473</p> <p>CAGGTGACGTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAAGCTCTGGATTCACTTCACTTACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGAA GTAATAAATACTATGACAGCTCCGTGAAGGGCC GCTTCAACCATCCAGAGACAATTCCAAGAACCA CGTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACAGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTGGAGTGTCTTGGGGGACTACT GGGGCCAGGGAACCCCTGGTCAACCTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGACACAGC GGCCCTGGCTGCCCTGGTCAAGGACTACTTCCC CGAACCCGTGACGGTGTGCGTGAACCTCAGGCGC CCTGACCAAGCGGTGTGCAACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCTCAGCAGC GTGTTGACCTGCCCCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTGTGACAAAACTCACACATGCCACAC GTGCCACGACCTGAACCTCTGGGGGACCGTCT AGTCTTCTCTTCCCCCAAAACCCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCAATG CGTGGTGGTGACGTGAGCCACGAAAGACCTGA</p>
IPS:335938	6H1	NA			

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			GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGCAGCGT CCTCACCGTCTGCACCAAGACTGGCTGAATGG CAAGGAGTACAAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCATCCCGGAGGAGATGACCA AGAACAGGTCAAGCTGACCTGCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGAGACAACACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
		SEQ ID NO: 1887	SEQ ID NO: 2044
	AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTEFT LTISLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR TVAAPSVFIIPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSYSTLSST LTLKADYEEKHKVYACEVTHQGLSSPVTKSFNRG EC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDGSNKYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGLTVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVVFSCSVMEALHNHYTQKS LSLSPGK
		SEQ ID NO: 317	SEQ ID NO: 474
!PS:335 941 2F11	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCAATCTGTAGGAGACAGAGTCACCATCATT GCCAGGCGAGTCAGGACATTAGCAACTATTAA ATTGGTATCAGCAGAAACCAAGGAAAGCCCTA	CAGTGCAACTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCAACCTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG

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AGCTCTGATCTACGATGCATCCAAATTTGGAAA CAGGGTCCCATCAAGGTTCAAGTGGAGTGGAT CTGGGACAGATTTTAGTTTCACCATCAGCAGCCT GCAGCCTGAAGATATTGCAACATATTACTGTCA ACAGTATGATATTCTCTCCTCCTCTTCGGCGGAGG GACC AAGTGGAGATCAAGCGAACGGTGGCTG CACCATCTGTCTTCATCTTCCCGCCATCTGATGA GCAGTTGAAATCTGGAACCTGCCCTCTGTTGTGTC CTGCTGAATAACTTCTATCCAGAGAGGCCAAA GTACAGTGGAGGTGGATAACGCCCTCCCAATCG GGTA ACTCCCAGGAGAGTGTACAGAGCAGGAC AGCAAGGACAGCACCTACAGCCTCAGCAGCAC CTGACGCTGAGCAAAAGCAGACTACGAGAAACA CAAAGTCTACGCCTGCGAAGTCAACCCATCAGGG CCTGAGCTCGCCCGTCACAAAGAGCTTCAACAG GGGAGAGTGT	CTGGAGTGGTGGCAGTTATATGGTATGATGGA AGTAATAAATACTATGCAGACTCCGTGAAGGGC CGATTCACCATCTCCAGCGACAATTCCAAGAAC ACGCTGATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGACGATTTTGGAGTGGTCTTGGACTACTGG GGCCAGGGAACCTGGTCAACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA CCCTCTCCAAAGAGCAACCTCTGGGGGCACAGCG GCCCCTGGCTGCCCTGGTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCTGTGGAACCTCAGGGGCC CTGACCAAGCGGTGCACACCTTCCCCGGCTGTC CTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAAGCCC AGCAACACCAAGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACACC GTGCCAGCACCTGAACCTCTGGGGGACCGTCT AGTCTTCTCTTCCCCCAAAACCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGGTGGTGACGTGAGCCACGAAGACCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACAGGTCAAGCTGACCTGCCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGAGCGCGGAGAACAACTACAAG ACCAGCCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
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			SEQ ID NO: 1888	TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTA
			SEQ ID NO: 2045	QVQLVESGGGVVQPGRSLRLSCAASGFTSSYGM HWVRQAPGKGLEWVAWIYDGSNKYYADSVKG RFTISDNSKNTLYLQMNLSRAEDTAVYYCARDR TIFGVLDYWGGQTLVTVSSASTKGPSVFPLAPSS KSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKEVPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDSDGSEFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
			SEQ ID NO: 475	CAGTGCCGCTGGTGAGTCTGGGGTGAGGTG AAGAAGCTGGGCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATCCACTGGTGCGACAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATCAACCTGACAGT GGTGGCACAGACTATTACAGAGGTTTCAGGGC AGGTTACCATGACCAAGGACACGTCATCAGC ACAGCTACATGGAACCTGAACAGGCTGAGATCT GACGACACGGCGTGATTAATGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGAAACCTGGTCAACCGTCT CCTCAGCTCCACCAAGGGCCATCGGTCTTCCC CCTGGACCCCTCCTCCAGAGACCTCTGGGGG CACAGCGCCCTGGGTGCTGGTCAAGGACTA CTTCCCAGAACCGGTGACGGTGTCTGGAACTC AGCGCCCTGACCAAGCGGTGACACCTTCCC GGGTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG
			SEQ ID NO: 318	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGCTCTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAGAACTACATAGCTTGGTACCAGCAG CAACAGGACATCTCCTAAGCTGCTCATTTACT GGGCATCTACCCGGGAATCCGGGTCCCTGACC GATTCAAGTGGCAGCGGTCTGGGACAGATTTC CTCTCACCATCAGCAGCGCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATAATTATAGTAC TCCGTGGACGTTCCGGCCAGGGACCAAGGTGGA AATCAAAACGAACGGTGGCTGCACCATCTGTCTT CATCTTCCCGCATCTGTATGAGCAGTTGAAATCT GGAACCTGCCCTGTGTGTGCTGCTGAATAACT TCTATCCAGAGAGGCCAAAGTACAGTGGAAAG TGGATAACGCCCTCCATCGGGTAACCTCCAGG AGAGTGTACAGAGCAGGACAGCAAGGACAGC ACCTACAGCTCAGCAGCACCTGACGCTGAGC AAAGCAGACTACGAGAAACACAAGTCTACGC
		AA		
	5C2	NA		
IPS:335970				

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		<p>CTGCGAAGTCACCCATCAGGGCCTGAGCTCGCC CGTCACAAAGAGCTTCAACAGGGGAGAGTGT</p>	<p>GGACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCAATCTTGTGACAAACTCACACATG CCCACCGTGCCAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGGACGTGAGCCACGAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTG AGCTCTCACCCTCTTGCACCAAGGACTGGCTG AATGGCAAGGAGTCAAGTGAAGGTCTCCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGCAGCCCCGAGAACACACA GGTGTACACCTGCCCATCCCGGAGGAGAT GACCAAGAACAGGTACGCTGACCTGCCTGGT CAAAGGCTTCTATCCAGCGACATCGCCGTGGA GTGGAGAGCAATGGGAGCCGAGAGACAACACT ACAAGACCAGCTTCCCGTGTGGACTCCGACG GCTCTTCTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGATGAGGCTCTGCACAACCA CTACACGCAAGAGAGCCTCTCCCCTGTCTCCGGG TAAA</p>
	AA	<p>DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQPGHPPKLLIYWASTRESGVPDFSGS GSGTDFLTIISSLAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC</p>	<p>SEQ ID NO: 1889</p> <p>SEQ ID NO: 2046</p> <p>QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVVRQAPGQGLEWMGWINPDSGGTDYSQRFQGR FTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF</p>

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				YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
				SEQ ID NO: 476
				CAGTGCCGCTGGTGCACTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATCCACTGGTGCGACAGGCCCTGGACAAAGGA CTTGAGTGGATGGGTGGATCAACCTGACAGT GGTGGCACAGACTATTACAGAGGTTTCAGGGC AGGTTACCATGACCAAGGACACGTCCATCAGC ACAGCTACATGGAACCTGAGCAGGCTGAGATCT GACGACACGGCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTT ACTACTGGGGCCAGGAAACCTGGTCAACCGTCT CCTCAGCTCCACCAAGGGCCATCGGTCTTCCC CCTGGACCTCTCTCCAGAGCACTCTGGGGG CACAGCGGCTGGCTGCTGGTCAAGGACTA CTTCCCGAACCGGTGACGGTGTCTGGAACTC AGCGGCTTGACAGCGGGGTGACACCTTCCC GGTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCAAGCCTACATCTGCAACGTGAATCAC AAGCCAGCAACCAAGGTGGACAAAGAAAGT TGAGCCCAATCTTGTGACAAACTCACACATG CCCACCGTGCCAGCACCTGAACTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAA GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGACGTGAGCCACGAAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCGTGT GAGGAGCAGTACGGCAGCAGTACCGTTGTGTC AGGTCCTCAGCGTCTGACCAAGGACTGGCTG AATGGCAAGGAGTCAAGTGAAGGTCTCCAAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGGCAGCCCCCGAGAACACAA
				SEQ ID NO: 319
				GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTATATCCAGCTCC AACATAAAGAACTACATAGCTTGGTACACAGCAG AAACAGGACATCTCTCCTAAGCTGCTCATTTACT GGGCATCTACCCGGGAATCCGGGTCCCTGACC GATTCAAGTGGCAGCGGTCTGGGACAGATTTC CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATAATTATAGTAC TCCGTGGACGTTCCGGCCAAAGGACCAAGGTGGA AATCAACGAACGGTGGCTGCACCATCTGTCTT CATCTTCCCGCCATCTGATGAGCAAGTTGAAATCT GGAACCTGCTCTGTGTGTGCTGCTGAATAACT TCTATCCAGAGAGGCCAAAGTACAGTGGAAAG TGGATAACGCCCTCCAATCGGGTAACCTCCAGG AGAGTGTACAGAGCAGGACAGCAAGGACAGC ACCTACAGCTCAGCAGCAGCCTGACGCTGAGC AAAGCAGACTACGAGAAACACAAAGTCTACGC CTGCGAAGTCAACCATCAGGGCTGAGCTCGCC CGTCACAAAGAGCTTCAACAGGGGAGAGTGT
				NA
				13H12
				IPS:335978

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			GGGTACACCCTGCCCCCATCCCGGAGGAGAT GACCAAGAACAGGTGAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCACATCGCCGTGGA GTGGGAGAGCAATGGCAGCCGGAGAACAACT ACAAGACCAGCCTCCCGTGTGCTGACTCCGACG GCTCCTTCTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGATGAGGCTCTGCACAACCA CTACACGAGAAAGAGCCTCTCCCCTGTCTCCGGG TAAA
		SEQ ID NO: 1890	SEQ ID NO: 2047
	AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQKPGHPPKLLIYWASTRESGVPDFRFGS GSGTDFLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYI HWVRAQPGGLEWGMWINPDSGGTDYSQRFQGR FTMTRDTSISTAYMELSLRSDDTAVYYCAREATI FGMVIVPFDYWGGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSGDSFFLY SKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPGK
		SEQ ID NO: 320	SEQ ID NO: 477
IPS:335986	11C1	NA	CAGGTCCCGCTGGTACAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCACCCGGCTACTAT ATACACTGGTGCCTCAGGCCCTGGACAAGGG CTTGTGTGATGGGTGGATCAGCCCTAACAGT GGTGACACAAAGCTATGCACAGAAAGTTTCAGGAC AGGTCACCATGACAGGGACACGTCCATCAGC ACAGCCTATATGAGCTGAGCAGACTGAGATCT GACGACACGGCGGTGTATTTCTGTACGAGAG

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	<p>CTCCGTGGACGTTCCGGCCAAAGGGACCAAGGTGG AAATCAAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAAC TGCTCTGTTGTGTGCCTGCTGAATAAC TTCTATCCAGAGAGGCCAAAGTACAGTGGGAAG GTGGATAACGCCCTCCAAATCGGGTAACTCCAG GAGAGTGTACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCCCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCAACCATCAGGGCCTGAGCTCGC CCGTCAACAAGAGCTTCAACAGGGGAGAGTGT</p>	<p>SEQ ID NO: 1891</p>
AA	<p>DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQOKPGQPPNLLIYWTSTRDSGVDPDRFSG</p>	<p>SEQ ID NO: 2048</p>
	<p>GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCAACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCTCTCTCCAAAGAGCACCTCTGGGGG CACAGGGCCCTGGGTGCTGCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCTGTGGAATC AGCGCCCTGACCAAGCGGGCTGCACACCTTCCC GGCTGTCTACAGTCTCTCAGGACTCTACTCCCTC AGCAGCTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCAATCTTGTGACAAAACTCACACATG CCCACCGTGCCAGCACCTGAACCTCTGGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTCT ACATGCGTGGTGGACGTGAGCCACGAAAGAC CCTGAGGTCAAAGTTCAAACCTGGTACGTGGACGGC GTGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCTCTCTCACCTCTCTGCAACCAAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAGGGCAGCCCCGAGAACCAACA GGTGTACACCTTGCCCCCATCCCGGGAGGAGAT GACCAAGAACCAAGGTACGCTGACCTGCCTGGT CAAGGCTTCTATCCCAAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGACGCCGGAGAACAACT ACAAGACCAACGCTCCCGTGTGGACTCCGACG GCTCTTCTTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGAGAAAGAGCCTCTCTCCCTGTCTCCGGG TAAA</p>	<p>QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYI HWVROAPGQGLVWMGWISPNSGDTSYAOKFQDR</p>

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			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKRTVAAPSVFIFFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSYLSSTLTLSKADYEEKHKVYACEVTHQQLSS PVTKSFNRGEC	VTMTRDTSISTAYMELSRLSDDTAVYFCTREATI FGMLIVPFDYWGGQTLVTVSSASTKGPSVFPLAPS SKSTSGGTAAAGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITMISRTPETCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
			SEQ ID NO: 321	SEQ ID NO: 478
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGCGAGAGGGCCACCAATCAAC TGCAAGTCCAGCCAGAGTGTITATCCAGCTCC AACATAAGAACTACTTAGCTTGGTACCAGCAG AAACGAGGACAGCTCTCAACCTGCTCAATTTAC TGGACTTCTACCCGAGATTCCGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTACCATCAACAGCCTGCAAGGCTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTCCGGCCAGGGACCAAGGTGG AAATCAACAGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACCTGCCCTCTGTTGTGTGCTGCTGAATAAC TTCTATCCAGAGAGGCCAAAGTACAGTGGAAG GTGGATAACGCCCTCCAAATCGGGTAACTCCCA GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCCTGACGCTGAG CAAAAGCAGACTACGAGAAACACAAGTCTACG CCTGCGAAGTCAACCATCAGGGCCTGAGCTCGC CCGTCAAAAGAGCTTCAACAGGGGAGAGTGT	CAGTGCCGCTGGTGCACTCTGGGGCTGAGGTG AAGAAGCTGGGGCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATACACTGGTGCGTCAGGCCCTGGACAAAGG CTTAGTGATGGGTGGATAAGCCCTAACAAAT GGTGACACAACTATGCACAGAAATTTTCAGGAC AGGTCAACATGACAGGACACGTCCTCATCAGC ACAGCTATATGGAGCTGAGCAGGCTGAGATCT GACGACACGGCGTGTATTACTGTACGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCAATTTG ACTACTGGGGCCAGGGAACCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCTCTCTCCAGAGCACCTCTGGGGG CACAGCGCCCTGGGTGCTGGTCAAGGACTA CTTCCCGAACCGGTGACGGTGTGCGTGGAACTC AGCGCCCTGACACAGCGGTGTGACACCTTCCC GGTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCAATCTTGTGACAAACTCACACATG CCCACCGTGCCAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAG
IPS:335994	12H11	NA		

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					<p>GACACCCCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGGACGTGAGCCACGAAAGAC CCTGAGGTCAGTTCAACTGGTACGTGGACGGC GTGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCGTCTCACCGTCTTGCACCAAGACTGGCTG AATGGCAAGGAGTACAAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGCAGCCCCGAGAACACACA GGGTACACCCCTGCCCATCCCGGAGGAGAT GACCAAGAACAGGTACGCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGAGCCGGAGAACAACT ACAAGACCAGCCTCCCGTGTGCTGACTCCGACG GCTCCTTCTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGATGAGGCTCTGCACAACCA CTACACGAGAAAGAGCCTCTCCCCTGTCTCCGGG TAAA</p>
				<p>SEQ ID NO: 1892</p> <p>DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDFSG SGSGTDFTLTINSLQAEDVAVYCCQQYYRTPTWF GQGTKVEIKRTVAAPSVFIPTPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYLSSTLTLSKADYEKHKVYACEVTHQQLSS PVTKSFNRGEC</p>	<p>SEQ ID NO: 2049</p> <p>QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWISPNNGDTNYAQKFQD RVTMTRDTSISTAYMELSRLSDDTA VYCTREA TIFGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGT AALGCLVKDYFPEPTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLEPPPKKDTLMISRTPEVTCVVVDVSH DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFEL YSKLTVDKSRWQQGNVVFSCSVMEALHNHYTQK SLSLSPGK</p>
			AA		

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			SEQ ID NO: 322	SEQ ID NO: 479
IPS:336024	18E3	NA	GAAATTGTGTGACGCAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCAGACAGGTTTCAGTGGCAGTG GGTCTGGGACAGACTTCACTCTCACCATCAGCA GACAGGAGCCTGATGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGTTTCAACCGCTCACTTCCGG CGGAGGGACCAAGGTGGAGATCAACGAACGG TGGCTGCACCATCTGTCTTCATCTTCCCGCCATC TGATGAGCAGTTGAAATCTGGAACCTGCCTCTGT TGTGTGCCTGCTGAATAACTTCTATCCAGAGA GGCCAAAGTACAGTGGAGGTGGATAACGCCCT CCAATCGGGTAACCTCCAGGAGAGTGTACACAGA GCAGGACAGCAAGGACAGCACCTACAGCCTCA GCAGCACCCCTGACGCTGAGCAAAAGCAGACTACG AGAAACACAAAGTCTACGCTGCGAAGTCAACC ATCAGGGCCTGAGCTCGCCCGTCCACAAAGAGCT TCAACAGGGGAGAGTGT	CAGGTGCAGTTGCAGGAGTCGGGGCCAGGACTG GTGAAGCCCTTACAGAGCCCTGTCCCTCACCTGC ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCACCCAGGGA AGGGCCTGGAGTGGATTGGGTACATCTATTACA GTGGGAGCACCTACTACAACCCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGTCCTAAGA ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGGGGACACGGCCGTGTATTACTGTGCGAGAGA TCGTATTACGATTTTGGAGTGGTTATGGGGGGC GGTATGGACGTCTGGGGCCAAAGGACCAACGGTC ACCGTCTCCTCAGCCTCCACCAAGGGCCCATCG GTCCTCCCCCTGGCACCCCTCCTCCAAGAGCACCT CTGGGGGCACAGCGGCCCTGGGCTGCCCTGGTCA AGGACTACTTCCCCGAACCGGTGACGGTGTCTGT GGAACCTCAGGGCCCTGACCAAGCGGCGTGCACA CCTTCCCGGTGTCTCAGTCTCAGTCTCAGGACTCTA CTCCCTCAGCAGCGTGTGACCGTCCCTCCAG CAGCTTGGGCACCCAGACCTACATCTGCAACGT GAATCACAAAGCCAGCAACCAAGGTGGACA AGAAAGTTGAGCCCAATCTTGTGACAAACTC ACACATGCCACCCGTGCCAGCACCTGAACCTC TGGGGGACCGTCACTCTTCTTCTTCCCCCAA ACCCAAGGACACCCCTCATGATCTCCCGGACCC TGAGGTACATGCGTGGTGGTGGACGTGAGCCA CGAAGACCCCTGAGGTCAAGTTCAACTGGTACGT GGACGGCTGGAGGTGCATAATGCCAAGACAA AGCCGTGTGAGGAGCAGTACGGCAGCACGTACC GTTGTGTACGCTCTCACCGTCTTGCACCCAGG ACTGGCTGAATGGCAAGGAGTACAAGTGCAAG GTCTCCAACAAGCCCTCCAGCCCCCATCGAG AAAACCATCTCCAAGCCAAAGGGCAGCCCCGA GAACCCACAGGTGTACACCTGCCCCCATCCCGG GAGGAGATGACCAAGAACCAAGGTGAGCTGAC CTGCTGGTCAAGGCTTCTATCCAGCGGACAT

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				CGCCGTGGAGTGGGAGAGCAATGGCAGCCGG AGAACAACTACAAGACCACGCCTCCCGTGTGG ACTCCGACGGCTCCTTCTTCTCTATAGCAAGCT CACCGTGACAAGAGCAGGTGGCAGCAGGGGA ACGTCTTCTCATGTCTCCGTGATGCATGAGGCTCT GCACAACCACTACACGCAGAAAGAGCCTCTCCCT GTCTCCGGGTAAA
		SEQ ID NO: 1893	SEQ ID NO: 2050	
		EIVLTQSPGTLSPGERATLSCRASQISYSYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGTDF TLTISRQEPDDFAVYYCQQYGSPLTFGGGKVEI KRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSYSL STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGE	QVQLQESGPGLVKPSQTLSTCTVSGDISSSGGYY WSWIRQHPGKGLEWIGYIYSGSTYYNPSLKSRT ISVDTSKNQFSLKLSVTAADTA VYCARDRITIFG VVMGGMDVWVGQTTVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI AKQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK	
	AA	SEQ ID NO: 323	SEQ ID NO: 480	
		GAAATAGTGATGACGCAGTCTCCAGCCACCCCTG TCTGTGTCCTCAGGGGAAAGAGCCACCCCTCTCC TGACGGCCAGTCAGAGTGTTAGCAGCAACTTA GCCTGTACCAAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACCAAGGCC ACTGGTATCCCAGCCAGGTCA GTGGCAGTGGG TCTGGGACAGAGTTCACCTCACCATCAGCAGC CTGCAGTCTGAAGATTTTGCAAGTTTATTACTGTC AGCAGTATAATACTGGCCTCTCACTTTCGGCG GAGGGACCAAGGTGGAGATCAACGAACGGTG GCTGCACCATCTGTCTTCATCTTCCCGCCATCTG ATGAGCAGTTGAATCTGGAACCTGCCTCTGTTG TGTGCCTGCTGAATAACTTCTATCCCAGAGAGG	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACTTTCAGTAACATATGGC ATGCACTGGTCCGCCAGGCTCCAGGCGAGGGG CTGGAGTGGTGGCAGCTATATGTTTGATGGA AGTGATAAATACTATGCAGACTCCGTGAAGGGC CGATTCACCATCTCCAGAGACAACTCCAAAGAAC ACGCTGATCTGCAATGAACAGACCTGAGAGCC GAGGACACGGCTGTGTAATTACTGTGCGAGAGAT CAGGCGATTTTGGAGTGTGTCCTCCGACTACTGG GGCCAGGGAACCCCTGGTCAACCGTCTCCTCAGCC TCCACCAAGGCCCATCGGTCTTCCCCCTGGCA CCCTCCTCCAAAGAGCACCTCTGGGGGCACAGCG	
IPS:336041	2G10_LC1	NA		

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	<p>CCAAAGTACAGTGGAAGGTGGATAACGCCCTCC AATCGGGTAACCTCCAGGAGAGTGTCACAGAGC AGGACAGCAAGGACAGCACCTACAGCCTCAGC AGCACCTGACGCTGAGCAAAAGCAGACTACGAG AAACACAAAGTCTACGCTGCGAAGTCACCCAT CAGGGCTGAGCTCGCCCGTCACAAAGAGCTTC AACAGGGGAGAGTGT</p>	<p>GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCTGTGGAACCTCAGGGCC CTGACCAGCGGCTGCACACCTTCCCCTGCTC CTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCTTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACAC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAAACCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCATCCCGGAGGAGATGACCA AGAACAGGTGAGCTGACCTGCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGACAACATACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTA</p>
	<p>SEQ ID NO: 1894</p>	<p>SEQ ID NO: 2051</p>
AA	<p>EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLIYGAAATRAATGIPARVSGSGGTE FTLTISLSQSEDFAVYQCQYNNWPLTFGGGKVE IKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYP REAKVQWVKVDNALQSGNSQESVTEQDSKDSITYSL SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEN</p>	<p>QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAIWFDGSDKYADSVKGG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVDPDYWGQGLVTVSSASTKGPSVFPLAPSS KSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCTCPPEPELLG</p>

[illegible]

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				<p>SEQ ID NO: 1895</p> <p>DIQMTQSPSSLSASVGDRVTITCRASQGI RNELGW YQQKPGKAPKRLIYGASSLSQSGVPSRFSGSGSGTE FTLTISLQPEDFVITYYCLQHNSYPFTFGPGTKVDV KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEK</p>	<p>SEQ ID NO: 1895</p> <p>CCTCACCGTCTGCACCAAGGACTGGCTGAATGG CAAGGAGTACAAAGTGCAAGGTCTCCACAAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACAGGTACGCTGACCTGCCTGGTCAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGACAAATGGCAGCCGAGAACAACTACAAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
		AA		<p>SEQ ID NO: 2052</p> <p>QVQLVESGGGVVQPGRSRLRSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIYDGSNKYYADSVKG RFTISRDNKNTLYLQMNSLR AEDTAVYYCARDG TIFGVLLGDYWGQGTLLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLMISRTPETCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFELY SKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPGK</p>	<p>SEQ ID NO: 2052</p> <p>QVQLVESGGGVVQPGRSRLRSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIYDGSNKYYADSVKG RFTISRDNKNTLYLQMNSLR AEDTAVYYCARDG TIFGVLLGDYWGQGTLLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLMISRTPETCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFELY SKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPGK</p>
	IP:336088	6A5.004	NA	<p>SEQ ID NO: 325</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCAATCTGTGGGGACAGAGTCACCAATCATT GCCAGGCGAGTCAGGACATTACCAACTATTAA ATTGGTATCAGCAGAAACCAAGGAAAGCCCTA AACTCCTGATCTACGATGCTTCCAAATTTGGAGCC AGGGTCCCATCAAGGTTTCAGTGGAAAGTGGATC TGGGACAGATTTTACTTTTACCAATCAGCAGCCTG</p>	<p>SEQ ID NO: 482</p> <p>CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGCTATATGGTATGATGGAA ATAATAAACTATGCAGACTCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTTCCAAAGACA</p>

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CAGCCTGAAGATATTGCAACATATTACTGTCAA CAGTATGATGATCTATTCACTTTCGGCCCTGGGA CCAAAGTGGATATCAAACGAACGGTGGCTGCAC CATCTGCTTTCATCTTCCCGCCATCTGATGAGCA GTTGAAATCTGGAACCTGCTCTGTTGTGCTG CTGAATAACTTCTATCCCAGAGAGGCCAAAGTA CAGTGGAAGGTGGATAACGCCCTCCAATCGGGT AACTCCAGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGCAGCACCTT GACGCTGAGCAAAAGCAGACTACGAGAAACACA AAGTCTACGCCCTGCGAAGTCAACCCATCAGGGCC TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGG GAGAGTGT	CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGGTGTGATTACTGTGCGAGAGATC GGACGATTTTGGAGTGGTCCTTGAGTACCTCG GCCAGGAACCTTGGTCAACCGTCTCCTCAGCCT CCACCAAGGGCCATCGGTCTTCCCCCTGGCAC CCTCTCCAAGAGCACCTCTGGGGGACACAGGG CCCTGGGCTGCCGTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCC TGACCAGCGGGTGCACACCTTCCCCGGCTGTCC TACAGTCTCAGGACTCTACTCCTCAGCAGCGT GGTGACCGTGGCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAAGCCAG CAACACCAAGGTGGACAAAGAAAGTTGAGCCCCA AATCTTGTGACAAAACTCACACATGCCACCGT GCCCAGCACCTGAACCTCCTGGGGGACCGTCAG TCTTCTCTTCCCCCACAACCCAAAGGACACCT CATGATCTCCGGACCCCTGAGGTACATGCGT GGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCTGGAGGT GCATAATGCCAAGACAAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTACGCTCC TCACCGTCTGCACCAAGGACTGGGTGAATGGCA AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC TCCCAGCCCCCATCGAGAAACCATCTCCAAAG CCAAAGGCGAGCCCCGAGAACCCACAGGTGTAC ACCTGCCCCCATCCCGGGAGGAGATGACCAAG AACCAGGTCAGCCTGACCTGCCCTGGTCAAAGGC TTCTATCCCAAGCAGATCGCCGTGGAGTGGGAG AGCAATGGGCAAGCCGGAACAACACTACAAGAC CACGCCCTCCGTGTGTGACTCCGACGGCTCCTTC TTCCTCTATAGCAAGCTCACCGTGGACAAAGC AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACAG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
SEQ ID NO: 1896	SEQ ID NO: 2053

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		AA	<p>DIQMTQSPSSLSASVGDRVTITCQASQDITNLYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGGTD FTFTISLQPEDIATYYCQQYDDLFTFGPGTKVDIK RTVAAPSVFIAPPDEQLKSGTASVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSLSS TLTLKADYEEKHKVYACEVTHQGLSSPVTKSNR GEC</p>	<p>QVQLVESGGGVVQGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLVWVAIWDGNNKYYADSVKG RFTISRDSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYLGGTLVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN HKPSNTKVDKKEPKSCDKTHTCPPCPAPPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVFSQSVMHREALHNHYTQKLSL SPGK</p>
			<p>SEQ ID NO: 326</p> <p>GACATCCAGATGACCCAGTCTCCATCTTCCGTGT CTGCATCTGTAGGAGACAGAGTACCATCACTT GTCGGCGAGTCAGGGTCTTATCATCTGGTTAG CCTGGTATCAGCAGAAACCGGGGAAAGCCCCA AACTCTGATCTATGCTGCATCCAGTTTGCAAAG TGGGTCCCATCAAGGTTCAAGCGGCGAGTGGCTC TGGGACAGATTTCACCTCTCAACCATCAGCAGCCT ACAGCCTGAAGATTTTGCAACTTACTATTGTCAA CAGACTAACAGTTTCCCTCCGACGTTCCGGCCAA GGGACCAAGGTGGAAATCAACGAAACGGTGGC TGCAACCATCTGTCTTCATCTTCCCGCCATCTGAT GAGCAGTTGAAATCTGGAACTGCCTCTGTTGTG TGCCTGCTGAAATAACTTCTATCCAGAGAGGCC AAAGTACAGTGGAAAGGTGGATAACGCCCTCCAA TCGGGTAACTCCAGGAGAGTGTACAGAGCAG GACAGCAAGGACAGCACCTACAGCCTCAGCAGC ACCCGTGACGCTGAGCAAGCAGACTACGAGAA ACACAAAGTCTACGCTGCGAAGTCAACCCATCA GGGCTGAGCTCGCCCGTCAAAAGAGCTTCAA CAGGGGAGAGTGT</p>	<p>SEQ ID NO: 483</p> <p>CAGTGCAGCTGCAGGAGTCGGGCCAGGACTG GTGAAGCCTTCGGAGACCTGTCCCTCACCTGC ACTGTCTCTCAGGGTCCATCAGTAGTTACTACT GGAGCTGGATCCGACAGCCCGCGGGAAGGGA CTAGAGTGGATTGGCCGTATCTATACAGTGGG AGCACCAACTACAACCCCTCCCTCAAGAGTCGA GTCACCATGTCAATAGACACGTCCCAAGAACCCAG TTCTCCCTGAACCTGAACCTGTGACCCGCCGCG GACACGGCCGTGATTACTGTGCGAGAGATGTA GCAGTGGCTGGCTTTGACTACTGGGGCCAGGGA ACCTGGTCAACCGTCTCCTCAGCTCCACCAAG GGCCATCGGTCTTCCCTCCCTGGCACCCCTCCCA AGAGCACCTCTGGGGCACAGCGGCCCTGGGCT GCCTGGTCAAGGACTACTTCCCGCAACCGGTGA CGGTGTCTGGAACCTCAGGGCCCTGACCAAGC GCGTGACACCTTCCCGGCTGTCTACAGTCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT GCCCCTCCAGCAGCTTGGGACCCAGACCTACAT CTGCAACGTGAATCAAGCCCAAGCAACACCAA GGTGGACAAGAAAGTTGAGCCCAATCTTGTGA CAAACCTCACACATGCCACACCGTGCCCAAGCACC</p>
IPS:336099	17H11.004	NA	<p>SEQ ID NO: 326</p> <p>GACATCCAGATGACCCAGTCTCCATCTTCCGTGT CTGCATCTGTAGGAGACAGAGTACCATCACTT GTCGGCGAGTCAGGGTCTTATCATCTGGTTAG CCTGGTATCAGCAGAAACCGGGGAAAGCCCCA AACTCTGATCTATGCTGCATCCAGTTTGCAAAG TGGGTCCCATCAAGGTTCAAGCGGCGAGTGGCTC TGGGACAGATTTCACCTCTCAACCATCAGCAGCCT ACAGCCTGAAGATTTTGCAACTTACTATTGTCAA CAGACTAACAGTTTCCCTCCGACGTTCCGGCCAA GGGACCAAGGTGGAAATCAACGAAACGGTGGC TGCAACCATCTGTCTTCATCTTCCCGCCATCTGAT GAGCAGTTGAAATCTGGAACTGCCTCTGTTGTG TGCCTGCTGAAATAACTTCTATCCAGAGAGGCC AAAGTACAGTGGAAAGGTGGATAACGCCCTCCAA TCGGGTAACTCCAGGAGAGTGTACAGAGCAG GACAGCAAGGACAGCACCTACAGCCTCAGCAGC ACCCGTGACGCTGAGCAAGCAGACTACGAGAA ACACAAAGTCTACGCTGCGAAGTCAACCCATCA GGGCTGAGCTCGCCCGTCAAAAGAGCTTCAA CAGGGGAGAGTGT</p>	<p>SEQ ID NO: 483</p> <p>CAGTGCAGCTGCAGGAGTCGGGCCAGGACTG GTGAAGCCTTCGGAGACCTGTCCCTCACCTGC ACTGTCTCTCAGGGTCCATCAGTAGTTACTACT GGAGCTGGATCCGACAGCCCGCGGGAAGGGA CTAGAGTGGATTGGCCGTATCTATACAGTGGG AGCACCAACTACAACCCCTCCCTCAAGAGTCGA GTCACCATGTCAATAGACACGTCCCAAGAACCCAG TTCTCCCTGAACCTGAACCTGTGACCCGCCGCG GACACGGCCGTGATTACTGTGCGAGAGATGTA GCAGTGGCTGGCTTTGACTACTGGGGCCAGGGA ACCTGGTCAACCGTCTCCTCAGCTCCACCAAG GGCCATCGGTCTTCCCTCCCTGGCACCCCTCCCA AGAGCACCTCTGGGGCACAGCGGCCCTGGGCT GCCTGGTCAAGGACTACTTCCCGCAACCGGTGA CGGTGTCTGGAACCTCAGGGCCCTGACCAAGC GCGTGACACCTTCCCGGCTGTCTACAGTCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT GCCCCTCCAGCAGCTTGGGACCCAGACCTACAT CTGCAACGTGAATCAAGCCCAAGCAACACCAA GGTGGACAAGAAAGTTGAGCCCAATCTTGTGA CAAACCTCACACATGCCACACCGTGCCCAAGCACC</p>

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		TGAACTCCTGGGGGACCGTCAGTCTTCTCTCTC CCCCAAAACCCAAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTACATGCGTGGTGGTGAC GTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCC AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG CACGTACCGTTGTGTACGCGTCTCACCGTCTCTG CACCAGGACTGGCTGAATGGCAAGGAGTACAA GTGCAAGGTCTCCAACAAAGCCCTCCAGCCCC CATCGAGAAACCATCTCCAAGCCAAAGGCA GCCCCGAGAACACAGGTGTACACCTGCCCCC ATCCCGGAGGAGATGACCAAGAACAGGTCA GCCTGACCTGCCCTGGTCAAAGGCTTCTATCCCA GCGACATCGCCGTGGAGTGGGAGAGCAATGGG CAGCCGGAGAACAACTACAAGACCACGCCCTCCC GTGCTGGACTCCGACGGCTCCTTCTTCTCTATA GCAAGCTCACCGTGGAACAAGACAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAAACCACTACACGCAAGAGAGC CTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1897	SEQ ID NO: 2054
	DIQMTQSPSSVSASVGDRVTITCRASQGLIWLAW YQQKPGKAPKLLIYAASSLQSGVPSRFSGSGGTD FTLTISLQPEDFATYYCQQTNISFPPTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSITYSL STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGECA	QVQLQESGPGLVKPSETLSLTCTVSQGSISYYWS WIRQPAGKGLEWIGRIYTSGSTNYPNPSLKSRTMS IDTSKNQFSLKLSVTAADTA VYCARDVAVAGF DYWGQGTLLVTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHCTCPPELPGGSPVFLFP PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQ DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYVTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKKS RWQQGNVFSCSVMHEALHNHYTOKLSLSLSPGK
		AA

			SEQ ID NO: 327	SEQ ID NO: 484
IPS:359621	17H11.004.001	NA	GACATCCAGATGACCCAGTCTCCATCTTCCGTGT CTGCATCTGTAGGAGACAGAGTCAACCATCACTT GTCGGCGAGTCAGGGTCTTATCATCTGGTTAG CCTGGTATCAGCAGAAACCGGGGAAAGCCCCTA AACTCTGATCTATGCTGCATCCAGTTTGCAAAG TGGGTCCCATCAAAGTTTCAGCGGGCAGTGGCTC TGGGACAGATTTCACCTCTCAACCATCAGCAGCCT ACAGCCTGAAGATTTTGCAACTTACTATTGTCAA CAGACTAACAGTTTCCCTCCGACGTTTCGGCCAA GGGACCAAGGTGGAAATCAACGAACGGTGGC TGCACCATCTGTCTTCATCTTCCCGCCATCTGAT GAGCAGTTGAAATCTGGAACTTCCCTCTGTTGTG TGCCCTGCTGAATAACTTCTATCCAGAGAGGCC AAAGTACAGTGGAAAGGTGGATAACGCCCTCCAA TCGGGTAACTCCAGGAGAGTGTACAGAGCAG GACAGCAAGGACAGCACCTACAGCCTCAGCAGC ACCCTGACGCTGAGCAAGCAGACTACGAGAA ACACAAAGTCTACGCTGCGAAGTCAACCCATCA GGGCTGAGCTCGCCCGTCAACAAGAGCTTCAA CAGGGGAGAGTGT	CAGGTGCAGCTGCAGGAGTCGGGCCAGGACTG GTGAAGCCTTCGGAGAGCCCTGTCCCTCACCTGC ACTGTCTCTGGGGCTCCATCAGTAGTACTACT GGAGCTGGATCCGCGACGCCCGCGGAAAGGGA CTAGAGTGGATTGGCCGTATCTATACAGTGGG AGCACCAACTACAACCCCTCCCTCAAGAGTCA GTCACCATGTCAATAGACACGTCCCAAGAACCAG TTCTCCCTGAACCTGAACCTCTGTGACCGCCGCG GACACGGCCGTGTAATTACTGTGCGAGAGATGTA GCAGTGGCTGGCTTTGACTACTTGGGGCCAGGGA ACCCGTGTCACCGTCTCCCTCAGCCTCCACCAAG GGCCCATCGGTCTTCCCTGGCACCCCTCCCTCCA AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT GCCGTGTCAGGACTACTTCCCGCAACCGGTGA CGGTGTCGTGGAACCTCAGGGCCCTGACCAAGCG GCGTGACACACCTTCCCGGCTGTCTACAGTCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT CTGCAACGTGAATCAACAAGCCACGCAACACCAA GGTGACACAAGAAAGTTGAGCCCAATCTTGTGA CAAACTCACACATGCCACCCGTGCCACGACCC TGAACTCTGGGGGACCGTCAGTCTTCTCTTC CCCCAAAACCAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTACATGCGTGGTGGTGGAC GTGAGCCACGAAGACCCCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCC AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG CACGTACCGTTGTGTCAAGCGTCTCACCGTCTG CACCAGGACTGGCTGAATGGCAAGGAGTACAA GTGCAAGGTCTCCAACAAGCCCTCCAGCCCC CATCGAGAAACCATCTCCAAGCCAAAGGCA GCCCCGAGAACCAAGGTGTACACCTGCCCCC ATCCCGGGAGGAGATGACCAAGAACCAAGTCA GCCTGACCTGCCTGGTCAAGAGGCTTCTATCCCA GCGACATCGCCGTGGAGTGGGAGAGCAATGGG

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					CAGCCGGAGAACAACTACAAGACCACGCCTCCC GTGCTGGACTCCGACGGCTCCTTCTTCTCTATA GCAAGCTCACC GTGGACAAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACCACTACACGCAAGAGAGC CTCTCCCTGTCTCCGGTAAA
				SEQ ID NO: 1898	SEQ ID NO: 2055
				DIQMTQSPSSVSASVGDRVTITCRASQGLIWLAW YQQKPGKAPKLLIYAASSLQSGVPSRFSGSGGTD FTLTISLQPEDFATYYCQQTNFPPTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEK	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWS WIRPAGKGLEWIGRIYTSGSTNYPNPSLKSRVTMS IDTSKNQFSLKLSNVTAAADTA VYYCARDVA VAGF DYWGQGTLLVTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNT KVDKKVEPKSCDKTHITCPPCPAPELGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQ DWLNGKEYKCKVSNKALPAPIEK TISKAKGQPREP QVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
			AA	SEQ ID NO: 328	SEQ ID NO: 485
				GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCAATCTGTAGGAGACAGAGTCACCATCCTT GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG GCTGTATCAGCAGAAACCAAGGAAAGCCCTA AACTCCTGATCTATGGTGATCCAGTTTGCAAA GTGGGTCCCATCAAGGTTTCAGCGGCAGTGGAT CTGGGACAGAGTTCACTCTCACAAATCAGCAGCC TGACGCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAATAGTTACCCATTCACTTTCGGCCA AGGACCAAAAGTGATGTCAAAACGAACGGTGG CTGCACCATCTGTCTTTCATCTTCCCGCCATCTGA TGAGCAGTTGAAAATCTGGAACTGCCTCTGTGTGT GTGCTGTGTAATAACTTCTATCCCAGAGAGGC CAAAAGTACAGTGAAGGTGGATAACGCCCTCCA ATCGGGTAACTCCCAAGGAGAGTGTACAGAGCA	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTTACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAAA GTAATAAAATACTATGCAGACGCCGTGAAGGGCC GCTTCAACCATCTCCAGAGACAATTCCAAGAAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTGGAGTGTCTTGGGGGACTACT GGGGCAGGGAACCTGGTCAACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCTGGC ACCTCTCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGCTGCCGTGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGTGGAACTCAGGCGC
!PS:359781	4H9.004.001	NA			

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	<p>GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCTGACGCTGAGCAAGAGCAGACTACGAGA AACACAAAGTCTACGCCCTGCGAAGTCACCCATC AGGCCTGAGCTCGCCCGTCACAAAGAGCTTCA ACAGGGGAGAGTGT</p>	<p>CCTGACCAGCGGCGTGACACACCTTCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACAC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAAACCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAGAACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCAATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCATCCCGGAGGAGATGACCA AGAACAGGTGACCTGACCTGCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGGAGAACAACTACAAG ACCAGCCTCCCGTGCTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTA</p>
	<p>SEQ ID NO: 1899</p> <p>DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSTE FTLTISLQPEDFVITYYCLQHNSYPFTFGQGTKVD VKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWVKVDNALQSGNSQESVTEQDSKDSSTYS LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF NRGEC</p>	<p>SEQ ID NO: 2056</p> <p>QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIYDASNKYADAVKVG RFTISRDNSKNTLYLQMNSLRAEDTAVYVCARDG TIFGVLLGDYWGQGTLLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLMISRTPETVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV</p>

[illegible]

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				<p>SEQ ID NO: 1900</p> <p>DIQMTQSPSSLSASVGDRVTITCRASQGINELGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSTE FTLTISLQPEDFVITYYCLQHNSYPFTFGQGTKVD VKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYS LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF NRGEC</p>		<p>SEQ ID NO: 1900</p> <p>CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCATCCCGGAGGAGATGACCA AGAACAGGTGAGCCTGACCTGCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGACAAATGGCAGCCGAGAACAACTACAAG ACCAGCCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTAA</p>
		AA		<p>SEQ ID NO: 2057</p> <p>QVQLVESGGGVVQPGRLSLRSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIYDASNKYIYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYCARDG TIFGVLLGDYWGQGTLLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPGK</p>		<p>SEQ ID NO: 2057</p> <p>QVQLVESGGGVVQPGRLSLRSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIYDASNKYIYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYCARDG TIFGVLLGDYWGQGTLLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPGK</p>
	IPS:360936	4H9.004.003	NA	<p>SEQ ID NO: 330</p> <p>GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCAATCTGTAGAGAGACAGAGTCACCATCATT GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG GCTGTATCAGCAGAAACCAAGGAAAGCCCTTA AACTCCTGATCTATGGTGATCCAGTTTGCAAA GTGGGTCCCATCAAGGTTTCAGCGGCAGTGGAT CTGGGACAGAGTTCACTCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAAATAGTTACCCATTCACTTTCGGCCA</p>		<p>SEQ ID NO: 487</p> <p>CAGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAAGCTCTGGATTCACTTTCAGTTACTTTGGCA TGC ACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGGA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCAACCATCTCCAGAGACAATTCACAAGAAC CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG</p>

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	AGGACCAAAGTGGATGTCAAACGAACGGTGG CTGCACCATCTGTCTTCATCTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCCTCTGTTGT GTGCTGTCTGAATAACTTCTATCCACAGAGGC CAAAGTACAGTGAAGGTGGATAACGCCCTCCA ATCGGTAACCTCCAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCTGACGCTGAGCAAGCAGACTACGAGA AACACAAAGTCTACGCCTGCGAAGTCAACCATC AGGCCTGAGCTCGCCCGTCAACAAAGAGCTTCA ACAGGGGAGAGTGT	GGACGATTTTGGAGTGCTCTTGGGGGACTACT GGGGCAGGGAACCCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGCTGCCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGC CCTGACCAAGCGCGTGCACACCTTCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACACC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAAACCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAGACCCCTGA GGTCAAGTTCAACTGTACGTGGACGGCGTGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACAGGTCAAGCTGACCTGCCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGACAACATACAAG ACCAAGCTTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCATAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1901 DIQMTQSPSSLSASVGDRTVTITCRASQGINELGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSTE FTLTISSLQPEDFVITYYCLQHNSYPFTFGQGTKVD	SEQ ID NO: 2058 QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIYDGSNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG
AA		

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			VKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTS LSSTLTLKADYEKHKVYACEVTHQGLSSLSPVTKSF NRGEC	TIFGVLLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDLMISRTPEVTCVVVDVSHED PEVKFNWYVVDGVEVHNAKTKPCEEQYGYSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
			SEQ ID NO: 331 GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACCAAGGAAAGCCCTA AACTCCTGATCTATGGTGCAATCCAGTTTGCAA GTGGGTCCCATCAAGGTTTCAGCGGCAGTGGAT CTGGGACAGAGTTCACTCTCACAAATCAGCAGCC TGCAAGCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAATAGTTACCCATTCACTTTCGGCCCT GGGACCAAAAGTGGATGTCAAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACCTGCCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	SEQ ID NO: 488 CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTCAAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGATGATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCAACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTGGAGTGTCTTGGGGGACTACT GGGGCCAGGAACCTGGTCAACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCTCTCAAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGTGCCGTGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGTGGAACTCAGGCG CCTGACCAAGCGGTGTCAACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACCTCACACATGCCACC GTGCCCAGCACCTGAACCTCTGGGGGACCGTCT AGTCTTCTCTTCCCCCACAACCCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACTG
IPS:360943	4H9.004.004	NA		

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				<p>CGTGGTGGTGACGTGAGCCACGAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTGACCGT CCTCACCGTCTGCACCAAGACTGGCTGAATGG CAAGGAGTACAAAGTGCAAGGTCTCCAAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACAGGTGAGCCTGACCTGCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGAGAGACAACATACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
				<p>SEQ ID NO: 1902</p> <p>DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFVITYYCLQHNSYPFTFGPGTKVDV KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLS STLTLSKADYEKHKVYACEVTHQGLSPVTKSFN RGEN</p>
		AA		<p>SEQ ID NO: 2059</p> <p>QVQLVESGGGVVQPGRSRLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIYDASNKYADAVKKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKS LSLSPGK</p>

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				<p>AGAGCAATGGGAGCCGGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCCTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTAAA</p> <p>SEQ ID NO: 2060</p>
				<p>QVQLVESGGGVVQGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIYDASNKYAYADA VKG RFTISRDNSKNTLYLQMNSLRAEDTAVYCARDG TIFGVLGDYWGQGTLLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGGSFFLY SKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPGK</p> <p>SEQ ID NO: 490</p>
				<p>DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGW YQQKPGKAPKRLIYGASSLQSGVPSRFSGSGTE FTLTISLQPEDFVITYCLQHNSYPFTFGQGTQVD VKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWVKVDNALQSGNSQESVTEQDSKDSSTYS LSSTLTLSKADYEKHKVYACEVTHQGLSSLSPVTKSF NRGEC</p> <p>AA</p> <p>SEQ ID NO: 1903</p>
				<p>GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCACTCTGTAGGAGACAGAGTCACCATCACCTT GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG GCTGTATCAGCAGAAACCAAGGGAAGCCCCCTA AACTCCTGATCTATGGTGATCCAGTTTGC AAA GTGGGTCCCATCAAGGTTTCAGCGGCAGTGGAT CTGGACAGAGTTCACTCTCACAAATCAGCAGCC TGACGCTGAAGATTTTGTAACTTAATTACTGTCT ACAGCATAATAGTTACCCATTCACTTTCGGCCA AGGACCATAAGTGATGTCAAAACGAACGGTGG CTGCACCATCTGTCTTCACTTCCCCGCCATCTGA TGAGCAGTTGAAAATCTGGAACTGCCTCTGTGTGT GTGCTGTGTAATAACTTCTATCCCCAGAGAGGC CAAAAGTACAGTGGAAGGTGGATAACGCCCTCCA</p> <p>NA</p> <p>SEQ ID NO: 333</p>
IPS:359761	4H9.004.006			<p>CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTTACTTTGGCA TGC ACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCAACCATCTCCAGAGACAATTCACAAGAAC CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATA GGACGATTTTGGAGTGTCTTTGGGGGACTACT GGGGCAGGGAACCTGGTCAACCGTCTCCTCAG CCTCCACCAAGGGGCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTTGGGGGCACAGC GGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCC</p>

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	<p>ATCGGGTAACTCCAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCCTGACGCTGAGCAAGCAGACTACGAGA AACACAAAAGTCTACGCCCTGCGAAGTCAACCCATC AGGCCCTGAGCTCGCCCGTCAACAAAGAGCTTCA ACAGGGGAGAGTGT</p>	<p>CGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGC CCTGACCAGCGCGTGCACACCTTCCCGGTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACCTACACATGCCACAC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAAACCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCCTGTGTGTCAGCGT CCTCACCGTCTGCACCAAGACTGGCTGAATGG CAAGGAGTACAAAGTGCAAGGTCTCCAAACAAGC CCTCCAGCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCATCCCGGAGGAGATGACCA AGAACAGGTGACCTGACCTGCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGACAACATACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
AA	<p>DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFVITYYCLQHNSYPFTFGQGTKVD VKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWVKVDNALQSGNSQESVTEQDSKDSSTYS LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF NRGEC</p>	<p>SEQ ID NO: 1904</p> <p>SEQ ID NO: 2061</p> <p>QVQLVESGGGVVQGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIYDASNKYADAVKYG RFTISRDNSKNTLYQMNSLRAEDTAVYFCARDR TIFGVLLGDYWGQGTLLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED</p>

IPS:360955	4B1.010	NA	<div> <div>SEQ ID NO: 334</div> <div> GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAAGGAAAGCCCCTA AGCTCCTGATCTATGGTGATCCAGTTGCAAA GTGGGTCCCTTCAAGGTTCAAGCGCAGTGGAT CTGGGACAGAAATTCAC'TCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTTCGGCCAA GGGACCAAAGTGAGATATCAAAACGAAACGGTGCT GCACCATCTGTCTTCAATCTTCCC GCCATCTGATG AGCAGTTGAAATCTGGAACCTGCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAGTGGATAACGCCCTCCAAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAAGCAGACTACGAGAAAC ACAAAAGTCTACGCCCTGCGAAGTCAACCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT </div> </div>	<div> <div>SEQ ID NO: 334</div> <div> GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAAGGAAAGCCCCTA AGCTCCTGATCTATGGTGATCCAGTTGCAAA GTGGGTCCCTTCAAGGTTCAAGCGCAGTGGAT CTGGGACAGAAATTCAC'TCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTTCGGCCAA GGGACCAAAGTGAGATATCAAAACGAAACGGTGCT GCACCATCTGTCTTCAATCTTCCC GCCATCTGATG AGCAGTTGAAATCTGGAACCTGCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAGTGGATAACGCCCTCCAAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAAGCAGACTACGAGAAAC ACAAAAGTCTACGCCCTGCGAAGTCAACCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT </div> </div>
IPS:360955	4B1.010	NA	<div> <div>SEQ ID NO: 491</div> <div> CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGAGGTCCTTGAGACTCTCCTGT GCAGGCTCTGGATTACATTTCAGTAACCTTTGGCA TGCACCTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGATGATGATGCAA GTAATGAAAACATATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAAATTCCAAGAATA CGCTGTATCTGCAAAATGAACAGCCTGAGAGTCG CGGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTTGGGGACTACT GGGGCCAGGAAACCTGGTCAACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTTCTCCAAAGACACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC CGAAACGGTGACGGTGTCTGTGGAACTCAGGCGC CCTGACCAGCGGCTGCACACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAACTTTGTGACAAAACCTCACACATGCCACCC GTGCCCAGCACCTGAACTCCTGGGGGACCGTC AGTCTTCTCTTCCCCCCTCAAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCAACATG CGTGGTGGTGGACGTGAGCCACGAAAGACCCCTGA GGTCAAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCAATAATGCCAAGACAAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCGACTGGCTGAATGG </div> </div>	<div> <div>SEQ ID NO: 491</div> <div> CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGAGGTCCTTGAGACTCTCCTGT GCAGGCTCTGGATTACATTTCAGTAACCTTTGGCA TGCACCTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGATGATGATGCAA GTAATGAAAACATATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAAATTCCAAGAATA CGCTGTATCTGCAAAATGAACAGCCTGAGAGTCG CGGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTTGGGGACTACT GGGGCCAGGAAACCTGGTCAACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTTCTCCAAAGACACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC CGAAACGGTGACGGTGTCTGTGGAACTCAGGCGC CCTGACCAGCGGCTGCACACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAACTTTGTGACAAAACCTCACACATGCCACCC GTGCCCAGCACCTGAACTCCTGGGGGACCGTC AGTCTTCTCTTCCCCCCTCAAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCAACATG CGTGGTGGTGGACGTGAGCCACGAAAGACCCCTGA GGTCAAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCAATAATGCCAAGACAAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCGACTGGCTGAATGG </div> </div>

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			<p>CAAGGAGTACAAAGTGCAAGGTCTCCAAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACAGGTGACCTGACCTGCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGAGAACAACTACAAG ACCAGCCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
			<p>SEQ ID NO: 1905</p> <p>DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSTEFT LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSITYSLSS TLTLTKADYEKHKVYACEVTHQGLSPVTKSFNR GEC</p>
		AA	<p>SEQ ID NO: 2062</p> <p>QVQLVESGGGVVQPGRLSLRSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDNSKNTLYLQMNSLRVADTA VYYCARDG TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPGK</p>
IPS:360962	4B1.011	NA	<p>SEQ ID NO: 335</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCATT GCCGGGCAAGTCAGGACATTAGAGATTATTAG GCTGTATCAGCAGAAACCAAGGAAAGCCCTA AGCGCTGATCTATGGTGATCCAGTTTGCAAA GTGGGTCCCTTCAAGGTTTCAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT</p>
			<p>SEQ ID NO: 492</p> <p>CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTTCAGTAACTTTGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAATA CGCTGTATCTGCAAAATGAACAGCCTGAGAGTCG</p>

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	ACAGCATAAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAACGAACGGTGGCT GCACCATCTGTCTTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACCTGCCCTCTGTTGT GCCTGCTGAATAACTTCTATCCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCCTGCCGAAATCAGCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	CGGACACGGCTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTTGGGGGACTACT GGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCAG CCTCCACCAAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGACACAGC GGCCCTGGCTGCTTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGTGGAATCAGAGCGC CCTGACCAAGCGGCTGCACACCTTCCC GGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGGCTTCCAGCAGCTTGGGCACC CAGACCTACATCTGCACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACAC GTGCCAGCACCTGAATCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAACCCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAGACCCCTGA GGTCAAGTTCAACTGTACGTGGACGGCGTGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCCTGTGTGTCAGCGT CCTCACCGTCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCACAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCATCCCGGAGGAGATGACCA AGAACCAAGTCAAGCTGACCTGCCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGAGCCGGAGACAACATACAAG ACCACGCTTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1906	SEQ ID NO: 2063
AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLSQSGVPSRFSGSGSGTEFT	QVQLVESGGGVVQPGSRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAWIWYDASNENYADAVKGG

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			<p>LTISLQPEDFATYYCLQHNPNYPFTFGQGTKVDIK RTVAAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSYLSLSS TLTLKADYKHKVYACEVTHQGLSSPVTKSFNR GEC</p>	<p>RFTISRDN SKNTLYLQMNSLRVADTA VYYCARDG TIFGVVLGDYWGQGT LVTVSSASTKGPSVFP LAPS SKSTSGGT AALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQSSGL YLSVVTVVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKD TLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK</p>
			<p>SEQ ID NO: 336</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACCAAGGAAAGCCCTA AGCTCTGATCTATGGTGCAATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTCAAGCGGCAGTGGAT CTGGGACAGAAATCACTCTCACAAATCAGCAGCC TGACGCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAACGAAACGGTGGCT GCACCATCTGTCTTCACTTCCCGCCATCTGATG AGCAGTTGAATCTGGAACCTGCCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCAAAAGAGCTTCAACA GGGGAGAGTGT</p>	<p>SEQ ID NO: 493</p> <p>CAGTGCAGCTGGTGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAACATATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAATA CGCTGATCTGCAAAATGAACAGCCTGAGAGTCG CGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCTGGTCAACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCTGGCTGCCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTGTTGGAACTCAGGCGC CCTGACCAAGCGGTGTGCAACCTTCCCGGTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTTGACCGTGGCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCACCC GTGCCAGCACCTGAACCTCTGGGGGACCGTCT AGTCTTCTCTTCCCCCCTCAAAACCCCAAGGACAC</p>
IPS:360968	4B1.012	NA	<p>SEQ ID NO: 336</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACCAAGGAAAGCCCTA AGCTCTGATCTATGGTGCAATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTCAAGCGGCAGTGGAT CTGGGACAGAAATCACTCTCACAAATCAGCAGCC TGACGCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAACGAAACGGTGGCT GCACCATCTGTCTTCACTTCCCGCCATCTGATG AGCAGTTGAATCTGGAACCTGCCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCAAAAGAGCTTCAACA GGGGAGAGTGT</p>	<p>SEQ ID NO: 493</p> <p>CAGTGCAGCTGGTGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAACATATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAATA CGCTGATCTGCAAAATGAACAGCCTGAGAGTCG CGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCTGGTCAACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCTGGCTGCCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTGTTGGAACTCAGGCGC CCTGACCAAGCGGTGTGCAACCTTCCCGGTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTTGACCGTGGCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCACCC GTGCCAGCACCTGAACCTCTGGGGGACCGTCT AGTCTTCTCTTCCCCCCTCAAAACCCCAAGGACAC</p>

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IP:360974	4B1.013	NA
<div> <div>SEQ ID NO: 337</div> <div> GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGAAAGCCCCTA AGCTCCTGATCTATGGTGATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTCAAGCGGCAGTGGAT CTGGGACAGAAATTCAC'TCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCAC'TTTCGGCCAA GGGACCAAAGTGGATATCAAACGAAACGGTGGCT GCACCATCTGTCTTCAATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAAC'TGCCCTCTGTTGTGT GCCTGCTGAATAACTTCTATATCCAGAGAGGCCA AAGTACAGTGAAGGTGGATAACGCCCTCCAAT CGGGTAAC'TCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCAACCATCAGG GCCTGAGCTCGCCCGTCAAAAGAGCTTCAACA GGGGAGAGTGT </div> </div>		
<div> <div>SEQ ID NO: 494</div> <div> CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGAGGTCCTTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTTCAGTAAC'TTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGATGATGCAA GTAATGAAAACTATGCAGACTCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAATA CGCTGTATCTGCACATGAACAGCCTGAGAGTCG CGGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGACTACT GGGGCCAGGAACCTGGTCAACCGTCTCCTCAG CCTCCACCAAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCTCTCCAAAGACACCTCTGGGGGCACAGC GGCCCTGGGTGCCTGGTCAAGGACTACTTCCCTCC CGAAACGGTGACGGTGTCTGTGGAAC'TCAGGCGC CCTGACACAGCGGCTGCACACCTTCCCCGGCTGT CCTACAGTCTCAAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGAC'TACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAAGGTGGACAAGAAAGTTGAGCC CAAACTTTGTGACAAAAC'TCACACATGCCACCC GTGCCCAGCACCTGAAACTCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCCAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTCAAGCGT CCTCACCGTCTGCACCAAGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC CCTCCAGCCCCATCGAGAAAACCATCTCCAA AGCCAAAGGCGAGCCCCGAGAAACACAGGTGT ACACCTGCCCCCATCCCCGGGAGGAGATGACCA AGAAACAGGTACGCTGACCTGCCTGGTCAAAAG GCTTCTATCCCAAGCACAATGCCCGTGGAGTGCGG </div> </div>		

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				<p>AGAGCAATGGGAGCCGGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCCTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTAAA</p> <p>SEQ ID NO: 2065</p>
				<p>QVQLVESGGGVVQGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAWIWYDASNENYADSVKVG RFTISRDNSKNTLYLHMNSLRVADTA VYYCARDG TIFGVVLGDYWGQGTLLTVSSASTKGPSVFPLAPS SKSTSGGT AALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGGSFFLY SKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPGK</p> <p>SEQ ID NO: 495</p>
				<p>DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSITYSLSS TLTL SKADYEEKHKVYACEVTHQGLSSPVTKSFNR GEC</p> <p>SEQ ID NO: 1908</p>
		AA		<p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCA TCTATAGGAGACAGAGTCACCAATCATT GCCGGGCAAGTCAGGACATTAGAGATTATTAG GCTGTATCAGCAGAAACCAAGGAAAGCCCTA AGCTCCTGATCTATGGTGATCCAGTTTGCAAA GTGGGTCCCTTCAAGGTTCAAGGCGCAGTGGAT CTGGACAGAAATTCATCTCACAAATCAGCAGCC TGACGCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATA TCAACGAACGGTGGCT GCACCATCTGTCTTCACTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACCTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAAT</p> <p>SEQ ID NO: 338</p>
IPS:360978	4B1.014	NA		<p>CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTTCAGTAACTTTGGCA TGC ACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGGAA GTAATGAA AACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCACAAGAATA CGCTGTATCTGCACATGAACAGCCTGAGAGTCG CGGACACGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCTTGGTCAACCGTCTCCTCAG CCTCCACCAAAGGGCCCATCGGTCTTCCCGCTGGC ACCTCCTCCAAGAGCACCTCTGTGGGGCACAGC GGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCC</p>

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		<p>CGGGTAACTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCGAAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT</p>	<p>CGAACCGGTGACGGTGTCTGTGGAACCTCAGGCG CCTGACCAGCGGCGTGACACACCTTCCCGGTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACCTACACATGCCACAC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAAACCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCAATATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAAGACTGGCTGAATGG CAAGGAGTACAAAGTGCAAGGTCTCCACACAAGC CCTCCAGCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCATCCCGGAGGAGATGACCA AGAACAGGTGACCTGACCTGCTGCTGCTCAAAG GCTTCTATCCAGCGCATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGGAGACAACATACAAG ACCAGCTTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
	AA	<p>DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLS TLTLTKADYEEKHKVYACEVTHQGLSPVTKSFNR GEC</p>	<p>SEQ ID NO: 1909</p> <p>SEQ ID NO: 2066</p> <p>QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAWIYDGSNENYADAVKG RFTISRDNSKNTLYLHMNSLRVADTAVYYCARDG TIFGVVLGDYWGQGTLLTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLSQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED</p>

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					PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK			
				SEQ ID NO: 339	SEQ ID NO: 496			
				GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAAGGAAAGCCCCTA AGCTCTGATCTATGGTGCAATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTCAAGCGGCAGTGGAT CTGGGACAGAAATTCACCTCTCACAAATCAGCAGCC TGCAAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAGTGGATAACAACGAACGGTGGCT GCACCATCTGTCTTCACTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACCTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAAGTCAACCCATCAGG GCCTGAGCTCGCCCCGTCAAAAGAGCTTCAACA GGGGAGAGTGT	4B1.015	IPS:359785	NA	CAGTGCAGCTGGTGGAGTCTGGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGTATGATGCAA GTAATGAAAACATATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAATA CGCTGATCTGCAAAATGAACAGCCTGAGAGTCG AGGACACGGCTGTGTATTATTGTGCGCGAGATA GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGAAACCCGTGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCTCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGTGCCTGTGTCAAAGGACTACTTCCC CGAACCCGGTGACGGTGTCTGTGGAACTCAGGCG CCTGACCAAGCGGTGCAACACTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACCTCACACATGCCACCC GTGCCACGACCTGAACCTCTGGGGGACCGTCTC AGTCTTCTCTTCCCCCAAAACCCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGCGCTGGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAAGGACTGGCTGAATGG

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			<p>CAAGGAGTACAAAGTGCAAGGTCTCCAAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACAGGTGAGCCTGACCTGCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGAGAACAACTACAAG ACCAGCCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCCTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
			<p>SEQ ID NO: 1910</p> <p>DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSTEFT LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLS TLTLTKADYEKHKVYACEVTHQGLSPVTKSFNR GEC</p>
		AA	<p>SEQ ID NO: 2067</p> <p>QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDNSKNTLYQMNSLRVEDTAVYYCARDR TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFELY SKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPGK</p>
IPS:360982	4B1.016	NA	<p>SEQ ID NO: 340</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCATT GCCGGGCAAGTCAGGACATTAGAGATTATTAG GCTGTATCAGCAGAAACCAAGGAAAGCCCTA AGCTCCTGATCTATGGTGATCCAGTTTGCAAA GTGGGTCCCTTCAAGGTTTCAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT</p>
			<p>SEQ ID NO: 497</p> <p>CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAATA CGCTGTATCTGCAAAATGAACAGCCTGAGAGTCG</p>

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	ACAGCATAAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAACGAACGGTGGCT GCACCATCTGTCTTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACCTGCCCTCTGTGTGT GCCTGCTGAATAACTTCTATCCCCAGAGAGGCCA AAGTACAGTGGAAAGGTGGATAACGCCCTCCAAAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCCGAAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	AGGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTTGGGGGACTACT GGGGCCAGGGAACCCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGCTGCCCTGGTCAAGGACTACTTCCC CGAACGGTGACGGTGTCTGTGGAACCTCAGGCGC CCTGACCAAGCGGCGTGACACCTTCCC GGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACAC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAGACCCCTGA GGTCAAGTTCAACTGTACGTGGACGGCGTGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCACAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCATCCCGGAGGAGATGACCA AGAACAGGTCAAGCTGACCTGCCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGACAACATAAAG ACCACGCTTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1911	SEQ ID NO: 2068
AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLSQSGVPSRFSGSGSGTEFT	QVQLVESGGGVVQPGRSRLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKGG

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			<div>LTISLQPEDFATYYCLQHNNYPFTFGQGTKVDIK RTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSYLSLS TLTLKADYEEKHKVYACEVTHQGLSSPVTKSFNR GEC</div>	<div>RFTISRDN SKNTLYLQMNSLRVEDTAVYYCARDG TIFGVVLGDYWGQGT LVTVSSASTKGPSVFPLAPS SKSTSGGT AALGCLVKDYFPEPVT VSWNSGALTS GVHTFPAVLQSSGLYSLSSVTV PSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPAPELL GGPSVFLFPPKPKD TLMISRTPETCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK</div>
			<div>SEQ ID NO: 341</div> <div>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCACAGAAACCAAGGAAAGCCCCTA AGCGCTGATCTATGGTGATCCAGTTTGC AAA GTGGGTCCCTTCAAGGTTCAAGCGGCAGTGGAT CTGGGACAGAAATTCAC'TCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAGTGGATATCAAAACGAAACGGTGGCT GCACCATCTGTCTTCAATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAAC TGGCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT CGGGTA ACTCCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAAGCAGACTACGAGAAAC ACAAAAGTCTACGCCTGCGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCAAAAGAGCTTCAACA GGGGAGAGTGT</div>	<div>SEQ ID NO: 498</div> <div>CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCACTAACCTTTGGCA TGCACTGGGTCCGCCAGGCCCAAGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGGAA GTAATGAAAACTATGCAGACTCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCACAAGAACA CGCTGTATCTGCACATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGAACCCCTGGTCAACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCTCTCCAAAGACACCTCTGGGGGCACAGC GGCCCTGGGTGCCCTGGTCAAGGACTACTTCCC CGAAACGGTGACGGTGTCTGTGGAAC TCAAGGCG CCTGACACAGCGGTGTCAACACTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAAGAAAGTTGAGCC CAAACTTTGTGACAAAACTCACACATGCCACCC GTGCCCAGCACCTGAAC TCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCCCCAAAACCCCAAGGACAC</div>
IPS:335922	18F2	NA		

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		<p>SEQ ID NO: 1912</p> <p>DIQMTQSPSSLSASIGDRVTITCRASQDLRNLYLGW YHQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTE FTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSITYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEN</p>	<p>SEQ ID NO: 2069</p> <p>QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAWIYDGSNENYADSVKVG RFTISRDNSKNTLYLHMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLLTVVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK</p>
	AA		

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SEQ ID NO: 342	SEQ ID NO: 499
GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGTATCAACAGAAACCAAGGGAAGCCCTA AGCTCTGATCTATGGTGCATCCAGTTTGC AAA GTGGGTCCCTTCAAGGTTCAAGGGCAGTGGAT CTGGGACAGAAATTCACCTCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTGCAACTTATTACTGTCT ACAGCATAAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAGTGGATATCAACGAACGGTGGCT GCACCATCTGTCTTCACTCTCCCGCCATCTGATG AGCAGTTGAATCTGGAACCTGCCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAGTCTACGCTGCGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCAAAAGAGCTTCAACA GGGGAGAGTGT	CAGGTGAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCACTAATTTGGCA TGCACCTGGTCCGCCAGGCCCAAGGAGGCG TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGCAGACGCCGTGAAGGCGC GATTCAACCATCTCCAGAGACAATTCCAAGAAACA CGCTGATCTGCAAAATGAACAGCCTGAGAGCCG CGGACACGGCTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGCTGCCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGC CCTGACCAAGCGGTGTGCAACCTTCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGGCTTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACAC GTGCCACGACCTGAACTCTGGGGGACCCGTC AGTCTTCTCTTCCCCCAAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAAGACCTGA GGTCAGTTCAACTGGTACGTGGACGGCGTGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTGACGCT CCTCACCGTCTGCACCAGGACTGGTGGTGAATGG CAAAGGAGTACAAAGTGCAAGGTCTCCAAACAAGC CCTCCAGCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAAGCCCCGAGAACCCAGGTGT ACACCTGCCCTTCCCGGAGGAGATGACCA AGAACCAAGTCAAGCTGACCTGCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG
18F2.002	NA
IPS:360986	

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				<p>AGAGCAATGGGAGCCGGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCCTGGACAAG AGCAGGTGGCAGCAGGGAACGCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTAAG</p> <p>SEQ ID NO: 1913</p>	
				<p>DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSTE FTLTISLQPEDFATYYCLQHNHYPTFGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEK</p> <p>AA</p> <p>SEQ ID NO: 2070</p> <p>QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAWIYDASNENYADAVKG RFTISRDNSKNTLYLQMNSLRAADTA VYYCARDG TIFGVVLGDYWGQGTLLVTVSSASTKGPSVFPLAPS SKSTSGGT AALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNKEYKCKVSNKALPAPIEKTIISK AKQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPGK</p>	
IPS:36095	18F2.003	NA		<p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCATT GCCGGGCAAGTCAGGACCTTAGAAAATTATTAG GCTGTATCAACAGAAACCAAGGAAAGCCCTA AGCTCCTGATCTATGGTGATCCAGTTTGCAAA GTGGGTCCCTTCAAGGTTCAAGGCGCAGTGGAT CTGGACAGAAATTCATCTCACAAATCAGCAGCC TGACGCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTCGGCCCT GGGACCAAAGTGGATAACAACGAACGGTGGCT GCACCATCTGTCTTCACTTCGCCCATCTGATG AGCAGTTGAAATCTGGAACCTGCCTCTGTGTGT GCCTGCTGAATAACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT</p> <p>SEQ ID NO: 343</p> <p>CAGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTTCAGTAACTTTGGCA TGC ACTGGTCCGCCAGGCCCAAGGAGGCG TGGAGTGGTGGCAGTTATATGGTATGATGCAAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCACAAGAACAA CGCTGTATCTGCACATGAACAGCCTGAGAGCCG CGGACACGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCAGGGAACCTGGTCAACCGTCTCCTCAG CCTCCACCAAAGGGCCCATCGGTCTTCCCGCAG ACCTCCTCCAAGAGCACCTCTGCGGGGCACAGC GGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCC</p>	

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		<p>CGGGTAACTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCGAAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT</p>	<p>CGAACCGGTGACGGTGTCTGTGGAACCTCAGGCG CCTGACCAGCGCGTGCACACCTTCCCGGTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACCTCACACATGCCACCC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAAACCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCAATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCATCCCGGAGGAGATGACCA AGAACAGGTGAGCCTGACCTGCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGGAGACAACATACAAG ACCAGCCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
		<p>SEQ ID NO: 1914</p>	<p>SEQ ID NO: 2071</p>
	AA	<p>DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YQQKPGKAPKLLIYGASSLSQGVPSRFSGSGSTE FTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP EAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC</p>	<p>QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAWIYDASNENYADAVKGG RFTISRDNSKNTLYLHMNSLRAADTA VYYCARDG TIFGVVLGDYWGQGTLLTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLSQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLMISRTPETVTCVVVDVSHED</p>

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				<p>PEVKFNWYVVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFNCSVMHEALHNHYTQKS LSLSPGK</p>
				<p>SEQ ID NO: 344</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCACAGAAACCAAGGAAAGCCCCTA AGCTCTGATCTATGGTGCAATCCAGTTTGCAA GTGGGTCCCCTTCAAGGTTCAAGGCGAGTGGAT CTGGGACAGAATTCACTCTCACAAATCAGCAGCC TGACGCCCTGAAGATTTGCAACTTATTACTGTCT ACAGCATAAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAGTGGATATCAACGAACGGTGGCT GCACCATCTGTCTTCACTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACCTGCCCTCTGTTGT GCCTGCTGAAATACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCAAAAGAGCTTCAACA GGGGAGAGTGT</p>
				<p>SEQ ID NO: 501</p> <p>CAGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCACTTTTCACTAACCTTTGGCA TGCACTGGTCCGCCAGGCCCAAGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAACTATGACAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGATCTGCAAAATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTTGGGGGACTACT GGGGCCAGGGAACCCCTGGTCAACCTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCTCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGCTGCCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTGTTGGAACCTCAGGCGC CCTGACCAAGCGGCGTGCAACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACAC GTGCCAGCACCTGAACTCTGGGGGAGACCGTC AGTCTTCTCTTCCCCCAAAACCCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGCGGTGGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTACGCGT CCTCACCGTCTTGCAACAGGACTGGCTGAATGG</p>

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				<p>CAAGGAGTACAAAGTGCAAGGTCTCTCCAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACAGGTGACCTGACCTGCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGAGAACAACTACAAG ACCAGCCTCCCGTCTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCCTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
				<p>SEQ ID NO: 1915</p> <p>DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YHQKPGKAPKLLIYGASSLQSGVPSRFSGSGGTE FTLTISLQPEDFATYYCLQHNHYPTFTGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEK</p>
			AA	<p>SEQ ID NO: 2072</p> <p>QVQLVESGGGVVQPGRSRLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAWIYDASNENYADAVKG RFTISRDNSKNTLYQMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAAAGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPGK</p>
				<p>SEQ ID NO: 345</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCATT GCCGGGCAAGTCAGGACCTTAGAAAATTATTTAG GCTGTATCAACAGAAACCAAGGAAAGCCCTTA AGCGCTGATCTATGGTGATCCAGTTTGCAAA GTGGGTCCCTTCAAGGTTTCAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCACAATCAGCAGCC TGACGCCTGAAGATTTCGCAACTTATTACTGTCT</p>
IPS:361005	18F2.005	NA		<p>SEQ ID NO: 502</p> <p>CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCAAGGAGGCGC TGGAGTGGTGGCAGTTATATGGTATGATGCAAA GTAATGAAAACATATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG</p>

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	ACAGCATAAATAATTACCCCTTCACCTTTCGGCCCT GGGACCAAAGTGGATATCAACGAACGGTGGCT GCACCATCTGTCTTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACCTGCCCTCTGTTGT GCCTGCTGAATAACTTCTATCCCCAGAGAGGCCA AAGTACAGTGGAAAGGTGGATAACGCCCTCCAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCCTGCCGAAATCAGCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	CGGACACGGCTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTTGGGGGACTACT GGGGCCAGGGAACCCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGCTGCCCTGGTCAAGGACTACTTCCC CGAACGGTGACGGTGTCTGTGGAACCTCAGGCGC CCTGACCAAGCGGCGTGACACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACAC GTGCCAGCACCTGAACCTCTGGGGGGACCGTC AGTCTTCTCTTCCCCCAAAACCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAGACCCCTGA GGTCAAGTTCAACTGTACGTGGACGGCGTGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCACAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCATCCCGGAGGAGATGACCA AGAACAGGTGACCTGACCTGCCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGAGCCGGAGACAACATAAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1916	SEQ ID NO: 2073
AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YQQKPGKAPKRLIYGASSLSQGVPSRFSGSGSGTE	QVQLVESGGGVVQPGSRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAWIWYDASNENYADAVKGG

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			FTLTISSLQPEDFATYYCLQHNNYPFTGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSYLSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEN	SEQ ID NO: 346	RFTISRDNKNTLYLQMNSLRAADTA VYYCARDG TIFGVVLGDYWGQGT LVTVSSASTKGPSVFP LAPS SKSTSGGT AALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQSSGL YLSVVTVVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKD TLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHN A KTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
				SEQ ID NO: 503	CAGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTTCAGTAACTTTGGCA TGCACTGGTCCGCCAGGCCCAAGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAA AACTATGCAGACGCCGTGAAGGGCC GATTACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCACATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCTGGGTGCTGCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTGCGTGAACCTCAGGCGC CCTGACCAAGCGGTGTCACACCTTCCCCGGTGT CCTACAGTCTCAGGACTCTACTCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAA AACTCACACATGCCACC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTCTCCCCCAAAACCC AAGGACAC
IPS:361009	18F2.006	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGATCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTAATTAG GCTGGTATCAACAGAAACCAAGGAAAGCCCTA AGCCCTGATCTATGGTGATCCAGTTTGCAAA GTGGGTCCCTTCAAGGTTCAAGCGGCAGTGGAT CTGGGACAGAAATCACTCTCACAAATCAGCAGCC TGACGCTGAAGATTTGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAGTGGATATCAACGAACGGTGGCT GCACCATCTGTCTTCACTTCCCGCCATCTGATG AGCAGTTGAATCTGGAACCTGCCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCGGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCAAAAGAGCTTCAACA GGGGAGAGTGT		

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		<p>SEQ ID NO: 1917</p> <p>DIQMTQSPSSLSASIGDRVTITCRASQDLRNLYLGW YQQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTE FTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSITYSL STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEN</p>	<p>SEQ ID NO: 2074</p> <p>QVQLVESGGGVVQPGRSRLRSCAASGFTFSNFGM HWVRQAPGKGLEWVAWIYDASNENYADAVKVG RFTISRDNKNTLYLHMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLLTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSGGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK</p>
	AA		

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SEQ ID NO: 347	SEQ ID NO: 504
<p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCAACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCACAGAAACCAAGGAAAGCCCCTA AGCTCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGTCCCTTCAAGGTTCAAGGCGAGTGGAT CTGGGACAGAAATTCACCTCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTGCAACTTATTACTGTCT ACAGCATAAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAGTGGATATCAACGAACGGTGGCT GCACCATCTGTCTTCACTCTCCCGCCATCTGATG AGCAGTTGAATCTGGAACCTGCCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCAAAAGAGCTTCAACA GGGGAGAGTGT</p>	<p>CAGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCACTTTTCAGTAACTTTGGCA TGCACCTGGTCCGCCAGGCCCAAGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAAACA CGTGTATCTGCACATGAACAGCCTGAGAGCCG CGGACACGGCTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTTGGGGGACTACT GGGGCCAGGGAACCCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGCTGCCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGC CCTGACCAAGCGGCTGCAACACCTTCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGGCTTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACC GTGCCACGACCTGAACTCTGGGGGACCGTCTC AGTCTTCTCTTCCCCCAAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAAGACCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTGACGCT CCTCACCGTCTGCACCAGGACTGGTGGTGAATGG CAAGGAGTACAAAGTGCAAGGTCTCCAAACAAGC CCTCCAGCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCGAGCCCCGAGAACCCAGGTGT ACACCTGCCCCATCCCGGGAGGAGATGACCA AGAACCAAGTCAAGCTGACCTGCCTGGTCAAAG GCTTCTATCCCAAGCGACATCGCCGTGGAGTGGG</p>
IPs:361013	18F2.007
NA	

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				<p>AGAGCAATGGGAGCCGGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCCTGGACAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTAAA</p> <p>SEQ ID NO: 1918</p> <p>DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YHQKPGKAPKLLIYGASSLQSGVPSRFSGSGGTE FTLTISLQPEDFATYYCLQHNYPFTFGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLS STLTLSKADYEKHKVYACEVTHQGLSPVTKSFN RGEK</p>	<p>AGAGCAATGGGAGCCGGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCCTGGACAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTAAA</p> <p>SEQ ID NO: 2075</p> <p>QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAWIYDASNENYADA VKG RFTISRDNSKNTLYLHMNSLRAADTA VYYCARDG TIFGVVLGDYWGQGTLLTVSSASTKGPSVFPLAPS SKSTSGGT AALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGGSFFLY SKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPGK</p>
	AA			<p>SEQ ID NO: 348</p> <p>GACATCCAGATACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCCTT GCCGGGCAAGTCAGGACCTTAGAAAATTATTAG GCTGTATCACAGAAACCCAGGGAAGCCCTTA AGCCCTGATCTATGGTGATCCAGTTTGCAAA GTGGGTCCCTTCAAGGTTTCAGGGCAGTGGAT CTGGGACAGAAATTCATCTCACAAATCAGCAGCC TGACGCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATA TCA AACGAACGGTGGCT GCACCATCTGTCTTCACTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACCTGCCTCTGTGTGT GCCTGCTGAATAACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCCAAT</p>	<p>SEQ ID NO: 505</p> <p>CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCAAGGAGGCG TGGAGTGGTGGCAGTTATATGGTATGATGCAAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG CGGACACGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCAGGGAACCCCTGGTCAACGCTCTCCTCAG CCTCCACCAAAGGGGCCATCGGTCTTCCCGCTGGC ACCTCCTCCAAGAGCACCTCTTGGGGGCACAGC GGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCC</p>

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	<p>CGGGTAACTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCGAAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT</p>	<p>CGAACCGGTGACGGTGTCTGTGGAACCTCAGGCG CCTGACCAGCGGCGTGACACACCTTCCCGGTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACCTCACACATGCCACAC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAAACCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCAATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAAGACTGGCTGAATGG CAAGGAGTACAAAGTGCAAGGTCTCCAAACAAGC CCTCCAGCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCATCCCGGAGGAGATGACCA AGAACAGGTGACCTGACCTGCTGCTGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGAGCCGGAGACAACATACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
	<p>SEQ ID NO: 1919</p> <p>DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YHQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTE FTLTISLQPEDFATYYCLQHNHYPTFTGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP EAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEK</p>	<p>SEQ ID NO: 2076</p> <p>QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAWIYDASNENYADAVKG RFTISRDNKNTLYLQMNSLRAADTAVYYCARDG TIFGVLDGYWGQGTLTIVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED</p>

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				SEQ ID NO: 349 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCAACAGAAACCAAGGGAAGCCCCA AGCTCTGATCTATGGTGCAATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTCAAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAAATCAGCAGCC TGACGCTGAAGATTTGCAACTTATTACTGTCT ACAGCATAAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAGTGGATATCAACGAACGGTGGCT GCACCATCTGTCTTCACTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACCTGCCTCTGTTGTGT GCCTGCTGAAATACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT			SEQ ID NO: 506 CAGGTGACGTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTTTCACTAACCTTTGGCA TGCACTGGTCCGCCAGGCCCAAGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGGAA GTAATGAAACATATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCACAGAACAA CGCTGATCTGCAAAATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTTGGGGGACTACT GGGGCCAGGGAACCCCTGGTCAACCTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCTCTCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGCTGCCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTGTTGGAACCTCAGGCGC CCTGACCAAGCGGCGTGCAACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACCTCACACATGCCACAC GTGCCACGACCTGAACCTCTGGGGGAGACCGTC AGCTTCTCTCTCCCCCAAAACCCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGCGGTGGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTACGCGT CCTCACCGTCTTGCACCAAGGACTGGCTGAATGG
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			<p>CAAGGAGTACAAAGTGCAAGGTCTCTCCAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACAGGTCAAGCTGACCTGCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGAGAACAACTACAAG ACCAGCCTCCCGTCTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCCTGGACAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
			<p>SEQ ID NO: 1920</p> <p>DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSTE FTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSITYSL STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEK</p>
		AA	<p>SEQ ID NO: 2077</p> <p>QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAWIYDGSNENYADAVKG RFTISRDNSKNTLYQMNSLRAADTA VYCARDG TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYITLPPSRREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPGK</p>
			<p>SEQ ID NO: 507</p> <p>CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTTCAGTAACCTTTGGCA TGCACTGGGTCCGCCAGGCCCAAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAAA GTAATGAAAACATATGCAGACTCCCGTGAAGGGCC GATTCACCATCTCCAGAGACAAATTCACAAGAACAA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG</p>
		NA	<p>SEQ ID NO: 350</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCATT GCCGGGCAAGTCAGGACCTTAGAAAATTATTTAG GCTGTATCAACAGAAACCAAGGAAAGCCCTTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGTCCCTTCAAGGTTTCAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT</p>
IPS:361028	18F2.010		

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	ACAGCATAAATAATTACCCCTTCACCTTTCGGCCCT GGGACCAAAGTGGATATCAACGAACGGTGGCT GCACCATCTGTCTTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACCTGCCCTCTGTTGT GCCTGCTGAATAACTTCTATCCCCAGAGAGGCCA AAGTACAGTGGAAAGGTGGATAACGCCCTCCAA CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCCGAAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	CGGACACGGCTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTTGGGGGACTACT GGGGCCAGGGAACCCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGCTGCCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGC CCTGACCAAGCGGCGTGACACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACAC GTGCCAGCACCTGAACCTCTGGGGGGACCGTC AGTCTTCTCTTCCCCCAAAACCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAGACCCCTGA GGTCAAGTTCAACTGTACGTGGACGGCGTGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCACAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCATCCCGGGAGGAGATGACCA AGAACAGGTGACCTGACCTGCCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGAGCCGGAGACAACATAAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1921	SEQ ID NO: 2078
AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGTE	QVQLVESGGGVVQPGSRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAWIWYDASNENYADSVKGG

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			FTLTISSLQPEDFATYYCLQHNNYPFTGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEK	SEQ ID NO: 351	RFTISRDN SKNTLYLQMNSLRAADTA VYYCARDG TIFGVVLGDYWGQGT LVTVSSASTKGPSVFP LAPS SKSTSGGT AALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQSSGL YLSVVTVVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKD TLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHN AAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
				SEQ ID NO: 508	CAGGTG CAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCAAGGCGC TGGAGTGGTGGCAGTTATATGGTATGATGCA GTAATGAA AACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAA CGCTGATCTGCAAAATGAACAGCCTGAGAGCG AGGACACGGCTGTGTATTACTGTGCGAGAGATA GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCTGGTCAACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAAGAGACCTCTGGGGGACACAGC GGCCTGGGTGCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTGCGAACCTCAGGCGC CCTGACCAGCGGCGTGACACACTTCCCCGGCTGT CCTACAGTCTCCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAAGGCC AGCAACACCAAGGTGGACAAAGAAAGTTGAGCC CAAATCTTGTGACAA AACTCACACATGCCACCC GTGCCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTCCTCTTCCCCCCCAAAACCCCAAGGACAC
IPS:360535	18F2.011	NA			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCCTT GCCGGGCAAGTCAGGACCTTAGAAAATTATTAG GCTGTATCAACAGAAACCAAGGAAAGCCCTA AGCTCCTGATCTATGGTGATCCAGTTTGCAAA GTGGGTCCCTTCAAGGTTGAGCGGCAGTGGAT CTGGGACAGAAATCACTCTCACAAATCAGCAGCC TGACGCTGAAGATTTGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAGTGGATATCAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACCTGCCTCTGTGTGT GCCTGTGAAATAACTTCTATCCCAAGAGAGGCCA AAGTACAGTGGAAAGGTGGATAACGCCCTCCAAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCAAAAGAGCTTCAACA GGGGAGAGTGT

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				<p>AGAGCAATGGGAGCCGGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCCTGGACAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTAAA</p> <p>SEQ ID NO: 2080</p>
				<p>QVQLVESGGGVVQPGSRSLRSCAASGFTFSNFGM HWVRQAPGKGLEWVAWIYDASNENYADA VKG RFTISRDNSKNTLYLQMNSLRAEDTAVYCARDG TIFGVVLGDYWGQGTLLTVSSASTKGPSVFPLAPS SKSTSGGT AALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPGK</p> <p>SEQ ID NO: 510</p>
				<p>DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISLQPEDFATYYCLQHNYPFTFGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSITYSL STLTLSKADYEKHKVYACEVTHQGLSSLSPVTKSFN RGEK</p> <p>SEQ ID NO: 1923</p>
			AA	<p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCACTCTGTAGGAGACAGAGTCACCATCATT GCCAGGCGAGTCAGGACATTAGCAACTATTAA ATTGGTATCAGCAGAAACCAAGGAAAGCCCTA AGCTCTGATCTACGATGCATCCAAATTTGGAAA CAGGGTCCCATCAAAGGTTCAAGTGAAGTGGAT CTGGGACAGATTTTAGTCTCACCATCAGCAGCC TGCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATATTCTCTCCTCATTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGAACGGTGGCTG CACCATCTGTCTTCATCTTCCCGCCATCTGATGA GCAGTTGAAAATCTGGAACCTGCTCTGTTGTGTC CTGCTGAATAACTTCTATCCAGAGAGGCCAAA GTACAGTGAAGGTGGATAACGCCCTCCCAATCG</p> <p>SEQ ID NO: 353</p>
IPS:35940	2F11.002	NA		<p>CAGGTGCAACTGGTGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAGCTATGGC ATGCACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAATACTATGCAGACGCCGTGAAGGGC CGATTACCATCTCCAGGGACAAATCCAAAGAAC ACGCTGATCTGCAAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTGGAGTGGTTCTTGACTACTGG GGCCAGGGAACCTGGTCAACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC</p>

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	GGTA ACTCCCAGGAGAGTGTCACAGAGCAGGAC AGCAAGGACAGCACCTACAGCCTCAGCAGCACC CTGACGCTGAGCAAGAGAGACTACGAGAAACA CAAAGTCTACGCCTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCACAAAGAGCTTCAACAG GGGAGAGTGT	GAACCGGTGACGGTGTCTGTGGAACCTCAGGGGCC CTGACCAGCGCGTGCACACCTTCCCGGCTGTC CTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACCTACACATGCCCCACC GTGCCCAGCACCTGAACCTCTGGGGGACCCGTC AGTCTTCTCTTCCCCCAAAACCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCAATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAAGTGCAAGGTCTCCAAACAAGC CCTCCAGCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCATCCCGGAGGAGATGACCA AGAACAGGTGACCTGACCTGCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGAGCCGGAGACAACACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1924 DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSTRFSGSGGTD FSLTISSLQPEDFATYYCQQYDILLTFGGGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLS TLTLTKADYEKHKVYACEVTHQGLSPVTKSFNR GEC	SEQ ID NO: 2081 QVQLVESGGGVVQGRSLRLSCAASGFTSSYGM HWVRQAPGKGLEWVAWIYDASNKYADAVKVG RFTISRDNKNTLYLQMNSLRAEDTAVYVCARDR TIFGVLDYWQGGLVTVSSASTKGPSVFPLAPSS KSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKEPKSCDKTHTCTCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE

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					VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEVESNGQPENNYKTTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK			
					SEQ ID NO: 354	SEQ ID NO: 511		
				NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCAATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTAA ATTGGTATCAGCAGAAACCAAGGAAAGCCCCTA AGCTCTGATCTACGATGCATCCAATTTGGAAA CAGGGTCCCATCAAGGTTCAAGTGGAAGTGGAT CTGGGACAGATTTTAGTCTCACCATCAGCAGCC TGCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATATTCTCCTCACTTTCGGCGGAGG GACC AAGGTGGAGATCAAGCGAACGGTGGCTG CACCATCTGTCTTCACTCTCCCGCCATCTGATGA GCAGTTGA AATCTGGA ACTGCCCTCTGTTGTGTC CTGCTGAATAACTTCTATCCCAGAGAGGCCAAA GTACAGTGG AAGGTGGATAACGCCCTCCAATCG GGTA ACTCCCAGGAGAGTGTCAAGAGCAGGAC AGCA AGGACAGCACCTACAGCCTCAGCAGCACCC CTGACGCTGAGCA AAGCAGACTACGAGAAACA CAAA GTCTACGCC TCGAAGTCAACCATCAGGG CCTGAGCTCGCCCGTCACAAAGAGCTTCAACAG GGGAGAGTGT		2F11.003	IPS:361039

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			<p>CAAGGAGTACAAAGTGCAAGGTCTCCAAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACAGGTGAGCCTGACCTGCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGAGAACAACTACAAG ACCAGCCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCCTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
			<p>SEQ ID NO: 1925</p> <p>DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFGSGSGTD FSLTISLQPEDFATYYCQQYDILLTFGGGTKEIK RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSITYSLSS TLTLTKADYEEKHKVYACEVTHQGLSPVTKSFNR GEC</p>
		AA	<p>SEQ ID NO: 2082</p> <p>QVQLVESGGGVVQPGRSRLRSCAASGFTFSYGM HWVRQAPGKGLEWVAWIYDASNKYAYADA VKG RFTISSDNSKNTLYLQMNLSRAEDTAVYYCARDR TIFGVLDYWQGQTLVTVSSASTKGPSVFPLAPSS KSTSGGTAAALGCLVKDYFPEPTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCTPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK</p>
IPS:361043	2F11.004	NA	<p>SEQ ID NO: 355</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCAATCTGTAGGAGACAGAGTCACCATCCTT GCCAGGCGAGTCAGGACATTAGCAACTATTAA ATTGGTATCAGCAGAAACCAAGGAAAGCCCTA AGCTCCTGATCTACGATGCATCCCAATTTGAAA CAGGGGTCCCATCAAGGTTTCAGTGGAAGTGGAT CTGGGACAGATTTTAGTCTCACCATCAGCAGCC TGCAGCCTGAAGATATTGCAACATATTACTGTC</p>
			<p>SEQ ID NO: 512</p> <p>CAGGTGCAACTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCAACCTTCAGTAGCTATGGC ATGCACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAATACTATGCAGACGCCGTGAAGGGC CGATTACCATCTCCAGGGGACAATTCCAAGAAC ACGCTGATCTGCAAAATGAACAGCCTGAGAGCC</p>

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	<p>AACAGTATGATATTCTCCTCACTTTCGGCGGAG GGACCAAGGTGGAGATCAAGCGAACGGTGGCT GCACCATCTGTCTTTCATCTTCCCGCCATCTGATG AGCAGTTGAATCTGGAACCTGCCCTCTGTTGT GCCTGCTGAATAACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCCGAAAGTCAACCATCAGG GCCTGAGCTCGCCCGTCAAAAGAGCTTCAACA GGGAGAGTGT</p>	<p>GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGACGATTTTGGAGTGGTCTTGACTACTGG GGCCAGGGAACCTGGTCAACCGTCTCCTCAGCC TCCACCAAGGCCCATCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCTCTGGGGGCACAGG GCCCTGGCTGCCCTGGTCAAGGACTACTTCCCC GAACCGGTACGGTGTCTGTGGAACCTCAGGGCC CTGACCAAGCGGTGCACACCTTCCCCGGCTGTC CTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGGCTTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAAGCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACCC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAAACCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGGTGGGACGTGAGCCACGAGAACCCCTGA GGTCAAGTTCAACTGTACGTGGACGGCGTGA GGTGCATAATGCCAAGACAAGCCGTGTAGGA GCAGTACGGCAGCAGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCA AGCCAAAGGCGAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCATCCCGGAGGAGATGACCA AGAACAGGTCAACCTGACCTGCCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGAGCGCGGAGACAACATAAAG ACACGCTTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCTGTCTCCGGGTAAA</p>
	<p>SEQ ID NO: 1926</p>	<p>SEQ ID NO: 2083</p>
AA	<p>DIQMTQSPSSLSASVGDRTVTITCQASQDISNYLNW YQOKPGKAPKLLIYDASNLETGVPSRFSGSGGTD</p>	<p>QVQLVESGGGVVQPRSLRLSCAASGFTFSSYGM HWVRQAPGKGLEWVAWIYDASNKYADA VKG</p>

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			<p>FSLTISSLQPEDIATYYCQYDILLTFGGGKVEIKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNFFYPREA KVQWKVDNALQSGNSQESVTEQDSKSDSTYLSST LTLKADYEEKHKVYACEVTHQGLSSPVTKSFNRG EC</p>	<p>RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLDYWGQGLTVTVSSASTKGPSVFPLAPSS KSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHCTPCPPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK</p>
			<p>SEQ ID NO: 356</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTAA ATTGGTATCAGCAGAAACCAAGGAAAGCCCCTA AGCTCCTGATCTACGATGCATCCAAATTTGGAAA CAGGGTCCCATCAAGGTTCAAGTGAAGTGGAT CTGGGACAGATTTTAGTTTCAACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATATTCTCCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGAACGGTGGCTG CACCATCTGTCTTCACTCTCCCGCCATCTGATGA GCAGTTGAAAATCTGGAACCTGCCCTCTGTTGTGTC CTGCTGAATAACTTCTATCCAGAGAGGCCAAA GTACAGTGGAAAGGTGGATAACGCCCTCCAAATCG GGTAACTCCAGAGAGAGTGTCACAGAGCAGGAC AGCAAGGACAGCACCTACAGCCTCAGCAGCACCC CTGACGCTGAGCAAAAGCAGACTACGAGAAACA CAAAGTCTACGCTGCGAAGTCAACCCATCAGGG CCTGAGCTCGCCCGTCACAAAGAGCTTCAACAG GGGAGAGTGT</p>	<p>SEQ ID NO: 513</p> <p>CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTCAGTAGCTATGGC ATGCACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGTTATGATGCA AGTAATAATACTATGCAGACGCCGTGAAGGGC CGATTCAACCATCTCCAGGGACAATTCCAAGAAC ACGCTGATCTGCAAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTGGAGTGGTCTTGACTACTGG GGCCAGGGAACCTGGTCAACGCTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCTCTGGGGGACACAGCG GCCCTGGCTGCCTGGTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCC CTGACCAGCGCGTGCACACCTTCCCCGGCTGTC CTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAACTTTGTGACAAAACCTCACACATGCCACCC GTGCCCAGCACCTGAACCTCTGGGGGACCGTCT AGTCTTCTCTTCCCCCCCCAAAACCCCAAGGACAC</p>
IPS:361049	2F11.005	NA		

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IPs:361055	2F11.006	NA	<p>SEQ ID NO: 357</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCAACCATCACTT GCCAGCGAGTCAAGGACATTAGCAACTATTAA ATTGGTATCAGCAGAAACAGGGAAGCCCTA AGCTCTGATCTACGATGCATCCAAATTTGAAA CAGGGTCCCATCAAGGTTCAAGTGAAGTGGAT CTGGGACAGATTTTAGTCTCAACCATCAGCAGCC TGCAGCCTGAAGATATTGCAACATATTACTGTG AACAGTATGATATTCTCTCACTTTCGGCGGAG GGACCAAGGTGGAGATCAAGCGAAGGTGGCT GCACCATCTGTCTTCAATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACTGCCCTCTGTTGTG GCCTGCTGAATAACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT CGGGTAACTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCGAAGTCAACCATCAGG GCCTGAGCTCGCCGTCAACAAGAGCTTCAACA GGGGAGAGTGT</p>	<p>SEQ ID NO: 514</p> <p>CAGGTGCAACTGGTGGAGTCTGGGGAGGCGTGT GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGATTACCTTCAGTAGCTATGCC ATGCACCTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGTTATGATGCA AGTAATAAATACTATGACAGACGCCGTGAAGGGC CGATTCAACCATCTCCAGCGACAATTCCAAGAAC ACGCTGTATCTGCAATGAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTGGAGTGTCTTGACTACTGG GGCCAGGGAACCTGGTCAACCGTCTCCTCAAGCC TCCACCAAGGGCCCATCGGTCTTCCCCTGGCA CCCTCTCTCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGCTGCCCTGGTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCC CTGACCAAGCGCGTGCACACCTTCCCGGCTGTC CTACAGTCTCAGGACTCTACTCCTCTCAGCAGC GTGTTGACCGTGCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGTGGACAAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCACCC GTGCCCAGCACCTGAACCTCCTGGGGGACCGTCT AGTCTTCTCTTCCCCCACAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCCTGA GGTCAAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCAATAATGCCAAGACAAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTCAAGCGT CCTCACCGTCTGCAACGAGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCCATCGAGAAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCTTATCCCGGAGGAGATGACCA AGAACAGGTACGCTGACCTGCCTGGTCAAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG</p>
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				<p>AGAGCAATGGGAGCCGGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCCTGGACAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTAAA</p> <p>SEQ ID NO: 1928</p> <p>DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGTID FSLTISSLQPEDIATYYCQQYDILLTFGGGTKVEIKR TVAAPSVFIIPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSITYLSST LTLTKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC</p>		<p>AGAGCAATGGGAGCCGGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCCTGGACAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTAAA</p> <p>SEQ ID NO: 2085</p> <p>QVQLVESGGGVVQPGRSLRLSCAASGFTSSYGM HWVRQAPGKGLEWVAWIYDASNKYAYADA VKG RFTISDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLDYWGQGLVTVSSASTKGPSVFP LAPSS KSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKEPKSCDKTHCTCPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEK TISKA KGQPREPQVYITLPPSRREMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPVLDSDGSEFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK</p>
				<p>AA</p>		
IPS:361059	2F11.007	NA		<p>SEQ ID NO: 358</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCA TCTGTAGGAGACAGAGTCACCAATCATT GCCAGGCGAGTCAGGACATTAGCAACTATTAA ATTGGTATCAGCAGAAACCAAGGAAAGCCCTA AGCTCTGATCTACGATGCATCCAAATTTGGAAA CAGGGTCCCATCAAAGGTTCAAGTGAAGTGGAT CTGGGACAGATTTTAGTTTCACCAATCAGCAGCCT GCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATATTCTCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGAAACGGTGGCTG CACCATCTGTCTTCACTTCCCGCCATCTGATGA GCAGTTGAAAATCTGGAACCTGCTCTGTTGTGTC CTGCTGAATAACTTCTATCCAGAGAGGCCAAA GTACAGTGGAAGGTGGATAACGCCCTCCCAATCG</p>		<p>SEQ ID NO: 515</p> <p>CAGGTGCAACTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAGCTATGGC ATGCACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAATACTATGCAGACGCCGTGAAGGGC CGATTACCACTCTCCAGCGACAAATTCAGAAC ACGCTGATCTGCAAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTGGAGTGGTTCTTGACTACTGG GGCCAGGGAACCTGGTCAACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCGCTGGCA CCCTCCTCCAAAGAGCACCTCTGGGGGACAGCG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC</p>

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	GGTA ACTCCCAGGAGAGTGTCACAGAGCAGGAC AGCAAGGACAGCACCTACAGCCTCAGCAGCACC CTGACGCTGAGCAAGAGAGACTACGAGAAACA CAAGTCTACGCCTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCACAAAGAGCTTCAACAG GGGAGAGTGT	GAACCGGTGACGGTGTCTGTGGAACCTCAGGGGCC CTGACCAGCGGCGTGACACACCTTCCCGGCTGTC CTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACCTCACACATGCCACAC GTGCCAGCACCTGAACCTCTGGGGGACCGTCTC AGTCTTCTCTTCCCCCAAAACCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCAATAAGCCAAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAAGTGCAAGGTCTCCAAACAAGC CCTCCAGCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCATCCCGGAGGAGATGACCA AGAACAGGTGACCTGACCTGCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGGAGACAACATACAAG ACACGCCCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
AA	SEQ ID NO: 1929 DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSTRFSGSGGTD FSFTISLQPEDFATYYCQQYDILLTFGGGTKVEIK RTVAAPSVFIFPPSDAEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLS TLTLTKADYEKHKVYACEVTHQGLSPVTKSFNR GEC	SEQ ID NO: 2086 QVQLVESGGGVVQPRSLRLSCAASGFTSSYGM HWVRQAPGKGLEWVAWIYDASNKYADA VKG RFTISSDNKNTLYLQMNLSRAEDTAVYYCARDR TIFGVLDYWQGGLVTVSSASTKGPSVFP LAPSS KSTSGGTAAALGCLVKDYFPEPTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKEPKSCDKTHTCTCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE

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					<div>VFKNWYVVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDSDGSFELYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK</div>
					<div>SEQ ID NO: 516 CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCAACCTTCAGTAGCTATGGC ATGCACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGCAAGACGCCGTGAAGGGC CGATTACCAATCTCCAGGGGACAATTCCAAGAAC ACGCTGATCTGCAAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTGGAGTGGTCTTGACTACTGG GGCAGGGAACCTGGTCAACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA CCCTCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGCTGCCGTGGTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCTGTGGAACCTCAGGGCC CTGACCAAGCGGTGCACACCTTCCCGGCTGTC CTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCACCC GTGCCAGCACCTGAACCTCTGGGGGACCCGTC AGTCTCTCTTCCCCCAAAACCCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCAATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTACGCGT CCTCACCGTCCCTGCACCAGGACTGGCTGAATGG</div>
					<div>SEQ ID NO: 359 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCAATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTAA ATTGGTATCAGCAGAAACCAAGGAAAGCCCTA AGCTCTGATCTACGATGCATCCCAATTTGGAAA CAGGGTCCCATCAAGGTTCAAGTGGAAGTGGAT CTGGGACAGATTTTAGTTTCACCATCAGCAGCCT GCAGCCTGAAGATAATTGCAACATAATTACTGTCA ACAGTATGATATTCTCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGAACGGTGGCTG CACCATCTGTCTTCACTCTCCCGCCATCTGATGA GCAGTTGAAATCTGGAACCTGCTCTGTTGTGTC CTGCTGAATAACTTCTATCCAGAGAGGCCAAA GTACAGTGAAGGTGGATAACGCCCTCCAATCG GGTAACTCCAGGAGAGTGTACAGAGCAGGAC AGCAAGGACAGCACCTACAGCCTCAGCAGCACC CTGACGCTGAGCAAAAGCAGACTACGAGAAACA CAAAAGTCTACGCTGCGAAGTCAACCCATCAGGG CCTGAGCTCGCCCGTCAACAAAGAGCTTCAACAG GGGAGAGTGT</div>
				NA	
		2F11.008			

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			<p>CAAGGAGTACAAAGTGCAAGGTCTCTCCAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACAGGTACGCTGACCTGCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGAGAACAACTACAAG ACCAGCCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCCTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
			<p>SEQ ID NO: 1930</p> <p>DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGGTD FSFTISLQPEDIATYYCQQYDILLTFGGGKVEIKR TVAAPSVFIPIPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSITYLSST LTLTKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC</p>
		AA	<p>SEQ ID NO: 2087</p> <p>QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM HWVRQAPGKGLEWVAWIYDASNKYAYADA VKG RFTISRDNSKNTLYLQMNSLRAEDTAVYVCARDR TIFGVLDYWQGGLVTVSSASTKGPSVFPLAPSS KSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCTPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEK TISKA KGQPREPQVYITLPPSRREEMTKNQVSLTCL VKGFYP SDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK</p>
			<p>SEQ ID NO: 517</p> <p>CAGGTGCAACTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCAACCTTCAGTAGCTATGGC ATGCACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAATACTATATGCAGACTCCCGTGAAGGC CGATTACCACTCTCCAGGGGACAATTCCAAGAAC ACGCTGATCTCTGCAAAATGAACAGCCTGAGAGCC</p>
		NA	<p>SEQ ID NO: 360</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCACTCTGTAGGAGACAGAGTCACCAATCATT GCCAGGCGAGTCAGGACATTAGCAACTATTAA ATTGGTATCAGCAGAAACCAAGGAAAGCCCTA AGCTCCTGATCTACGATGCATCCCAATTTGGAAA CAGGGGTCCCATCAAGGTTTCAGTGGAAGTGGAT CTGGGACAGATTTTAGTCTCACCATCAGCAGCC TGCAGCCTGAAGATTTTGCAACATATTACTGTCA</p>
	2F11.009	IPS:359949	

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	<p>ACAGTATGATATTCTCCTCACCTTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGAACGGTGGCTG CACCATCTGTCTTCATCTTCCCGCCATCTGATGA GCAGTTGAAATCTGGAACTGCCTCTGTGTGTGC CTGCTGAATAACTTCTATCCAGAGAGGCCAAA GTACAGTGGAAAGGTGGATAACGCCCTCCAAATCG GGTAACCTCCAGGAGAGTGTACAGAGCAGGAC AGCAAGGACAGCACCTACAGCCTCAGCAGCACCC CTGACGCTGAGCAAAAGCAGACTACGAGAAACA CAAAGTCTACGCTGCGAAGTCAACCCATCAGGG CCTGAGCTCGCCCGTCACAAAGAGCTTCAACAG GGGAGAGTGT</p>	SEQ ID NO: 1931	
AA	<p>DIQMTQSPSSLSASVGDRTVTITCQASQDISNYLNW YQOKPGKAPKLLIYDASNLETGVPSRFSGSGGTD</p>	SEQ ID NO: 2088	<p>GAGGACACGGCTGTGTATTACTGTGCGGAGAGAT AGGACGATTTTGGAGTGGTCTTGACTACTGG GGCCAGGGAACCTGGTCAACCGTCTCCTCAGCC TCCACCAAGGCCCATCGGTCTTCCCCCTGGCA CCCTCTCCAAAGAGCACCTCTGGGGGCACAGCG GCCCTGGCTGCCTGGTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCTGTGGAACCTCAGGGGCC CTGACCAAGCGGTGCACACCTTCCCGGCTGTC CTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGGCTTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACC GTGCCAGCACCTGAACCTCTGGGGGACCGTCT AGTCTTCTCTTCCCCCAAAACCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAGACCCCTGA GGTCAAGTTCAAACTGGTACGTGGACGGCGTGA GGTGCAATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAAGTGCAAGGTCTCCACAAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCGAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCATCCCGGAGGAGATGACCA AGAACAGGTCAACCTGACCTGCCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGACAACATACAAG ACCACGCCCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCTCCGGTAAA</p>

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			FSLTISSLQPEDFATYYCQQYDILLTFGGGKVEIK RTVAAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSYSLSS TLTLKADYEEKHKVYACEVTHQGLSSPVTKSFNR GEC	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLDYWGQGLTVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHCTCPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKA KGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEVESNGQPENNYKTTTPPVLDSDGSEFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
			SEQ ID NO: 361	SEQ ID NO: 518
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCACTCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTAA ATTGGTATCAGCAGAAACCAAGGAAAGCCCCA AGCTCTGATCTACGATGCATCCAAATTTGGAAA CAGGGTCCCATCAAGGTTCAAGTGGAAGTGGAT CTGGGACAGATTTTAGTCTCACCATCAGCAGCC TGACGCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATATTCTCCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGAACGGTGGCTG CACCATCTGCTTCACTCTCCCGCCATCTGATGA GCAGTTGAAATCTGGAACCTGCTCTGTGTGTGC CTGCTGAATAACTTCTATCCAGAGAGGCCAAA GTACAGTGGAGGTGGATAACGCCCTCCCAATCG GGTAACCTCCAGGAGAGTGTCACAGAGCAGGAC AGCAAGGACAGCACCTACAGCCTCAGCAGCAC CTGACGCTGAGCAAAAGCAGACTACGAGAAACA CAAAAGTCTACGCTGCGAAGTCAACCATCAGGG CCTGAGCTCGCCCGTCACAAAGAGCTTCAACAG GGGAGAGTGT	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCAACCTTCAGTAGCTATGGC ATGCACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGGA AGTAATAATACTATGCAGACGCCGTGAAGGGC CGATTACCATCTCCAGGGACAATTCCAAGAAC ACGCTGATCTGCAAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTGGAGTGGTCTTGACTACTGG GGCCAGGGAACCTGGTCAACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCTCTGGGGGACACAGG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCTGTGGAACCTCAGGGCC CTGACCAAGCGGTGCACACCTTCCCCGGCTGTC CTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTTGACCGTGGCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCACCC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCCCCAAACCCCAAGGACAC
IPS:359956	2F11.010	NA		

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				SEQ ID NO: 362	SEQ ID NO: 519
IPS:359865	6H1.002	NA		<p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACCAAGGAAAGCCCTA AGCCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGTCCCTTCAAGGTTCAAGCGGCAGTGGAT CTGGGACAGAAATTCACCTCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAGTGGATATCAACGAACGGTGGCT GCACCATCTGTCTTCACTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACTGCCCTCTGTTGTGT GCCTGCTGAAATACTTCTATATCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCGAAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCAACAAGAGCTTCAACA GGGGAGAGTGT</p>	<p>CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGTCCCTGAGACTCTCCTGT GCAAGCTCTGGATTCAACCTTCAAGTTACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCAACCATCTCCAGAGACAATTCCAAGAACAA CGTGTATCTGCAAAATGAACAAGCCTGAGAGCCG AGGACAGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTGGAGTGTCTTTGGGGGACTACT GGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGCTGCCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGC CCTGACCAAGCGGCGTGCAACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGGCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCACC GTGCCAGCACCTGAACCTCTGGGGGACCGTCTC AGTCTTCTCTTCCCCCAAAACCCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGCGGTGGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAAACAAGC CCTCCAGCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAAGCCCCGAGAACCCAGGTGT ACACCTGCCCCATCCCGGAGGAGATGACCA AGAACGAGTCAAGCTGACCTGCCTGGTCAAAG GCTTCTATCCAGCGGACATCGCCGTGGAGTGGG</p>

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				<p>AGAGCAATGGGAGCCGGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCCTGGACAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTAAA</p> <p>SEQ ID NO: 1933</p> <p>DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR TVAAPSVFIIPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSITYLSST LTLTKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC</p>		<p>AGAGCAATGGGAGCCGGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCCTGGACAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTAAA</p> <p>SEQ ID NO: 2090</p> <p>QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIWYDASNKYAYADA VKG RFTISRDNSKNTLYLQMNSLRAEDTAVYVCARDG TIFGVLGDIYWGQGTLLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKS LSLSPGK</p>
		AA		<p>SEQ ID NO: 363</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCACTCTATAGGAGACAGAGTCACCATCCTT GCCGGGCAAGTCAGGACATTAGAGATTATTAG GCTGTATCAGCAGAAACCAAGGGAAGCCCTA AGCGCTGATCTATGGTGATCCAGTTTGCAAA GTGGGTCCCTTCAAGGTTCAAGGCGCAGTGGAT CTGGACAGAAATTCATCTCACAAATCAGCAGCC TGACGCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATAACAACGAACGGTGGCT GCACCATCTGTCTTCACTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACCTGCCTCTGTGTGT GCCTGCTGAATAACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAAT</p>	6H1.003	IPS:359869
		NA		<p>SEQ ID NO: 520</p> <p>CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTCACTTACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAAA GTAATAAACTATGACAGACGCCGTGAAGGGCC GCTTCAACCATCTCCAGAGACAATTCACAAGAAC CGCTGATCTGCAAAATGAACAGCCTGAGAGCCG AGACACGGCTGTGTATTACTGTGCGCGAGATA GGACGATTTTGGAGTGTCTTGGGGGACTACT GGGGCAGGGAACCTTGGTCAACCTCTCCTCAG CCTCCACCAAGGGGCCATCGGTCTTCCCTCCG ACCTCCTCCAAAGAGCACCTCTTGGGGGCACAGC GGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCC</p>		

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	<p>CGGGTAACTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCGAAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT</p>	<p>CGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGC CCTGACCAGCGCGTGCACACCTTCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACCTCACACATGCCCCACC GTGCCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAAACCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCAATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCCTGTGTCTCAGCGT CCTCACCGTCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAAGTGCAAGGTCTCCACACAAGC CCTCCAGCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCATCCCGGAGGAGATGACCA AGAACAGGTGAGCTGACCTGCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGGAGACAACATACAAG ACCAGCTTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
	<p>SEQ ID NO: 1934</p> <p>DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR TVAAPSVFIIPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSITYLSST LTLKADYEEKHKVYACEVTHQGLSSPVTKSFNRG EC</p>	<p>SEQ ID NO: 2091</p> <p>QVQLVESGGGVVQGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIYDASNKYADAVKVG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED</p>

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						PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK			
					SEQ ID NO: 364	SEQ ID NO: 521			
					GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAAGGGAAGCCCCTA AGCTCTGATCTATGGTGCAATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTCAAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCTCACAAATCAGCAGCC TGACGCCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAGTGGGATATCAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACCTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCCAGAGAGGCCA AAGTACAGTGGAAAGGTGGATAACGCCCTCCAAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAAGTCACCCATCAGG GCCTGAGCTCGCCCCGTCAAAAGAGCTTCAACA GGGGAGAGTGT	NA	6H1.004	IPS:359873	CAGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAAGCTCTGGATTCACTTCACTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCAACCATCTCCAGAGACAATTCCAAAGAACA CGTGTATCTGCAAAATGAACAAGCCTGAGAGCCG AGGACACGGCTGTATTACTGTGCGCGAGATG GGACGATTTTGGAGTGTCTTGGGGGACTACT GGGGCAGGGAACCTGGTCAACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCTCTCCAAGAGCACCTCTGGGGGCACAGC GGCCTGGGTGCTGTGTCAAGGACTACTTCCCC CGAACCGGTGACGGTGTCTGTGGAACTCAGGCGC CCTGACCAAGCGGTGTGCACACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCACAC GTGCCAGCACCTGAACCTCTCTGGGGGACCGTCT AGCTTTCCTCTTCCCCCAAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGCGCTGGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAAGGACTGGCTGAATGG

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			<p>CAAGGAGTACAAAGTGCAAGGTCTCCACAAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACAGGTGAGCCTGACCTGCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGAGAACAACTACAAG ACCAGCCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCCTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTAAA</p> <p>SEQ ID NO: 2092</p>
			<p>QVQLVESGGGVVQGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIYDASNKYAYADA VKG RFTISRDNSKNTLYQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGLTVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPGK</p> <p>SEQ ID NO: 522</p>
			<p>DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT LTISLQPEDFATYYCLQHNNYPFTFGQGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSITYSLSS TLTLTKADYEKHKVYACEVTHQGLSSLSPVTKSFNR GEC</p> <p>SEQ ID NO: 1935</p>
		AA	<p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCCTT GCCGGGCAAGTCAGGACATTAGAGATTATTAG GCTGTATCAGCAGAAACCAAGGAAAGCCCTTA AGCTCCTGATCTATGGTGATCCAGTTTGCAAA GTGGGTCCCTTCAAGGTTTCAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT</p> <p>SEQ ID NO: 365</p>
!PS:359877	6H1.005	NA	<p>CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCA GCGTCTGGATTCAACCTTCACTTCTTGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAAA GTAATAAACTACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAAGAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG</p> <p>SEQ ID NO: 522</p>

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	<p>ACAGCATAAATAATTACCCCTTCACTTTTCGGCCAA GGGACCAAAGTGGATATCAACGAACGGTGGCT GCACCATCTGTCTTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACCTGCCCTCTGTTGT GCCTGCTGAATAACTTCTATCCCCAGAGAGGCCA AAGTACAGTGGAAAGGTGGATAACGCCCTCCAA CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCCGAAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT</p>	<p>AGGACACGGCTGTGTATTACTGTGCGCGAGATA GGACGATTTTGGAGTGTCTTGGGGGACTACT GGGGCAGGGAACCCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGCTGCTTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGTGGAATCAGGCGC CCTGACCAAGCGGCTGCACACCTTCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGGCTTCCAGCAGCTTGGGCACC CAGACCTACATCTGCACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACAC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAAACCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAGACCCCTGA GGTCAAGTTCAACTGTACGTGGACGGCGTGA GGTGCATAATGCCAAGACAAGCCGTGTAGGA GCAGTACGGCAGCAGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCACAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCGAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCATCCCGGAGGAGATGACCA AGAACAGGTGACCGTGAACCTGCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGAGCGCGGAGACAACATACAAG ACACGCTTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
AA	<p>DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QOKPGKAPKLLIYGASSLSQSGVPSRFSGSGSGTEFT</p>	<p>SEQ ID NO: 1936</p>
		<p>SEQ ID NO: 2093</p>
		<p>QVQLVESGGGVVQPGRSRLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIWYDASNKYYADA VKG</p>

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			<p>LTISLQPEDFATYYCLQHNHNNYPFTFGQGTKVDIK RTVAAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKSDSTYSLSS TLTLKADYKHKVYACEVTHQGLSSPVTKSFNR GEC</p>	<p>RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGT AALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKD TLMISRTPETCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTKISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK</p>
			<p>SEQ ID NO: 366</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACCAAGGAAAGCCCTA AGCTCTGATCTATGGTGCAATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTCAAGGCGCAGTGGAT CTGGGACAGAAATCACTCTCACAAATCAGCAGCC TGACGCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAACGAAACGGTGGCT GCACCATCTGTCTTCACTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACCTGCCTCTGTTGTGT GCCTGCTGAAATACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAAGTGGATACGCCCTCCCAAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCAAAAGAGCTTCAACA GGGGAGAGTGT</p>	<p>SEQ ID NO: 523</p> <p>CAGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGTCCCTGAGACTCTCCTGT GCAAGCTCTGGATTCACTTCACTTACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGGA GTAATAATACTATGCAGACTCCGTGAAGGGCC GCTTCACTATCCAGAGACAATTCACAAAGACA CGTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTGGAGTGTCTTGGGGGACTACT GGGGCCAGGGAACCTGGTCAACCTCTCCTCAG CCTCCACCAAGGGCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCTGGCTGCCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTGTTGGAACCTCAGGCGC CCTGACCAAGCGGTGTGCAACCTTCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCTCAGCAGC GTGTGACCGTGGCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCACCC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAAACCCAAAGGACAC</p>
IPS:361067	6H1.006	NA	<p>SEQ ID NO: 366</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACCAAGGAAAGCCCTA AGCTCTGATCTATGGTGCAATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTCAAGGCGCAGTGGAT CTGGGACAGAAATCACTCTCACAAATCAGCAGCC TGACGCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAACGAAACGGTGGCT GCACCATCTGTCTTCACTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACCTGCCTCTGTTGTGT GCCTGCTGAAATACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAAGTGGATACGCCCTCCCAAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCAAAAGAGCTTCAACA GGGGAGAGTGT</p>	<p>SEQ ID NO: 523</p> <p>CAGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGTCCCTGAGACTCTCCTGT GCAAGCTCTGGATTCACTTCACTTACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGGA GTAATAATACTATGCAGACTCCGTGAAGGGCC GCTTCACTATCCAGAGACAATTCACAAAGACA CGTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTGGAGTGTCTTGGGGGACTACT GGGGCCAGGGAACCTGGTCAACCTCTCCTCAG CCTCCACCAAGGGCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCTGGCTGCCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTGTTGGAACCTCAGGCGC CCTGACCAAGCGGTGTGCAACCTTCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCTCAGCAGC GTGTGACCGTGGCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCACCC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAAACCCAAAGGACAC</p>

		<p>SEQ ID NO: 1937</p> <p>DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVVQWKVDNALQSGNSQESVTEQDSKDSITYLSST LTLISKADYEEKHKVYACEVTHQGLSSPVTKSFNRG EC</p>	<p>SEQ ID NO: 2094</p> <p>QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAIVWYDGSNKYYADSVKGG RFTISRDN SKNTLYLQMNLSRAEDTAVYYCAR DGTIFGVLLGDYWGQGLTVTVSSASTKGPSVFPLA PS SKTSSGGTAAALGCLVKDYFPEPTVSWNSGALT S GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICN VNHKPSNTKVDKKEPKSCDKTHITCPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTIVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSGFFLY SKLTVDKSRWQQGNVVFSCSVMHREALHNHYTQKS LSLSPGK</p>
	AA		

IPs:361071	401,007	NA
SEQ ID NO: 367	<p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGAAAGCCCCTA AGCTCCTGATCTATGGTGATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTCAAGCGCAGTGGAT CTGGGACAGAAATTCAC'TCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCAC'TTTCGGCCCT GGGACCAAAGTGGATATCAAACGAAACGGTGGCT GCACCATCTGTCTTCAATCTTCCC GCCATCTGATG AGCAGTTGAAATCTGGAAC'TGCTCTGTTGTGT GCCTGCTGAATACTTCTATCCAGAGAGGCCA AAGTACAGTGAAGGTGGATAACGCCCTCCAAT CGGGTAAC'TCCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCAACCATCAGG GCCTGAGCTCGCCCGTCAAAAGAGCTTCAACA GGGGAGAGTGT</p>	<p>SEQ ID NO: 524</p> <p>CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGAGGTCCTTGAGACTCTCCTGT GCAGGCTCTGGATTACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAAGACTCCGTGAAGGGCC GCTTCAACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGGCGAGATG GGACGATTTTGGAGTGCCTTTGGGGGACTACT GGGGCCAGGAACCTGGTCAACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCTCTCCAAAGACACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC CGAAACGGTGACGGTGTCTGTGGAAC'TCAGGCG CCTGACACGCGGTGCACACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGAC'TACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAACTTTGTGACAAAAC'TCACACATGCCACCC GTGCCCAGCACCTGAAACTCCTGGGGGACCGTC AGTCTTCTCTTCCCCCCAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAAGTTCAA'CTGGTACGTGGACGGCGTGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTCAAGCGT CCTCACCGTCTGCACCAAGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC CCTCCAGCCCCATCGAGAAAACCATCTCCAA AGCCAAAGGCGAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCCGGGAGGAGATGACCA AGAAACAGGTACGCTGACCTGCCTGGTCAAAAG GCTTCTATCCCAAGCAGACATGCCCGTGGAGTG</p>

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				<p>AGAGCAATGGGAGCCGGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTAAA</p> <p>SEQ ID NO: 1938</p>			<p>AGAGCAATGGGAGCCGGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTAAA</p> <p>SEQ ID NO: 2095</p>
			AA	<p>DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT LTISLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR TVAAPSVFIPTPSDEQLKSGTASVVCLLNFPREA KVQWKVDNALQSGNSQESVTEQDSKDSYSTLSST LTLKADYEEKHKVYACEVTHQGLSSPVTKSFNRG EC</p>			<p>QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIWYDASNKYIYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGLTVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGGSFFLY SKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPGK</p> <p>SEQ ID NO: 525</p>
IPS:361075	6H1.008	NA		<p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCACTCTATAGGAGACAGAGTCACCATCATT GCCGGGCAAGTCAGGACATTAGAGATTATTAG GCTGTATCAGCAGAAACCAAGGAAAGCCCTA AGCTCTGATCTATGGTGATCCAGTTTGCAAA GTGGGTCCCTTCAAGGTTCAAGGCGAGTGGAT CTGGACAGAAATTCATCTCACAAATCAGCAGCC TGACGCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTCGGCCCT GGGACCAAAGTGGATAACAACGAACGGTGGCT GCACCATCTGTCTTCACTTCGCCCATCTGATG AGCAGTTGAATCTGGAACCTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAAT</p> <p>SEQ ID NO: 368</p>			<p>CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTCACTTACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGGA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCAACCATCTCCAGAGACAATCCAAAGAACA CGCTGATCTGCAAAATGAACAGCCTGAGAGCCG AGACACGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTGGAGTGTCTTTGGGGGACTACT GGGGCAGGGAACCTTGGTCACTCCCTCTCCTCAG CCTCCACCAAAGGGCCCATCGGTCTTCCCTCCG ACCTCTCTCCAAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCC</p> <p>SEQ ID NO: 525</p>

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	<p>CGGGTAACTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCCGAAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT</p>	<p>CGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGC CCTGACCAGCGGCGTGACACACCTTCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACCTCACACATGCCACAC GTGCCCAGCACCTGAACCTCTGGGGGACCCGTC AGTCTTCTCTTCCCCCAAAACCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCAATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAAGACTGGCTGAATGG CAAGGAGTACAAAGTGCAAGGTCTCCACACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCATCCCGGAGGAGATGACCA AGAACAGGTGACCTGACCTGCTGCTGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGAGCCGGAGACAACATACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
	<p>SEQ ID NO: 1939</p> <p>DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR TVAAPSVFIAPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSITYLSST LTLKADYEEKHKVYACEVTHQGLSSPVTKSFNRG EC</p>	<p>SEQ ID NO: 2096</p> <p>QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIYDGSNKYYADA VKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED</p>
	<p>AA</p>	

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				<p>SEQ ID NO: 369</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCACTCTGTGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTAA ATTGGTATCAGCAGAAACCAAGGAAAGCCCCA AACTCTGATCTACGATGCTTCCAATTGGAGCC AGGGTCCCATCAAGGTTCAAGTGGAAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAGTGGATATCAACGAACGGTGGCTGCA CCATCTGCTTCTCATCTTCCCGCCATCTGATGAGC AGTTGAAATCTGGAACTGCCTCTGTTGTGTCCT GCTGAATAACTTCTATCCAGAGAGGCCAAAGT ACAGTGGAAAGGTGGATAACGCCCTCCAAATCGGG TAAC'TCCAGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGCAGCACCT GACGCTGAGCAAGCAGACTACGAGAAACACA AAGTCTACGCTGCGAAGTCAACCCATCAGGGCC TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGG GAGAGTGT</p>
				<p>SEQ ID NO: 526</p> <p>CAGTGCAGCTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCTCCTTCACTAGCTATGGCA TGCACTGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGTGGCAGCTATATGGTATGATGCAA ATAATAAATACTATGCAGAGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTATTACTGTGCGAGAGATC GGACGATTTTGGAGTGGTCTTGGAGTACTGGG GCCAGGAAACCTGTGTACCGCTCTCCTCAGCCT CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC CCTCCTCCAAGAGCACTCTGGGGGACAGCGG CCCTGGGTGCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCTGTGGAACCTCAGGCGCC TGACCAGCGGCTGCACACCTTCCCCGCTGTCC TACAGTCTCAGGACTCTACTCCTCAGCAGCCT GGTGACCGTGCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAGCCCCA CAACCAAGGTGGACAAAGAAAGTTGAGCCCCA AATCTGTGACAAAACTCACACATGCCACCCGT GCCCAGCACTGAACTCCTGGGGGACCGTCAG TCTTCTCTTCCCCCAAAACCAAGGACACCT CATGATCTCCCGGACCCCTGAGGTACATGCGT GGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCTGGAGGT GCATAATGCCAAGACAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTACGCTCC TCACCGTCTGCAACCAAGGACTGGCTGAATGGCA</p>

IPS:361079

6A5.004.001

NA

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			<p>AGGAGTACAAGTGCAAGGTCTCCAAACAAAGCCC TCCAGCCCCCATCGAGAAACCATCTCCAAAG CCAAAGGCAGCCCCGAGAACACACAGGTGTAC ACCTGCCCCCATCCCGGAGGAGATGACCAAG AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC TTCTATCCAGCGACATCGCCGTGGAGTGGGAG AGCAATGGCAGCCGAGAACAACTACAAGAC CACGCCTCCGTGCTGACTCCGACGGCTCCTTC TTCCTATAGCAAGCTCACCGTGGACAAGAGC AGTGCGACGAGGGGAACGTCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACAG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
			<p>SEQ ID NO: 1940</p> <p>DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGGTD FTLTISLQPEDFATYYCQYDDLFTFGPGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLS TLTLKADYEKHKVYACEVTHQGLSPVTKSFNR GEC</p>
		AA	<p>SEQ ID NO: 2097</p> <p>QVQLVESGGGVVQPGRSRLRSLSCAASGFSFSYGM HWVRQPPGKGLWVAAIWYDANNKYVADAVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLEYWGQGLTVTVSSASTKGPSVFPLAPSS KSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCTPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKA KQPREPQVYVTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK</p>
			<p>SEQ ID NO: 527</p> <p>CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGCTATATGGTATGATGCAAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTTCCAAAGAAC CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG</p>
		NA	<p>SEQ ID NO: 370</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCACTCTGTGGGGACAGAGTCACCAATCATT GCCAGGCGAGTCAGGACATTACCAACTATTAA ATTGGTATCAGCAGAAACCAAGGAAAGCCCTA AACTCCTGATCTACGATGCTTCCAAATTGGAGCC AGGGTCCCATCAAGGTTTCAGTGGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATATTGCAACATATTACTGTCA</p>
	IPS:361085	6A5,004,002	

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	AA	ACAGTATGATGATCTATTACATTTCGGCCCTGGG ACCAAGTGGATATCAACGAACGGTGGCTGCA CCATCTGTCTTTCATCTCCCGCCATCTGATGAGC AGTTGAAATCTGGAACTGCCTCTGTTGTGTCCT GCTGAATAACTTCTATCCAGAGAGGCCAAAGT ACAGTGGAAAGGTGGATAACGCCCTCCAAATCGGG TAAC'TCCAGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGCAGCACCT GACGCTGAGCAAGCAGACTACGAGAAACACA AAGTCTACGCTGCGAAGTCAACCCATCAGGGCC TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGG GAGAGTGT	AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTGGAGTGGTCTTGAGTACTGGG GCCAGGAACCTTGGTCAACCGTCTCCTCAGCCT CCACCAAGGGCCATCGGTCTTCCCCCTGGCAC CCTCTCCAAGAGCACCTCTGGGGGACACAGGG CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG AACCGTGAACGGTGTCTGTGGAAC'TCAGGCGCC TGACCAGCGGCTGCACACCTTCCCCGGCTGTCC TACAGTCTCAGGACTCTACTCCTCAGCAGCGT GGTGACCGTGCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAGCCAG CAACACCAAGTGGACAAAGAAAGTTGAGCCCA AATCTTGTGACAAAACTCACACATGCCACCGT GCCAGCACCTGAAC'TCCTGGGGGACCGTCAG TCTTCTCTTCCCCCAAACCCAAAGGACACCT CATGATCTCCGGACCCCTGAGGTACATGCGT GGTGGTGGACGTGAGCCACGAAGACCC'TGAGGT CAAGTTCAACTGTACGTGGACGGCTGGAGGT GCATAATGCCAAGACAAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTACGCGTCC TCACCGTCTGCACCAAGGACTGGGTGAATGGCA AGGAGTACAAGTGCAAGTCTCCAACAAAGCCC TCCCAGCCCCCATCGAGAAACCATCTCCAAG CCAAAGGCGAGCCCCGAGAACCCACAGGTGTAC ACCTGCCCCCATCCCGGGAGGAGATGACCAAG AACCAGGTCAGCCTGACCTGCC'TGGTCAAAGGC TTCTATCCAGCGACATCGCCGTGGAGTGGGAG AGCAATGGGCAGCCGGAACAAC'TACAAGAC CACGCCCTCCGTGTCTGGACTCCGACGGCTCCTC TTCCTCTATAGCAAGTCAACCGTGGACAAAGC AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACAG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
		SEQ ID NO: 1941	SEQ ID NO: 2098
	AA	DIQMTQSPSSLSASVGDRTVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGGTD	QVQLVESGGGVVQPGRSRLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAIWYDANNKYVADAVKG

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			FTLTISSLQPEDIAITYCQQYDDLFTFGPGTKVDIK RTVAAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSLSS TLTLKADYKHKVYACEVTHQGLSSPVTKSFNR GEC	SEQ ID NO: 371	RFTISRDSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGQGLTVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHCTCPPELPG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
				SEQ ID NO: 528	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCTTCAGTAGCTATGGCA TGCACTGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGTGGCAGCTATATGGTATGATGCAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTACCATCTCCAGAGACAGTTCCAAAGAAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTGGAGTGGTCCCTTGAGTACCTCG GCCAGGGAACCTGGTCAACCCTCTCCCTCCAGCCT CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC CCTCTCCAAAGACACCTCTGGGGGACAGCGG CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCTGGAACCTCAGGCGCCC TGACACGCGGTGCACACCTTCCCGGCTGTCC TACAGTCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCAACCA GACCTACATCTGCAACGTGAATCACAAGCCCCAG CAACACCAAGGTGGACAAAGAAAGTTGAGCCCCA AATCTGTGACAAAACTCACACATGCCACCCGT GCCCAGCACCTGAACCTCTGGGGGACCCGTACG TCTTCCCTCTTCCCCCCCAAAACCCAAAGGACACCT
IPS:361091	6A5.004.003	NA			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCACTCTGTGGGGACAGAGTCACCACTACTT GCCAGGCGAGTCAGGACATTACCAACTATTAA ATTGGTATCAGCAGAAACCAAGGAAAGCCCCA AACTCTGATCTACGATGCTTCCAAATTGGAGCC AGGGTCCCATCAAGGTTCAAGTGGAAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCACACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAGTGGATATCAACGAACGGTGGCTGCA CCATCTGTCTTCACTTCCCGCCATCTGATGAGC AGTTGAAATCTGGAACTGCCTCTGTTGTGTGCT GCTGAATAACTTCTATCCAGAGAGGCCAAAGT ACAGTGGAAAGTGGATAACGCCCTCCAAATCGGG TAAC'TCCAGGAGAGTGTACAGCAGGACAGAG CAAGGACAGCACCTACAGCCTCAGCAGCACCT GACGCTGAGCAAGAGCAGACTACGAGAAACACA AAGTCTACGCTGCGAAGTCAACCCATCAGGGCC TGAGCTCGCCCCGTACAAAGAGCTTCAACAGGG GAGAGTGT

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				<p>CATGATCTCCCGGACCCCTGAGGTACATGCGT GGTGGTGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGAGGTT GCATAATGCCAAGACAAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTACGCGTCC TCACCGTCTGCACCAAGGACTGGCTGAATGGCA AGGAGTACAAGTGCAAGGTCTCCAAACAAAGCCC TCCCAGCCCCCATCGAGAAACCATCTCCAAAG CCAAAGGCAGCCCCCGAGAACACACAGGTGTAC ACCTGCCCCCATCCCGGAGGAGATGACCAAG AACCAGGTCAGCCTGACCTGCCTGGTCAAGGC TTCTATCCAGCGACATCGCCGTGGAGTGGGAG AGCAATGGGCAGCCGAGAACAACTACAAGAC CACGCCTCCGTGTGACTCCGACGGCTCCTTC TTCCTCTATAGCAAGCTCACCGTGGACAAAGC AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACAG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
				<p>SEQ ID NO: 1942</p> <p>DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGGTD FTLTISLQPEDFATYYCQQYDDLFTFGPGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLS TLTLSKADYEKHKVYACEVTHQGLSPVTKSFNR GEC</p>
		AA		<p>SEQ ID NO: 2099</p> <p>QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLVVAAIWYDANNKYYADAVKG RFTISRDSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYLGQGTLVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCDKTHTCPCPAPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVVFSCSVMHEALHNHYTQKSLSL SPGK</p>

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IP:361095	6A5.004.004	NA	SEQ ID NO: 372	SEQ ID NO: 529
			<p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAACCCAGGGAAGCCCCA AACTCTGATCTACGATGCTTCCAAATTTGGAGCC AGGGTCCCATCAAGGTTCAAGTGGAAAGTGGATC TGGGACAGATTTTACTTTCAACCATCAGCAGCCTG CAGCCTGAAGATTTTGCACACATAATTACTGTCAA CAGTATGATGATCTATTCACITTCGGCCCTGGGA CCAAAGTGGATATCAACGAAACGGTGGCTGCAC CATCTGCTTTCATCTTCCCGCCATCTGATGAGCA GTTGAAATCTGGAACCTGCCTCTGTTGTGTGCTG CTGAATAACTTCTATCCCAGAGAGGCCAAAGTA CAGTGGAAAGTGGATAACGCCCTCCAATCGGGT AACTCCAGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGCAGCACCTT GACGCTGAGCAAGCAGACTACGAGAAACACA AAGTCTACGCTGCGAAGTCAACCCATCAGGGCC TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGG GAGAGTGT</p>	<p>CAGGTGACGTGGTGGAGTCTGGGGGAGGCGGTG GTCCAGCCTGGGAGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCTTTCAGTAGCTATGGCA TGCACCTGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGTGGCAGCTATATGGTATGATGCAA ATAATAATACTATGCAGAGCCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAAGAAACA CGTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACAGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTGGAGTGGTCTTGGAGTACTGGG GCCAGGAAACCTGGTCAACCGTCTCCTCAGCCT CCACAAAGGGCCATCGGTCTTCCCCCTGGCAC CCTCTCCAAGAGCACTCTGGGGGACAGCGG CCCTGGGTGCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCTGTGGAACCTCAGCGCCC TGACACGGCGTGCACACCTTCCCGGCTGTCC TACAGTCTCAGGACTCTACTCCTCAGCAGCGT GGTGACCGTGGCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAGCCCCAG CAACCAAGGTGGACAAAGAAAGTTGAGCCCCA AATCTGTGACAAAACTCACACATGCCACCGT GCCCAGCACCTGAACCTCCTGGGGGACCGTCAG TCTTCTCTTCCCCCACAACCCAAAGGACACCT CATGATCTCCCGGACCCCTGAGGTACATGCGT GGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGT GCATAATGCCAAGACAAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTACGCGTCC TCACCGTCTGCAACGAGGACTGGGTGAATGGCA AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC TCCCAGCCCCATCGAGAAACCATCTCCAAAG CCAAAGGCGACGCCCGAGAACCCACAGGTGTAC ACCTGCCCCCATCCCCGGGAGGAGATGACCAAG AACCAGGTACGCTGACCTGCCTGGTCAAGGC TTCTATCCCAAGCGACATCGCCGTGGAGTGGGAG</p>

A-2124-WO-PCT

				<p>AGCAATGGGCAGCCGGAGAACAACTACAGAC CACGCCTCCCTGCTGGACTCCGACGGCTCCTTC TTCCTCTATAGCAAGCTCACCCTGGACAAAGAGC AGTGGCAGCAGGGGAACGTCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACACG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA</p> <p>SEQ ID NO: 2100</p>
				<p>QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLVVAAIWYDANNKYYADA VKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWQQGLVTVSSASTKGPSVFPLAPSS KSTSGGTAAALGCLVKDYFPEPTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKEPKSCDKTHCTCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDSGDSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK</p> <p>SEQ ID NO: 530</p>
				<p>DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGGTD FTFTISLQPEDFATYYCQQYDDLFTFGPGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSITYSLSS TLTLTKADYEEKHKVYACEVTHQGLSSPVTKSFNR GEC</p> <p>SEQ ID NO: 1943</p>
		AA		<p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGACAGATCACCATCCTT GCCAGGCGAGTCAGGACATTACCAACTATTAA ATTGGTATCAGCAGAAACCAAGGAAAGCCCCA AACTCTGATCTACGATGCTTCCAAATTGGAGCC AGGGTCCCATCAAGGTTCAAGTGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATAATTGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAGTGGATATCAACGAACGGTGGCTGCA CCATCTGTCTTCATCTTCCCGCCATCTGATGAGC</p> <p>SEQ ID NO: 373</p>
IP:361101	6A5,004,005	NA		<p>CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGTCCGCCAGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGCTATATGGTATGATGCAA ATAATAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCACAGAAACA CGCTGATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGATTACTGTGCGAGAGATC GGACGATTTTGGAGTGGTCTTGTGAGTACCTCG GCCAGGGAACCTGGTCAACCGTCTCCTCAGCCT</p>

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	AGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCT GCTGAATAACTTCTATCCACAGAGAGGCCAAAGT ACAGTGGAAGGTGGATAACGCCCTCCAATCGGG TAAC'TCCACGAGAGGTGTCACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGCAGCACCT GACGCTGAGCAAAGCAGACTACGAGAAACACA AAGTCTACGCTGCGAAGTCACCCATCAGGGCC TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGG GAGAGTGT	CCACCAAGGGCCCCATCGGTCTTCCCCCTGGCAC CCTCTCCAAGAGCACCTCTGGGGCACAGCGG CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCTGTGGAAC'TCAGGCGCCC TGACCAGCGGCTGCACACCTTCCCCGGCTGTCC TACAGTCTCAGGACTCTACTCTCCCTCAGCAGCGT GGTGACCGTGGCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAGCCACG CAACACCAAGGTGGACAAAGAAAGTTGAGCCCCA AATCTTGTGACAAAACTCACACATGCCACCGT GCCCAGCACCTGAATCTCTGGGGGACCGTCAAG TCTTCTCTTCCCCCACAACCCAAAGGACACCT CATGATCTCCCGGACCCCTGAGGTACATGCGT GGTGGTGACGTGAGCCACGAAGACCC'TGAGGT CAAGTTCAACTGGTACGTGGACGGCTGGAGGT GCATAATGCCAAGACAAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTACGCTCC TCACCGTCTGCACCAAGGACTGGCTGAATGGCA AGGAGTACAAGTGCAAGTCTCCAACAAAGCCC TCCCAGCCCCCATCGAGAAACCATCTCCAAG CCAAAGGCAGCCCCCGAGAACACAGGTGTAC ACCTGCCCCCATCCCGGAGGAGATGACCAAG AACAGGTCAGCCTGACCTGCC'TGGTCAAAGGC TTCTATCCACGACATCGCCGTGGAGTGGGAG AGCAATGGGCAGCCGGAACAACACTACAAGAC CACGCCTCCGTGCTGGACTCCGACGGCTCCTTC TTCCTCTATAGCAAGCTCACCGTGGACAAAGC AGTGGCAGCAGGGGAACGTCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACAG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1944 DIQMTQSPSSLSASVGDRTVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGGTD FTLTISLQPEDIATYYCQQYDDLFTFGPGTKVDIK RTVAAPSVFIPPSDEQLKSGTASVCLLNFFPRE AKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLS	SEQ ID NO: 2101 QVQLVESGGGVVQGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAIIWYDANNKYYADA VKG RFTISRDSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYLGQGTLT VTVSSASTKGPSVFPLAPSSK STSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGV
AA		

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			TLTLISKADYEHKHYACEVTHQGLSSPVTKSFNR GEC		HTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCDKTHTCPPCPAPPELLGGP SVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVFSQSVMHREALHNHYTQKSLSL SPGK
					SEQ ID NO: 531
					SEQ ID NO: 374
					SEQ ID NO: 361105
					SEQ ID NO: 645.004.006
					NA

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				GCATAATGCCAAGACAAAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTACGCGTCC TCACCGTCTGCACACGAGACTGGCTGAATGGCA AGGAGTACAAGTGCAAGGTCTCCACAAAGCCC TCCCAGCCCCCATCGAGAAAACCATCTCCAAAG CCAAAGGCAGCCCCGAGAACACACAGGTGTAC ACCTGCCCCCATCCCGGAGGAGATGACCAAG AACAGGTCAGCCTGACCTGCCTGGTCAAAGGC TTCTATCCAGCGACATCGCCGTGGAGTGGGAG AGCAATGGCAGCCGAGAACAACTACAAGAC CACGCTCCCGTGTGACTCCGACGGCTCCTTC TTCCTCTATAGCAAGCTCACCGTGGACAAGAGC AGTGCGCAGCAGGGGAACGTCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACAG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
				SEQ ID NO: 1945 DIQMTQSPSSLSASVGDRVTITCQASQDITNLYNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGGTD FTFTISLQPEDFATYYCQQYDDLFTFGPGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLS TLTLTKADYEKHKVYACEVTHQGLSPVTKSFNR GEC
			AA	SEQ ID NO: 2102 QVQLVESGGGVVQGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLWVAAIWYDANNKYYADA VKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYLGQGTLVTVSSASTKGPSVFPLAPSSK STSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVN HKPSNTKVDKVKVEPKSCDKTHTCPPCPAPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYITLPPSRREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVVFSCSVMHEALHNHYTQKSLSL SPGK
				SEQ ID NO: 375 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCAATCTGTGGGGACAGAGTCACCAATCATT GCCAGGCGAGTCAGGACATTACCAACTATTAA ATTGGTATCAGCAGAAACCAAGGGAAGCCCTA AACTCCTGATCTACGATGCTTCCAAATTGGAGCC
		9 IPS:36110	6A5,004.00 7	NA

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		AGGGGTCCCATCAAGGTTTCAGTGGAAAGTGGATC TGGGACAGATTTTACTTTTCAACCATCAGCAGCCTG CAGCCTGAAGATATTGCAACATATTACTGTCAA CAGTATGATGATCTATTCACTTTCCGCCCTGGGA CCAAAGTGGATATCAACGAAACGGTGGCTGCAC CATCTGCTTTCATCTTCCCGCCATCTGATGAGCA GTTGAAATCTGGAACCTGCTCTGTTGTGCTG CTGAATAACTTCTATCCAGAGAGGCCAAAGTA CAGTGGAAAGTGGATAACGCCCTCCAATCGGGT AACTCCAGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGCAGCACCT GACGCTGAGCAAGCAGACTACGAGAAACACA AAGTCTACGCTGCGAAGTCAACCCATCAGGGCC TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGG GAGAGTGT	ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAAGAAC CGCTGATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGATTACTGTGCGAGAGATC GGACGATTTTGGAGTGGTCTTGGAGTACTGGG GCCAGGAACCTTGGTCAACGCTCTCTCAGCCT CCACCAAGGGCCATCGGTCTTCCCCCTGGCAC CCTCTCCAAGAGCACCTCTGGGGGACACAGCG CCTGGGCTGCCGTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCTGTGGAACCTCAGCGCCC TGACCAGCGGCTGCACACCTTCCCCGGCTGTCC TACAGTCTCAGGACTCTACTCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAGCCCCAG CAACACCAAGGTGGACAAAGAAAGTTGAGCCCCA AATCTTGTGACAAAACTCACACATGCCACCGT GCCCAGCACCTGAACCTCCTGGGGGACCGTCAG TCTTCTCTTCCCCCACAACCCAAAGGACACCT CATGATCTCCGGACCCCTGAGGTACATGCGT GGTGGTGGACGTGAGCCACGAAGACCCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCTGGAGGT GCATAATGCCAAGACAAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTACGCGTCC TCACCGTCTGCACCAAGGACTGGGTGAATGGCA AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC TCCCAGCCCCCATCGAGAAACCATCTCCAAAG CCAAGGCGAGCCCCGAGAACCCACAGGTGTAC ACCTGCCCCCATCCCGGGAGGAGATGACCAAG AACAGGTCAGCCTGACCTGCCCTGGTCAAAGGC TTCTATCCAGCGACATCGCCGTGGAGTGGGAG AGCAATGGGCAGCCGGAACAACACTACAAGAC CAGCCTCCCTGTGTGACTCCGACGGCTCCTTC TTCCTCTATAGCAAGCTCACCGTGGACAAAGC AGTGGCAGCAGGGGAACGTCTTCTCATGTCTC GTGATGCATGAGGCTCTGCACAACCACTACAG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
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		SEQ ID NO: 1946	SEQ ID NO: 2103
	AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGGTD FTFTISLQPEDIAITYCQQYDDLFTFGPGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSITYSLSS TLTLKADYEKHKVYACEVTHQGLSSLSPVTKSFNR GEC	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLVVAIWDANNKYADA VKG RFTISRDSKNTLYLQMNLSRAEDTAVYYCARDR TIFGVVLEYWGQGLVTVSSASTKGPSVFP LAPSS KSTSGGTAAALGCLVKDYFPEPTVSWNSGALTSG VHTFPAVLQSSGLYSLSVVTPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCTPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEK TISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPVLDSDGSEFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
		SEQ ID NO: 376	SEQ ID NO: 533
IPS:361113	6A5.004.008	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGACAGAGTCACCAATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTAA ATTGGTATCAGAGAAACCAAGGAAAGCCCCA AACTCTGATCTACGATGCTTCCAAATTTGGAGCC AGGGTCCCATCAAGGTTCAAGTGGAAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAGTGGATATCAACGAACGGTGGCTGCA CCATCTGTCTTCACTTCCCGCCATCTGATGAGC AGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCT GCTGAATAACTTCTATCCAGAGAGGCCAAAAGT ACAGTGGAAAGGTGGATAACGCCCTCCAAATCGGG TAACCTCCAGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGCAGCACCT GACGCTGAGCAAAAGCAGACTACGAGAAACACA AAGTCTACGCTGCGAAGTCAACCCATCAGGGCC TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGG GAGAGTGT	CAGTGCAGCTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCTCTTCAGTAGCTATGGCA TGCACTGGTCCGCCAGCCTCCAGGCAAGGGC TGGAGTGGTGGCAGCTATATGGTATGATGGAA ATAATAAATACTATGCAGAGCCTGGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAAGAAC CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTGGAGTGGTCCCTTGAAGTCTGGG GCCAGGGAACCTTGTCAACCTCTCCCTCCAGCCT CCACCAAGGGCCCATCGGTCTTCCCTCCGAC CCTCCTCCAAAGACACCTCTGGGGGACAGCGG CCCTGGGCTGCCTGGTCAAGGACTACTTCCCGG AACCGGTGACGGTGTCTGTGGAACCTCAGCGGCC TGACACGCGGTGCACACCTTCCCGGCTGTCC TACAGTCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAGCCCA CAACACCAAGGTGGACAAAGAAAGTTGAGCCCA
	NA		

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			<p>AAATCTTGTGACAAACTCACACATGCCCACCGT GCCCAGCACCTGAACCTCCTGGGGGACCGTCAG TCTTCTCTTCCCCCAAACCCAAAGGACACCT CATGATCTCCGGACCCCTGAGGTACATGCGT GGTGGTGGACGTGAGCCACGAAGACCCGTAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGT GCATAATGCCAAGACAAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTACGCGTCC TCACCGTCTGCACCAAGGACTGGCTGAATGGCA AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC TCCCAGCCCCCATCGAGAAACCATCTCCAAG CCAAGGGCAGCCCCGAGAACACAGGTGTAC ACCTGCCCCCATCCGGGAGGAGATGACCAAG AACAGGTACGCTGACCTGCCTGGTCAAAGGC TTCTATCCAGCGACATCGCCGTGGAGTGGGAG AGCAATGGGCAAGCGGAGAACAACTACAAGAC CACGCTCCCGTGTGACTCCGACGGCTCCTTC TTCCTCTATAGCAAGCTCACCGTGGACAGAGC AGTGCGCAGCAGGGGAACGTCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACAG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
		SEQ ID NO: 1947	SEQ ID NO: 2104
	AA	<p>DIQMTQSPSSLSASVGDRVTITCQASQDITNLYNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGGTD FTLTISSLQPEDFATYYCQQYDDLFTFGPGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNFPYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLS TLTLTKADYEKHKVYACEVTHQGLSPVTKSFNR GEC</p>	<p>QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDGNKKYYADA VKG RFTISRDSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAAALGCLVKDYFPEPTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK</p>

			SEQ ID NO: 377	<p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGACAGAGTCACCATCACTT GCCAGCGAGTCAGGACATTACCAACTATTAA ATTGGTATCAGCAGAAACCAGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAAATTGGAGCC AGGGTCCCATCAAGGTTTCAGTGGAAGTGGATC TGGGACAGATTTTACTCTCAACCATCAGCAGCCT GCAGCCTGAAGATTTTGC AACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAAGTGGATATCA AACGAACGGTGGCTGCA CCATCTGCTTCATCTTCCCGCCATCTGATGAGC AGTTGAAATCTGGAAC'TGCCCTCTGTTGTGTGCT GCTGAATAACTTCTATCCAGAGAGGCCAAAGT ACAGTGGAAGTGGATAACGCCCTCCAATCGGG TAACTCCCAGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGCAGCACCCCT GACGCTGAGCA AAGCAGACTACGAGAAACACA AAGTCTACGCC'TGCCGAAGTACCCATCAGGGCC TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGG GAGAGTGT</p>	SEQ ID NO: 534	<p>CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGAGGTCCTTGAGACTCTCCTGT GCAGGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGATGATGCAAA ATAATAAATACTATGCAAGACTCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCTCAAGAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGGGAGAGATC GGACGATTTTGGAGTGGTCTTGTGAGTACTGGG GCCAGGAAACCTGTGTACACCGTCTCCTCAGCCT CCACCAAGGGCCCATCGGTCTTCCCTCGGCAC CCTCTCC AAGAGCACCTCTGGGGGCACAGCGG CCCTGGGTGCC'TGGTCAAGGACTACTTCCCG AACC'GGTGACGGTGTGTGTGGAACTCAGGCGCC TGACCAGCGCGTGCACACCTTCCCGGTGTCC TACAGTCTCAGGACTCTACTCCTCAGCAGCAGT GGTGACCGTGGCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCAACAAGCCAG CAACAACCAAGTGGACAAGAAAGTTGAGCCCA AATCTTGTGACA AAAC'TCACACATGCCCAACGT GCCAGCACCTGAAC'TCCTGGGGGACCGTCAG TCTTCTCTTCCCCCAAAACCAAGGACACCCCT CATGATCTCCCGACCCCTGAGGTACATGCGT GGTGTGGACGTGAGCCACGAAGACCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGT GCATAATGCCAAGACA AAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTGACGCTCC TCACCGTCTGCACCAAGGACTGGCTGAATGGCA AGGAGTACAAGTGCAAGGTCTCCAACAAGGCC TCCAGCCCCCATCGAGAAAACCATCTCCAAG CCAAAGGGCAGCCCCGAGAACACAGGTGTAC ACCCTGCCCCCATCCCGGGAGGAGATGACCAAG AACCAGGTACGCTGACCTGCCTGGTCAAAGGC TTCTATCCCAGCGACATCGCCGTGGAGTGGGAG</p>
6A5,004,009	NA		SEQ ID NO: 377	<p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGACAGAGTCACCATCACTT GCCAGCGAGTCAGGACATTACCAACTATTAA ATTGGTATCAGCAGAAACCAGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAAATTGGAGCC AGGGTCCCATCAAGGTTTCAGTGGAAGTGGATC TGGGACAGATTTTACTCTCAACCATCAGCAGCCT GCAGCCTGAAGATTTTGC AACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAAGTGGATATCA AACGAACGGTGGCTGCA CCATCTGCTTCATCTTCCCGCCATCTGATGAGC AGTTGAAATCTGGAAC'TGCCCTCTGTTGTGTGCT GCTGAATAACTTCTATCCAGAGAGGCCAAAGT ACAGTGGAAGTGGATAACGCCCTCCAATCGGG TAACTCCCAGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGCAGCACCCCT GACGCTGAGCA AAGCAGACTACGAGAAACACA AAGTCTACGCC'TGCCGAAGTACCCATCAGGGCC TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGG GAGAGTGT</p>	SEQ ID NO: 534	<p>CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGAGGTCCTTGAGACTCTCCTGT GCAGGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGATGATGCAAA ATAATAAATACTATGCAAGACTCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCTCAAGAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGGGAGAGATC GGACGATTTTGGAGTGGTCTTGTGAGTACTGGG GCCAGGAAACCTGTGTACACCGTCTCCTCAGCCT CCACCAAGGGCCCATCGGTCTTCCCTCGGCAC CCTCTCC AAGAGCACCTCTGGGGGCACAGCGG CCCTGGGTGCC'TGGTCAAGGACTACTTCCCG AACC'GGTGACGGTGTGTGTGGAACTCAGGCGCC TGACCAGCGCGTGCACACCTTCCCGGTGTCC TACAGTCTCAGGACTCTACTCCTCAGCAGCAGT GGTGACCGTGGCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCAACAAGCCAG CAACAACCAAGTGGACAAGAAAGTTGAGCCCA AATCTTGTGACA AAAC'TCACACATGCCCAACGT GCCAGCACCTGAAC'TCCTGGGGGACCGTCAG TCTTCTCTTCCCCCAAAACCAAGGACACCCCT CATGATCTCCCGACCCCTGAGGTACATGCGT GGTGTGGACGTGAGCCACGAAGACCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGT GCATAATGCCAAGACA AAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTGACGCTCC TCACCGTCTGCACCAAGGACTGGCTGAATGGCA AGGAGTACAAGTGCAAGGTCTCCAACAAGGCC TCCAGCCCCCATCGAGAAAACCATCTCCAAG CCAAAGGGCAGCCCCGAGAACACAGGTGTAC ACCCTGCCCCCATCCCGGGAGGAGATGACCAAG AACCAGGTACGCTGACCTGCCTGGTCAAAGGC TTCTATCCCAGCGACATCGCCGTGGAGTGGGAG</p>

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				<p>AGCAATGGGCAGCCGAGAACAACTACAGAC CACGCCTCCCTGCTGGACTCCGACGGCTCCTTC TTCCTCTATAGCAAGCTCACCCTGGACAAAGC AGTGGCAGCAGGGGAACGTCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACAG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA</p> <p>SEQ ID NO: 2105</p> <p>QVQLVESGGGVVQPGRLSLRSCAASGFSFSSYGM HWVRQPPGKGLVVAIWIYDANNKYVADSVKVG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWQQGTLVTSSASTKGPSVFP LAPSS KSTSGGTAAALGCLVKDYFPEPTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKEPKSCDKTHCTCPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEK TISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEVESNGQPENNYKTTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK</p>
				<p>DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGGTD FTLTISLQPEDFATYYCQYDDLFTFGPGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSITYSLSS TLTL SKADYEEKHKVYACEVTHQGLSSPVTKSFNR GEC</p> <p>SEQ ID NO: 1948</p>
	AA			<p>SEQ ID NO: 378</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCA TCTGTGGGGACAGAGTCACCAATCATT GCCAGGCGAGTCAGGACATTACCAACTATTAA ATTGGTATCAGCAGAAACCAAGGAAAGCCCTA AACTCCTGATCTACGATGCTTCCAAATTTGGAGCC AGGGTCCCATCAAGGTTTCAGTGGAAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATGATCTATTACCTTTCGGCCAAAG GACCAAAAGTGGATATCAAAAGAACGGTGGCTGC ACCATCTGTCTTCAATCTTCCCGCCATCTGATGAG CAGTTGAAAATCTGGAACTGCCTCTGTTGTGTGCC TGCTGAATAAATTCTATCCAGAGAGGCCAAAG TACAGTGGAAAGTGGATAACGCCCTCCCAATCGG</p>
IPS:359896	6A5.004.010	NA		<p>SEQ ID NO: 535</p> <p>CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGC ACTGGGTCCGCCAGCTTCCAGCAAGGGGC TGGAGTGGTGGCAGCTATATGGTATGATGCAAA ATAATAAATACTATGCAGAGCCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTTCCAAAGAAC CGCTGATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTGGAGTGGTCTTGGTACTGGG GCCAGGGAACCTGGTCAACCGTCTCCTCAGCCT CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC CCTCCTCCAAGAGCACCTCTGGGGGCACAGCGG CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG</p>

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	<p>GTAATCCAGGAGAGTGTCACAGAGCAGGACA GCAAGGACAGCACCTACAGCCTCAGCAGCACCC TGACGCTGAGCAAAAGCAGACTACGAGAAACAC AAAGTCTACGCCCTGCGAAGTCACCCATCAGGGC CTGAGCTCGCCCGTCACAAAGAGCTTCAACAGG GGAGAGTGT</p>	<p>AACCGGTGACGGTGTCTGGAACCTCAGGCGCCC TGACCAGCGGCTGCACACCTTCCCAGGCTGTCC TACAGTCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAGCCAG CAACACCAAGTGGACAAAGAAAGTTGAGCCCA AATCTGTGACAAAACTCACACATGCCACCGT GCCCAGCACCTGAACCTCCTGGGGGACCGTCAG TCTTCTCTTCCCCCAAACCCAAAGGACACCT CATGATCTCCGGACCCCTGAGGTACATGCGT GGTGTGACGTGAGCCACGAAGACCTGAGGT CAAGTTCAACTGTACGTGGACGGCTGGAGGT GCATAATGCCAAGACAAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTACGCTCC TCACCGTCTGCCACGAGGACTGGCTGAATGGCA AGGAGTACAAGTGCAAGTCTCCACAAAGCCC TCCCAGCCCCATCGAGAAACCATCTCCAAAG CCAAAGGCAGCCCCGAGAACACAGGTGTAC ACCTGCCCTCATCCGGGAGGAGATGACCAAG AACCAGGTACGCTGACCTGCCTGGTCAAAGGC TTCTATCCAGCGACATCGCCGTGGAGTGGGAG AGCAATGGGCAGCCGAGAACACTACAAGAC CACGCTCCCTGTCTGGACTCCGACGGCTCCTC TTCCTCTATAGCAAGCTCACCGTGGACAGAGC AGTGGCAGCAGGGGACGCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACAG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
	<p>SEQ ID NO: 1949</p> <p>DIQMTQSPSSLSASVGDRVTITCQASQDITNLYNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGGTD FTLTISLQPEDFATYYCQQYDDLFTFGQGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEK</p>	<p>SEQ ID NO: 2106</p> <p>QVQLVESGGGVVQPGSRSLRSLSCAASGFSFSSYGM HWVRQPPGKGLEWVAIIWYDANNKYVADAVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWQQGTLVTVSSASTKGPSVFPPLAPSS KSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCTPCPAPELLG GPSVFLFPPKPKDITLMISRTPETVTCVVVDVSHEDPE</p>

AA

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					VKFNWYV DGV EVHNAKTKPCEEQY GSTYRCVSV LTVLHQDWL NGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDSGDSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
					SEQ ID NO: 536 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGTGGCAGCTATATGGTATGATGCAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAAGAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTGGAGTGGTCTTGAAGTACCTCG GCCAGGGAACCCGTGTCAACCGTCTCCTCAGCCT CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC CCTCCTCCAAGACACCTCTGGGGGACACAGCGG CCCTGGGTGCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCTGTGGAACCTCAGGCGCC TGACCAGCGCGTGCACACCTTCCCCGGTGTCC TACAGTCTCAGGACTCTACTCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAGGCCAG CAACACCAAGGTGGACAAAGAAAGTTGAGCCCA AATCTTGTGACAAAACTCACACATGCCACCGT GCCCAGCACTGAACCTCCTGGGGGACCGTCAG TCTTCTCTTCCCCCAAAACCCAAGGACACCCCT CATGATCTCCCGGACCCCTGAGGTACATGCGT GGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGT GCATAATGCCAAGACAAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTCA GCGTCC TCACCGTCTGCACCAAGGACTGGCTGAATGGCA

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			<p>AGGAGTACAAGTGCAAGGTCTCCACAAAGCCC TCCAGCCCCCATCGAGAAACCATCTCCAAAG CCAAAGGCAGCCCCGAGAACACACAGGTGTAC ACCTGCCCCCATCCCGGAGGAGATGACCAAG AACCAGGTCAGCCTGACCTGCCTGGTCAAGGC TTCTATCCAGCGACATCGCCGTGGAGTGGGAG AGCAATGGCAGCCGAGAACAACTACAAGAC CACGCCTCCGTGCTGACTCCGACGGCTCCTTC TTCCTCTATAGCAAGCTCACCGTGGACAAGAGC AGTGCGCAGCAGGGGAACGTCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACAG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
			<p>SEQ ID NO: 1950</p> <p>DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGGTD FTLTISLQPEDFATYYCQQYDDLFTFGQGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEN</p>
		AA	<p>SEQ ID NO: 2107</p> <p>QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLWVAAIWYDANNKYADA VKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYLGQGTLVTVSSASTKGPSVFPLAPSSK STSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVN HKPSNTKVDKKEPKSCDKHTHTCPCPAPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVVFSCSVMHAEALHNHYTQKSLSL SPGK</p>
IPS:359567	2A11.002	NA	<p>SEQ ID NO: 380</p> <p>GAAATTGTGTTGACGCAAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCT GCAGGGCCAGTCAGATTTTACACAGCACCTACT TAGCCTGGTACACAGCAGAAACCTGGCCAGGCTC CCAGGCTCCTCATCTATGTGTCATCCAGCAGGG CCACTGGCATCCAGACAGGTTTCAGTGGCAGTG GGTCTGGGACAGACTTCACTCTCAACCATCAGCA GATTGGAGCCTGAAGATTTTGCAAGTGTAATTACT</p>
			<p>SEQ ID NO: 537</p> <p>CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCAAGTTTCAGTAGCTATGGC ATGCACTGGTCCGCCAGGCTCCAGGCAAGGGA CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAATACTATGAAGACGCCGTGAAGGGC CGATTACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTTTCTGCAAGTGAACAGCCTGAGAGCC</p>

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	AA	<p>GTCAGCAGTATGGTAGCTCACCTCGCTTCGGCC AAGGACACGACTGGAGATTAAACGAACGGTG GCTGCACCATCTGTCTTCATCTTCCCGCCATCTG ATGAGCAGTTGAAATCTGGAACCTGCCTCTGTTG TGTGCTGTGCTGAATACTTCTATCCAGAGAGG CCAAAGTACAGTGAAGGTGGATAACGCCCTCC AATCGGGTAACCTCCAGGAGAGTGTCACAGAGC AGGACAGCAAGGACAGCACCTACAGCCTCAGC AGCACCTGACGCTGAGCAAGCAGACTACGAG AAACACAAAGTCTACGCTGCGAAGTCAACCCAT CAGGGCCTGAGCTCGCCCGTCAACAAAGAGCTTC AACAGGGGAGAGTGT</p>	<p>GAGGACACGGCTGTGTATTACTGTGCGAGAGGG ATTACGATTTTGGTCATGGGTTTGAATATTGGG GCCAGGAACCTGGTCAACCGTCTCCTCAGCCT CCACCAAGGGCCATCGGTCTTCCCCCTGGCAC CCTCTCCAAGACACCTCTGCGGGCACAGCGG CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCTGTGGAACCTCAGCGCCC TGACCAGCGGCTGCACACCTTCCCCGGCTGTCC TACAGTCTCAGGACTCTACTCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAGCCCCAG CAACACCAAGGTGGACAAAGAAAGTTGAGCCCCA AATCTGTGACAAAACTCACACATGCCACCGT GCCAGCACCTGAACCTCCTGGGGGACCGTCAG TCTTCTCTTCCCCCAAACCCAAAGGACACCT CATGATCTCCGGACCCCTGAGGTACATGCGT GGTGGTGACGTGAGCCACGAAGACCCCTGAGGT CAAGTTCAACTGTAAGTGGACGGCGTGGAGGT GCATAATGCCAAGACAAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTACGCTCC TCACCGTCTGCACCAAGGACTGGGTGAATGGCA AGGAGTACAAGTGCAAGTCTCCAACAAAGCCC TCCCAGCCCCCATCGAGAAACCATCTCCAAG CCAAGGGCAGCCCCGAGAACCCACAGGTGTAC ACCTGCCCCCATCCCGGGAGGAGATGACCAAG AACAGGTCAGCCTGACCTGCCCTGGTCAAGGC TTCTATCCAGCGACATCGCCGTGGAGTGGGAG AGCAATGGGCAGCCGGAACAACACTACAAGAC CACGCTCCCGTGTGTGACTCCGACGGCTCCTTC TTCCTCTATAGCAAGCTCACCGTGGACAAAGC AGTGGCAGCAGGGGAACGTCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACAG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
		<p>SEQ ID NO: 1951</p> <p>EIVLTQSPGTLSPGERATLSCRASQIFTSTYLAW YQOKPGQAPRLLIYGASSRATGIPDRFSGSGGTDF</p>	<p>SEQ ID NO: 2108</p> <p>QVQLVESGGGVQPGRSLRLSCAASGFSFSSYGM HWVRQAPGKGLEWVAWIYDASNKYYEDAVKGG</p>

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		TLTISRLEPEDFAVYQCQYGSSPRFGQGRLEIKR TVAAPSVFIPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKSDSTYSLSST LTLKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC	SEQ ID NO: 381	RFTISRDN SKNTLFLQVNSLRAEDTAVYVCARGITI FGHGFYWGQGTLVTVSSASTKGPSVFPLAPSSKS TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVPSSSLGTQYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP GK
IPS:335965	2A11.003	NA	SEQ ID NO: 538	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCAAGTTTCAGTAGCTATGGC ATGCACTGGTCCGCCAGGCTCCAGGCAAGGGA CTGGAGTGGTGGCAGTTATATGGTATGATGGA AGTAATAATACTATGAAGACTCCGTGAAGGGC CGATTACCACTCCAGAGACAATTCCAAGAAC ACGCTGTTCTGCAAGTGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTAAGTGTGCGAGAGGG ATTACGATTTTGGTCAATGGGTTTGAATATTGGG GCCAGGGAACCTGGTCAACCGTCTCCCTCAGCCT CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC CCTCCTCCAAGAGCACTCTGGGGGACAGCGG CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCTGGAACCTCAGGCGCCC TGACCAGCGGCTGCACACCTTCCCGGCTGTCC TACAGTCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCAACCA GACCTACATCTGCAACGTGAATCACAAGCCCCAG CAACCAAGGTGGACAAGAAAGTTGAGCCCCA AATCTGTGACAAACTCAGACATGCCACCGCT GCCCCAGCACTGAATCTCTGGGGGACCGCTCAG TCTTCCCTCTTCCCCCAAAACCAAGGACACCT

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				<p>CATGATCTCCCGGACCCCTGAGGTACATGCGT GGTGGTGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGAGGTT GCATAATGCCAAGACAAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTACGCGTCC TCACCGTCTGCACCAAGGACTGGGTGAATGGCA AGGAGTACAAGTGCAAGGTCTCCAAACAAAGCCC TCCCAGCCCCCATCGAGAAACCATCTCCAAAG CCAAAGGCAGCCCCCGAGAACACAGGTGTAC ACCTGCCCCCATCCCGGAGGAGATGACCAAG AACCAGGTCAGCCTGACCTGCCTGGTCAAGGC TTCTATCCCAAGCACATCGCCGTGGAGTGGGAG AGCAATGGGCAAGCGGAGAACAACTACAAGAC CACGCCTCCGTGTGACTCCGACGGCTCCTTC TTCCTCTATAGCAAGCTCACCGTGGACAAAGC AGTGCGCAGCAGGGGAACGTCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACAG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
				<p>SEQ ID NO: 1952</p> <p>EIVLTQSPGTLSPGERATLSCRAEQIFTSTYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGTDF TLTISRLEPEDFAVYYCQQYGSSPRFGQGRLEIKR TVAAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSYSTLSST LTLKADYEEKHKVYACEVTHQGLSSPVTKSFNRG EC</p>
		AA		<p>SEQ ID NO: 2109</p> <p>QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQAPGKGLEWVAWIYDGSNKYYEDSVKG RFTISRDNSKNTFLQVNSLRAEDTAVYYCARGITI FGHGFYWGQGTLVTVSSASTKGPSVFPLAPSSKS TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKG QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEVESNGQPENNYKTTTPVLDSDGSGFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKLSLSP GK</p>

	SEQ ID NO: 382	SEQ ID NO: 539
PS:361158	<p>2A11.004</p> <p>NA</p>	<p>361158</p>

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				<p>AGCAATGGGCAGCCGGAGAACAACTACAAGAC CACGCCTCCCTGCTGGACTCCGACGGCTCCTTC TTCCTCTATAGCAAGCTCACCCTGGACAAAGC AGTGGCAGCAGGGGAACGTCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACAG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA</p> <p>SEQ ID NO: 2110</p>
				<p>QVQLVESGGGVVQPGSRSLRSLSCAASGFSFSSYGM HWVRQAPGKGLEWVAWIYDGSNKYYEDA VKG RFTISRDNKNTLFLQVNSLRAEDTA VYYCARGITI FGHGFYWGQGTLVTVSSASTKGPSVFPLAPSSKS TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKG QPREPVYTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKLSLSP GK</p> <p>SEQ ID NO: 540</p>
				<p>EIVLTQSPGTLSLSPGERATLSCRASQIFTSTYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDF TLTISRLEPEDFAVYYCQQYGSSPRFGQGTREIKR TVAAPSVFIIPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSITYLSST LTLISKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC</p> <p>AA</p> <p>SEQ ID NO: 1953</p>
				<p>GAAATTGTGTTGACGCAAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCT GCAGGGCCAGTCAGATTTTACAGCACCTACT TAGCCTGGTACCAAGCAAGAACCTGGCCAGGCTC CCAGGCTCCTCATCTATGTGTCATCCAGCAGGG CCACTGGCATCCAGACAGGTTCAAGTGCAGTG GGTCTGGGACAGACTTCACTCTCAACCATCAGCA GATTGGAGCCTGAAAGATTTTGCAGTGATTAAT GTCAGCAGTATGGTAGCTCACCTCGCTTCGGCC AAGGGACACGACTGGAGATTAAACGAACGGTG GCTGCACCATCTGTCTTCACTTCCCGCCATCTG ATGAGCAGTTGAAATCTGGAACTGCCCTCTGTG TGTGCTGTGTAATACTTCTATCCCAAGAGAGG CCAAAGTACAGTGAAGGTGGATAACGCCCTCC</p> <p>NA</p> <p>SEQ ID NO: 383</p>
IPS:361165	2A11.005			<p>CAGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCAAGTTTCAGTAGCTATGGC ATGCACTGGTCCGCCAGGCTCCAGGCAAGGGA CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGAAGACTCCGTGAAGGGC CGATTACCACTCTCCAGAGACAATTCCAAGAAC ACGCTGTTCTGCAAGTGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGGG ATTACGATTTTGGTTCATGGGTTTGAATATTGGG GCCAGGGAACCTGGTCAACCGTCTCCTCAGCCT CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC CCTCCTCCAAGAGCACCTCTGGGGGCAACAGCGG CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG</p>

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	<p>AATCGGGTA ACTCCAGGAGAGTGTCACAGAGC AGGACAGCAAGGACAGCACCTACAGCCTCAGC AGCACCCCTGACGCTGAGCAAAAGCAGACTACGAG AAACACAAAGTCTACGCCTGCGAAGTCAACCCAT CAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTC AACAGGGGAGAGTGT</p>	<p>AACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCC TGACCAGCGGGGTGCACACCTTCCCAGGCTGTCC TACAGTCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAAGCCAG CAACACCAAGGTGGACAAAGAAAGTTGAGCCCA AATCTGTGACAAAACTCACACATGCCACCGT GCCCAGCACCTGAATCCTGGGGGACCGTCAG TCTTCTCTTCCCCCAAACCCAAAGGACACCT CATGATCTCCGGACCCCTGAGGTACATGCGT GGTGTGACGTGAGCCACGAAGACCCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCTGGAGGT GCATAATGCCAAGACAAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTACGCTCC TCACCGTCTGCACCAAGGACTGGCTGAATGGCA AGGAGTACAAGTGCAAGTCTCCACAAAGCCC TCCCAGCCCCCATCGAGAAACCATCTCCAAAG CCAAAGGCAGCCCCCGAGAACACAGGTGTAC ACCTGCCCCCATCCGGGAGGAGATGACCAAG AACCAGGTCAGCTGACCTGCCTGGTCAAAGGC TTCTATCCCAAGCAGATCGCCGTGGAGTGGGAG AGCAATGGGCAAGCCGAGAACACTACAAGAC CACGCCTCCGTGTGTGACTCCGACGGCTCCTTC TTCCTCTATAGCAAGCTCACCGTGGACAAAGC AGTGGCAGCAGGGGAACGTCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACAG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
	<p>SEQ ID NO: 1954</p> <p>EIVLTQSPGTLSPGERATLSCRAQIFTSTYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGTDF TLTISRLEPEDFAVYYCQQYGSSPRFGQGRLEIKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSYSTYLSST LTLKADAYEKHKVYACEVTHQGLSSPVTKSFNRG EC</p>	<p>SEQ ID NO: 2111</p> <p>QVQLVESGGGVVQPGRLSLRSLSCAASGFSFSSYGM HWVRQAPGKGLEWVAWIYDASNKYVEDSVKGG RFTISRDNSKNTFLQVNSLRAEDTAVYYCARGITI FGHGFYWGQGTLTVTSSASTKGPSVFPLAPSSKS TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK</p>

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					FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLT VLHQDWLNKEYKCKVSNKALPAPIEKTISKAKG QPREQVYTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSP GK
				SEQ ID NO: 384	SEQ ID NO: 541
			2G10_LC1.003	NA	CAGTGCAGCTGGTGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCAACCTTCAAGTAACTATGGC ATGCACTGGTCCGCCAGGCTCCAGGCGAGGGG CTGGAGTGGTGCGCAGCTATATGGTTTGTATGCA AGTGATAAATACTATGCAAGACGCCGTGAAGGGC CGATTACCAATCTCCAGAGACAACTCCAAGAAC ACGCTGTATCTGCAAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGGAGAGAT CAGCGGATTTTGGAGTGGTCCCGGACTACTGTG GGCCAGGGAACCTGGTCAACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA CCCTCTCCAAGACACCTCTGGGGGCACAGCG GCCCTGGCTGCCCTGGTCAAGGACTACTTCCCC GAACCGGTACGGTGTCTGTGGAACCTCAGGCGCC CTGACCAAGCGGTGCACACCTTCCCCGGCTGTC CTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTACAAAACCTCACACATGCCACCC GTGCCAGCACCTGAACCTCTGGGGGACCCGTC AGTCTTCTCTTCCCCCCAAACCCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCAATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAGGACTGGCTGAATGG

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			<p>SEQ ID NO: 1955</p> <p>EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLIYGAAATRAATGIPARFSGSGSGTE FTLTISLSQSEDFAVYYCQQYNNWPLTFGGGKVE IKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKDSITYSL SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEK</p>	<p>SEQ ID NO: 1955</p> <p>CAAGGAGTACAAAGTGCAAGGTCTCCAAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACAGGTACGCTGACCTGCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGGAGAACAACTACAAG ACCAGCCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
		AA	<p>SEQ ID NO: 2112</p> <p>QVQLVESGGGVVQPGRSRLRSCAASGFTFSNYGM HWVRQAPGEGLEWVAIIWFDASDKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVDPDYWQGGLVTVSSASTKGPSVFPLAPSS KSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCTPPCAPPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKA KGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK</p>	<p>SEQ ID NO: 2112</p> <p>QVQLVESGGGVVQPGRSRLRSCAASGFTFSNYGM HWVRQAPGEGLEWVAIIWFDASDKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVDPDYWQGGLVTVSSASTKGPSVFPLAPSS KSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCTPPCAPPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKA KGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK</p>
IPS:361178	2G10_LC1.004	NA	<p>SEQ ID NO: 385</p> <p>GAAATAGTGATGACGCAGTCTCCAGCCACCCCTG TCTGTGTCTCCAGGGGAAGAGCCACCCCTCTCC TGACGGGCCAGTCAGAGTGTAGCAGCAACTTA GCCTGTACCAAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACCAAGGGCC ACTGGTATCCAGCCAGGTTCACTCAGGAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGCA GTCTGAAGATTTTGCAGTTTATTACTGTC</p>	<p>SEQ ID NO: 542</p> <p>CAGGTGCACTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACTTTCAGTAACATATGGC ATGCACTGGTCCGCCAGGCTCCAGGCGAGGGG CTGGAGTGGTGGCAGCTATATGGTTTGTATGCA AGTGATAAATACTATGACAGACTCCCGTGAAGGC CGATTACCATCTCCAGAGACAACTCCAAGAAC ACGCTGATCTGCAAAATGAACAGCCTGAGAGCC</p>

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	AGCAGTATAATAACTGGCCTCTCACTTTCGGCG GAGGGACCAAGGTGGAGATCAAACGAAACGGTG GCTGCACCATCTGTCTTCACTTCCCGCCATCTG ATGAGCAGTTGAAATCTGGAACCTGCCTCTGTTG TGTGCTGTGCTGAATACTTCTATCCAGAGAGG CCAAAGTACAGTGAAGGTGGATAACGCCCTCC AATCGGGTAACCTCCAGGAGAGTGTCACAGAGC AGGACAGCAAGGACAGCACCTACAGCCTCAGC AGCACCTGACGCTGAGCAAAGCAGACTACGAG AAACACAAAGTCTACGCCCTGCGAAGTCAACCCAT CAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTC AACAGGGGAGAGTGT	GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTGGAGTGGTCCCGGACTACTGG GGCCAGGGAACCTGGTCAACCGTCTCCTCAGCC TCCACCAAGGGCCATCGGTCTTCCCCCTGGCA CCCTCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCCTGGCTGCCTGGTCAAGGACTACTTCCCC GAACCGGTACGGTGTCTGTGGAACCTCAGGGCC CTGACCAAGCGGTGCACACCTTCCCGGCTGTC CTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAAGCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACCC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGGTGGGACGTGAGCCACGAGAACCCCTGA GGTCAAGTTCAACTGTACGTGGACGGCGTGA GGTGCATAATGCCAAGACAAGCCGTGTAGGA GCAGTACGGCAGCAGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCATCCCGGAGGAGATGACCA AGAACCAAGGTACGCTGACCTGCCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGACAACATAAAG ACCAAGCTTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
AA	SEQ ID NO: 1956 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQOKPGQAPRLLIYGAATRAATGIPARFSGSGSGTE	SEQ ID NO: 2113 QVQLVESGGGVVQPGRSRLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAIWFDASDKYYADSVKKG

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			FTLTISSLQSEDAVYYCQQYNNWPLTFGGGKVE IKRTVAAPSVFIPPSDEQLKSGTASVVCLLNNFY REAKVQWKVDNALQSGNSQESVTEQDSKDSYSL SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEK	SEQ ID NO: 386	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWQGGLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG VHTFPAVLQSSGLYSLSVTVPPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHCTCPPEPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEVESNGQPENNYKTTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
IPS:361185	2G10_LC1.005	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCCTG TCTGTGCTCCAGGGGAAAGAGCCACCCCTCTCC TGACGGGCCAGTCAGAGTGTAGCAGCAACTTA GCCTGTACACAGCAAACTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACCAAGGCC ACTGGTATCCCAGCCAGGTTCAAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGCAGTCTGAAGATTTTGCAAGTTTATTACTGTC AGCAGTATAATAACTGGCCTCTCACTTTCCGGCG GAGGGACCAAGGTGGAGATCAACGAAACGGTG GCTGCACCATCTGTCTTCACTTCCCGCCATCTG ATGAGCAGTTGAAATCTGGAACTGCCCTCTGTTG TGTGCCCTGCTGAATAACTTCTATCCCAGAGAGG CCAAAGTACAGTGGAAAGGTGGATAACGCCCTCC AATCGGGTAACCTCCAGGAGAGTGTACAGAGC AGGACAGCAAGGACAGCACCTACAGCCTCAGC AGCACCCCTGACGCTGAGCAAGCAGACTACGAG AAACACAAAGTCTACGCCTGCGAAAGTACCCCAT CAGGGCCTGAGCTCGCCCGTCAACAAAGAGCTTC AACAGGGGAGAGTGT	SEQ ID NO: 543	CAGGTGCAGCTGGTGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCAACCTTCAAGTAATATGGC ATGCACTGGTCCGCCAGGCTCCAGCGGAGGGG CTGGAGTGGTGCGAGCTATATGGTTTGTATGGA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTACCATCTCCAGAGACAACCTCCAAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTAAGTGTGCGAGAGAT CAGGCGATTTTGGAGTGGTCCCGGACTACTGG GGCCAGGGAACCTGGTCAACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCTCTGGGGGACACAGG GCCCTGGGCTGCCCTGGTCAAGGACTACTTCCCC GAACCGGTGACGGTGTGCTGGAACCTCAGGGGCC CTGACCAAGCGGTGCAACACCTTCCCCGGCTGTC CTACAGTCTCAGGACTCTACTCCTCAGCAGC GTGTTGACCGTGGCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAGGCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCACAC GTGCCCAGCACCTGAACCTCTGGGGGACCGTCT AGTCTTCTCTTCCCCCCCCAAACCCCAAGGACAC

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			IPs:361192	2G10_LC1.006	
		NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCCTG TCTGTGTCCTCAGGGGAAAGAGCCACCCCTCTCC TGACGGGCCAGTCAGAGTGTAGCAGCAACTTA GCCTGTACCAAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACCAAGGGCC ACTGGTATCCCAGCCAGGGTCAAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGCAGTCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTGGCCTCTCACTTTCGGCG GAGGGACCAAGGTGGAGATCAACGAAACGGTG GCTGCACCATCTGTCTTCATCTTCCCGCCATCTG ATGAGCAGTTGAAATCTGGAACTGCCCTCTGTTG TGTGCCCTGCTGAATACTTCTATCCCAGAGAGG CCAAAGTACAGTGAAGGTGGATAACGCCCTCC AATCGGGTAACCTCCAGGAGAGTGTCACAGAGC AGGACAGCAAGGACAGCAACCTACAGCCTCAGC AGCACCCCTGACGCTGAGCAAGCAGACTACGAG AAACACAAAGTCTACGCCCTGCGAAGTCAACCCAT CAGGGCCTGAGCTCGCCCGTCAACAAAGAGCTTC AACAGGGGAGAGTGT		
			GAGTGCAGCTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACTTCACTAAGTAACTATGGC ATGCACTGGTCCGCCAGGCTCCAGGCGAGGGG CTGGAGTGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAAGCGCGTGAAGGGC CGATTCAACATCTCCAGAGACAACCTCAAAGAAC ACGCTGATCTGCAAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGCGATTTTGGAGTGGTCCCGCACTACTGG GGCCAGGGAACCTGGTCAACCGTCTCCTCAGCC TCCACCAAGGCCCATCGGTCTTCCCCCTGGCA CCCTCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGCTGCCCTGGTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCC CTGACCAAGCGGTGCACACCTTCCCGGCTGTC CTACAGTCTCAGGACTCTACTCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTACAAAACTCACACATGCCCACCC GTGCCAGCACCTGAACCTCTGGGGGACCGTCTC AGTCTTCCCTCTCCCCCAAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAAGTGCAAGGTCTCCAAACAAGC CCTCCAGCCCCCATCGAGAAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACACAGGTGT ACACCTGCCCATCCCGGAGGAGATGACCA AGAACAGGTCAAGCTGACCTGCCTGGTCAAAG GCTTCTATCCCAAGCGACATCGCCGTGGAGTGGG		

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			<div>SEQ ID NO: 1958</div> <div>EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAAATRAATGIPARVSGSGGTE FTLTISLQSEDFAVYCYQQYNNWPLTFGGGKVE IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKDSITYSL SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEK</div>		<div>SEQ ID NO: 1958</div> <div>AGAGCAATGGCAGCCGGAGAACAACTACAAG ACCACGCTCCCGTGTCTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAAA</div>
		AA	<div>SEQ ID NO: 388</div> <div>GAAATAGTGATGACGCAGTCTCCAGCCACCCCTG TCTGTGTCCTCAGGGAAAGAGCCACCCCTCTCC TGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACCAAGGCC ACTGGTATCCCAAGCCAGGTTCAAGTGCCAGTGGG TCTGGGACAGAGTTCACCTCACCATCAGCAGC CTGGAGCCTGAAGATTTTGCAAGTTTATTACTGTC AGCAGTATAATAACTTCCCTCTCACTTTCCGGCGG AGGGACCAAGGTGGAGATCAAAACGAACGGTGG CTGCACCATCTGTCTTCATCTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACCTGCCTCTGTTGT GTGCTGTGTAATAACTTCTATATCCCAAGAGAGC CAAAAGTACAGTGGAAAGGTGGATAACGCCCTCCA</div>		<div>SEQ ID NO: 388</div> <div>AGAGCAATGGCAGCCGGAGAACAACTACAAG ACCACGCTCCCGTGTCTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAAA</div>
IPS:359609	2G10_LC1.007	NA	<div>SEQ ID NO: 545</div> <div>CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACTTCAGTAACATATGGC ATGCACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGCTATATGTTTGTATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCAACATCTCCAGAGACAACCTCCAAAGAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTGGAGTGTCCCGGACTACTTGG GGCCAGGGAACCTGGTCAACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCGCTGGCA CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC</div>		<div>SEQ ID NO: 545</div> <div>CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACTTCAGTAACATATGGC ATGCACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGCTATATGTTTGTATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCAACATCTCCAGAGACAACCTCCAAAGAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTGGAGTGTCCCGGACTACTTGG GGCCAGGGAACCTGGTCAACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCGCTGGCA CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC</div>

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	<p>ATCGGGTAACTCCAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCTGACGCTGAGCAAGCAGACTACGAGA AACACAAAAGTCTACGCCCTGCGAAGTCAACCCATC AGGCCCTGAGCTCGCCCCGTACAAAAGAGCTTCA ACAGGGGAGAGTGT</p>	<p>GAAACCGGTACGGTGTCTGTGGAACCTCAGGGGCC CTGACCAGCGGCTGCACACCTTCCCGGCTGTC CTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAAGTGGACAAGAAGTTGAGCC CAAATCTTGTGACAAAACCTACACATGCCACAC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAAACCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCAATAAGCCAAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAAGGACTGGCTGAATGG CAAGGAGTACAAAGTGCAAGGTCTCCAAACAAGC CCTCCAGCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAAGCCCCGAGAACCCACAGGTGT ACACCTGCCCATCCCGGAGGAGATGACCA AGAACAGGTGACCTGACCTGCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAAGCCGAGACAACATACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
	<p>SEQ ID NO: 1959</p> <p>EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQKPGQAPRLLIYGAAATRAATGIPARFSGSGSGTE FTLTISSELEPEDAVYYCQQYNFPLTFGGGKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEK</p>	<p>SEQ ID NO: 2116</p> <p>QVQLVESGGGVVQPRSLRLSCAASGFTFSNYGM HWVRQAPGKGLEWVAIWFDASDKYYADAVKG RFTISRDNSKNTLYQMNSLRRAEDTAVYYCARDQ AIFGVDPDYWGQGLTVTVSSASTKGPSVFPLAPSS KSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNV NHKPSNTKVDKKEPKSCDKTHHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE</p>

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					VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDSGDSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK			
					SEQ ID NO: 389	SEQ ID NO: 546		
					GAAATAGTGATGACGCGAGTCTCCAGCCACCCCTG TCTGTGTCCTCAGGGGAAAGAGCCACCCCTCTCC TGCAGGGCCAGTCAGAGTGTAGCAGCAACTTA GCCTGTACCAAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACCAAGGGCC ACTGGTATCCCAGCCAGGTTCAAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGGAGCCTGAAGATTTTGCAAGTTTATTACTGTC AGCAGTATAATAACTATCCTCTCACTTTCGGCGG AGGGACCAAGGTGGAGATCAACGAACGGTGG CTGCACCATCTGCTTTCATCTTCCCAGCATCTGA TGAGCAGTTGAAATCTGGAACTGCGCTCTGTTGT GTGCTGCTGAATAACTTCTATCCCAGAGAGGC CAAAAGTACAGTGAAGGTGGATAACGCCCTCCA ATCGGGTAACCTCCAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCTGACGCTGAGCAAGCAGACTACGAGA AACACAAAGTCTACGCCCTGCGAAGTCACCCATC AGGGCCTGAGCTCGCCCGTCAACAAAGAGCTTCA ACAGGGGAGAGTGT	NA	2G10_LC1.008	IP:359615
					CAGGTGACGTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCAACCTTCAAGTAACATATGGC ATGCACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGAGCCGTGAAGGGC CGATTCAACATCTCCAGAGACAACCTCCAAGAAC ACGCTGATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGCGATTTTGGAGTGGTCCCGGACTACTGG GGCCAGGAAACCTGGTCAACCGTCTCCTCAGCC TCCACAAAGGCCCATCGGTCTTCCCCCTGGCA CCCTCTCCAAGAGCAACCTCTGGGGGACACAGCG GCCCTGGCTGCCTGGTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCC CTGACCAAGCGGTGCACACCTTCCCCGGCTGTC CTACAGTCTCAGGACTCTACTCTCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAGCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACCTCACACATGCCACCC GTGCCAGCACCTGAACCTCTGGGGGACCGTGC AGTCTTCTCTTCCCCCAAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGCGCTGGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAAGGACTGGCTGAATGG			

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			<p>SEQ ID NO: 1960</p> <p>EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAAATRAATGIPARFSGSGSGTE FTLTISLSEPEDFAVYYCQQYNMYPLTFGGGKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSYSTYLS STLTLSKADYEKHKVYACEVTHQGLSPVTKSFN RGEK</p>	<p>SEQ ID NO: 1960</p> <p>CAAGGAGTACAAAGTGCAAGGTCTCTCAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACAGGTCAAGCTGACCTGCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
		AA	<p>SEQ ID NO: 2117</p> <p>QVQLVESGGGVVQPGRSRLRSCAASGFTFSNYGM HWVRQAPGKGLWVAIWFDASDKYYADAVKG RFTISRDNSKNTLYQMNSLRRAEDTAVYYCARDQ AIFGVDPDYWGQGLVTVSSASTKGPSVFPLAPSS KSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCTPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTKSKA KGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK</p>	<p>SEQ ID NO: 2117</p> <p>QVQLVESGGGVVQPGRSRLRSCAASGFTFSNYGM HWVRQAPGKGLWVAIWFDASDKYYADAVKG RFTISRDNSKNTLYQMNSLRRAEDTAVYYCARDQ AIFGVDPDYWGQGLVTVSSASTKGPSVFPLAPSS KSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCTPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTKSKA KGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK</p>
IPS:361196	2G10_LC1.009	NA	<p>SEQ ID NO: 390</p> <p>GAAATAGTGATGACGCAGTCTCCAGCCACCCCTG TCTGTGTCCTCAGGGGAAGAGCCACCCCTCTCC TGACGGGCCAGTCAGAGTGTAGCAGCAACTTA GCCTGTGTACAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACCAAGGGCC ACTGGTATCCCAGCCAGGTTCACTCAGCAGTGGG TCTGGGACAGAGTTCACTCAGCAGTGGGAGCAGC CTGGAGCCTGAAGATTTTGCAGTTTATTACTGTC</p>	<p>SEQ ID NO: 547</p> <p>CAGGTGACGTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCAACCTTCACTAATATGGC ATGCACTGGTCCGCCAGGCTCCAGGCGAGGGG CTGGAGTGGTGGCAGCTATATGGTTTGTATGCA AGTGATAAATACTATGACAGACGCCGTGAAGGGC CGATTACCATCTCCAGAGACAACTCCAAAGAAC ACGCTGATCTGCAAAATGAACAGCCTGAGAGGCC</p>

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	AGCAGTATAATAACTGGCCTCTCACTTTCGGCG GAGGGACCAAGGTGGAGATCAAACGAACGGTG GCTGCACCATCTGTCTTCATCTTCCCGCCATCTG ATGAGCAGTTGAAATCTGGAACTGCCTCTGTTG TGTGCCCTGCTGAATAACTTCTATCCAGAGAGG CCAAAGTACAGTGGAAAGGTGGATAACGCCCTCC AATCGGGTAACCTCCAGGAGAGTGTACAGAGC AGGACAGCAAGGACAGCACTACAGCCTCAGC AGCACCTGACGCTGAGCAAGCAGACTACGAG AAACACAAAGTCTACGCTGCGAAGTCAACCCAT CAGGGCCTGAGCTCGCCGTCACAAAGAGCTTC AACAGGGGAGAGTGT	SEQ ID NO: 1961	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQOKPGQAPRLLIYGAAATRAATGIPARFSGSGSGTE	AA
GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTGGAGTGGTCCCGGACTACTGG GGCCAGGGAACCTGGTCAACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA CCCTCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGCTGCCTGGTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCC CTGACCAAGCGGCGTGCACACCTTCCCGGCTGTC CTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACCTCACACATGCCACCC GTGCCAGCACCTGAACCTCTGGGGGACCGTCC AGTCTTCCCTCTTCCCCCAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACACATG CGTGGTGGTGGACGTGAGCCACGAGAACCCCTGA GGTCAAGTTCAAACTGGTACGTGGACGGCGTGA GGTGCAATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTCAAGCGT CCTCACCGTCTGCACCAAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCCATCGAGAAAACCATCTCCAA AGCCAAGGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACCAAGGTCAACCTGACCTGCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACACTACAAG ACCACGCCCTCCCGTGTGTGACTCCGACGGCTCC TTCTTCTCTCTATAGCAAGCTCACCCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA	SEQ ID NO: 2118	QVQLVESGGGVVQPRSLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAAIWFDASDKYYADAVKVG		

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			FTLTISSELEPEFAVYYCQQYNNWPLTFGGGKVE IKRTVAAPSVFIPPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKSDSTYSL SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEN	SEQ ID NO: 391	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWQGGLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHCTCPPEPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
IPS:361202	2G10_LC1.010	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCCTG TCTGTGCTCCAGGGGAAAGAGCCACCCCTCTCC TGACGGGCCAGTCAGAGTGTAGCAGCAACTTA GCCTGTACCAAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACCAAGGGCC ACTGGTATCCCAGCCAGGTTCAAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGGAGCCTGAAGATTTTGCAAGTTTATTACTGTC AGCAGTATAATAACTGGCCTCTCACTTTCCGGCG GAGGGACCAAGGTGGAGATCAACGAAACGGTG GCTGCACCATCTGTCTTCACTTCCCGCCATCTG ATGAGCAGTTGAAATCTGGAACTGCCCTCTGTTG TGTGCCCTGCTGAATAACTTCTATCCCAGAGAGG CCAAAGTACAGTGGAAAGGTGGATAACGCCCTCC AATCGGGTAACCTCCAGGAGAGTGTACAGAGC AGGACAGCAAGGACAGCACCTACAGCCTCAGC AGCACCCCTGACGCTGAGCAAGCAGACTACGAG AAACACAAAGTCTACGCCTGCGAAAGTACCCCAT CAGGGCCTGAGCTCGCCCGTCAACAAAGAGCTTC AACAGGGGAGAGTGT	SEQ ID NO: 548	CAGGTGCAGCTGGTGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCAACCTTCAAGTAATATGGC ATGCACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGCGAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTACCATCTCCAGAGACAACCTCCAAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTGGAGTGGTCCCGGACTACTGG GGCCAGGGAACCTGGTCAACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCTCTGGGGGACACAGG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCTGTGGAACCTCAGGGGCC CTGACCAAGCGGTGCAACACCTTCCCCGGCTGTC CTACAGTCTCAGGACTCTACTCCTCAGCAGC GTGTTGACCGTGGCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCACACC GTGCCAGCACCTGAACCTCTGGGGGACCGTCTC AGTCTTCTCTCTCCCCCCCCAAACCCCAAGGACAC

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				CGCCGTGGAGTGGGAGAGCAATGGGCAGCCGG AGAACAACTACAGACACGCCTCCCGTGTGG ACTCCGACGGCTCTTCTTCTCTATAGCAAGCT CACCGTGGACAAGACAGGTGGCAGCAGGGGA ACGTCTTCTCATGCTCCGTGATGCATGAGGCTCT GCACAACCACTACACGAGAGAGCCTCTCCCT GTCTCCGGGTAAA
			SEQ ID NO: 1963	SEQ ID NO: 2120
			EIVLTQSPGTLSPGERATLSCRASQISYSYLA YQQKPGQAPRLIYGASSRATGIPDRFSGSGTDF TLTISRLEPDDFAVYYCQQYGSSPLTFGGGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSITYSLSS TLTLKADYEEKHKVYACEVTHQGLSSPVTKSFNR GEC	QVQLQESGPGLVKPSETLSLTCTVSGDSISGGYY WSWIRPPGKGLEWIGIYYSGSTYYNPSLKSRT ISVDTSKNQFSLKLSVTAADTA VYYCARDRITIFG VVMGGMDVWVGQGT VTVSSASTKGPSVFPPLAP SSKSTSGGT AALGCLVKDYFPEP VTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGGSFFLY SKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPGK
		AA	SEQ ID NO: 393	SEQ ID NO: 550
			GAAATTGTGTTGACGCA GTCTCCAGGCAACCCGTG TCTTTGTCTCCAGGGAAAGAGCCACCCCTCTCCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACAGCAGAAACCTGGCCAGGCTC CCCGCTCCTCATCTATGTTGTCATCCAGCAGGG CCACTGGCATCCAGACAGGTTCA GTGGCAGTG GGTCTGGGACAGACTTCACTCTCAACCATCAGCA GACAGGAGCCTGATGATTTTGCAGTGTATTACT GTACAGCAGTATGGTAGTTACCCGCTCACTTTCGG CGGAGGGACCAAGGTGGAGATCAACGAAACGG TGGCTGCACCATCTGTCTTCATCTTCCCGCCATC TGATGAGCAGTTGAAATCTGGAAC TGCCTCTGT TGTGTGCCTGCTGAATAACTTCTATCCAGAGA	CAGGTGCAGTTGCAGGAGTCGGGCCAGGACTG GTGAAGCCTTCAGAGACCCCTGTCCCTCACCTGC ACTGTCTCTGTTGACTCCATCAGCAGTGTGTT ACTACTGGAGCTGGATCCGCCAGCCCCAGGGA AGGCCCTGGAGTGGATTGGGTACATCTATTACA GTGGGAGCACCTACTACAACCCGCTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGCTCAAGA ACCAAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGGACACGGCCGTGTAATTACTGTGCGAGAGA TCGTATTACGATTTTGGAGTGGTTATGGGGGC GGTATGGAGCTGTGGGGCCCAAGGACACACGGTC ACCGTCTCTCAGCCTCCACCAAGGGCCCATCG GTCTTCCCCCTGGCACCCCTCCTCCAGAGCACCT
IPS:361206	18E3.003	NA		

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	<p>GGCCAAAGTACAGTGGAAGGTGGATAACGCCCT CCAATCGGGTAACCTCCAGGAGAGTGTACAGA GCAGGACAGCAAGGACAGCACCTACAGCCTCA GCAGCACCTTGACGCTGAGCAAGCAGACTACG AGAAACACAAAGTCTACGCTGCGAAGTCAACC ATCAGGGCCTGAGCTCGCCCGTCAACAAAGAGCT TCAACAGGGGAGAGTGT</p>	<p>CTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCA AGGACTACTTCCCCGAACCGGTACGGTGTCTGT GGAATCAGCGGCCCTGACCAGCGGCGTGCACA CCTCCCGGCTGTCTACAGTCTCAGGACTCTA CTCCCTCAGCAGCGTGTGACCGTGCCCTCCAG CAGCTTGGGACCCAGACCTACATCTGCAACGT GAATCACAAGCCCAAGCAACCAAGGTGGACA AGAAGTTGAGCCCAATCTTGTGACAAACTC ACATATGCCACCGTGCCAGCACCTGAACCTC TGGGGGACCGTCAAGTCTTCTTCCCCCCTCAA ACCAAGGACACCTCATGATCTCCCGGACCCC TGAGGTACATGCGTGGTGGTGGACGTGAGCCA CGAAGACCTGAGGTCAAAGTTCAAAGTGTACGT GGACGGCTGGAGGTGCATAATGCCAAGACAA AGCCGTGAGGAGCAGTACGGCAGCACGTACC GTTGTGTCAGCGTCTCACCGTCTTGACCCAGG ACTGGCTGAATGGCAAGGAGTACAAGTGCAAG GTCTCCAACAAGCCCTCCAGCCCCCATCGAG AAACCATCTCCAAGCCAAGGGCAGCCCCGA GAACACAGGTGTACACCTGCCCCCATCCCCG GAGGAGATGACCAGAACCAAGGTACGCTGAC CTGCTGGTCAAAGGCTTCTATCCAGCGACAT CGCCGTGGAGTGGGAGAGCAATGGGCAGCCGG AGAACAACTACAAGACCACGCTCCCGTGTGG ACTCCGACGGCTCTTCTTCTCTATAGCAAGCT CACCGTGGACAAGAGCAGGTGGCAGCAGGGGA ACGTCTTCTCATGCTCCGTGATGCATGAGGCTCT GCACAACCACTACACGCAAGAGAGCCTCTCCCT GTCTCCGGGTAAA</p>
AA	<p>SEQ ID NO: 1964</p> <p>EIVLTQSPGTLSPGERATLSCRASQISYSYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGTDF TLTSRQEPDDFAVYYCQQYGSSPLTFGGGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSYLSLS</p>	<p>SEQ ID NO: 2121</p> <p>QVQLQESGPGLVKPSETLSLTCTVSGDSISSGGYY WSWIRPPGKGLEWIGIYIYSGSTYYPNPSLKSRTV ISVDTSKNQFSLKLSVTAADTA VYCARDRITIFG VVMGGMDVWVGQGTTVTVSSASTKGPSPVPLAP SSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN</p>

PS:359628	18E3.004	NA	<p>STLTLISKADYEHKHKVYACEVTHQGLSSPVTKSFN RGE</p> <p>SEQ ID NO: 394</p> <p>GAAATTGTGTTGACGCAGTCTCCAGGCACCCCTG TCTTTGCTCCAGGGGAAAGAGCCACCCCTCTCCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAAGCAGAAACCTGGCCAGGCTC CCCGGCTCCTCATCTATGGTGTCATCCAGCAGGG CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG GGTCTGGGACAGACTTCACTCTCACCATCAGCA GACTGGAGCCTGATGATTTTGCAGTGTTACTG TCAGCAGTATGATGTTCAACCGCTCACTTTCCGGC GGAGGGACCAAGGTGGAGATCAAAACGAACGGT GGCTGCACCATCTGTCTTCACTTCCCGCCATCT GATGAGCAGTTGAAATCTGGAACCTGCCCTCTGTT GTGTGCCCTGCTGAATAACTTCTATCCACAGAGAG GCCAAAGTACAGTGAAGGTGGATAACGCCCTC CAATCGGGTAACTCCAGGAGAGTGTACACAGAG CAGGACAGCAAGGACAGCACCTACAGCCTCAGC AGCACCTGACGCTGAGCAAAAGCAGACTACGAG AAACACAAAGTCTACGCTGCGAAGTCAACCCAT CAGGGCCTGAGCTCGCCGTACACAAAGAGCTTC AACAGGGGAGAGTGT</p>
			<p>SEQ ID NO: 551</p> <p>CAGGTGCAGTTGCAGGAGTCGGGCCACGGACTG GTGAAGCCTTCACAGACCCTGTCCCTCACCTGC ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCCCCAGGGA AGGCCCTGGAGTGGATTGGTACATCTATTACA GTGGGAGCACCTACTACAACCCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGTCTAAGA ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGGACACGGCCGTGTTACTGTGCGAGAGA TCGTATTACGATTTTTGGAGTGGTTATGGGGGC GGTATGGAGCTCTGGGCCAAGGACACACGGTC ACCGTCTCCTCAGCCTCCACCAAGGGCCCCATCG GTCTTCCCCCTGGCACCCCTCCTCCAAAGACACCT CTGGGGCACACGCGCCCTGGGCTGCCGTGGTCA AGGACTACTTCCCGCAACCGGTGACGGTGTCTGT GGAACTCAGCGGCCCTGACCAAGCGGCTGCACA CCTTCCCCGGTGTCTACAGTCTCAGGACTCTA CTCCCTCAGCAGCTGGTGACCGTGCCCTCCAG CAGCTTGGGCACCCAGACCTACATCTGCAACGT GAATCAACAAGCCCAACAACCAAGGTGGACA AGAAAGTTGAGCCCAAACTTTGTGACAAAACCTC ACACATGCCCCACCGTGGCCAGCACCTGAACCTCC TGGGGGACCGTCAGTCTTCTCTCTTCCCCCAA ACCAAGGACACCCCTCATGATCTCCCGGACCCC TGAGGTCACATGCGTGGTGGTGGACGTGAGCCA CGAAGACCCCTGAGGTCAAGTTCAACTGGTACGT GGACGGCGTGGAGGTGCATAATGCCAAGACAA</p>

A-2124-WO-PCT

			AGCCGTGTGAGGAGCAGTACGGCAGCACGTACC GTTGTGTACAGCTCCTCACCGTCTGCACACGAG ACTGGCTGAATGGCAAGGAGTACAAGTGCAAG GTCTCAACAAGCCCTCCAGCCCCCATCGAG AAAAACATCTCCAAGGCCAAAGGGCAGCCCCGA GAACCAAGGTGTACACCTGCCCTCCCATCCCGG GAGGAGATGACCAAGAACCAGGTACAGCCTGAC CTGCCTGGTCAAGGCTTCTATCCACAGCGACAT CGCCGTGGAGTGGGAGAGCAATGGGCAGCCGG AGAACAACTACAAGACACGCTCCCGTGTCTGG ACTCCGACGGCTCTTCTTCTCTATAGCAAGCT CACCGTGGACAAGACAGGTGGCAGCAGGGGA ACGTCTTCTCATGCTCCTCGTGATGATGAGGCTCT GCACAACCACTACACGCAGAAAGAGCCTCTCCCT GTCTCCGGGTAAA
		SEQ ID NO: 1965	SEQ ID NO: 2122
	AA	EIVLTQSPGTLSPGERATLSCRASQISYSYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGTDF TLTISRLEPDDFAVYYCQQYGSPLTFGGGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSLSS TLTLISKADYEEKHKVYACEVTHQGLSSPVTKSFNR GEC	QVQLQESGPGLVKPSQTLSTCTVSGDISSGGVY WSWIRQPPGKGLEWIGIYYSGSTYYPNLSKSRVT ISVDTSKNQFSLKLSSTAAADTA VYYCARDRITIFG VVMGGGMDVWVGQGTITVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTSIK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKS LSLSPGK
		SEQ ID NO: 395	SEQ ID NO: 552
	NA	GAAATTGTGTGACGCAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAAGCAGAAACCTGGCCAGGCTC CCCGGCTCCTCATCTATGTTGATCCAGCAGGG GAGGCTGGAGTGGATTGGGTACATCTATTACA	CAGGTGCAGTTGCAGGAGTCGGGCCACGACTG GTGAAGCCTTCAGAGACCCCTGTCCCTCACCTGC ACTGTCTCTGGTGACTCCATCAGCAGTGGTGTT ACTACTGGAGCTGGATCCGCCAGCACCCAGGGA AGGGCTGGAGTGGATTGGGTACATCTATTACA
IPS:35963 7 18E3.005			

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CCACTGGCATCCAGACAGGTTTCAGTGGCAGTG GGTCTGGGACAGACTTCACTCTCACCATCAGCA GACTGGAGCCTGATGATTTTGCAGTGATTAATG TCAGCAGTATGGTAGTTCACCGCTCACTTTCCGGC GGAGGGACCAAGGTGGAGATCAACGAACGGT GGCTGCACCATCTGTCTTCACTTCCCGCCATCT GATGAGCAGTTGAATACTGGAACTGCCCTCTGTT GTGTCCCTGCTGAATAACTTCTATCCAGAGAG GCCAAGTACAGTGGAAGGTGGATAACGCCCTC CAATCGGGTAACCTCCAGGAGAGTGTACACAGAG CAGGACAGCAAGGACAGCACCTACAGCCTCAGC AGCACCTGACGCTGAGCAAGCAGACTACGAG AAACACAAAGTCTACGCCTGCGAAGTCAACCCAT CAGGGCCTGAGCTCGCCCGTCAACAAAGAGCTTC AACAGGGGAGAGTGT	GTGGAGCACCTACTACAACCCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGTCCTAAGA ACAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGGGACACGGCCGTGTATTACTGTGCGAGAGA TCGTATTACGATTTTGGAGTGGTTATGGGGGGC GGTATGGACGTCTGGGGCCAAGGACCAACGGTC ACCGTCTCTCAGCCTCCACCAAGGGCCCATCG GTCCTCCCTGGCACCTCCCTCCAAGAGCACCT CTGGGGGCACAGCGGCCCTGGGCTGCCCTGGTCA AGGACTACTTCCCGCAACCGGTGACGGTGTCTGT GGAATCAGGGCCCTGACCAAGCGGCGTGCACA CCTCCCGGCTGTCTACAGTCTCAGGACTCTA CTCCCTCAGCAGCGTGTGACCGTGCCCTCCAG CAGCTTGGGACCCAGACCTACATCTGCAACGT GAATCACAAGCCCAAGCAACCAAGGTGGACA AGAAAGTTGAGCCCAATCTTGTGACAAACTC ACATATGCCACCGTGCCCAAGCACTGAACCTC TGGGGGACCGTCAAGTCTCTTCCCTCCCAAA ACCAAGGACACCTCATGATCTCCCGGACCCC TGAGGTACATGCGTGGTGGTGGACGTGAGCCA CGAAGACCTGAGGTCAAAGTTCAAAGTGTACGT GGACGGCGTGGAGGTGCATAATGCCAAGACAA AGCGGTGAGGAGCAGTACGGCAGCACGTACC GTTGTGTACGCTCTCACCGTCTGCAACAGG ACTGGCTGAATGGCAAGGAGTACAAGTGCAAG GTCCTCAACAAGCCCTCCAGCCCCCATCGAG AAACCATCTCCAAGCCAAGGGCAGCCCCGA GAACCAAGGTGTACACCTGCCCCCATCCCCG GAGGAGATGACCAGAACCAGGTCAACCTGAC CTGCTGGTCAAGGCTTCTATCCAGCGACAT CGCCGTGGAGTGGGAGAGCAATGGGCAGCCGG AGAACAACTACAAGACCAAGCCTCCCGTGTGG ACTCCGACGGCTCTTCTTCTCTATAGCAAGCT CACCGTGGACAAGAGCAGGTGGCAGCAGGGGA ACGTCTTCTCATGCTCCGTGATGCATGAGGCTCT
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[illegible]

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		<p>CAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTC AACAGGGGAGAGTGT</p>	<p>CAGCTTGGGCACCCAGACCTACATCTGCAACGT GAATCACAAGCCCAAGCAACACCAAGGTGGACA AGAAAGTTGAGCCCAAATCTTGTGACAAACTC ACATATGCCACCGTGCCAGCACCTGAACCTCC TGGGGGACCGTCAAGTCTTCTCTTCCCCCAAA ACCAAGGACACCTCATGATCTCCCGGACCCC TGAGGTACATGCGTGGTGGTGGACGTGAGCCA CGAAGACCTGAGGTCAAAGTTCAAAGTGTACGT GGACGGCTGGAGGTGATATGCCAAAGACAA AGCCGTGAGGAGCAGTACGGCAGCACGTACC GTTGTGTCAGCTCCTCACCGTCTTGCACCAAG ACTGGCTGAATGGCAAGGAGTACAAGTGCAAG GTCTCCAACAAGCCCTCCAGCCCCATCGAG AAACCATCTCCAAGCCAAGGGCAGCCCCGA GAACACAGGTGTACACCTGCCCCCATCCCCG GAGGAGATGACCAAGAACCAAGTCAAGCTGAC CTGCTGGTCAAGGCTTCTATCCAGCGACAT CGCCGTGGAGTGGGAGAGCAATGGGCAGCCGG AGAACAACTACAAGACCACGCTCCCGTGTGG ACTCCGACGGCTCTTCTTCTCTATAGCAAGCT CACCGTGGACAAGACAGGTGGCAGCAGGGGA ACGTCTTCTCATGCTCCGTGATGCATGAGGCTCT GCACAACCACTACACGCAAGAGAGCCTCTCCCT GTCTCCGGGTAAA</p>
	AA	<p>SEQ ID NO: 1967</p> <p>EIVLTQSPGTLSPGERATLSCRASQISYSYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGTDF TLTISRLEPDDFAVYYCQQYGSSPLTFGGGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSLSS TLTLSKADYEKHKVYACEVTHQGLSPVTKSFNR GEC</p>	<p>SEQ ID NO: 2124</p> <p>QVQLQESGPGLVKPSQTLSTCTVSGDSISSGGYY WSWIRQHPGKGLEWIGYIYSGSTYYPNPSLKSRVT ISVDTSKNQFSLKLSVTAADTA VYCARDRITIFG VVMGGMDVWVGQGTTVTVSSASTKGPSVPFLAP SSKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLMISRTPETCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF</p>

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				YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
				SEQ ID NO: 554
				CAGTGCAGTTGCAGGAGTCGGGCCAGGACTG GTGAAGCCTTCAGAGAGACCTGTCCCTCACCTGC ACTGTCTCTGGTACTCCATCAGAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCACCCAGGGA AGGCCCTGGAGTGGATTGGGTACATCTATTACA GTGGAGCACCTACTACAACCCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGCTAAGA ACCAAGTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGACACGGCCGTGTATTACTGTGCGAGAGA TCGTATTACGATTTTGGAGTGGTTATGGGGGGC GGTATGGAGCTCTGGGGCCAAAGGACACAGGTC ACCGTCTCCTCAGCCTCCACCAAGGGCCCATCG GTCCTCCCTGGCAGCCTCCCTCCAAAGACACCT CTGGGGCACAGCGGCCCTGGGCTGCCTGGTCA AGGACTACTTCCCGCAACCGGTGACGGTGTCTGT GGAACACAGCGCCCTGACACAGCGCGCTGCACA CCTTCCCGGTGTCTCTACAGTCTCAGGACTCTA CTCCCTCAGCAGCGTGTGACCGTGCCCTCCAG CAGCTTGGGACCCAGACCTACATCTGCAACGT GAATCACAAGCCCAAGCAACCAAGGTGGACA AGAAAGTTGAGGCCAAATCTTGTGACAAAATC ACATATGCCACCGTGCCCAAGCACCTGAACCTC TGGGGGACCGTCAAGTCTTCTTCTCCCGGACCC ACCAAGGACACCTCATGATCTCCCGGACCC TGAGGTACATGCGTGGTGGTGGACGTGAGCCA CGAAGACCTGAGGTCAAATTCAACTGGTACGT GGACGGCGTGGAGGTGCAATAATGCCAAGACAA AGCGGTGTAGGAGCAGTACGGCAGCACGTACC GTTGTGTGAGGTCTCACCCTGCTGCACCCAGG ACTGGCTGATGGCAAGGAGTACAAAGTGCAAG GTCTCCAACAAGCCCTCCCAAGCCCCCATCGAG AAACCATCTCTCCAAGCCAAAGGGCAGCCCCGA
				SEQ ID NO: 397
				GAAATTGTGTGACGCGAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCTCTCCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCCGCTCCTCATCTATGGTGATCCAGCAGGG CCACTGGCATCCAGACAGGTTCAAGTGGCAGTG GGTCTGGGACAGACTTCACTCTCACCATCAGCA GACAGGACCTGATGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGTTACCCGCTCACTTTCGG CGAAGGACCAAGTGGAGATCAACGAAACGG TGGCTGCACCATCTGTCTTCACTCTCCCGCCATC TGATGAGCAGTTGAAATCTGGAACTGCCTCTGT TGTGTCCCTGCTGAATAACTTCTATCCCAAGAGA GGCCAAAGTACAGTGGAAAGTGGATAACGCCCT CCAAATCGGGTAACCTCCAGGAGAGTGTACAGA GCAGGACAGCAAGGACAGCACCTACAGCCTCA GCAGCACCTGACGCTGAGCAAAAGCAGACTACG AGAAACACAAAGTCTACGCTGCGAAGTCAACC ATCAGGGCCTGAGCTCGCCCGTCAACAAAGAGCT TCAACAAGGGGAGAGTGT
			18E3.007	NA
			IPS:361214	

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			<p>GAACCACAGGTGTACACCTGCCCCCATCCCCG GAGGAGATGACCAAGAACCAAGGTACGCTGAC CTGCTGGTCAAGGCTTCTATCCCAGCGACAT CGCCGTGAGTGGGAGAGCAATGGGACGCCGG AGAACAACTACAAAGACACGCTCCCGTGTGG ACTCCGACGGCTCTTCTTCTCTATAGCAAGCT CACCGTGGACAAGACAGGTGGCAGCAGGGGA ACGTCTTCTCATGCTCCGTGATGCATGAGGCTCT GCACAACCACTACACGACAGAGAGCCTCTCCCT GTCTCCGGGTAAA</p>
			<p>SEQ ID NO: 1968</p> <p>EIVLTQSPGTLSPGERATLSCRASQISYSYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGTDF TLTISRQEPDDFAVYYCQQYGSSPLTFGGGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSYSTYSL STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEN</p>
	AA		<p>SEQ ID NO: 2125</p> <p>QVQLQESGPGLVKPSETLSLTCTVSGDSISSGGYY WSWIRQHPGKGLEWIGYIYYSGSTYYPNPSLKSRVT ISVDTSKNQFSLKLSVTAADTA VYYCARDRITIFG VVMGGMDVWGQGTITVTVSSASTKGPSVPFLAP SSKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYITLPPSRREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPGK</p>
IPS:361218	18E3.008	NA	<p>SEQ ID NO: 398</p> <p>GAAATTGTGTTGACGCAAGTCTCCAGGCAACCCTG TCTTTGTCTCCAGGGAAAGAGCCACCCCTCTCCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACACGACAGAAACCTGGCCAGGCTC CCCGGCTCCTCATCTATGTTGTCATCCAGCAGGG CCACTGGCATCCAGACAGGTTCAAGTGGCAGTG GGTCTGGGACAGACTTCACTCTCAACCATCAGCA GACAGGAGCCTGATGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGTTACCCGCTCACTTTCGG CGGAGGGACCAAGGTGGAGATCAACGGAACGG</p>
			<p>SEQ ID NO: 555</p> <p>CAGGTGCAGTTGCAGGAGTCGGGCCAGGACTG GTGAAGCCTTACAGACCTGTGCCCTCACCTGC ACTGTCTCTGTGACTCCATCAGCAGTGTGGTT ACTACTGGAGCTGGATCCGCCAGCCCCCAGGGA AGGCCTGGAGTGGATTGGGTACATCTATTACA GTGGAGCACCTACTACAACCCGCTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGCTCAAGA ACCAAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGGACACGGCCGTGATTACTGTGCGAGAGA TCGTATTACGATTTTTTGGAGTGGTTATGGGGGC</p>

A-2124-WO-PCT

	TGGCTGCACCATCTGTCTTCATCTTCCCGCCATC TGATGAGCAGTTGAAATCTGGAACCTGCCTCTGT TGTGTGCCCTGCTGAATAACITCTATCCCCAGAGA GGCCAAAGTACAGTGAAGGTGGATAACGCCCT CCAATCGGGTAACCTCCAGGAGAGTGTACACAGA GCAGGACAGCAAGGACAGCACCTACAGCCTCA GCAGCACCTTGACGCTGAGCAAGCAGACTACG AGAAACACAAAGTCTACGCTGCGAAGTCAACCC ATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCT TCAACAGGGGAGAGTGT	GGTATGGACGTCTGGGGCCAAAGGACCACGGTC ACCGTCTCTCAGCCTCCACCAAGGGCCCATCG GTCCTCCCCCTGGCACCTCTCTCCAAGAGCACCT CTGGGGCACAGGGCCCTGGGCTGCCCTGGTCA AGGACTACTTCCCCGAACCGGTACGGTGTCTGT GGAATCAGGGGCCCTGACCAGCGGCGTGCACA CCTTCCGGCTGTCTCTACAGTCTCAGGACTCTA CTCCCTCAGCAGCGTGTGACCGTGCCCTCCAG CAGCTTGGGACCCAGACCTACATCTGCAACGT GAATCACAAGCCAGCAACCAAGGTGGACA AGAAAGTTGAGCCCAATCTTGTGACAAACTC ACATATGCCACCGTGCCAGCACCTGAACCTC TGGGGGACCGTCAAGTCTCTCTTCCCCCAAA ACCAAGGACACCTCATGATCTCCCGGACCCC TGAGGTACATGCGTGGTGGACGTGAGCCA CGAAGACCTGAGGTCAAAGTTCAAAGTGTACGT GGACGGCTGGAGGTGCATAATGCCAAGACAA AGCGGTGAGGAGCAGTACGGCAGCACGTACC GTTGTGTCAGCGTCTCACCGTCTTGACCCAGG ACTGGCTGAATGGCAAGGAGTACAAGTGCAAG GTCCTCAACAAGCCCTCCAGCCCCCATCGAG AAACCATCTCCAAGCCAAGGGCAGCCCCGA GAACACAGGTGTACACCTGCCCCCATCCCCG GAGGAGATGACCAGAACCAAGGTACGCTGAC CTGCTGGTCAAGGCTTCTATCCCAGCGACAT CGCCGTGGAGTGGGAGAGCAATGGGCAGCCGG AGAACAACTACAAGACCACGCTCCCGTGTGG ACTCCGACGGCTCTTCTTCTCTATAGCAAGCT CACCGTGGACAAGAGCAGGTGGCAGCAGGGGA ACGTCTTCTCATGCTCCGTGATGCATGAGGCTCT GCACAACCACTACACGCAAGAGAGCCTCTCCCT GTCCTCCGGGTAAA
	SEQ ID NO: 1969	SEQ ID NO: 2126
AA	EIVLTQSPGTLSPGERATLSCRASQISYSYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGTDF TLTISRQEPDDFAVYYCQQYGSPLTFGGGTKVEI	QVQLQESGPGLVKPSQTLSTCTVSGDSISSGGYY WSWIRPPGKGLEWIGYIYSGSTYYNPSLKSRT ISVDTSKNQFSLKLSVTAADTAVYYCARDRTIFG

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			KRTVAAPSFIFFPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSYSL STLTLKADYEKHKVYACEVTHQGLSSPVTKSFN RGE	VVMGGMDVWVQGTTVTVSSASTKGPSVFP SSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFNCSVMHEALHNHYTQKS LSLSPGK
			SEQ ID NO: 399	SEQ ID NO: 556
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGCTCTGGCGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAGAACTACATAGCTTGGTACACAGCAG CAACAGGACATCTCTAAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGGTCCCTGACC GATTCAAGTGGCAGCGGTCTGGGACAGATTTC CTCTCACCATCAGCAGCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAGGGACCAAGGTGGA AATCAACGAACGGTGGCTGCACCATCTGTCTT CATCTTCCCGCCATCTGATGAGCAGTTGAAATCT GGAACCTGCCCTCTGTTGTGTGCTGCTGAATACT TCTATCCAGAGAGGCCAAAGTACAGTGGAAAG TGGATAACGCCCTCCAATCGGGTAACCTCCAGG AGAGTGTACAGAGCAGGACAGCAAGGACAGC ACCTACAGCTCAGCAGCAGCCTGACGCTGAGC AAAGCAGACTACGAGAAACACAAAGTCTACGC CTGCGAAGTCAACCATCAGGGCCTGAGCTCGCC CGTCACAAAGAGCTTCAACAGGGGAGAGTGT	CAGTGCAGCTGGTGCACTGCGGCTGAGGTG AAGAAGCTGGGGCTCAGTGAAAGTCTCCTGC AAGCTTCTGGATACACCTTCAACCGGCTACTAT ATCCACTGGTGCGACAGGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATCAACCTGAAAGT GGTGGCACAGACTATTCACAGAGGTTTCAGGGC AGGTCAACATGACAGGACACGTCATCAGC ACAGCTACATGGAACAGACAGGCTGAGATCT GACGACAGCGGCTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTT ACTACTGGGGCCAGGAAACCTGGTCAACCGTCT CCTCAGCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCTCTCTCCAGAGCACCTCTGGGGG CACAGCGGCTGGGTGCTGCTGGTCAAGGACTA CTTCCCGAACCGGTGACGGTGTGCGGAACTC AGCGGCTTGACAGCGGCTGACACCTTCCC GGTGTCTCAGTCTCAGGACTCTACTCCCTC AGCAGGTGGTGAACGCTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCAATCTTGTGACAAACTCACACATG CCCACCGTGGCCAGCACCTGAACCTCTGGGGG ACCGTCACTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTG
IPS:361222	5C2.006	NA		

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			<p>ACATGCGTGGTGGACGTGAGCCACGAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGC AGCGTCTCACCGTCTGCACCAAGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAGCCAAAGGCAGCCCCGAGAACACACA GGTGTACACCTGCCCTCCCTCCGGGAGGAGAT GACCAAGAACAGGTACGCTGACCTGCCTGGT CAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGCAGCCGAGAGACAACCT ACAAGACCAGCTCCCGTGTGGACTCCGACG GCTCTTCTTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGATGAGGCTCTGCACAACCA CTACACGAGAAAGCCCTCTCCCCTGTCTCCGGG TAAA</p>
		SEQ ID NO: 1970	SEQ ID NO: 2127
	AA	<p>DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQPGHPPKLLIYWASTRESGVPDFSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC</p>	<p>QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRAQPGQGLEWMGWINPESGTDYISQRFQGR VTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI FGMVIVPFDYWQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKS LSLSPGK</p>
		SEQ ID NO: 400	SEQ ID NO: 557

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IP:361229	5C2.007	NA	<div>GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAGAACTACATAGCTTGGTACCAGCAG CAACAGGACATCCTCCTAAGCTGCTCATTTACT GGGCATCTACCCGGGAATCCGGGTCCCTGACC GATTCAAGTGGCAGCGGTCTGGGACAGATTTCATCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAAGGACCACAGGTGGA AATCAACGAACGGTGGCTGCACCATCTGTCTT CATCTCCCGCCATCTGATGAGCAGTTGAAATCT GGAACCTGCCCTCTGTTGTGTGCTGCTGAATAACT TCTATCCAGAGAGGCCAAAGTACAGTGGAAAG TGGATAACGCCCTCCAATCGGGTAACCTCCAGG AGAGTGTACAGACGAGGACAGCAAGGACAGC ACCTACAGCCTCAGCAGCACCCCTGACGCTGAGC AAAGCAGACTACGAGAAACACAAAGTCTACGC CTGCGAAGTCAACCATCAGGGCCTGAGCTCGCC CGTCACAAAGAGCTTCAACAGGGGAGAGTGT</div>
			<div>CAGTGCCCGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGTGCAGACAGGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATCAACCTGAAAGT GGTGGCACAGACTATTACAGAGGTTTCAGGGC AGTTTACCATTGACCAAGGACACGTCCATCAGC ACAGCCTACATGGAACCTGAACAGGCTGAGATCT GACGACACGGCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGAAACCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCTCTCTCCAAGAGCACCTCTGCGGG CACAGCGGCCCTGGGTGCTGGTCAAGGACTA CTTCCCGCAACCGGTGACGGTGTCTGGAACTC AGCGCCCTGACCAAGCGGTGCAACCTTCCC GGTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCAAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCAAATCTTGTGACAAACTCACACATG CCCACCGTGCCCAAGCCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGACGTGAGCCACGAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCAGTACCGTTGTGTC AGGTCTCTACCGTCTTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACACACA GGTGTACACCTGCCCTCCATCCCGGAGGAGAT GACCAAGAACCAAGGTGAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGACAACACT</div>

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				<p>ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGAGAAAGCCCTCTCCCCTGTCTCCGGG TAAA</p> <p>SEQ ID NO: 2128</p> <p>QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYI HWVRQAPQGGLWGMWINPESGGTDYSQRFQGR FTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGLVKDYFPEPVTVSWNSGALTS SKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLISRTPETVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPGK</p> <p>SEQ ID NO: 558</p> <p>CAGGTGCAGCTGGTGCGAGTCTGGGGCTGAGGTG AAGAAGCCTGGGCGCTCAGTGAAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATCCACTGGTGCGACAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATCAACCTGACGCT GGTGGCACAGACTATTACAGAGGTTTCAGGGC AGGTCAACCATGACAGGACACGTCATCAGC ACAGCCTACATGGAACCTGAACAGGCTGAGATCT GACGACACGGCGTGATTAATGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGCGCAGGAAACCTGGTACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCCTCCTCCAAAGAGCACCTCTGGGGG CACAGCGGCCCTGGGCTGCCCTGGTCAAGGACTA</p>
				<p>DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQHPGPKLLIYWASTRESGVPDFRFGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC</p> <p>SEQ ID NO: 1971</p> <p>AA</p>
				<p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGCGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAGAACTACATAGCTTGGTACCAGCAG CAACAGGACATCCTCCTAAGCTGCTCATTTACT GGGCATCTACCCGGGAATCCGGGTCCCTGACC GATTCAGTGGCAGCGGTCTGGGACAGATTCA CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATAATTATAGTAC TCCGTGGACGTTCCGCCAAGGGACCAAGGTGGA AATCAAAACGAACGGTGGCTGCACCATCTGTCTT CATCTTCCCGCCATCTGATGAGCAGTTGAAATCT GGAACCTGCCCTCTGTTGTGTGCTGCTGAATACT TCTATCCACAGAGAGGCCAAAGTACAGTGGAAAG</p> <p>SEQ ID NO: 401</p> <p>NA</p>
IPS:361236	5C2.008			

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	<p>TGGATAACGCCCTCCAAATCGGGTAACCTCCCAGG AGAGTGTACAGACGAGCAGGACAGCAAGGACAGC ACCTACAGCCTCAGCAGCACCCCTGACGCTGAGC AAAGCAGACTACGAGAAACACAAAGTCTACGC CTGCGAAGTCAACCATCAGGGCCTGAGCTCGCC CGTCACAAAGAGCTTCAACAGGGGAGAGTGT</p>	<p>CTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTC AGCGCCCTGACCAGCGGGCTGCACACCTTCCC GGTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGGTGGTACCCTGCCCTCCAGCAGCTTG GGCACCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCAATCTTGTGACAAACTCACACATG CCCACCGTGCCACAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGACGTGAGCCACGAAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCTCTCACCCTCTGCACCAAGGACTGGCTG AATGGCAAGGAGTACAAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGCAGCCCCGAGAACACACA GGTGTACACCTGCCCATCCCGGAGGAGAT GACCAAGAACAGGTGAGCCTGACCTGCCTGGT CAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGAGCCGAGACAACACT ACAAGACCAGCTTCCGTGCTGGACTCCGAGC GCTCTTCTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGATGAGGCTCTGCACAACCA CTACACGAGAAAGAGCCTCTCCCCTGTCTCCGGG TAAA</p>
AA	<p>SEQ ID NO: 1972</p> <p>DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQPGHPPKLLIYWASTRESGVPDFRFGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC</p>	<p>SEQ ID NO: 2129</p> <p>QVQLVQSGAEVKKPGASVKVSKASGYTFTGYYI HWVRQAPGQGLEWMGWINPDAGGTDYSQRFQG RVMTTRDTSISTAYMELNRLRSDDTA VYYCAREA TIFGMVIVPFDYWGGQTLVTVSSASTKGPSVFPLA PSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL</p>

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				<p>AGCGTCCTACCGTCCTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAAGTGCAAGGTCTCCAAC AAGCCCTCCAGCCCATCGAGAAACCATC TCCAAGCCAAAGGCAGCCCCGAGAACACA GGTGACACCTGCCCATCCCGGAGGAGAT GACCAAGAACAGGTGAGCCTGACCTGCCTGGT CAAGGCTTCTATCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGAGCCGAGAACAACT ACAAGACCAGCCTCCCGTGTGGACTCCGACG GCTCCTTCTCTATAGCAAGCTACCCGTGGA CAAGAGCAGGTGGCAGCAGGGAACGTCTTCTC ATGCTCCGTGATGATGAGGCTCTGCACAACCA CTACACGAGAAAGAGCCTCTCCCCTGTCTCCGGG TAAA</p>
				<p>SEQ ID NO: 1973</p> <p>DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQPGHPKLLIYWASTRESGVPDFRSGS GSGTDFLTIISSLAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIIPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSLTLTKADYEEKHKVYACEVTHQGLSSP VTKSFNRGEC</p>
			AA	<p>SEQ ID NO: 2130</p> <p>QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYI HWVRAQPGGLEWMGWINPDAGGTDYSQRFQG RFTMTRDTSISTAYMELNRLRSDDTAVYVCAREA TIFGMVIVFDYWGGQTLTVSSASTKGPSVFPLA PSSKSTSGGTAAALGCLVKDYFPEPTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLEPPKPKDTLMISRTPETCVVVDVSH DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFEL YSKLTVDKSRWQQGNVVFSCSVMEALHNHYTQK SLSLSPGK</p>
				<p>SEQ ID NO: 560</p> <p>CAGGTGCAGCTGGTGCGAGTCTGGGGCTGAGGTG AAGAAGCCTGGGCGCTCAGTGAAAGGTCTCCTGC AAGGCTTCTGGATACACCTTTCACCGGCTACTAT ATCCACTGGGTGCGACAGGCCCTTGACAAAGGG CTTGAGTGGATGGGTGGATCAACCTGACAGT GGTGGCACAGACTATTACACAGAGGTTTCAGGGC</p>
			NA	<p>SEQ ID NO: 403</p> <p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGCTCTGGCGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAGAACTACATAGCTTGGTACCAGCAG CAACCAGGACATCCTCCTAAGCTGCTCATTTACT GGGCATCTACCCGGGAATCCGGGTCCCTGACC</p>
		5C2.010	IPS:361240	

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GATTGAGTGGCAGCGGGTCTGGGACAGATTTCATCTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTTTACTGTCAACAATATTATAGTACTCCGTGGACGTTCCGGCCAAAGGACCAAGGTGGAATCAAAACGAACGGTGGCTGCACCATCTGTCTTCATCTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCCAATCGGGTAACCTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCAACCCATCAGGGCCTGAGCTCGCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	AGGGTCACCATGACCAGGACACGTCCTCATCAGCACAGCCTACATGGAACCTGAACAGGCTGAGATCTGACGACACGGCCGTGATTACTGTGCGAGAGAGGCCACGATTTTGGAAATGGTTATTGTACCGTTTGACTACTGGGGCCAGGAACCCCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCTGGCACCCCTCTCCAAGAGCACCTCTTGGGGGCACAGGGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGCGCCCTGACCAGCGGCTGCACACCTTCCCAGGCTGTCTACAGTCTTCAGGACTCTACTCCCCTCAGAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAAGCCAGCAACCAAGGTGGACAAAGAAAGTTGAGCCCAATCTTGTGACAAACTCACACATGCCCACCGTGCCCAAGCCTGAACCTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAGGACCCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGAGCGTGAGCCACGAAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCCTGAGGTGCATAATGCCAAGACAAGCCGTGTGAGGACAGTACGGCAGCACGTACCGTTGTGTCAGCTCTCACCGTCTTGCAACAGGACTGGCTGAATGGCAAGGAGTACAAAGTGCAAGGTCTCCAACAAGCCCTCCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCCAGGTGTACCCCTGCCCATCCCGGGAGGAGATGACCAAGAACAGGTGAGCCTGACCTGCCCTGGTCAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGACAACACTACAAGACCACGCCCTCCCGTGTGGACTCCGACGGCTCTTCTCTATAGCAAGCTCACC GTGGAAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAAGAGCCCTCTCCCCTGTCTCCCGG
	TAAA

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		SEQ ID NO: 1974	SEQ ID NO: 2131
	AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQPGHPPKLLIYWASTRESGVPDFRSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWINPDGGTDYSQRFQGR VTMRDTSISTAYMELNRLRSDDTAVYVCAREATI FGMVVPFDYWGGQGLVVDYFPEPVTVSWNSGALTS SKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLISRTPETVTVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTKSK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGGSFFLY SKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPGK
		SEQ ID NO: 404	SEQ ID NO: 561
IPS:361247	5C2.011	NA	CAGTGCAGCTGGTGCGAGTCTGGGGCTGAGGTG AAGAAGCTGGGGCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATCCACTGGTGCGACAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATCAACCTGACAGT GGTGGCACAGACTATTACAGAGGTTTCAGGGC AGGTTACCATGACCAAGGACACGTCATCAGC ACAGCTACATGGAATGAACTGACAGGCTGAGATCT GACGACAGGGCGGTGTTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCTGGTACCGTCT CCTCAGCTCCACCAAGGGCCATCGGTCTTCCC CCTGGACCTCTCTCCAGAGACCTCTGGGGG CACAGGGCCCTGGGTGCTGCTGGTCAAGGACTA CTTCCCAGAACCGGTGACGGTGTGCTGGAACTC AGCGCCCTGACCAAGCGGTGCAACACCTTCCC GGCTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTAATCAC AAGCCCAGCAACACCAAGGTGGACAAGAAAGT

	<div>SEQ ID NO: 1975</div> <div>DIVMTQSPDLSLAVSLGERATINCKSSQSVLSSSNK NYLAWYQQPGHPKLLIYWASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSTLTLSKADYEKHKVYACEVTHQGLSP VTKSFNRGEC</div>	<div>SEQ ID NO: 2132</div> <div>TGAGCCCAAATCTTGTGACAAAACTCACACATG CCCACCGTGCCAGCACTGAACCTCTGGGGG ACCGTCAAGTCTTCCCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCTGGTGGTGGACGTGAGCCACGAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCGTCCTACCGTCTCTGCCACGAGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAAACCATC TCCAAAGCCAAAGGCAGCCCCGAGAACCCACA GGTGTACACCTGCCCTCCCATCCCGGAGGAGAT GACCAAGAAACAGGTACGCTGACCTGCCTGGT CAAGGCTTCTATCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGAACAACT ACAAAGACCACGCTCCCGTGTCTGACTCCGACG GCTCCTTCTTCTCTATAGCAAAGCTCAACGTGGA CAAGAGCAGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAAGAGCCTCTCCCTGTCTCCGGG TAAA</div>
AA	<div>SEQ ID NO: 1975</div> <div>DIVMTQSPDLSLAVSLGERATINCKSSQSVLSSSNK NYLAWYQQPGHPKLLIYWASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSTLTLSKADYEKHKVYACEVTHQGLSP VTKSFNRGEC</div>	<div>SEQ ID NO: 2132</div> <div>QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYI HWVRRAPGGGLEWMGWINPDSGGTDYSQRFQGR FTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHSTCPCPAPELL GGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHED PEVKFNWYVVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYCKKVSNAKALPAIEKTIK AKGQPREPQVYVYTLPPSRHEMTKNQVSLTCLVKGF YPSDIAVEFESNGQPENNYKTTTPPVLDSDGSFFLY</div>

A-2124-WO-PCT

					SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
					SEQ ID NO: 562
					CAGTGCCGCTGGTGCAAGTCTGGGGCTGAGGTG AAGAAGCTGGGGCTCAGTGAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATCCACTGGTGCGACAGGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATCAACCTGACAGT GGTGGCACAGACTATTCACAGAGGTTTCAGGGC AGGTCAACATGACAGGACACGTCATCAGC ACAGCTACATGGAACAGAGGCTGAGATCT GACGACACGGCGTGATTAATGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTT ACTACTGGGGCCAGGAAACCTGGTCACCGTCT CCTCAGCTCCACCAAGGGCCATCGGTCTTCCC CCTGGACCTCTCTCCAGAGCACTCTGGGG CACAGCGCCCTGGGTGCTGGTCAAGGACTA CTTCCCGAACCGGTGACGGTGTCTGGAACTC AGCGCCCTGACAGCGGGGTGCACACCTTCCC GGTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGGTGGTGACGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCAATCTTGTGACAAACTCACACATG CCCACCGTGCCAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGTGACGTGAGCCACGAAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGGTCTCTACCGTCTTGCACCAAGGACTGGCTG AATGGCAAGGAGTCAAGTGAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACCCACA GGTGTACACCTGCCCCCATCCCCGGGAGGAGAT
					SEQ ID NO: 405
					GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTATATCCAGCTCC AACATAAGAACTACATAGCTTGGTACCAGCAG CAACAGGACATCTCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGTCCCTGACC GATTCAAGTGGCAGCGGTCTGGGACAGATTTC CTCTACCATCAGCAGCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAGGGACCAAGGTGGA AATCAACGAAACGGTGGCTGCACCATCTGTCTT CATCTTCCCGCCATCTGATGAGCAAGTTGAAATCT GGAACCTGCTCTGTGTGTGCTGCTGAATAACT TCTATCCAGAGAGGCCAAAGTACAGTGGAAAG TGGATAACGCCCTCCAATCGGGTAACCTCCAGG AGAGTGTACAGAGCAGGACAGCAAGGACAGC ACCTACAGCTCAGCAGCACCTGACGCTGAGC AAAGCAGACTACGAGAAACACAAAGTCTACGC CTGCGAAGTCAACCATCAGGGCCTGAGCTCGCC CGTCACAAAGAGCTTCAACAGGGGAGAGTGT
				NA	
			5C2.012		
			IPS:361254		

A-2124-WO-PCT

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	<p>CATCTTCCCGCCATCTGATGAGCAGTTGAAATCT GGAAC TGCTGTGTGCTGCTGCTGAATAACT TCTATCCAGAGAGGCCAAAGTACAGTGGAAAG TGGATAACGCCCTCCAATCGGGTAACCTCCAGG AGAGTGTACAGAGCAGGACAGCAAGGACAGC ACCTACAGCCTCAGCAGCACCTGACGCTGAGC AAAGCAGACTACGAGAAACACAAAGTCTACGC CTGCGAAGTCAACCATCAGGGCCTGAGCTCGCC CGTCACAAAGAGCTTCAACAGGGGAGAGTGT</p>	<p>CCTACGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGG CACAGCGCCCTGGGCTGCCGTGGTCAAGGACTA CTTCCCGCAACCGGTGACGGTGTCTGTGGAATC AGCGCCCTTGACAGCGGGCTGCACACCTTCCC GGTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCAATCTTGACAAACTCACACATG CCCACCGTGCCAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGACGTGAGCCACGAAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCAGTACCGTTGTGTC AGCTCTCACCGTCTTGCAACAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAGCCAAAGGCAGCCCCGAGAACACACA GGTGTACACCTGCCCTCCCTGAGGAGGAGAT GACCAAGAACAGGTGACGCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGAGCGCGGAGACAACAT ACAAGACCAGCTCCCTGCTGGACTCCGACG GCTCTTCTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGCTTCTC ATGCTCCGTGATGATGAGGCTCTGCACAACCA CTACACGAGAAAGAGCCTCTCCCCTGTCTCCGGG TAAA</p>
	<p>SEQ ID NO: 1977</p>	<p>SEQ ID NO: 2134</p>
AA	<p>DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQHPKLLIYWASTRESGVPDFRFSGS GSGTDFLTIISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL</p>	<p>QVQLVQSGAEVKKPGASVKVSKKASGYTFTGYYI HWVRQAPGQGLEWMGWINPDAGGTDYSQRFQF RFTMTRDTSISTAYMELNRLRSDDTAVYYCAREA TIFGMVIVPFDYWGQGTTLVTVSSASTKGPSVFPLA</p>

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			NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYLSSTLTLSKADYEHKVVYACEVTHQGLSSP VTKSFNRGEC	SEQ ID NO: 407 GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGCTCTGGCGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAAATAAGAACTACATAGCTTGGTACCAGCAG CAACCAAGGACATCTCTAAGCTGCTCATTTACT GGGCATCTACCCGGGAATCCGGGGTCCCTGACC GATTCAAGTGGCAGCGGGTCTGGGACAGATTTC CTCTCACCATCAGCAGCTGCAGGCTGAAGATG TGGCAGTTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAAAGGACCAAGGTGGA AATCAACGAAACGGTGGCTGCACCATCTGTCTT CATCTTCCCGCCATCTGATGAGCAGTTGAAATCT GGAACCTGCCCTCTGTTGTGTGCCTGCTGAATAACT TCTATCCCAAGAGAGGCCAAAGTACAGTGGAAAG TGGATAACGCCCTCCAATCGGGTAACTCCCAAG AGAGTGTCAAGAGCAGGACAGCAAGGACAGC ACCTACAGCCTCAGCAGCACCTTGACGCTGAGC AAAGCAGACTACGAGAAACACAAAGTCTACGC CTGCGAAGTCAACCATCAGGGCCTGAGCTCGCC CGTCACAAGAGCTTCAACAGGGGAGAGTGT	SEQ ID NO: 564 CAGGTGCCGCTGGTGCAAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCCTCAGTGAAGTCTCCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATCCACTGGGTGCACAGGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATCAACCTGACGCT GGTGGCACAGACTATTACAGAGGTTTCAGGGC AGGGTCAACATGACCAAGGACACGTCCATCAGC ACAGCCTACATGAACTGAACAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGTTATTGTACCGTTTG ACTACTGGGGCCAGGAAACCTGGTCAACCGTCT CCTCAGCCTCCACC AAGGGCCCATCGGTCTTCCC CCTGGCACCTCTCTCCAAGAGCACCTCTGGGG CACAGCGCCCTGGGTGCGTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTGCTGGAACTC AGCGCCCTGACACAGCGGCTGCACACCTTCCC GGCTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCAAAATCTTGTGACAAAACTCACACATG CCCACCGTGGCCAGCACCTGAACTCCTGGGGG ACCGTCAAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTG ACATGCGTGGTGGAGCTGAGCCACGAAAGAC
IPS:361268	5C2.014	NA			

A-2124-WO-PCT

		<p>SEQ ID NO: 1978</p> <p>DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQPGHPPKLLIYWASTRESGVPDFRFGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSLTTLISKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC</p>	<p>SEQ ID NO: 2135</p> <p>QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYVI HWVRQAPGQGLEWMGWINPDAGGTDYSQRFQG RVMTTRDTSISTAYMELNRLRSDDTA VYYCAREA TIFGMVIVPFDYWGQGLTVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNPKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDITLMISRTPETCVVVDVSH DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFL YSKLTVDKSRWQQGNVVFSCSVMEALHNHYTQK SLSLSPGK</p>
	AA		

A-2124-WO-PCT

			SEQ ID NO: 408	SEQ ID NO: 565
IPS:359669	5C2.015	NA	<p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGCTCTGGCGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTATATCCAGCTCC AACATAAGAACTACATAGCTTGGTACCAGCAG AAACGAGACAACCTCCTAAGCTGCTCATTTAC TGGGCATCTACCCGGGAATCCGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTT ACTCTACCATCAGCAGCCTGCAAGGCTGAAGAT GTGGCAGTTTTTACTGTCAACAATATTATAGTA CTCCGTGGACGTTCCGGCCAGGGACCAAGGTGG AAATCAACGAAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACCTGCCCTCTGTTGTGTGCTGCTGAATAAC TTCTATCCAGAGAGGCCAAAGTACAGTGGAAAG GTGGATAACGCCCTCCAAATCGGGTAACTCCAG GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAGTCTACG CCTGCCGAAGTCAACCCATCAGGGCCTGAGCTCGC CCGTCAACAAGAGCTTCAACAGGGGAGAGTGT</p>	<p>CAGTGCAGCTGGTGACGTCTGGGGCTGAGGTG AAGAAGCTGGGGCTCAGTGAAAGTCTCCTGC AAGGTTCTGGATACACCTTCAACCGGCTACTAT ATCCACTGGTGCGACAGGGCCCTGGACAAAGG CTTAGTGGATGGGTGGATCAACCTTGACGCT GGTGGCACAGACTATTACACAGAGGTTTCAGGGC AGGTACCATGACACAGGACACGTCATCAGC ACAGCTACATGGAACCTGAACAGCTGAGATCT GACGACACGGCGGTGATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTT ACTACTGGGGCCAGGAAACCTGGTCAACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGACCCCTCCTCCAAGAGCACTCTGGGGG CACAGGGCCCTGGGTGCTGGTCAAGGACTA CTTCCCGCAACCGGTGACGGTGTCTGGAACTC AGCGCCCTGACACAGCGGTGCAACCTTCCC GGTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCAATCTTGTGACAAACTCACACATG CCCACCGTGCCAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGTGACGTGAGCCACGAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCAGTACCGTTGTGTC AGCTCTCTACCGTCTTGCACCAAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAAACACA GGTGTACACCTGCCCTCCCATCCCGGAGGAGAT GACCAAGAACCAAGGTGACGCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA</p>

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				GTGGGAGCAATGGGCAGCCGGAGAACAACT ACAAGACCACGCTCCCGTGGTGGACTCCGACG GCTCCTTCTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGAGAAAGCCCTCTCCCCTGTCTCCGGG TAAA
			SEQ ID NO: 1979	SEQ ID NO: 2136
			DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQKPGQPPKLLIYWASTRESGVPDFRFGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWINPDAGGTDYSQRFQG RVMTTRDTSISTAYMELNSLRSDDTAVYYCAREA TIFGMVIVPFDYWGGQTLVTVSSASTKGPSVFPLA PSSKSTSGGT AALGCLVKDYFPEPTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGPSVFLFPPKPKDITLMISRTPETCVVVDVSH DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGPQREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEVESNGQPENNYKTTPPVLDSDGSFEL YSKLTVDKSRWQQGNVFCSSVMHEALHNHYTQK SLSLSPGK
		AA	SEQ ID NO: 409	SEQ ID NO: 566
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGCGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAGAACTACATAGCTTGGTACCAGCAG AAACAGGACAACTCCTAAGCTGCTCATTTAC TGGGCATCTACCCGGGAATCCGGGGTCCCTGAC CGATTCAAGTGCGAGCGGGTCTGGGACAGATTTC ACTCTCAACCATCAGCAGCCCTGCAAGGCTGAAGAT GTGGCAGTTTTTTACTGTCAACAATATTATAGTA CTCCGTGGACGTTCCGGCCAAGGGACCAAGGTGG AAATCAAAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCCATCTGATGAGCAGTTGAAATC TGGAACCTGCTCTGTGTGTGTGCCTGCTGAATAAC	CAGGTGCAGTGGTGCGAGTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATCCACTGGTGCGACAGGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATCAACCTGAAAGT GGTGGCACAGACTATTACAGAGGTTTCAGGGC AGGTACACCATGACAGGACACGTCATCAGC ACAGCCTACATGGAACCTGAACGCTGAGATCT GACGACAGCCGCTGTATTACTGTGCGAGAGAG GCCACGATTTTIGGAAATGGTTATTGACCGTTTG ACTACTGGGGCCAGGGAACCTGGTACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCCTCCTCCAAGAGCACCTCTCGGGG
IPS:359678	SC2.016	NA		

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	<p>TTCTATCCAGAGAGGCCAAAGTACAGTGGAAG GTGGATAACGCCCTCCAAATCGGGTAACTCCCCAG GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAGTCTACG CCTGCGAAGTCAACCATCAGGGCCTGAGCTCGC CCGTCAACAAGAGCTTCAACAGGGGAGAGTGT</p>	<p>CACAGCGGCCCTGGGCTGCCGTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCTGTGGAATC AGCGCCCTTGACCAGCGGCGTGACACCTTCCC GGTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAGAAAGT TGAGCCCAATCTTGTGACAAACTCACACATG CCCACCGTGCCAGCACCTGAATCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGACGTGAGCCACGAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCTCTCACCCTCTGCACCAAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAGCCAAAGGCAGCCCCGAGAACACACA GGTGTACACCTGCCCATCCCGGAGGAGAT GACCAAGAACAGGTGACGCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGACAACCT ACAAGACCAGCTTCCCGTGTGGACTCCGACG GCTCCTTCTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAAGAGAGCCTCTCCCCTGTCTCCGGG TAAA</p>
	<p>SEQ ID NO: 1980</p> <p>DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQKPGQPPKLLIYWASTRESGVPDFRFGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK</p>	<p>SEQ ID NO: 2137</p> <p>QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWINPESGTDYSQRFQGR VTMTRDTSISTAYMELNSLRDDTAVYYCAREATI FGMVIVPFDYWGQGLVTVSSASTKGPSVFPLAPS SKSTSGGTAAAGCLVKDYFPEPVTVSWNSGALT GVHTFPAVLQSSGLYSLSVSVTVPSSSLGTQTYICN</p>

AA

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		DSTYLSSTLTL\$KADY\$KHKVYACEVTHQGLSSP VTK\$FNRGEC	SEQ ID NO: 410	SEQ ID NO: 567	VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKD\$TL\$MISRTPEVTCVVVDV\$SHED PEVKFNWY\$VDGVEVHN\$AKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVY\$TLP\$PSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYK\$TTPPVLDSDGSFFLY SKLTV\$DKSRWQ\$QGNVFSC\$VMHEALHNHYTQKS LSLSPGK
		GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGGCAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGT\$TTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCACACAG AAACCAAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGAAATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTTC ACTCTCACCATCAACAGCCTGCAAGGCTGAAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTCCGGCCAGGGACCAAGGTGG AAATCAAAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAAGTGCCTCTGTGTGTGCGCTGCTGAATAAC TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAG GTGGATAACGCCCTCCAAATCGGGTAACTCCCAG GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCTTGACGCTGAG CAAAAGCAGACTACGAGAAACACAAGTCTACG CCTGCGAAGTCAACCCATCAGGGCCTGAGCTCGC CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT		CAGGTGCCGCTGGTACAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGTCTCCTGTC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATACACTGGTGCGTCAAGCCCCCTGGACAAGGG CTTGTGTGGATGGGTGGATCAGCCCTAACAGT GGTGAAACAAGCTATGCACAGAAGTTTCAGGAC AGGGTCAACCATGACCAGGGACACGTCCATCAGC ACAGCCTATATGAGCTGAGCAGACTGAGATCT GACGACACGGCCGTGTATTTCTGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGAAACCTGGTCAACCGTCT CCTCAGCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCTCCTCCTCAAGAGCACCTCTGGGGG CACAGCGCCCTGGGTGCGCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTGCTGGAACTC AGCGCCCTGACCAAGCGGTGCACACCTTCCC GGCTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCAAAATCTTGTGACAAAACTCACACATG CCCCCGTGGCCAGCACCTGAACCTCTGGGGGG ACCGTCAAGTCTTCTCTTCCCCCAAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTG ACATGCGTGGTGGAGCTGAGCCACGAAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAGCCGTGT	
IPS:361275	11C1.002	NA			

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TGGACTTCTACCCGAGAAATCCGGGGTCCCTGAC CGATTTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAAGGCTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTTCGGCCCAAGGACCACAGGTGG AAATCAAAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACCTGCCCTCTGTTGTGTGCCTGCTGAATAAC TTCTATCCAGAGAGGCCAAAGTACAGTGGAG GTGGATAACGCCCTCCAAATCGGGTAACTCCCA GAGAGTGTACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCAACCCATCAGGGCCTGAGCTCGC CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	GGTGACACAAAGCTATGCACAGAAAGTTTCAGGAC AGGTACACCATGACCAGGGACACGTCCATCAGC ACAGCCTATATGAGCTGAGCAGACTGAGATCT GACGACACGGCCGTGTATTCTGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGAAACCCCTGGTCAACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGG CACAGCGGCCCTGGGCTGCCCTGGTCAAGGACTA CTTCCCGCAACCGGTGACGGTGTCTGTGGAACTC AGCGCCCTGACCAAGCGGCTGCACACCTTCCC GGTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCAATCTTGTGACAAACTCACACATG CCCACCGTGCCCAAGCCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGGACGTGAGCCACGAAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCAGTACCGTTGTGTG AGCTCTCTACCGTCTTGCAACAGGACTGGCTG AATGGCAAGGAGTCAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACACAA GGTGTACACCTGCCCTCCATCCCGGAGGAGAT GACCAAGAACAGGTGAGCCTGACCTGCCTGGT CAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGAGCCGGAGAACAACT ACAAGACCAGCCTCCCGTGTGGACTCCGAGC GCTCCTTCTCTCTATAGCAAGCTCACCCTGGA CAAGAGCAGGTGGCAGCAGGGGAACTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAAACCA
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				CTACACGCAGAAAGAGCCCTCTCCCTGTCTCCGGG TAAA
			SEQ ID NO: 2139	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLVWMGWISPNSGDTSYAQKFQDR VTMRDTSISTAYMELSRRLSDDTA VYFCAREATI FGMLIVPFDYWGGQTLVTVSSASTKGPSVFPLAPS SKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKD TLMISRTPETCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPGK
			SEQ ID NO: 412	CAGTGCCGCTGGTACAGTCTGGGGTGAGGTG AAGAAGCCTGGGCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATACACTGGTGCTCAGGCCCTGGACAAGGG CTTGTGTGGATGGGTGGATCAGCCCTAACAGT GGTGAAACAAGCTATGCACAGAA GTTTCAGGAC AGGTCACCATGACACAGGACACGTCATCAGC ACAGCCTATATGGAGCTGAGCAGACTGAGATCT GACGACACGGCGGTGATTCTGTGCGAGAGAG GCCACGATTTTGGAA TGCTTATTGTACCAATTG ACTACTGGGCCAGGAAACCTGGTCAACCGTCT CCTCAGCCTCCACCAAGGCCCATCGGTCTTCCC CCTGGCACCTCTCTCCAGAGACACCTCTGGGGG CACAGCGCCCTGGGTGCTGCTGGTCAAGGACTA CTTCCCAGAACCGGTGACGGTGTCTGGAACTC AGCGCCCTGACCAAGCGGTGACACACCTTCCC GGGTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG
			SEQ ID NO: 1982	DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLA WYQQKPGQPPNLLIYWTSTRESGVDRFSG SGSGTDFTLTINSLQAEDVA VYCCQQY YRTPWTF GQGTKVEIKRTVA APSVFIPPSDEQLKSGTASVVC LLNFFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSYLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC
			SEQ ID NO: 569	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGCGGAGAGGCCACCAATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAGAACTACTTAGCTTGGTACCAACAG AAACAGGACAGCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGTCCCTGAC CGATTCAAGTGCGAGCGGTCTGGGACAGATTTC ACTCTACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTCCGCCAAGGACCAAGGTGG AAATCAAACGAACGGTGGTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGA ACTGCTCTGTGTGTGCTGCTGCTGAATAAC TTCTATCCAGAGAGGCCAAA GTACAGTGGAAG GTGGATAACGCCCTCCAAATCGGTAACTCCAG GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAGTCTACG
		AA		
		NA	11C1.004	!PS:361289

A-2124-WO-PCT

		<p>CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT</p>	<p>GGACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCAATCTTGTGACAAACTCACACATG CCCACCGTGCCACAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGGACGTGAGCCACGAAGAC CCTGAGGTCAGTTCAACTGGTACGTGGACGGC GTGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTG AGCTCTCACCGTCTTGCACCAAGGACTGGCTG AATGGCAAGGAGTACAAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAGCCAAAGGCAGCCCCGAGAACACACA GGTGTACACCTGCCCATCCCGGAGGAGAT GACCAAGAACAGGTACGCTGACCTGCCTGGT CAAAGGCTTCTATCCAGCGACATCGCCGTGGA GTGGAGAGCAATGGCAGCCGAGAGACAACACT ACAAGACCAGCTTCCGTGCTGGACTCCGACG GCTCTTCTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAAGAGAGCCTCTCCCCTGTCTCCGGG TAAA</p>
	AA	<p>DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDFSG SGSGTDFTLTINSLQAEDVAVYCCQQYYRTPWTF GQGTKVEIKRTVAAPSVFIAPPDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSYLSSTLTLSKADYEKHKVYACEVTHQQLSS PVTKSFNRGEC</p>	<p>SEQ ID NO: 2140 QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYI HWVRQAPGQGLVWMGWISPNSETSYAQKFQDR VTMTRDTSISTAYMELSRLRSDDTAVYFCAREATI FGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLMISRTPETVTVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF</p>

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					YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
					SEQ ID NO: 570
					CAGTGCCGCTGGTACAGTCTGGGGCTGAGGTG AAGAAGCTGGGGCTCAGTGAAGTCTCCTGC AAGCTTCTGGATACACCTTCAACCGGTACTAT ATACACTGGTGCGTCAGGCCCTGGACAAGGG CTTGTGGATGGGGTGGATCAGCCCTAACAGT GGTGAAACAAGCTATGCACAGAAATTTTCAGGAC AGGTACCATGACACAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGACTGAGATCT GACGACACGGCGTGTATTTCTGTACGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCAATTTG ACTACTGGGCCAGGAAACCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCATCGGTCTTCCC CCTGGACCCCTCCTCCAAGACACCTCTGGGGG CACAGCGCCCTGGCTGCCCTGGTCAAGGACTA CTTCCCGAACCGGTGACGGTGTCTGGAACTC AGCGCCCTGACACAGCGGTGACACACCTTCCC GGTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCACGCAACCAAGGTGGACAAGAAAGT TGAGCCCAATCTTGTGACAACACTCACACATG CCCACCGTGCCAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGACGTGAGCCACGAAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCTCTCTCACCCTCTGCACCAAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGGCAGCCCCCGAGAACACACA
					SEQ ID NO: 413
					GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGCGGAGAGGGCCACCAATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAAGAACTACTTAGCTTGGTACCAACAG AAACGAGGACAGCTCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTT ACTCTACCATCAACAGCCTGCAAGGCTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTCCGGCCAGGGACCAAGGTGG AAATCAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAAGTTGAAATC TGGAAGTGGCTCTGTGTGTGCTGCTGCTGAATAAC TTCTATCCAGAGAGGCCAAAGTACAGTGGAAAG GTGGATAACGCCCTCCAATCGGGTAACTCCACAG GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCTCAGCAGCACCTGACGCTGAG CAAGCAGACTACGAGAAACACAAGTCTACG CCTGCGAAGTCAACCATCAGGGCTGAGCTCGC CCGTCAACAAGAGCTTCAACAGGGGAGAGTGT
				NA	
			11C1.005		
			IPS:359712		

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				GGGTACACCCTGCCCCATCCCGGAGGAGAT GACCAAGAACAGGTACAGCTGACCTGCCTGGT CAAAGGCTTCTATCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGCAGCCGGAGAACAACT ACAAGACCACGCTCCCGTGTGACTCCGACG GCTCCTTCTTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAAGAGCCTCTCCCTGTCTCCGGG TAAA
		SEQ ID NO: 1984	SEQ ID NO: 2141	QVPLVQSGAEVKKPGASVKVSKASGYTFTGYI HWVRQAPGQGLVWMGWISPNSETSYAQKFQDR VTMTRDTSISTAYMELSRLSDDTAVYFCTREATI FGMLIVPFDYWGQGLTVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTKISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVVFSCSVMEALHNHYTQKS LSLSPGK
	AA			
		SEQ ID NO: 414	SEQ ID NO: 571	CAGGTGCCGCTGGTACAGTCTGGGCTGAGGTG AAGAAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATACACTGGGTGCTCAGGCCCTTGACAAGGG CTTGTGTGGATGGGTGGATCAGCCCTAACAGT GGTGACACAAGCTATGCACAGAAAGTTTCAGGAC AGGGTCAACCATGACACGAGGACACGTCCATCAGC ACAGCCTATATGAGCTGAGCAGACTGAGATCT GACGACACGGCCGTGATTTCTGTACGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCAATTG
	NA	11Cl.006	IPS:361293	

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	<p>AAATCAAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACCTGCCCTGTGTTGTGCGCTGCTGAATAAC TTCTATCCACAGAGAGGCCAAAGTACAGTGAAG GTGGATAACGCCCTCCAAATCGGGTAACTCCACG GAGAGTGTACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCAACCATCAGGGCCTGAGCTCGC CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT</p>	<p>ACTACTGGGGCCAGGAACCCCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGG CACAGGGCCCTGGCTGCCCTGGTCAAGGACTA CTTCCCGAACCGGTGACGGTGTCTGTGGAATC AGCGCCCTGACCAAGCGGGCTGCACACCTTCCC GGTGTCTACAGTCTCTCAGGACTCTACTCCCTC AGCAGCTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCAAATCTTGTGACAAACTCACACATG CCCACCGTGCCCAAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGACGTGAGCCACGAAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCAGTACCGTTGTGTC AGCTCTCACCCTCTGCACCAAGGACTGGCTG AATGGCAAGGAGTCAAGTGCAGGTCTCCAAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACACACA GGTGTACACCTGCCCTCCCATCCCGGAGGAGAT GACCAAGAACAGGTGACGCTGACCTGCCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGAGCCGGAGAACAACT ACAAGACCAGCCTCCCGTGTGGACTCCGACG GCTCTTCTTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGAGAAAGACCTCTTCCCCTGTCTCCGGG TAAA</p>
	<p>SEQ ID NO: 1985</p>	<p>SEQ ID NO: 2142</p>
AA	<p>DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSTRESGVPDFSG SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF</p>	<p>QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYI HWVRQAPGQGLVWMGWISPNSGDTSYAQKFQDR VTMTRDTSISTAYMELSRRLSRDDTAVYFCTREATI</p>

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			<p>QGGTKVEIKRTVAAPSVFIFFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC</p>	<p>FGMLIVPFDYWGGQGLTVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPAPELL GGPSVFLFPPKPKDLMISRTP EVT CVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKS LSLSPGK</p>
			<p>SEQ ID NO: 415</p> <p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAAGAACTACTTAGCTTGGTACCAACAG AAACCAAGGACAGCTTCCTAACTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCA GTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCAAGGTGG AAATCAAAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACCTGCCCTCTGTTGTGTGCCCTGCTGAATAAC TTCTATCCCAAGAGAGGCCAAAGTACAGTGGAAAG GTGGATAACGCCCTCCAAATCGGGTAACTCCCAAG GAGAGTGTACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCCCTGACGCTGAG CAAAAGCAGACTACGAGAAACACAAGTCTACG CCTGCGAAGTCAACCATCAGGGCCTGAGCTCGC CCGTCAACAAAGAGCTTCAACAGGGGAGAGTGT</p>	<p>SEQ ID NO: 572</p> <p>CAGGTGCCGCTGGTACAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATACACTGGGTGCGTCAAGGCCCTGGACAAAGG CTTGTGTGGATGGGTGGATCAGCCCTAACAGT GGTGAACAAGCTATGACACAGAAGTTTCAGGAC AGGTACCATGACCAAGGACACGTCCATCAGC ACAGCTATATGAGCTGAGCAGACTGAGATCT GACGACACGGCGTGTATTTCTGTACGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCAGGGAACCTGGTCAACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCTCTCTCCAAAGAGCACCTCTGGGGG CACAGGGCCCTGGGTGCCGTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTGCTGGAACTC AGGCGCCCTGACCAAGCGGTGACACACTTCCC GGCTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCGTGTGACCGTGCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCAAAATCTTGTGACAAAACCTCACACATG CCCACCGTGGCCAGCACCTGAACCTCCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTG</p>
IPS:361297	11C1.007	NA		

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			<p>ACATGCGTGGTGGACGTGAGCCACGAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCGTCTCACCGTCTGCACCAAGACTGGCTG AATGGCAAGGAGTACAAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGCAGCCCCGAGAACACACA GGTGTACACCTGCCCTCCCATCCCGGAGGAGAT GACCAAGAACAGGTACGCTGACCTGCCTGGT CAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGCAGCCGAGAGACAACACT ACAAGACCAGCTCCCGTGTGCTGACTCCGACG GCTCCTTCTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGATGAGGCTCTGCACAACCA CTACACGAGAAAGACCTCTCCCCTGTCTCCGGG TAAA</p>
	SEQ ID NO: 1986	SEQ ID NO: 2143	
	<p>DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDFSG SGSGTDFTLTINSLQAEDVAVYCCQQYYRTPWTF GQGTKVEIKRTVAAPSVFIAPPDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYLSSTLTLSKADYEKHKVYACEVTHQQLSS PVTKSFNRGEC</p>	<p>QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRRQAPGQGLVWMGWISPNSETSYAQKFQDR VTMTRDTSISTAYMELSRLSDDTAIFYCTREATI FGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAAAGCLVKDYFPEPTVSWNSGALT GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVVFSCSVMEALHNHYTQKS LSLSPGK</p>	
	SEQ ID NO: 416	SEQ ID NO: 573	

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IP:361301	11C1.008	NA	<div>GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCCTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAGAACTACTTAGCTTGGTACCAACAG AAACCAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCAGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTC ACTCTACCATCAACAGCCTGCAAGGCTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCAGGTGG AAATCAAACGAAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACTGCCCTCTGTTGTGTGCTGCTGAATAAC TTCTATCCAGAGAGGCCAAAGTACAGTGGAG GTGGATAACGCCCTCCAAATCGGGTAACTCCAG GAGAGTGTACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAGTCTACG CCTGCGAAGTCAACCATCAGGGCCTGAGCTCGC CCGTCAAAAGAGCTTCAACAGGGGAGAGTGT</div>
			<div>CAGTGCCCGCTGGTACAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGTGCGTCAGGCCCTGGACAAGGG CTTGTGTGGATGGGTGGATCAGCCCTAACAGT GGTGACACAAAGCTATGCACAGAAATTTACAGGAC AGGTCAACATGACCAAGGACACGTCCATCAGC ACAGCCTATATGAGCTGAGCAGACTGAGATCT GACGACACGGCCGTGATTTCTGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGAAACCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCTCTCTCCAAGAGCACCTCTGGGGG CACAGCGCCCTGGGTGCTGCTGGTCAAGGACTA CTTCCCGCAACCGGTGACGGTGTCTGTGGAACTC AGCGCCCTGACCAAGCGGCTGCACACCTTCCC GGTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCAAGACCTACATCTGCAACGTGAATCAC AAGCCCAACAACCAAGGTGGACAAAGAAAGT TGAGCCCAATCTTGTGACAAACTCACACATG CCCACCGTGCCCAAGCACCTGAACTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGACGTGAGCCACGAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCAGTACCGTTGTGTC AGCTCTCTACCGTCTTGCACCAAGACTGGCTG AATGGCAAGGAGTCAAGTGAAGGTCTCCAAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGCAAGCCCCGAGAACCCACA GGTGTACACCTGCCCTCCATCCCGGAGGAGAT GACCAAGAACCAAGGTGAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGAACAACT</div>

A-2124-WO-PCT

				ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGAGAAGAGCCTCTCCCTGTCTCCGGG TAAA
			SEQ ID NO: 1987	SEQ ID NO: 2144
			DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLA WYQQKPGQPPNLLIYWTSRDSGVDRFSG SGSGTDFTLTINSLQAEDVA VYQCQQY YRTPWTF GQGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSYLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLVWMGWISPNSGDTSYAQKFQDR VTMTRDTSISTAYMELSRRLSDDTA VYFCAREATI FGMLIVPFDYWGGQTLVTVSSASTKGPSVFPLAPS SKSTSGGT AALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPGK
		AA	SEQ ID NO: 417	SEQ ID NO: 574
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGCGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAGAACTACTTAGCTTGGTACC AACAG AAACAGGACAGCCTCCTAAACTGCTCATTTAC TGGACTTCTACCCGAGAAATCCGGGGTCCCTGAC CGATTGAGTGCGAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAAGGCTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTCCGGCC AAGGACCAAGGTGG AAATCAAAACGAAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGA ACTGCCCTCTGTTGTGTGCCTGCTGAATAAC TTCTATCCACAGAGAGGCCAAAGTACAGTGAAG	CAGGTGCAGCTGGTACAGTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATACACTGGGTGCTCAGGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATCAGCCCTAACAGT GGTGAAACAAGCTATGCACAGAA GTTTCAGGAC AGGTACACCATGACACAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGCCTGAGATCT GACGACACGGCGGTGATTCTGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGAAACCTGGTACCGTCT CCTCAGCCTCCACCAAGGGCCATCGGTCTTCCC CCTGGCACCTCTCTCC AAGAGCACCTCTGGGGG CACAGCGGCCCTGGGCTGCCCTGGTCAAGGACTA
IPS:359703	11C1.009	NA		

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	<p>GTGGATAACGCCCTCC AATCGGGTAACTCCACAG GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCTGACGGCTGAG CAAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCAACCATCAGGGCCTGAGCTCGC CCGTCAACAAAGAGCTTCAACAGGGGAGAGTGT</p>	<p>CTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTC AGCGCCCTGACCAGCGGGCTGCACACCTTCCC GGTGTCTACAGTCTCAGGACTCTACTCCCTC AGACGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAGAAAGT TGAGCCCAATCTTGTGACAAACTCACACATG CCCACCGTGCCACAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGACGTGAGCCACGAAAGAC CCTGAGGTCAAGTTC AACTGGTACGTGGACGGC GTGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCTCTCTACCGTCTTGCACCAAGGACTGGCTG AATGGCAAGGAGTACAAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGCGACCCCGAGAACACACA GGTGTACACCTGCCCTCCCATCCCGGAGGAGAT GACCAAGAACAGGTGACGCTGACCTGCCTGGT CAAAGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGCGAGCCGGAGACAACCT ACAAGACCAGCTTCCCGTGTGGACTCCGACG GCTCTTCTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAAGAGCCTCTCCCCTGTCTCCGGG TAAA</p>
	<p>SEQ ID NO: 1988</p>	<p>SEQ ID NO: 2145</p>
AA	<p>DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYLA WYQQKPGQPPKLLIYWTSRESGVPDFSG SGSGTDFTLTINSLQAEDVA VYYCQQYYRTPTWTF GQGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVC LLNFPYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYLSSTLTLSKADYEKHKVYACEVTHQQLSS PVTKSFNRGEC</p>	<p>QVQLVQSGAEVKKPGASVKVSKASGYTFTGYYI HWVRQAPGQGLEWMGWISPNSETSYAQKFKDR VTMTRDTSISTAYMELSSLRDSDTAVYFCAREATI FGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL</p>

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				GGPSVFLFPPKPKD TLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVVFSCSVMHEALHNHYTQKS LSLSPGK		
			SEQ ID NO: 418	SEQ ID NO: 575		
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGGCAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAAGAACTACTTAGCTTGGTACCAACAG AAACCAAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGAAATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGTCTGGGACAGATTTTC ACTCTACCATCAACAGCCTGCGAGGCTGAAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTCTGGCCAAAGGACCAAGGTGG AAATCAAAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACCTGCCCTCTGTTGTGTGCCTGCTGAATAAC TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAG GTGGATAACGCCCTCCAAATCGGGTAACCTCCCAG GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCCCTGACGCTGAG CAAAAGCAGACTACGAGAAACACAAGTCTACG CCTGCGAAGTCAACCATCAGGGCCTGAGCTCGC CCGTCAAAAGAGCTTCAACAGGGGAGAGTGT	NA	11C1.010	IPS:361305
				CAGGTGCAGCTGGTACAGTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGTCTCCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATACACTGGGTGCGTCAAGCCCCCTGGACAAGGG CTTGAGTGGATGGGTGGATCAGCCCTAACAGT GGTGAAACAAGCTATGCACAGAAGTTTCAGGAC AGGGTCAACCATGACCAGGGGACACGTCCATCAGC ACAGCCTATATGAGCTGAGCAGACTGAGATCT GACGACACGGCCGTGTATTTCTGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCAATTTG ACTACTGGGGCCAGGAAACCTGGTCAACCGTCT CCTCAGCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGACCCCTCCTCCAAGAGCACCTCTGGGGG CACAGCGCCCTGGGTGCGCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTGTTGGAACTC AGCGCCCTGACCAAGCGGTGCACACCTTCCC GGCTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCTGGTGACCGTGCCTTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCCCAGCAACACCAAGGTGGACAAGAAAAGT TGAGCCCCAAATCTTGTGACAAAACTCACACATG CCCACCGTGCCCAAGCACCTGAACTCCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTG ACATGCGTGGTGGAGCTGAGCCACGAAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC		

A-2124-WO-PCT

				<p>AGCGTCCTCACCGTCTCTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAAGTGCAAGGTCTCCAAC AAGCCCTCCAGCCCATCGAGAAACCATC TCCAAGCCAAAGGCAGCCCCGAGAACACA GGGTACACCTGCCCATCCCGGAGGAGAT GACCAAGAACAGGTACGCTGACCTGCCTGGT CAAGGCTTCTATCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGCAGCCGGAGAACAACT ACAAGACCAGCTCCCGTGTGGACTCCGACG GCTCTTCTCTCTATAGCAAGCTACCCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGATGAGGCTCTGCACAACCA CTACACGAGAAAGAGCCTCTCCCTGTCTCCGGG TAAA</p>
				<p>SEQ ID NO: 1989</p> <p>DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSTRESGVDRFSG SGSGTDFTLTINSLQAEDVAVYCCQQYYRTPWTF GQGTKVEIKRTVAAPSVFIAPPDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSYSTLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC</p>
			AA	<p>SEQ ID NO: 2146</p> <p>QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWISPNSETSYAQKFKDR VTMTRDTSISTAYMELSRRLSDDTAVYFCAREATI FGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPGK</p>
				<p>SEQ ID NO: 576</p> <p>CAGTGCCGCTGGTGAGTCTGGGGCTGAGGTG AAGAAGCCTGGGCCCTCAGTGAAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATCCACTGGGTGCGACAGGCCCTTGACAAAGGA CTTGAGTGGATGGGTGGATCAACCCCTGAAAGT GGTGGCACAGACTATTACACAGAGGTTTCAGGGC</p>
			NA	<p>SEQ ID NO: 419</p> <p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAGAACTACATAGCTTGGTACCAGCAG AAACCAGGACATCCTCCTAAGCTGCTCATTTACT GGGCATCTACCCGGGAATCCGGGTCCCTGACC</p>
		13H12.002	IPS:361312	

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GATTCAGTGGCAGCGGTCTGGGACAGATTTCATCTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTTTACTGTCAACAATATTATAGTACTCCGTGGACGTTCCGCCAAGGGACCAAGGTGGAATCAAACGAACGGTGGCTGCACCATCTGTCTTCATCTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCCTGTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCCAATCGGGTAACCTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	AGGGTCACCATGACCAGGACACAGTCCATCAGCACAGCCTACATGGAACCTGAGCAGGCTGAGATCTGACGACACGGCCGTGATTACTGTGCGAGAGAGGCCACGATTTTGGAAATGGTTATTGTACCGTTTGACTACTGGGGCCAGGAACCCCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGGAACTCAGCGCCCTGACCAGCGGCTGCACACCTTCCCAGGTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAAGCCAGCAACCAAGGTGGACAAAGAAAGTTGAGCCCAATCTTGTGACAAACTCACACATGCCACCGTGCCAGCACCTGAACCTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCCAAAGGACCCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGAGCGTGAGCCACGAAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGAGGTGCATAATGCCAAGACAAGCCGTGTGAGGAGCAGTACGGCAGCACGTACCGTTGTGTCAGCTCCTCACCGTCTTGCAACAGGACTGGCTGAATGGCAAGGAGTACAAAGTGCAAGGTCTCCAAAGCCCTCCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCCAGGTGTACCCCTGCCCATCCCGGGAGGAGATGACCAAGAACAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGACAACACTCAAGACCACGCCCTCCCGTGTGGACTCCGACGGCTCTTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAAGAGCCTCTCCCTGTCTCCCGG
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TAAA

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		SEQ ID NO: 1990	SEQ ID NO: 2147
	AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQKPGHPPKLLIYWASTRESGVPDFRSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYI HWVRQAPGQGLEWMGWINPESGGTDYVSRFQGR VTMTRDTSISTAYMELSRRLSDDTAVYYCAREATI FGMVVPFDYWGGQGLVKDYFPEPVTVSWNSGALTS SKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTKISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPGK
	NA	SEQ ID NO: 420	SEQ ID NO: 577
IPS:359744	13H12.003	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCCTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG AAACAGGACATCCTCCTAAGCTGCTCATTTACT GGGCATCTACCCGGGAATCCGGGTCCCTGACC GATTCAGTGGCAGCGGTCTGGGACAGATTCA CTCTCAACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAGGGACCAAGGTGGA AATCAACGAACGGTGGCTGCACCATCTGTCTT CATCTTCCCGCCATCTGATGAGCAGTTGAAATCT GGAACTGCCCTCTGTTGTGTGCTGCTGAATAACT TCTATCCAGAGAGGCCAAAGTACAGTGGAAAG TGGATAACGCCCTCCAATCGGGTAACCTCCAGG AGAGTGTACAGAGCAGGACAGCAAGGACAGC ACCTACAGCCTCAGCAGCACCCTGACGCTGAGC AAAGCAGACTACGAGAAACACAAAGTCTACGC CTGCGAAGTCAACCCATCAGGGCCTGAGCTCGCC CGTCACAAAGAGCTTCAACAGGGGAGAGTGT	CAGTGCCGCTGGTGCGAGTCTGGGGCTGAGGTG AAGAAGCTGGGGCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATCCACTGGTGCGACAGGCCCTGGACAAAGGA CTTGAGTGGATGGGTGGATCAACCTGAAAGT GGTGGCACAGACTATTACAGAGGTTTCAGGGC AGGTTACCATGACCAAGGACACGTCATCAGC ACAGCTACATGGAATGAGCAGGCTGAGATCT GACGACAGGCCGCTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCTGGTACCGTCT CCTCAGCCTCCACCAAGGCCCATCGGTCTTCCC CCTGGCACCTCTCCACAGAGCACCTCTGGGGG CACAGCGCCCTGGGCTGCCCTGGTCAAGGACTA CTTCCCAGAACCGGTGACGGTGTGCGTGGAACTC AGCGCCCTGACCAAGCGGTGCAACACCTTCCC GGCTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGACAAAGAAAGT

[illegible]

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					SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
					SEQ ID NO: 578
					CAGTGCCGCTGGTGCACTCTGGGGCTGAGGTG AAGAAGCTGGGGCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATCCACTGGTGCAGACGGCCCTGGACAAAGGA CTTGAGTGGATGGGTGGATCAACCTTGACAGT GGTGGCACAGACTATTACACAGAGGTTTCAGGGC AGGTACCATGACACAGGACACGTCCATCAGC ACAGCTACATGGAACCTGAGCAGGCTGAGATCT GACGACACGGCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGAAACCTGGTCACCGTCT CCTCAGCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGACCCCTCCTCCAAGAGCACCTCTGGGGG CACAGCGCCCTGGGTGCTGGTCAAGGACTA CTTCCCGAACCGGTGACGGTGTCTGGAACTC AGCGCCCTGACACAGCGGTGACACACCTTCCC GGTGTCTCAGTCTCAGGACTCTACTCCCTC AGCAGGTGGTGACGTGCTCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCACGACACCAAGGTGGACAAAGAAAGT TGAGCCCAATCTTGTGACAAACTCACACATG CCCACCGTGCCAGCACCTGAACTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGTGACGTGAGCCACGAAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGGTCTCTACCGTCTTGCACCAAGGACTGGCTG AATGGCAAGGAGTCAAGTGAAGGTCTCCAAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACCCACA GGTGTACACCCCTGCCCCCATCCCCGGGAGGAGAT
					SEQ ID NO: 421
					GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTATATCCAGCTCC AACATAAAGAACTACATAGCTTGGTACCAGCAG AAACAGGACATCTCTCCTAAGCTGCTCATTTACT GGGCATCTACCCGGGAATCCGGGTCCCTGACC GATTCAAGTGGCAGCGGTCTGGGACAGATTTC CTCTACCATCAGCAGCTGCAAGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAAAGGACCAAGGTGGA AATCAACGAAACGGTGGCTGCACCATCTGTCTT CATCTTCCCGCCATCTGATGAGCAAGTTGAAATCT GGAACCTGCTCTGTGTGTGCTGCTGAATAACT TCTATCCAGAGAGGCCAAAGTACAGTGGAAAG TGGATAACGCCCTCCAATCGGGTAACCTCCAGG AGAGTGTACAGAGCAGGACAGCAAGGACAGC ACCTACAGCTCAGCAGCACCTGACGCTGAGC AAAGCAGACTACGAGAAACACAAAGTCTACGC CTGCGAAGTCAACCCATCAGGGCCTGAGCTCGCC CGTCACAAAGAGCTTCAACAGGGGAGAGTGT
				NA	
			13H12.004		
				IPS:361319	

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				<p>SEQ ID NO: 1992</p> <p>DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQKPGHPPKLLIYWASTRESGVPDFRFGS GSGTDFLTIISSLAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC</p>	<p>SEQ ID NO: 1992</p> <p>GACCAAGAACCAAGGTGAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGCAGCCGGAGAACAACT ACAAGACCACGCTCCCGTCTGCTGACTCCGACG GCTCCTTCTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGATGAGGCTCTGCACAACCA CTACACGAGAAAGCCCTCTCCCTGTCTCCGGG TAAA</p>
AA				<p>SEQ ID NO: 2149</p> <p>QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWINPDSGGTDYSQRFQGR VTMTRDTSISTAYMELSRLSDDTAVYYCAREATI FGMVIVPFDYWGQGLVKDYFPEPVTVSWNSGALTS SKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPGK</p>	<p>SEQ ID NO: 2149</p> <p>QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWINPDSGGTDYSQRFQGR VTMTRDTSISTAYMELSRLSDDTAVYYCAREATI FGMVIVPFDYWGQGLVKDYFPEPVTVSWNSGALTS SKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPGK</p>
!PS:359737	13HI2.005	NA		<p>SEQ ID NO: 422</p> <p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGCTCTGGCGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAGAACTACATAGCTTGGTACCAGCAG AAACAGGACAACTCTCTAAAGCTGCTCATTTAC TGGGCATCTACCCGGGAAATCCGGGGTCCCTGAC CGATTCAAGTGCGAGCGGGTCTGGGACAGATTTC ACTCTCAACCATCAGCAGCCTGCAAGGCTGAAGAT GTGGCAGTTTTTTACTGTCAACAATATTATAGTA CTCCGTGGACGTTCCGGCCAAGGGACCAAGGTGG AAATCAACGAACGGTGGCTGCACCATCTGTCT</p>	<p>SEQ ID NO: 579</p> <p>CAGGTGCAGTGGTGAGTCTGGGGCTGAGGTG AAGAAGCCTGGGCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATCCACTGGTGCGACAGGCCCTGGACAAAGGA CTTGAGTGGATGGGTGGATCAACCTGAAAGT GGTGGCACAGACTATTACAGAGGTTTCAGGGC AGGTACACCATGACAGGACACGTCCTCATCAGC ACAGCTACATGGAAGTGAAGCAGCTGAGATCT GACGACACGGCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCTGCTACCGTCT</p>

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	TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACCTGCCCTGTGTGCTGCTGCTGAATAAC TTCTATCCAGAGAGGCCAAAGTACAGTGGAAG GTGGATAACGCCCTCCAAATCGGGTAACTCCAG GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCAACCCATCAGGGCCTGAGCTCGC CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGG CACAGCGCCCTGGGCTGCCGTGGTCAAGGACTA CTTCCCGCAACCGGTGACGGTGTCTGTGGAATC AGCGCCCTTGACAGCGGGCTGCACACCTTCCC GGTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCAATCTTGTGACAAACTCACACATG CCCACCGTGCCAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCCGACCCCTGAGGTC ACATGCGTGGTGGACGTGAGCCACGAAAGAC CCTGAGGTCAGTTCACTGGTACGTGGACGGC GTGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCTCTCACCCTCTGCACCAAGGACTGGCTG AATGGCAAGGAGTACAAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGCGAGCCCCGAGAACACAA GGTGTACACCTGCCCTCCATCCCGGAGGAGAT GACCAAGAACAGGTGACGCTGACCTGCCTGGT CAAAGGCTTCTATCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGAGCGCGGAGAACAACT ACAAGACACGCTTCCGTGCTGGACTCCGACG GCTCTTCTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGCTTCTC ATGCTCCGTGATGATGAGGCTCTGCACAACCA CTACACGAGAAAGAGCCTCTCCCCTGTCTCCGGG TAAA
	SEQ ID NO: 1993	SEQ ID NO: 2150
AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQKPGQPPKLLIYWASTRESGVPDFRSGS GSGTDFLTLSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL	QVQLVQSGAEVKKPGASVKVSKKASGYTFTGYYI HWVRQAPGQGLEWMGWINPESGTDYSQRFQGR VTMTRDTSISTAYMELSSLRDSDTAVYYCAREATI FGMVIVPFDYWGQGLVTVSSASTKGPSVFPLAPS

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			<p>NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEHKVKVYACEVTHQGLSSP VTKSFNRGEC</p>	<p>SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVLELPPKPKDITLISRTPETVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFNCSVMHEALHNHYTQKS LSLSPGK</p>
<p>IPS:361326</p>	<p>13H12.006</p>	<p>NA</p>	<p>SEQ ID NO: 423</p> <p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGCGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG AAACGAGGACAACCTCCTAAGCTGCTCATTTAC TGGGCATCTACCCGGGAATCCGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAAGGCTGAAGAT GTGGCAGTTTTTTACTGTCAACAAATATTATAGTA CTCCGTGGACGTTCCGGCCAAAGGACCAGGTGG AAATCAAAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACCTGCCCTCTGTTGTGTGCTGCTGATTAAC TTCTATCCAGAGAGGCCAAAGTACAGTGGAAAG GTGGATAACGCCCTCCAAATCGGGTAACTCCACAG GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCCTGACGCTGAG CAAAAGCAGACTACGAGAAACACAAGTCTACG CCTGCGAAGTCAACCATCAGGGCCTGAGCTCGC CCGTCAACAAAGAGCTTCAACAGGGGAGAGTGT</p>	<p>SEQ ID NO: 580</p> <p>CAGTGCCGCTGGTGCGAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATCCACTGGTGCGACAGGCCCTGGACAAGGA CTTGAGTGGATGGGTGGATCAACCTGAAAGT GGTGGCACAGACTATTCACAGAGGTTTCAGGGC AGGTACCATGACACAGGACACGTCATCAGC ACAGCTACATGGAACCTGAGCAGGCTGAGATCT GACGACACGGCGGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCTCCTCCAGAGCACCTCTGGGGG CACAGCGGCCCTGGGTGCTGGTCAAGGACTA CTTCCCGAAACCGGTGACGGTGTGCGGAACTC AGCGGCCCTGACCAAGCGGTGCAACCTTCCC GGTGTCTCTACAGTCTCAGGACTCTACTCCCTC AGCAGGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACCAAGGTGGACAAGAAAGT TGAGCCCAATCTTGTGACAAACTCACACATG CCCACCGTGGCCAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTCT ACATGCGTGGTGGTGACGTGAGCCACGAGAC</p>

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			<p>SEQ ID NO: 1994</p> <p>DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQKPGQPPKLLIYWASTRESGVPDFRSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC</p>	<p>SEQ ID NO: 2151</p> <p>QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRAQPGQGLEWMGWINPESGTDYISQRFQGR VTMTRDTSISTAYMELSRLSDDTAVYYCAREATI FGMVIVPFDYWGQGLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLMISRTPETCVVDVSHED PEVKFNWYVDGVEVHNATKTPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVVFSCSVMEALHNHYTQKS LSLSPGK</p>
		AA	<p>SEQ ID NO: 424</p>	<p>SEQ ID NO: 581</p>

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IP:361330	12H11.002	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCCTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAGAACTACTTAGCTTGGTACCAGCAG AAACCAGGACAGCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCC TGAC CGATTCA GTGGCAGCGGGTCTGGGACAGATTTC ACTCTACCATCAACAGCCTGCAAGGCTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACC AAGGTGG AAATCAAACGAAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACTGCC TCTGTTGTGTGCTGCTGAATAAC TTCTATCCAGAGAGGCCAAAGTACAGTGGAAG GTGGATAACGCCCTCC AATCGGGTAACTCCCAAG GAGAGTGCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCCCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCACCCCATCAGGGCCTGAGCTCGC CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT
			CAGTGCCCGCTGGTGCGAGTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGTACTAT ATACACTGGTGCGTCAGGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATAAGCCCTAACCAA GGTGAAACA AACTATGCACAGAA GTTTTCAGGAC AGGTCAACCATGACCAGGACACGTCCATCAGC ACAGCCTATATGAGCTGAGCAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGAAACCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGG CACAGCGCCCTGGGTGCC TGGTCAAGGACTA CTTCCCGCAACCGGTGACGGTGTCTGGAACTC AGCGCCCTGACCAAGCGGCTGCACACCTTCCC GGTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCAAGACCTACATCTGCAACGTGAATCAC AAGCCCAACAACCAAGGTGGACAAGAAAGT TGAGCCCAAATCTTGTGACAAACTCACACATG CCCACCGTGCCCAAGCACCTGA ACTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAA AACCC AAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGGACGTGAGCCACGAAGAC CCTGAGGTC AAGTTC AACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACA AAGCCGTGT GAGGAGCAGTACGGCAGCAGTACCGTTGTGTC AGCTCCTCACCGTCTTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACACACA GGTGTACACCTGCCCCCATCCCGGGAGGAGAT GACCAAGAACCAAGGTGAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGACAACACT

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			<p>ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGAACGTCTTCTC ATGCTCCGTGATGATGAGGCTCTGCACAACCA CTACACGAGAAAGCCCTCTCCCCTGTCTCCGGG TAAA</p> <p>SEQ ID NO: 2152</p> <p>QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPQGGLWGMWISPNQGETNYAQKFQD RVMTTRDTSISTAYMELSRLSDDTAVYYCAREA TIFGMLIVPFDYWGGTTLVTYSSASTKGPSVFPLA PSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDITLMISRTPETCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGPQREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEVESNGQPENNYKTTTPVLDSDGSFEL YSKLTVDKSRWQQGNVVFSCSVMEALHNHYTQK SLSLSPGK</p>
		AA	<p>SEQ ID NO: 1995</p> <p>DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPNNLIYWTSTRDSGVDPDRFSG SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPTWTF GQGTKVEIKRTVAAPSVFIPTPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSITYLSSTLTLSKADYEKHKVYACEVTHQQLSS PVTKSFNRGEC</p>
		NA	<p>SEQ ID NO: 425</p> <p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAAGAACTACTTAGCTTGTAACGACAG AAACCAGGACAGCTCCTAACCTGCTCATTAC TGGACTTCTACCCGAGATTCCGGGGTCCCAGAC CGATTGAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCCTGCAAGGCTGAAGT GTGGCTGTTTATTACTGTGCAATATTATCGTA CTCCGTGGACGTTCCGCCAAGGGACCAAGGTGG AAATCAAAACGAACGGTGGTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACCTGCTCTGTGTGTGCTGCTGCTGAATAAC TTCTATCCAGAGAGGCCAAAGTACAGTGAAG</p>
IPS:361337	12H11.003		<p>SEQ ID NO: 582</p> <p>CAGGTCCCGCTGGTGCGAGTCTGGGGCTGAGGTG AAGAAGCCTGGGCGCTCAGTGAAGTCTCCTGC AAGGCTTCTGGATACACCTTCACCCGGCTACTAT ATACACTGGTGCGTCAAGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATAAGCCCTAACCAA GGTGACACAACTATGCACAGAAAGTTTCAGGAC AGGTCAACCATGACAGGACACGTCCTCAGC ACAGCCTATATGAGCTGAGCAGGCTGAGATCT GACGACACGGCGGTGATTACTGTGCGAGAGAG GCCACGATTTTGGAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGAACCCCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCCTCCTCCAAAGACACCTCTGGGGG CACAGCGGCCCTGGGCTGCCCTGGTCAAGGACTA</p>

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	<p>GTGGATAACGCCCTCC AATCGGGTAACTCCCAG GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCAACCATCAGGGCCTGAGCTCGC CCGTCAACAAAGAGCTTCAACAGGGGAGAGTGT</p>	<p>CTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTC AGCGCCCTGACCAGCGGGCTGCACACCTTCCC GGTGTCTACAGTCTCAGGACTCTACTCCCTC AGACGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCAATCTTGTGACAAACTCACACATG CCCACCGTGCCAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGACGTGAGCCACGAAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCTCTCTACCGTCTTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGCGAGCCCCGAGAACACACA GGTGTACACCTGCCCTCCCATCCCGGAGGAGAT GACCAAGAACAGGTGACGCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAAGCCGGAGACAACCT ACAAGACCAGCTTCCCGTGTGGACTCCGACG GCTCTTCTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAAGAGAGCCTCTCCCCTGTCTCCGGG TAAA</p>
	<p>SEQ ID NO: 1996</p> <p>DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLA WYQQKPGQPPNLLIYWTSTRDSGVPDFSG SGSGTDFTLTINSLQAEDVA VYYCQQYYRTPTWTF GQGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVC LLNFPYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC</p>	<p>SEQ ID NO: 2153</p> <p>QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYI HWVRQAPGQGLEWMGWISPNQGDNTYAQKFQD RVMTTRDTSISTAYMELSLRSDDDTA VYYCAREA TIFGMLIVPFDYWGQGLTVTVSSASTKGPSVFPLA PSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL</p>

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				LGPSVFLFPPKPKDTLMISRTPVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFEL YSKLTVDKSRWQQGNVFCFVSMHEALHNHYTQK SLSLSPGK
				SEQ ID NO: 426 GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGCGAGAGGGCCACCAATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAGAACTACTTAGCTTGGTACCAGCAG AAACGAGGACAGCTCTCAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGTCCCTGAC CGATTGAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTACCATCAACAGCCTGCAAGGCTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTCCGGCCAGGGACCAAGGTGG AAATCAACAGAACGGTGGTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACCTGCCCTCTGTTGTGTGCCTGCTGAATAAC TTCTATCCAGAGAGGCCAAAGTACAGTGGAAAG GTGGATAACGCCCTCCATCGGGTAACTCCCGAG GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCCCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAGTCTACG CCTGCGAAGTCAACCATCAGGGCCTGAGCTCGC CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT
				NA
		12H11.004	IPS:361344	SEQ ID NO: 583 CAGTGCCGCTGGTGCACTCTGGGGCTGAGGTG AAGAAGCTGGGGCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATACACTGGTGCGTCAGGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATAAGCCCTAACCAA GGTGAAACAACATATGCACAGAAAGTTTCAGGAC AGGTACCATGACACAGGACACGTCCTCATCAGC ACAGCCTATATGAGCTGAGCAGGCTGAGATCT GACGACACGGCGTGATTACTGTACGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCAATTG ACTACTGGGCCAGGAAACCTGGTCACCGTCT CCTACGCTCCACCAAGGGCCATCGGTCTTCCC CCTGGACCCCTCCTCCAAGAGCACCTCTGGGG CACAGCGCCCTGGGTGCTGCTGGTCAAGGACTA CTTCCCGAACCGGTGACGGTGTGTCGAGAACTC AGCGCCCTGACCAAGCGGCTGCACACCTTCCC GGTGTCTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCCAAGCAACCAAGGTGGACAAAGAAAGT TGAGCCCAATCTTGTGACAAACTCACACATG CCCACCGTGCCAGCACCTGAACTCTGGGGG ACCGTGAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTG ACATGCGTGGTGGACGTGAGCCACGAAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCAGTACCGTTGTGTC

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				AGCGTCCTCACCGTCTCTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCATCGAGAAAACCATC TCCAAAGCCAAAGGCAGCCCCGAGAACACA GGGTACACCTGCCCATCCCGGAGGAGAT GACCAAGAACAGGTACGCTGACCTGCCCTGGT CAAAGGCTTCTATCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGAACAACT ACAAGACCACGCCCTCCCGTGTGGACTCCGACG GCTCCTTCTTCTCTATAGCAAGCTACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCAATGAGGCTCTGCAACAACA CTACACGCAGAAAGAGCCTCTCCCTGTCTCCGGG TAAA	
				SEQ ID NO: 1997	SEQ ID NO: 2154
			AA	DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLA WYQQKPGQPPNLLIYWTSTRDSGVDRFSG SGSGTDFTLTINSLQAEDVA VYQCQQYYRTPTWF GQGTKVEIKRTVAAPS VFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC	QVPLVQSGAEVKKPGASVKVSKASGYTFTGYI HWVRQAPGQGLEWMGWISPNQGETNYAQKFQD RVTMRDTSISTAYMELSLRSLDDTA VYCTREA TIFGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGT AALGCLVKDYFPEPTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYIC NVN HKPSNTK VDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLEFPKPKDTLMISRTPETCVVVDVSH DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVVFSCSVMEALHNHYTQK SLSLSPGK
			NA	SEQ ID NO: 427	SEQ ID NO: 584
	12H11.005	IPS:361351		GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGCGGAGAGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACATAAGAACTACTTAGCTTGGTACCAAGCAG AAACCAAGGACAGCCTCCTAACCTTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC	CAGGTGCCGCTGGTGAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATACACTGGGTGCTCAGGCCCTTGACAAGGG CTTGAGTGGATGGGTGGATAAGCCCTAACAAAT GGTGAAACAAACTATGCACAGAAAGTTTCAGGAC

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CGATTTCAGTGGCAGCGGGTCTGGGACAGATTTTC ACTCTCACCATCAACAGCCTGCAAGGCTGAAGAT GTGGCTGTTTATTACTGTACGCAATATTATCGTA CTCCGTGGACGTTTCGGCCAAAGGACCACAGGTGG AAATCAAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACTGCCCTCTGTTGTGTGCCTGCTGAATAAC TTCTATCCAGAGAGGCCAAAGTACAGTGGAAAG GTGGATAACGCCCTCCAATCGGGTAACTCCCCAG GAGAGTGTACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCCCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCAACCCATCAGGGCCTGAGCTCGC CCGTACAAAGAGCTTCAACAGGGGAGAGTGT	AGGGTCACCATGACCAGGACACGTCCTCATCAGC ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT GACGACACGGCCGTGATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGAAACCCCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGG CACAGCGGCCCTGGGCTGCCCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCTGTGGAACTC AGCGCCCTGACCAAGCGGCTGCACACCTTCCC GGTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCAATCTTGTGACAAACTCACACATG CCCACCGTGCCCAAGCCTGAACTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGAGCGTGAGCCACGAAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCAGTACCGTTGTGTG AGCTCCTCACCGTCTTGCAACAGGACTGGCTG AATGGCAAGGAGTCAAGTGCAGGTCTCCAAAC AAAGCCCTCCAGCCCCCATCGAGAAACCCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACCCACA GGTGTACACCTGCCCTCCATCCCGGAGGAGAT GACCAAGAACAGGTGAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGAACAACT ACAAGACCAGCCTCCCGTGTGGACTCCGACG GCTCCTTCTCTCTATAGCAAGCTCACCCTGGA CAAAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAAGAGACCTCTCCCTGTCTCCCGG TAAA
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			SEQ ID NO: 1998	SEQ ID NO: 2155
	AA		DIVMTQSPDLSVSLGERATINCKSSQSVLSNNK NYLAWYQQKPGQPPNLLIYWTRSDSGVDRFSG SGSGTDFTLTINSLQAEDVAVYCCQQYYRTPWTF GQGTKVEIKRTVAAPSVFIIPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSYLSSTLTLSKADYEKHKVYACEVTHQQLSS PVTKSFNRGEC	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYI HWVRQAPGQGLEWMGWISPNNGETNYAQKFQD RVMTTRDTSISTAYMELSRRLSDDTA VYVCAREA TIFGMLIVPFDYWGQGLTVTVSSASTKGPSVFPLA PSSKSTSGGTAAALGCLVKDYFPEPTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNHNKPSNTKVDKKVEPKSCDKTHTCPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK FYPSDIAVEVESNGQPENNYKTTPPVLDSDGSF YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK
	NA	12H11.006	SEQ ID NO: 428	SEQ ID NO: 585
IPS:361358			GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGCGAGAGGGCCACCAATCAAC TGCAAGTCCAGCCAGAGTGTATCCAGCTCC AACATAAGAACTACTTAGCTTGGTACCAGCAG AAACGAGGACAGCTCTCACTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGTCCCTGAC CGATTGAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTACCATCAACAGCCCTGCAAGGCTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTCCGGCCAGGGACCAAGGTGG AAATCAACGAAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACCTGCTCTGTGTGTGCTGCTGCTGAATAAC TTCTATCCAGAGAGGCCAAAGTACAGTGGAAG GTGGATAACGCCCTCCAAATCGGGTAACTCCAG GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCCTGACGCTGAG CAAAAGCAGACTACGAGAAACACAAGTCTACG CCTGCGAAGTCAACCAATCAGGGCCTGAGCTCGC CCGTCAAAAGAGCTTCAACAGGGGAGAGTGT	CAGTGCCGCTGGTGAGTCTGGGGCTGAGGTG AAGAAGCTGGGGCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATACACTGGTGCGTCAGGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATAAGCCCTAACAAAT GGTGACACAACTATGCACAGAAAGTTTCAGGAC AGGTCAACATGACACAGGACACGTCATCAGC ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT GACGACACGGCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCAATTG ACTACTGGGCCAGGGAACCCCTGGTACCGTCT CCTCAGCCTCCACCAAGGCCCATCGGTCTTCCC CCTGGACCCCTCCTCCAAGAGCACCTCTGGGGG CACAGCGCCCTGGGTGCGGTGCTGCGTGAAGACTA CTTCCCGAAGCGGTGACGGTGTGCGTGAAGACTC AGCGCCCTGACCAAGCGGTGTGCAACACCTTCCC GGCTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCTGGTGACCGTGCCCTCCAGCAGCCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAAGAAAGT

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					TGAGCCCAAATCTTGTGACAAAACTCACACATG CCCACCGTGCCACAGCACCTGAACCTCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGACGTGAGCCACGAAGAC CCTGAGGTCAGTTCAACTGGTACGTGGACGGC GTGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCTCTCACCGTCTTGCACCAAGACTGGCTG AATGGCAAGGAGTACAAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGCAGCCCCGAGAACACACA GGTGTACACCTGCCCTCCCATCCCGGAGGAGAT GACCAAGAACAGGTACGCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGAGCCGGAGAACAACT ACAAGACCAGCTTCCCGTGTGCTGACTCCGACG GCTCTTCTTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGATGAGGCTCTGCACAACCA CTACACGAGAAAGAGCCTCTCCCCTGTCTCCGGG TAAA
				SEQ ID NO: 1999	SEQ ID NO: 2156
				DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLA WYQQKPGQPPNLLIYWTSTRDSGVPDFSG SGSGTDFLTINSLQAEDVA VYQCQQYYRTPTWTF GQGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVC LLNFIYPREA KQWKVDNALQSGNSQESVTEQDS KDSYLSSTLTLSKADYEKHKVYACEVTHQQLSS PVTKSFNRGEC	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWISPNNGDTNYAQKFQD RV/TMTRDTSISTAYMELSRLSDDTA VYYCAREA TIFGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPEL LGGPSVFLEPPPKKDTLMISRTPETCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFL
			AA		

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					YSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQK SLSLSPGK
					SEQ ID NO: 586
					CAGTGCCGCTGGTGCAAGTCTGGGGCTGAGGTG AAGAAGCTGGGGCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATACACTGGTGCGTCAAGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATAAGCCCTAACCAA GGTGACACAACTATGCACAGAAATTTTCAGGAC AGGTACCATGACACAGGACACGTCCATCAGC ACAGCTATATGGAGCTGAGCAGGCTGAGATCT GACGACACGGCGGTGATTAATGTACGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCAATTTG ACTACTGGGCCAGGAAACCTGGTCAACCGTCT CCTCAGCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGACCCCTCCTCCAAGAGCACCTCTGGGGG CACAGCGCCCTGGGTGCTGCTGGTCAAGGACTA CTTCCCGAACCGGTGACGGTGTCTGGAACTC AGCGCCCTGACACAGCGGTGACACACCTTCCC GGTGTCTCAGTCTCAGGACTCTACTCCCTC AGCAGGTGGTGACGTGCTGCTCCAGCAGCTTG GGCACCAGACCTACATCTGCAACGTGAATCAC AAGCCACGACACCAAGGTGGACAAAGAAAGT TGAGCCCAATCTTGTGACAAACTCACACATG CCCACCGTGCCAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGTGACGTGAGCCACGAAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGGTCTCTACCGTCTTGCACCAAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAGCCAAAGGGCAGCCCCGAGAACACACA GGTGTACACCCCTGCCCCCATCCCCGGGAGGAGAT
					SEQ ID NO: 429
					GACATCGTGAATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTATATCCAGCTCC AACATAAAGAACTACTTAGCTTGGTACCAGCAG AAACGAGGACGCTCTCAACCTGCTCAATTTAC TGGACTTCTACCCGAGATTCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTT ACTCTACCATCAACAGCCTGCAAGGCTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTCCGGCCAGGGACCAAGGTGG AAATCAACGAAACGGTGGTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAAGTTGAAATC TGGAACCTGCTCTGTGTGTGCTGCTGCTGAATAAC TTCTATCCAGAGAGGCCAAAGTACAGTGGAAAG GTGGATAACGCCCTCCAATCGGGTAACTCCACAG GAGAGTGTACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCTGACGCTGAG CAAAAGCAGACTACGAGAAACACAAGTCTACG CCTGCGAAGTCAACCATCAGGGCTGAGCTCGC CCGTCAACAAGAGCTTCAACAGGGGAGAGTGT
				NA	
			12H11.007		
				IPS:361365	

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					<p>GACCAAGAACCAAGGTGACCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGCAGCCGGAGAACAACT ACAAGACCACGCTCCCGTGTGCTGACTCCGACG GCTCCTTCTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGATGAGGCTCTGCACAACCA CTACACGAGAAAGCCCTCTCCCTGTCTCCGGG TAAA</p>
					<p>SEQ ID NO: 2000</p> <p>DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRDSGVPDFSG SGSGTDFLTINSLQAEDVAVYQCQQYYRTPWTF GQGTKVEIKRTVAAPSVFIIPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSYLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC</p>
				AA	<p>SEQ ID NO: 2157</p> <p>QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYI HWVRQAPGQGLEWMGWISPNQGDINYAQKFQD RVTMTRDTSISTAYMELSRLSRDDTAVYCTREA TIFGMLIVPFDYWGGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAAALGCLVKDYFPEPTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH E DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFEL YSKLTVDKSRWQQGNVVFSCSVMEALHNHYTQK SLSLSPGK</p>
					<p>SEQ ID NO: 430</p> <p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGCGAGAGGCCACCAATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAGAACTACTTAGCTTGGTACCAGCAG AAACGAGGACAGCTCTCAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGTCCCTGAC CGATTCAAGTGCGAGCGGGTCTGGGACAGATTTC ACTCTCAACCATCAACAGCCTGCAAGGCTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTCCGGCCAAGGGACCAAGGTGG AAATCAACGAACGGTGGCTGCACCATCTGTCT</p>
IPS:361372	12H11.008	NA			<p>SEQ ID NO: 587</p> <p>CAGTGCCGCTGGTGAGTCTGGGGTGAGGTG AAGAAGCCTGGGCCCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATACACTGGTGCTCAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATAAGCCCTAACCAAT GGTGAAACAAACTATGCACAGAAAGTTTCAGGAC AGGTCAACATGACACAGGACACGTCCATCAGC ACAGCCTATATGAGCTGAGCAGGCTGAGATCT GACGACACGGCGGTGTATTACTGTACGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGCCAGGGAACCCCTGGTACCCGTCT</p>

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	<p>TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAAC TGCTGTGTGCTGCTGCTGAATAAC TTCTATCCAGAGAGGCCAAAGTACAGTGGAAG GTGGATAACGCCCTCCAAATCGGGTAACTCCAG GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCAACCCATCAGGGCCTGAGCTCGC CCGTCAACAAGAGCTTCAACAGGGGAGAGTGT</p>	<p>CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCTCTCTCCAAAGAGCACCTCTGGGGG CACAGCGGCCCTGGGCTGCTGGTCAAGGACTA CTTCCCAGAACCGGTGACGGTGTCTGGAACTC AGCGCCCTGACCAAGCGGCTGCACACCTTCCC GGTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCAATCTTGACAAACTCACACATG CCCACCGTGCCAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCCGACCCCTGAGGTC ACATGCGTGGTGGACGTGAGCCACGAAAGAC CCTGAGGTCAGTTCACTGGTACGTGGACGGC GTGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCTCTCTACCGTCTTGCAACAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAGCCAAAGGCGAGCCCCGAGAACACACA GGTGTACACCTGCCCTCCCATCCCGGAGGAGAT GACCAAGAACCAAGGTACGCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGAGCGCGGAGACAACAT ACAAGACCAGCTTCCCTGCTGGACTCCGACG GCTCTTCTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGAGAAAGACCTCTTCCCCTGTCTCCGGG TAAA</p>
	<p>SEQ ID NO: 2001</p>	<p>SEQ ID NO: 2158</p>
AA	<p>DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDFSG SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPTWF GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC</p>	<p>QVPLVQSGAEVKKPGASVKVSKKASGYTFTGYI HWVRQAPGQGLEWMGWISPNNGETNYAQKFQD RVMTTRDTSISTAYMELSLRSDDTAVYYCTREA TIFGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLA</p>

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			LLNFPYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYKHKVYACEVTHQGLSS PVTKSFNRGEC			PSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFCFVSMHEALHNHYTQK SLSLSPGK
			SEQ ID NO: 431 GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACTTAGCTTGGTACCAGCAG AAACCAAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGAAATCCGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTACGCAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCAAGGTGG AAATCAAAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACCTGCCCTCTGTTGTGTGCCCTGCTGAATAAC TTCTATCCCAAGAGAGGCCAAAGTACAGTGGAAAG GTGGATAACGCCCTCCAAATCGGGTAACCTCCCAG GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCTGACGCTGAG CAAAAGCAGACTACGAGAAACACAAGTCTACG CCTGCGAAGTCAACCATCAGGGCCTGAGCTCGC CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	12H11.009	IPS:361379	SEQ ID NO: 588 CAGGTGCCGCTGGTGCGAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATACACTGGTGCGTCAAGGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATAAGCCCTAACCAA GGTGAACAACAATATGCACAGAAATTTTCAGGAC AGGTACCATGACACAGGACACGTCCATCAGC ACAGCCTATATGAGCTGAGCAGGCTGAGATCT GACGACACGGCCGTGATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCAATTG ACTACTGGGGCCAGGGAACCTGGTCAACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCTCTCTCCAAGAGCACCTCTGGGGG CACAGGGCCCTGGGTGCCCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTGCGTGGAACTC AGGCGCCCTGACCAAGCGGCGTGCACACCTTCCC GGCTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCGTGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCCAAATCTTGTGACAAAACTCACACATG CCCACCGTGGCCAGCACCTGAACTCCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTCT ACATGCGTGGTGGACGTGAGCCACGAAAGAC

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			<p>SEQ ID NO: 2002</p> <p>DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSTRESGVDRFSG SGSGTDFTLTINSLQAEDVAVYCCQQYYRTPWTF GQGTKVEIKRTVAAPSVFIQPPSDEQLKSGTASVVC LLNFIYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC</p>	<p>SEQ ID NO: 2159</p> <p>QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGGGLEWMGWISPNQGETNYAQKFQD RVTMTTRDTSISTAYMELSRLSDDDAVYVCAREA TIFGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAAALGCLVKDYFPEPTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNPKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPVFLFPPKPKDITLMISRTPEVTCVVVDVSH DEPKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFEL YSKLTVDKSRWQQGNVVFSCSVMEALHNHYTQK SLSLSPGK</p>
		AA	<p>SEQ ID NO: 432</p>	<p>SEQ ID NO: 589</p>

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IP:361383	12H11.010	NA	<p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTCTCTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAGAACTACTTAGCTTGGTACCAGCAG AAACCAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGAAATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTACCATCAACAGCCTGCAAGGCTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCAGAGTGG AAATCAAACGAAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACTGCCCTCTGTTGTGTGCTGCTGAATAAC TTCTATCCAGAGAGGCCAAAGTACAGTGGAG GTGGATAACGCCCTCCAAATCGGGTAACTCCAG GAGAGTGCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCAACCATCAGGGCCTGAGCTCGC CCGTCAAAAGAGCTTCAACAGGGGAGAGTGT</p>
IP:361383	12H11.010	NA	<p>CAGTGCCCGCTGGTGACGTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGTGCGTCAGGGCCCTGGACAAGGG CTTAGTGGATGGGTGGATAAGCCCTAACAAAT GGTGACACAACATATGCACAGAAATTTTCAGGAC AGGTACCATGACCAGGACACGTCATCAGC ACAGCCTATATGAGCTGAGCAGGCTGAGATCT GACGACACGGCGGTGATTACTGTGCGAGAGAG GCCACGATTTTGGAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGAAACCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCTCTCTCCAAGAGCACCTCTGGGGG CACAGCGGCCCTGGGTGCTGGTCAAGGACTA CTTCCCGCAACCGGTGACGGTGTCTGGAACTC AGCGCCCTGACAGCGGGCTGCACACCTTCCC GGTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCAAATCTTGTGACAAACTCACACATG CCCACCGTGCCCAAGCCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGACGTGAGCCACGAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCAGTACCGTTGTGTC AGCTCTCTACCGTCTTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACACACA GGTGTACACCTGCCCCCATCCCGGGAGGAGAT GACCAAGAACCAAGGTGAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGAACAACT</p>

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				<p>ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGAGAAGAGCCTCTCCCTGTCTCCGGG TAAA</p> <p>SEQ ID NO: 2160</p> <p>QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYI HWVRQAPQGGLWGMWISPNNGDNYAQKFQD RVMTTRDTSISTAYMELSRLSDDTAVYVCAREA TIFGMLIVPFDYWGGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAAALGCLVKDYFPEPTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPEL LGGPSVFLFPPKPKDITLMISRTPETCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEVESNGQPENNYKTTTPVLDSDGSFEL YSKLTVDKSRWQQGNVVFSCSVMEALHNHYTQK SLSLSPGK</p> <p>SEQ ID NO: 590</p> <p>CAGTGCCCGCTGGTGCACTCTGGGGCTGAGGTG AAGAAGCCTGGGCCCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATACACTGGGTGCTCAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATAAGCCCTAACCCAA GGTGACACAACTATGCACAGAAAGTTTCAGGAC AGGTACACCATGACACAGGACACGTCCATCAGC ACAGCCTATATGAGCTGAGCAGGCTGAGATCT GACGACACGGCGGTGATTAATGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATGTACCATTTG ACTACTGGGCCAGGAAACCTGGTCACCGTCT CCTCAGCCTCCACCAAGGCCCATCGGTCTTCCC CCTGGCACCTCTCTCCAAAGAGCACCTCTGGGGG CACAGCGGCCCTGGGCTGCCCTGGTCAAGGACTA</p>
				<p>SEQ ID NO: 2003</p> <p>DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPNNLIYWTSTRESGVDRFSG SGSGTDFTLTINSLQAEDVAVYCCQQYYRTPWTF GQGTKVEIKRTVAAPSVFIPTPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSITYLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC</p> <p>AA</p> <p>SEQ ID NO: 433</p> <p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGCGGAGAGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAGAACTACTTAGCTTGGTACCAGCAG AAACAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGAAATCCGGGGTCCCTGAC CGATTAGTGCGAGCGGGTCTGGGACAGATTTC ACTCTACCATCAACAGCCTGCAAGGCTGAAGAT GTGGCTGTTTATTAATGTCAAGCAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCAAGGTGG AAATCAAAACGAAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAATC TGGAAGTCCCTCTGTGTGTGCTGCTGAATAAC TTCTATCCAGAGAGGCCAAAGTACAGTGAAG</p>
			12H11.011	NA
		IPS:361387		

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	<p>GTGGATAACGCCCTCC AATCGGGTAACTCCCAG GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCAACCATCAGGGCCTGAGCTCGC CCGTCAACAAGAGCTTCAACAGGGGAGAGTGT</p>	<p>CTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTC AGCGCCCTGACCAGCGGGCTGCACACCTTCCC GGTGTCTACAGTCTCAGGACTCTACTCCCTC AGACGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCAAATCTTGTGACAAACTCACACATG CCCACCGTGCCAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAACCCAAAG GACACCTCATGATCTCCCCGACCCCTGAGGTC ACATGCGTGGTGGACGTGAGCCACGAAAGAC CCTGAGGTCAAGTTC AACTGGTACGTGGACGGC GTGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCTCTCTACCGTCTTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGCAGCCCCGAGAACACACA GGTGTACACCTGCCCTCCCATCCCGGAGGAGAT GACCAAGAACAGGTGACGCTGACCTGCCTGGT CAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGAGCCGGAGACAACACT ACAAGACCAGCTTCCGTGCTGGACTCCGACG GCTCTTCTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAAGAGCCTCTCCCCTGTCTCCGGG TAAA</p>
	<p>SEQ ID NO: 2004</p> <p>DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLA WYQQKPGQPPNLLIYWTSTRESGVPDFSG SGSGTDFTLTINSLQAEDVA VYYCQQYYRTPTWTF GQGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVC LLNFPYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC</p>	<p>SEQ ID NO: 2161</p> <p>QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYI HWVRQAPGQGLEWMGWISPNQGDNTYAQKFQD RVMTTRDTSISTAYMELSLRSLDDTA VYYCAREA TIFGMLIVPFDYWGQGLTVTVSSASTKGPSVFPLA PSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVN HKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL</p>

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				<p>LGPSVFLFPPKPKDTLMISRTPVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFEL YSKLTVDKSRWQQGNVFCFVSMHEALHNHYTQK SLSLSPGK</p>
				<p>SEQ ID NO: 434</p> <p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGCGAGAGGGCCACCAATCAAC TGCAAGTCCAGCCAGAGTGTATATCCAGCTCC AACATAAGAACTACTTAGCTTGGTACCAGCAG AAACGAGACAGCTCTCAACCTGCTCATTTAC TGGACTTCTACCCGAGAAATCCGGGGTCCCTGAC CGATTGAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTACCATCAACAGCCTGCAAGGCTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTCCGGCCAGGGACCAAGGTGG AAATCAACAGAACGGTGGTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAAGTTGAAATC TGGAAGTGGCTCTGTGTGTGCTGCTGCTGAATAAC TTCTATCCAGAGAGGCCAAAGTACAGTGGAAAG GTGGATAACGCCCTCCAAATCGGGTAACTCCCGAG GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCCTGACGCTGAG CAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCAACCATCAGGGCCTGAGCTCGC CCGTCAAAAGAGCTTCAACAGGGGAGAGTGT</p>
				<p>SEQ ID NO: 591</p> <p>CAGTGCCGCTGGTGCGAGTCTGGGGCTGAGGTG AAGAAGCTGGGGCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATACACTGGTGCGTCAAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATAAGCCCTAACAAAT GGTGAAACAACATATGCACAGAAAGTTTCAGGAC AGGTACCATGACACAGGACACGTCCTCATCAGC ACAGCCTATATGAGCTGAGCAGGCTGAGATCT GACGACACGGCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCAATTTG ACTACTGGGGCCAGGAAACCTGGTCAACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGACCCCTCTCTCCAAGAGCACCTCTGGGGG CACAGCGCCCTGGGTGCTGCTGGTCAAGGACTA CTTCCCGAAACGGGTGACGGTGTGCGACCTTCCC AGCGCCCTGACCAAGCGGGGTGCAACCTTCCC GGCTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCAGACCTACATCTGCAACGTGAATCAC AAGCCCAAGCAACCAAGGTGGACAAAGAAAGT TGAGCCCAATCTTGTGACAAACTCACACATG CCCACCGTGCCAGCACCTGAACTCTGGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTG ACATGCGTGGTGGACGTGAGCCACGAAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC</p>

NA

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				<p>AGCGTCCTCACCGTCTCTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAAGTGCAAGGTCTCCAAC AAGCCCTCCAGCCCATCGAGAAACCATC TCCAAGCCAAAGGCAGCCCCGAGAACACA GGGTACACCTGCCCTCCCATCCCGGAGGAGAT GACCAAGAACAGGTGAGCCTGACCTGCCTGGT CAAGGCTTCTATCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGCAGCCGAGAACAACT ACAAGACCAGCTCCCGTCTGCTGACTCCGACG GCTCTTCTCTCTATAGCAAGCTACCCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGATGAGGCTCTGCACAACCA CTACACGAGAAAGAGCCTCTCCCTGTCTCCGGG TAAA</p>
				<p>SEQ ID NO: 2005</p> <p>DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSTRESGVDRFSG SGSGTDFTLTINSLQAEDVAVYCCQQYYRTPTWTF GQGTKVEIKRTVAAPSVFIPTPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSYSTLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC</p>
			AA	<p>SEQ ID NO: 2162</p> <p>QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYI HWVRQAPQGGLWGMWISPNNGETNYAQKFQD RVMTTRDTSISTAYMELSLRSDDDTAVYVCAREA TIFGMLIVPFDYWGQGLTVTVSSASTKGPSVFPLA PSSKSTSGGTAAAGCLVKDYFPEPTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLEPPKPKDITLMISRTPETCVVVDVSH DPEVKFNWYVDGVEVHNAAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFEL YSKLTVDKSRWQQGNVVFSCSVMEALHNHYTQK SLSLSPGK</p>
				<p>SEQ ID NO: 435</p> <p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGCGAGAGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAGAACTACTTAGCTTGGTACCAAGCAG AAACCAGGACAGCTCTCTAAACTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC</p>
IPS:361395	12H11.013	NA		<p>SEQ ID NO: 592</p> <p>CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGCCCTCAGTGAAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATACACTGGGTGCTCAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATAGCCCTAACCCAA GGTGAAACAAACTATGCACAGAAAGTTTCAGGAC</p>

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CGATTTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAAGGCTGAAGAT GTGGCTGTTTATTACTGTACGCAATATTATCGTA CTCCGTGGACGTTTCGGCCAAAGGACCACAGGTGG AAATCAAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACTGCCCTCTGTTGTGTGCCTGCTGAATAAC TTCTATCCACAGAGAGGCCAAAGTACAGTGGAG GTGGATAACGCCCTCCAATCGGGTAACTCCCCAG GAGAGTGTACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCCCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCAACCCATCAGGGCCTGAGCTCGC CCGTCAACAAAGAGCTTCAACAGGGGAGAGTGT	AGGGTCACCATGACCAGGACACAGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGCCTGAGATCT GACGACACGGCCGTGATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGAAACCCCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGG CACAGCGGCCCTGGGCTGCCCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCTGTGGAACTC AGCGCCCTGACCAAGCGGCTGCACACCTTCCC GGTGTCTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCAATCTTGTGACAAACTCACACATG CCCACCGTGCCCAAGCCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGAGCGTGAGCCACGAAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCAGTACCGTTGTGTC AGCTCCTCACCGTCTTGCAACCAGGACTGGCTG AATGGCAAGGAGTACAAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACCCACA GGTGTACACCTGCCCTCCATCCCGGAGGAGAT GACCAAGAACAGGTGAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGAACAACT ACAAGACCAGCCTCCCGTGTGGACTCCGACG GCTCCTTCTCTCTATAGCAAGCTCACCCTGGA CAAAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAAGAGACCTCTCCCTGTCTCCCGG TAAA
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			SEQ ID NO: 2006	SEQ ID NO: 2163
	AA		DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPKLLIYWTSRDSSGVDPDRFSG SGSGTDFTLTINSLQAEDVAVYYCQQYRTPTWTF GQGTKVEIKRTVAAPSVFIIPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSYLSSTLTLSKADYEKHKVYACEVTHQQLSS PVTKSFNRGEC	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWISPNQGETNYAQKFQD RVMTTRDTSISTAYMELSSLRSDDTAVYYCAREA TIFGMLIVPFDYWGQGTLLVTVSSASTKGPSVFPLA PSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNHPKNTKVDKKVEPKSCDKTHTCPCPAPEL LGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGPQPREPVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEVESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQK SLSLSPGK
			SEQ ID NO: 436	SEQ ID NO: 593
!PS:361402	12H11.014	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGCTCTGGCGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTATCCAGCTCC AACATAAGAACTACTTAGCTTGGTACCAGCAG AAACGAGGACAGCTCTAACTGCTCATTTAC TGGACTTCTACCCGAGAAATCCGGGGTCCCTGAC CGATTGAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTACCATCAACAGCCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTCCGGCCAGGGACCAAGGTGG AAATCAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAATC TGGAACCTGCTCTGTTGTGTGCTGCTGAATAAC TTCTATCCAGAGAGGCCAAAGTACAGTGGAAG GTGGATAACGCCCTCCAAATCGGTTAACTCCAG GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCTGACGCTGAG CAAAAGCAGACTACGAGAAACACAAGTCTACG CCTGCGAAGTCAACCATCAGGGCCTGAGCTCGC CCGTCAAAAGAGCTTCAACAGGGGAGAGTGT	CAGTGCAGCTGGTGCGAGTCTGGGGCTGAGGTG AAGAAGCTGGGGCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATACACTGGTGCGTCAAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATAAGCCCTAACCAA GGTGAAACAACATATGCACAGAAAGTTTCAGGAC AGGTCAACATGACACAGGACACGTCCTCATCAGC ACAGCCTATATGGAGCTGAGCAGCCTGAGATCT GACGACACGGCGGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCAATTG ACTACTGGGGCCAGGAAACCCCTGGTCAACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGACCCCTCCTCCAAGAGCACCTCTGGGGG CACAGCGCCCTGGGTGCGGTGCGTGGTCAAGGACTA CTTCCCGCAACCGGTGACGGTGTGCGTGGAACTC AGCGCCCTGACCAAGCGGCTGCAACACCTTCCC GGCTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCGTGGTGACCGTGCCCTCCAGCAGCCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAAGAAAGT

[illegible]

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					Y SKLTVDKSRWQQGNVFSCSVMH EALHNHYTQK SLSLSPGK
					SEQ ID NO: 594
					CAGATCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCTGGGGCTCAGTGAAGTCTCCTGC AAGGCTCCGGATACACCTTCACCGGCTACTAT ATGCAATTGGTGCAGACGGCCCTGGACAAAGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGGCACAACTATGCACAGAAATTTCAAGGC AGGTCAACATGACACGGACACGTCCATCAGT ACAGCTACATGAGCTGAGCAGGCTGAGGTCT GACGACACGGCGTGATTACTGTGCGAGAGGG GGGATTACGTTTGGGGGACTTATCGGCCTCAC TACTACTCGGTATGGACGTCTGGGGCCAAAGG ACCAGGTCAACGCTCTCCTCAGCCTCCACCAA GGCCATCGGTCTTCCCCCTGGCACCTCTCCCA AGACACCTCTGGGGGCACAGCGGCCCTGGGT GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA CGGTGCTGTGGAACCTCAGGGCCCTGACCAAGC GCGTGACACCTTCCCCGGCTGTCTACAGTCTC AGGACTTACTCCCTCAGCAGGCTGGTGACCGT GCCCCTCCAGCAGCTTGGGCACCCAGACCTACAT CTGCAACGTGAATCAAGCCCAAGCAACACAA GGTGGACAAGAAAGTTGAGCCCAATCTTGTGA CAAACTCACACATGCCACCGTGGCCAGCACCC TGAACTCCTGGGGGACCGTCAGTCTTCTCTTC CCCCAAAACCAAGGACACCTCATGATCTCC CGGACCCCTGAGGTACATGCGTGGTGGTGAC GTGAGCCACGAAGACCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCC AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG CACGTACCGTTGTGTACAGCTCTCACCGTCTG CACCAGGACTGGCTGAATGGCAAGGAGTACAA GTGCAAGGTCTCCAAACAAAGCCCTCCCAAGCCC CATCGAGA AACCATCTCCAAAGCCAAAGGCA GCCCCGAGAACCAACAGGTGTACACCTGCCCC
					SEQ ID NO: 437
					CAGTCTGTGCTGACTAGCCACCTCAGCGTCTG GGACCCCGGCAGAGGGTCACCATCTCTTGT CTGGAAGTAGCTCCAAACATCGGAAGTCAAACTG TAAACTGGTACCAAGCACTCCCAAGAACGGCCC CCAAACTCCTCATCTATACATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGTGATTATTCTGTG CAACATTTCGATGAAGCCTGAGTGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCTCAGGT AGCCCAAGGTGCCCCCTCGGTCACTCTGTTC GCCCCTCTGAGGAGCTTCAAGCCAAACAAGGC CACACTGGTGTCTCATAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCTGGAAAGGCAGATAG CAGCCCCGTCAAGCGGGAGTGGAGACCAACAC ACCTTCCAAACAAGCAACAACAAGTACGGGC CAGCAGCTATCTGAGCCTGACGCTGAGCAGTG GAAGTCCACAGAAAGCTACAGTGGCAGGTCA GCATGAAGGGAGCACCGTGGAGAGACAGTGG CCCCACAGATGTTCA
				NA	
			2C2.005.001		
			IPS:361406		

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			<p>ATCCCGGAGGAGATGACCAAGAACAGGTCA GCTGACCTGCCTGGTCAAAGGCTTCTATCCCA GCGACATCGCCGTGGAGTGGGAGCAATGGG CAGCCGAGAACAACTACAAGACCACGCCTCCC GTGTGGACTCCGACGGCTCCTTCTTCTCTATA GCAAGCTCACCGTGACAAAGACAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACCACTACACGCAAGAGAGC CTCTCCCTGTCTCCGGTAAA</p> <p>SEQ ID NO: 2165</p>
			<p>QSVLTQPPSASGTPGQRVITISCSGSSNIGSQTVNW YQHLPGTAPKLLIYTNNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDESLSGPVFGGGTK LTVLGGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGA VTVAWKADSSPVKAGVETTTTPSKQSNKY AASSYLSLTPEQWKS HRSYSCQVTHEGSTVEKTV APTECS</p> <p>AA</p> <p>SEQ ID NO: 2008</p>
			<p>QMQVVQSGAEVKKPGASVKVSKASGYTFTGYY MHWVVRQAPGQGLEWMGWNPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLSDDTA VYYCARG GDYVWGTYRPHYYYGMDVWVGQGTTVTVSSAST KGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPV VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LSDSGSFFLYSKLTVDKSRWQQGNVVFSCVMHEA LHNHYTQKLSLSLSPGK</p> <p>SEQ ID NO: 595</p>
!PS:361412	2C2.005.002	NA	<p>CAGTGTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCCGGGCAGAGGTCACCACTCTCTTGT CTGGAAGTAGCTCCAAACATCGGAAGTCAAACTG TAAACTGGTACCAAGCACCTCCAGGAACGGCCC CCAAACTCTCATCTATATAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTCTGTG CAACATTGATGAAGCCTGCAAGGTCCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCCTAGGTC AGCCCCAAGGCTGCCCCCTCGGTCACTCTGTTC</p> <p>SEQ ID NO: 438</p>
			<p>CAGATGCAGGTGGTGCGAGTCTGGGCTGAGGTG AAGAAGCCTGGGCCTCAGTGAAAGTCTCCTGC AAGGCTTCCGGATACACCTTCAACCGGCTACTAT ATGCATTGGTGCGACAGGCCCTGGACAAAGG CTTGAGTGGATGGATGGATCAACCCATAACAGT GGTGGCACAACCTATGCACAGAAATTCAGGGC AGGTCAACATGACACAGGACACGTCCATCAGT ACAGCTACATGAGCTGAGCAGGCTGAGGTCT GACGACACGGCGGTGTTACTGTGCGAGAGGG GGGATTACGTTTGGGGGACTTATCGGCCTCAC TACTACTACGATGACAGCTCTGGGGCCAAAGG</p> <p>SEQ ID NO: 595</p>

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	<p>GCCCTCCTCTGAGGAGCTTCAAGCCAAACAAGGC CACACTGGTGTCTCATAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCTGGAAGGCAGATAG CAGCCCCGTCAAGCGGGAGTGGAGACCACAC ACCTCCAAACAAGCAACAACAAGTACGCGGC CAGCAGCTATCTGAGCCTGACGCCCTGAGCAGTG GAAGTCCACAGAAAGCTACAGCTGCCAGGTCAC GCATGAAGGGAGCACCGTGGAGAAAGACAGTGG CCCCTACAGATGTTCA</p>	<p>ACCACGGTCAACCGTCTCCTCAGCCTCCACCAAG GGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCA AGAGCACTCTGGGGGCACAGCGGCCCTGGGCT GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA CGGTGCTGTGAACTCAGGGGCCCTGACCAGCG GCGTGACACACCTTCCCCGGGTCTCCTACAGTCTC AGGACTCTACTCCTCAGCAGCGTGGTGACCGT GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT CTGCAACGTGAATCAAGCCACGCAACACCAA GGTGACAAAGAAAGTTGAGCCCAATCTTGTGA CAAACTCACACATGCCACCGTGCCACGACC TGAACTCCTGGGGGACCGTCAGTCTTCTCTTC CCCCCAAACCCAAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTCACATGCGTGGTGGTGGAC GTGAGCCACGAAGACCTGAGGTCAAGTTC AAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCC AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG CACGTACCGTTGTGACGCTCCTCACCGTCTCTG CACCAGGACTGGCTGAATGGCAAGGAGTACAA GTGCAAGGTCTCCAAACAAAGCCCTCCCAGCCCC CATCGAGAAACCATCTCTCCAAAGCCAAAGGGCA GCCCCGAGAACACAGGTGTACACCTGCCCCC ATCCCGGAGGAGATGACCAAGAACCAAGGTCA GCTTGACCTGCCCTGGTCAAAGGCTTCTATCCCA GCGACATCGCCGTGGAGTGGGAGAGCAATGGG CAGCCGAGAACAACTACAGACCACGCCCTCCC GTGCTGGACTCCGACGGCTCCTTCTTCTCTATA GCAAGCTCACCGTGGACAAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAAACCACTACACGCAAGAGAGC CTCTCCCTGTCTCCGGTAAA</p>
	<p>SEQ ID NO: 2009</p> <p>QSVLTQPPSASGTPGQRVTISCSGSSNIGSQTVNW YQHLPGTAPKLLIYTNNQRPSGVPDFRFSGSKSGTS ASLAISGLQSEDEADYFCA TFDESLOQPVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD</p>	<p>SEQ ID NO: 2166</p> <p>QMQVVQSGAEVKKPGASVKVSKKASGYTFTGYY MHWVVRQAPGQGLEWMGWNPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLSDDTAVYYCARG GDYVWGTYPHYYYGMDVWVGQGTITVTVSSAST</p>
AA		

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			FYPGAVTVAWKADSSPVKAGVETTTTPSKQSNKYY AASSYLSLTPEQWKSHRYSQCVTHEGSTVEKTV APTECS	KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYVTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LDSGDSFELYSKLTVDKSRWQQGNVVFSCSVMHEA LHNHYTQKSLSLSPGK
			SEQ ID NO: 439	SEQ ID NO: 596
			CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCCGGGCAGAGGGTCACCACTCTCTTGT CTGGAAGTAGCTCCAACATCGGAAGTAATTATG TAAACTGGTACCAAGCACTCCCAAGGAACGGCCC CCAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTCTGTG CAACATTCTGATGAAAGCCTGAGTGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCTCAGTGC AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCT GCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGC CACACTGGTGTGTCTCATAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCCTGGAAAGGCAGATAG CAGCCCCGTCAAGCGGGAGTGGAGACCAACCAC ACCTTCCAAACAAGCAACAACAAGTACGGGGC CAGCAGCTATCTGAGCCTGACGCTGAGCAGTG GAAGTCCACAGAAAGTACAGCTGCCAGGTAC GCATGAAGGGAGCACCGTGGAGAGACAGTGG CCCCACAGATGTTCA	CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAGTCTCCTGC AAGGCTCCGGATACACCTTCAACCGGCTACTAT ATGCAATTGGTGCAGAGGCCCTGGACAAGGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGGCACAACTATGCACAGAAATTTTCAGGGC AGGTCAACATGACACAGGACACGTCATCAGT ACAGCTACATGAGGTGAGCAGGCTGAGGTCT GACGACACGGCGTGTATTACTGTGCGAGAGGG GGGATTACGTTTGGGGGACTTATCGGCCTCAC TACTACTACGATATGGACGTCTGGGGCCAAAGG ACCAGGTCAACGCTCTCCTCAGCCTCCACCAAG GGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCA AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA CGGTGTCGTGGAACCTCAGGGGCCCTGACCAAGC GCCTGCACACCTTCCCCGGCTGTCTACAGTCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT GCCCCCAGCAGCTTGGGCACCCAGACCTACAT CTGCAACGTGAATCAAGCCACGCAACACCAA GGTGGACAAGAAAGTTGAGCCCAATCTTGTGA CAAACCTCACACATGCCACCGTGGCCAGCAC TGAACTCCTGGGGGACCGTCAGTCTTCTCTTC CCCCCAAACCAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTACATGCGTGGTGGTGGAC
IPS:361418	2C2.005.003	NA		

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		GTGAGCCACGAAGACCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCC AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG CACGTACCGTTGTGTGAGCGTCTCAACCGTCCTG CACCAGGACTGGCTGAATGGCAAGGAGTACAA GTGCAAGGTCTCCAACAAGCCCTCCCAAGCCCC CATCGAGAAAACCATCTCCAAGCCAAAGGGCA GCCCCGAGAACACAGGTGTACACCTGCCCCC ATCCCGGAGGAGATGACCAAGAACACAGGTCA GCCTGACCTGCCTGGTCAAAGGCTTCTATCCCCA GCGACATCGCCGTGGAGTGGGAGAGCAATGGG CAGCCGGAGAACAACTACAAGACCACGCCTCCC GTGCTGACTCCGACGGCTCCTTCTTCTCTATA GCAAGCTCACCGTGACAAAGACGAGGTGGCAG CAGGGAAACGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACCACTACACGCAGAAAGAGC CTCTCCCTGTCTCCGGGTA
	SEQ ID NO: 2010	SEQ ID NO: 2167
	QSVLTQPPSASGTPGQRVITISCSGSSNIGSNYVNW YQHLPGTAPKLLIYTNNQRPSGVDPDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDESLSGPVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS	QMQVVQSGAEVKKPGASVKVSKASGYTFTGY MHWVVRQAPGQGLEWMGWNPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLSDDTAVYYCARG GDYVWGTYPHYYYGMDVWVGQGTITVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEA LHNHYTQKSLSLSPGK
AA	SEQ ID NO: 440	SEQ ID NO: 597

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IPS:361424	2C2.005.004	NA	<p>CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGGTCACCATCTCTTGTT CTGGAAGTAGCTCCAAACATCGGAAGTAATTATG TAAACTGGTACCAGCACCTCCCAGGAACGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTCTGTG CAACATTTCGATGAAAGCCTGC AAGTCCGGTAT TCGGCGGAGGGACC AAGCTGACCGTCCTAGGTC AGCCCAAGGTGCCCCCTCGGTCACTCTGTTCCTC GCCCCTCCTCTGAGGAGCTTCAAGCCAAACAAGGC CACACTGGTGTCTCAT AAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCTGGAAAGGCAGATAG CAGCCCCGTC AAGCGGGAGTGGAGACCACAC ACCTTCCAAACAAGCAACAACAAGTACGGCGC CAGCAGCTATCTGAGCCTGACGCCCTGAGCAGTG GAAGTCCCACAGAAAGCTACAGCTGCCAGGTCAC GCATGAAGGGAGCACCGTGGAGAAAGACAGTGG CCCCACAGAAATGTTCA</p>
			<p>CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAACCTGGGGCCTCAGTGAAAGGTCTCCTGC AAGGCTCCGGATACACCTTCACCCGGCTACTAT ATGCATTGGTGCAGACGGCCCTGGACAAAGGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGGCACAACTATGCACAGAAAGTTTCAGGGC AGGTCAACCATGACCAGGGACACGTCCATCAGT ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGGGATTACGTTGGGGGACTTATCGGCCCTCAC TACTACTACGTATGGACGTCTGGGGCCCAAGG ACCACGGTCACCGTCTCCTCAGCCTCCACCAA GGCCCATCGTCTTCCCCCTGGCACCCCTCCTCCA AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT GCCGTGTC AAGACTACTTCCCCGAACCGGTGA CGGTGCTGTGGAAC TACAGGGGCCCTGACCAGCG GCGTGACACACCTTCCCCGGGTGTCCTACAGTCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT CTGCAACGTGAATCAACAGCCACGCAACACCAA GGTGGACAAGAAAGTTGAGCCCCAATCTTGTGA CAA AACTCACACATGCCCCACCGTGCCCCAGCAC TGAACTCCTGGGGGACCGTCAGTCTTCTCTTC CCCCCAAACCCAAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTACATGCGTGGTGGTGGAC GTGAGCCACGAAGACCCTGAGGTCAAGTTC AAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCC AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG CACGTACCGTTGTGTACGCTCCTCACCGTCTG CACCAGGACTGGCTGAATGGCAAGGAGTACAA GTGCAAGGTCTCCAAACAAGCCCTCCCAGCCCC CATCGAGAAACCATCTCTCCAAGCCAAAGGGCA GCCCCGAGAACACAGGTGTACACCTGCCCCC ATCCCGGAGGAGATGACCAAGAACACAGGTCA GCCTGACCTGCCTGGTCAAGGCTTCTATCCCCA GCGACATCGCCGTGGAGTGGGAGAGCAATGGG</p>

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			<p>SEQ ID NO: 2011</p> <p>QSVLTQPPSASGTPGQRVITISCGSSSNIGSNYVNW YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYFCAITFDESLOQPVFVGGGK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTTPSKQSNKY AASSYLSLTPEQWKSHRYSYSCQVTHEGSTVEKTV APTECS</p>		<p>CAGCCGGAGAACAACTACAAGACCACGCCTCCC GTGCTGGACTCCGACGGCTCCTTCTTCTCTATA GCAAGCTCACCGTGGACAAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCCGTGATGCAT GAGGCTCTGCACAACCACTACACGCAGAAAGAGC CTCTCCCTGTCTCCGGGTAAA</p>
		AA	<p>SEQ ID NO: 2168</p> <p>QMQVVQSGAEVKKPGASVKVSKASGYTFTGYY MHWVVRQAPGQGLEWMGWNPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLSDDTAVYYCARG GDYVWGTYPHYYYGMDVWVWQGGTTVTVSSAST KGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPV VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSLTVLHQDWLNGKEYKCKVSNK ALPAIEKTIKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LSDSGSFELYSKLTVDKSRWQQGNVVFCSVMHEA LHNHYTQKLSLSLSPGK</p>		<p>SEQ ID NO: 2168</p> <p>QMQVVQSGAEVKKPGASVKVSKASGYTFTGYY MHWVVRQAPGQGLEWMGWNPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLSDDTAVYYCARG GDYVWGTYPHYYYGMDVWVWQGGTTVTVSSAST KGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPV VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSLTVLHQDWLNGKEYKCKVSNK ALPAIEKTIKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LSDSGSFELYSKLTVDKSRWQQGNVVFCSVMHEA LHNHYTQKLSLSLSPGK</p>
		NA	<p>SEQ ID NO: 441</p> <p>CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGGTCACCACTCTCTTGT CTGGAAGTAGCTCCAAACATCGGAAGTCAAACTG TAAACTGGTACACGACACCTCCCAGGAACGGGCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTCTGTG CAACATTGATGACAGCCTGAATGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCCTAGGTC AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCT GCCCTCCTCTGAGGAGCTTCAAGCCCAACAAGGC CACACTGGTGTGTCTCATAAAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCTGGAAGGCAGATAG</p>	<p>2C2,005,005</p>	<p>!PS:361430</p> <p>SEQ ID NO: 441</p> <p>CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGGTCACCACTCTCTTGT CTGGAAGTAGCTCCAAACATCGGAAGTCAAACTG TAAACTGGTACACGACACCTCCCAGGAACGGGCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTCTGTG CAACATTGATGACAGCCTGAATGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCCTAGGTC AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCT GCCCTCCTCTGAGGAGCTTCAAGCCCAACAAGGC CACACTGGTGTGTCTCATAAAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCTGGAAGGCAGATAG</p>
			<p>SEQ ID NO: 598</p> <p>CAGATGCAGGTGGTGCGAGTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAAGTCTCCTGCG AAGGCTTCCGGATACACCTTCAACCGGCTACTAT ATGCATTGGGTGCGACAGGCCCTGGACAAAGGG CTTGAGTGGATGGATGGATGATCAACCTAACAGT GGTGGCACAACTATGCACAGAAAGTTTCAGGGC AGGTCAACCATGACACAGGACACGTCCTCATAGT ACAGCCTACATGAGAGCTGAGCAGGCTGAGGTCT GACGACACGGCGGTGTTACTGTGCGAGAGGGG GGGGATTACGTTTGGGGGACTTATCGGCCTCAC TACTACTACGATGAGACGTCTGGGGCCAAAGG ACCAAGGTCAACGCTCTCCTCAGCCTCCACCAAG GGCCCATCGGTCTTCCCGCTGGCACCTCCTCCCA AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT</p>		

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	<p>CAGCCCCGTC AAGCGGGAGTGGAGACCACCAC ACCCTCCAAACAAAGCAACAACAAGTACGCGGC CAGCAGCTATCTGAGCCTGACGCCCTGAGCAGTG GAA GTCCACAGAAAGCTACAGCTGCCAGGTCAC GCATGAAGGGAGCACCGTGGAGAAAGACAGTGG CCCCTACAGAAATGTTCA</p>	<p>GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA CGGTGTCGTGGAACCTCAGGGGCCCTGACCAGCG GCGTGACACACCTTCCCGGTGTCTCTACAGTCCTC AGACTCTACTCCCTCAGCAGCGTGGTGACCGT GCCCTCCAGCAGCTTGGGCAACCCAGACCTACAT CTGCAACGTGAATCAAGCCCAAGCAACACCAA GGTGGACAAGAAAGTTGAGCCCAATCTTGTGA CAAAACTCACACATGCCACCGTGCCACGACAC TGA ACTCTGGGGGACCGTCAGTCTTCTCTTC CCCCCAAAACCAAGGACACCTCATGATCTCC CGGACCCCTGAGGTACATGCGTGGTGGTGAC GTGAGCCACGAAGACCTGAGGTCAAGTTCAAC TGGTACGTGGACGCGGTGGAGGTGCATAATGCC AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG CACGTACCGTTGTGTCAGCGTCTCACCGTCTCTG CACCAGGACTGGCTGAATGGCAAGGAGTACAA GTGCAAGGTCTCCAAACAAGCCCTCCCAGCCCC CATCGAGAAACCATCTCCAAGCCAAGGGCA GCCCCGAGAACACAGGTGTACACCTGCCCCC ATCCCGGAGGAGATGACCAAGAACAGGTCA GCTTGACCTGCCGTGTCAAAGGCTTCTATCCCA GCGACATCGCCGTGGAGTGGGAGAGCAATGGG CAGCCGGAGAACAACTACAAGACCACGCTCCC GTGCTGGACTCCGACGGCTCTTCTTCTCTATA GCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACCACTACACGCAGAAAGAGC CTCTCCCTGTCTCCGGGTAAA</p>
AA	<p>QSVLTQPPSASGTPGQRVITISCGSSNIGSQTVNW YQHLPGTAPKLLIYTNNQRPSPGVPDFRFSKSGTS ASLAISGLQSEDEADYFCA TFDDSLNPGPVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTTPSKQSNKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS</p>	<p>SEQ ID NO: 2169 QMQVVQSGAEVKKPGASVKVSKKASGYTFTGYY MHWVRQAPGQGLEWMGWNPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLSDDTAVYYCARG GDYVWGTYPHYYYGMDVWVGQGTITVTVSSAST KGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPV VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPS SSLGTQTQYICNVNHNKPSNTKVDKKVEPKSCDKTH</p>

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				<p>TCPPCPAPELLGGPSVFLFPPKPKDITLMISRTPEVT CVVVDVSHEDPEVKFNWYVVDGVEVHNATKPCPE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAIEKTIKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LDSGSEFLYSKLTVDKSRWQQGNVVFSCSVMHEA LHNHYTQKSLSLSPGK</p>
				<p>SEQ ID NO: 442</p> <p>CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGGTCACCATCTCTTGT CTGGAAGTAGCTCCAAACATCGGAAGTAATTATG TAAACTGGTACCAAGCACTCCCAAGGAACGGGCC CCAAACTCCTCATCTATATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTCTGTG CAACATTTCGATGACAGCCTGAATGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCTCAGGTC AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCT GCCCCTCTCTGAGGAGCTTCAAGCCCAACAAGGC CACACTGGTGTGTCTCATAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCCTGGAAAGGCAGATAG CAGCCCCGTCAAGCGGGGAGTGGAGACCAACCAC ACCCCTCCAAACAAGCAACAACAAGTACGGGGC CAGCAGCTATCTGAGCCTGACGCTGAGCAGTG GAAGTCCACAGAAAGCTACAGCTGCCAGGTCA GCATGAAGGGAGCACCGTGGAGAGACAGTGG CCCCCTACAGATGTTCA</p>
				<p>SEQ ID NO: 599</p> <p>CAGATGCAAGTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCTGGGGCTCAGTGAAAGTCTCCTGC AAGGCTCCGGATACACCTTCAACCGGCTACTAT ATGCAITGGGTGCAGAGGCCCTGGACAAGGG CTTGAGTGGATGGGATGGATCAACCTAACAGT GGTGGCACAACTATGCACAGAAAGTTTCAGGGC AGGTGACCATGACAGGGACACGTCCTCATCAGT ACAGCTACATGAGGCTGAGCAGGCTGAGGTCT GACGACACGGCGTGTATTACTGTGCGAGAGGG GGGATTACGTTTGGGGGACTTATCGGCCTCAC TACTACTACGATATGGACGTCTGGGGCCAAAGG ACCAGGTCAACGCTCTCCTCAGCCTCCACCAAG GGCCATCGGTCTTCCCCCTGGCACCTCTCCCA AGAGCACTCTGGGGGCACAGCGGCCCTGGGCT GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA CGGTGTCGTGGAACCTCAGGGGCCCTGACCAAGC GCGTGACACACCTTCCCCGGCTGTCTACAGTCTC AGGACTCTACTCCCTCAGCAGGCTGGTGACCGT GCCCCCAGCAGCTTGGGCACCCAGACCTACAT CTGCAACGTGAATCAAGCCCAAGCAACACCAA GGTGACACAAGAAAGTTGAGCCCAATCTTGTGA CAAACTCACACATGCCACCGTGGCCAGCACCC TGAACTCCTGGGGGACCGTCAGTCTTCTCTTC CCCCCAAAACCAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTACATGCGTGGTGGTGGAC GTGAGCCACGAAGACCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCC AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG</p>

IPS:361436

2C2.005.006

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GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCGTG CAACATTCGATGAAAGCCTGAATGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCCTAGGTC AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCT GCCCCTCCTGAGGAGCTTCAAGCCAAACAAGGC CACACTGGTGTCTCATAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCTGGAAAGGCAGATAG CAGCCCCGTCAGCGGGAGTGGAGACCACCAC ACCCGCCAAACAAGCAACAACAAGTACGCGGC CAGCAGCTATCTGAGCCTGACGCCCTGAGCAGTG GAAGTCCACAGAAAGCTACAGCTGCCAGGTCAC GCATGAAGGGAGCACCGTGGAGAAAGACAGTGG CCCCACAGATGTTCA	AGGGTCACCATGACCAGGGACACGTCCATCAGT ACAGCCTACATGAGGCTGAGCAGGCTGAGGTCT GACGACACGGCGGTGATTACTGTGCGAGAGGG GGGATTACGTTTGGGGACTTATCGGCCTCAC TACTACTACGATATGGACGTCTGGGGCCAAAGG ACCACGGTCAACCGTCTCCCTCAGCCTCCACCAAG GGCCCATCGGTCTTCCCCCTGGCACCTCCCTCCA AGAGCCTCTGGGGGCACAGCGGCCCTGGGCT GCCGTGTCAGGACTACTTCCCCGAACCGGTGA CGGTGCTGTGGAACCTCAGGGGCCCTGACCAGCG GCGTGACACACCTTCCCCGGCTGTCTACAGTCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT GCCCCTCCAGCAGCTTGGGCACCCAGACCTACAT CTGCAACGTGAATCAAGCCACGCAACACCAA GGTGGACAAGAAAGTTGAGCCCAATCTTGTGA CAAACTCACACATGCCACCGTGCCACGACC TGAACTCTGGGGGACCGTCAGTCTTCTCTTC CCCCCAAACCCAAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTACATGCGTGGTGGTGGAC GTGAGCCACGAAGACCTGAGGTCAAGTTC AAC TGGTACGTGGACGGCGTGGAGGCAAGTACGGCAG AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG CACGTACCGTTGTGTGACGCTCTCACCGTCTCTG CACCAGGACTGGCTGAATGGCAAGGAGTACAA GTGCAAGGTCTCCAAACAAAGCCCTCCAGCCCC CATCGAGAAACCATCTCCAAGCCAAAGGGCA GCCCCGAGAACACAGGTGTACCCCTGCCCCC ATCCCGGGAGGAGATGACCAAGAACAGGTCA GCTTGACCTGCCCTGGTCAAAGGCTTCTATCCCCA GCGACATCGCCGTGGAGTGGGAGAGCAATGGG CAGCCGGAGAACAACTACAGACCACGCCCTCCC GTGCTGGACTCCGACGGCTCTTCTTCTCTATA GCAAGCTCACCGTGGACAAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACCACTACACGCAAGAGAGC CTCTCCCTGTCTCCGGGTAAA
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A-2124-WO-PCT

		SEQ ID NO: 2014	QSVLTQPPSASGTPGQRVTISCSGSSNIGSNTVNW YQHLPGTAPKLLIYTNNQRPSPGVPDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDESLNGPVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTTPSKQSNKY AASSYLSLTPEQWKSHRYSQVTHEGSTVEKTV APTECS	SEQ ID NO: 2171	QMQVVQSGAEVKKPGASVKVSKASGYTFTGYY MHWVVRQAPGQGLEWMGWNPNSGGTNYAQKFQ GRV/TMRDTSISTAYMELSRLSDDTA VYYCARG GDYVWGTYPHYYYGMDVWVGQGTTVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAIEKTIKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LDSGDSFFLYSKLTVDKSRWQQGNVVFSCSVMHEA LHNHYTQKLSLSLSPGK
	AA	SEQ ID NO: 444	CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGTCACCACTCTCTTGT CTGGAAGTAGCTCCAAACATCGGAAGTAATACTG TAAACTGGTACCAAGCACCTCCCAGGAACGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGG CTCCAGTCTGAGGATGAGCTGATTATTCTGTG CAACATTGATGACAGCCTGCAAGGTCCGGTAT TCGGCGGAGGACCAAGCTGACCGTCTCAGGTC AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCOC GCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGC CACACTGGTGTGTCTCATAAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCTGGAAGGCAGATAG CAGCCCCGTCAAGCGGGGAGTGGAGACCACCCAC ACCCTCCAAACA AAGCAACAACAAGTACGCGGC CAGCAGCTATCTGAGCCTGACGCTGAGCAGTG GAAGTCCACAGAAAGCTACAGTGCCAGGTCA GCATGAAGGAGCACCGTGGAGAAAGACAGTGG CCCCACAGAATGTTCA	SEQ ID NO: 601	CAGATGCAGTGGTGTGTCAGTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCCGGATACACCTTCAACCGGCTACTAT ATGCATTGGTGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGGCACAACATATGCACAGAAATTTTCAGGGC AGGTCAACATGACCAGGGACACGTCCATCAGT ACAGCCTACATGAGCTGAGCAGGCTGAGGTCT GACGACACGGCGTGTATTACTGTGCGAGAGGG GGGGATTACGTTTGGGGGACTTATCGGCCTCAC TACTACTACGGTATGGAGCTCTGGGGCCAAGGG ACCACGGTCAACGCTCTCCTCAGCCTCCACCAAG GGCCCATCGGTCTTCCCCCTGGCACCTCCTCCA AGAGCACCTCTGGGGGACACAGCGGCCCTGGGCT GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA CGGTGTCGTGGAACCTCAGGGCCCTGACCAAGCG GCGTGCACACCTTCCCCGGCTGTCTACAGTCCCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT CTGCAACGTGAATCACAAAGCCAGCAACACCAA
IPS:361448	2C2.005.008	NA			

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					GGTGGACAAGAAAGTTGAGCCCAATCTTGTGA CAAACATCACATGCCACCGTGCCACGACC TGAACTCTGGGGGACCGTCAGTCTTCCTCTTC CCCCAAAACCAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTACATGCGTGGTGGTGAC GTGAGCCACGAAGACCCTGAGGTCAAGTTC AAC TGGTACGTGGACGGCGTGAGGTGCATAATGCC AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG CACGTACCGTTGTGTCAGCGTCTCACCGTCTCTG CACCAGGACTGGCTGAATGGCAAGGAGTACAA GTGCAAGGTCTCCAAACAAAGCCCTCCAGCCCC CATCGAGAAACCATCTCCAAGCCAAAGGCA GCCCCGAGAACACAGGTGTACACCTGCCCCC ATCCCGGAGGAGATGACCAAGAACAGGTCA GCTTGACCTGCCCTGGTCAAAGGCTTCTATCCCCA GCGACATCGCCGTGGAGTGGGAGAGCAATGGG CAGCCGAGAACAACTACAGACACGCTCCC GTGCTGGACTCCGACGGCTCTTCTTCTCTATA GCAAGCTCACCGTGAGCAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAAACCACTACACGCAAGAGAGC CTCTCCCTGTCTCCGGGTAAA
				SEQ ID NO: 2015	SEQ ID NO: 2172
				QSVLTQPPSASGTPGQQRVTISCSGSSNIGSNTVNW YQHLPGTAPKLLIYTNNQRPSGVDPDRFSGSKSGTS ASLAISGLQSEDEADYFCA TFDDSLQGPVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGA VTVAWKADSSPVKAGVETTTTPSKQSNKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS	QMQVVQSGAEVKKPGASVKVSKASGYTFTGY MHWVRQAPGQGLEWMGWNPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLSDDTAVYYCARG GDYVWGTYPHYYYGMDVWVGQGTITVTVSSAST KGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPV
			AA		

[illegible]

A-2124-WO-PCT

				<p>ATCCCGGAGGAGATGACCAAGAACAGGTCA GCTGACCTGCCTGGTCAAAGGCTTCTATCCCA GCGACATCGCCGTGGAGTGGAGAGCAATGGG CAGCCGAGAACAACTACAAGACCACGCTCCC GTGTGGACTCCGACGGCTCCTTCTTCTCTATA GCAAGCTCACCGTGAGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACCACTACACGCAAGAGAGC CTCTCCCTGTCTCCGGGTAAA</p> <p>SEQ ID NO: 2173</p>
			AA	<p>QSVLTQPPSASGTPGQRVITISCSGSSNIGSNTVNW YQHLPGTAPKLLIYTNNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDDSLSGPVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGA VTVAWKADSSPVKAGVETTTTPSKQSNKYY AASSYLSLTPEQWKS HRYSYSCQVTHEGSTVEKTV APTECS</p> <p>SEQ ID NO: 446</p>
		2C2.005.010	!PS:361460	<p>CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCCGGGCAGAGGTCACCACTCTCTTGT CTGGAAGTAGCTCCAAACATCGGAAGTAATACTG TAAACTGGTACCAAGCACCTCCAGGAACGGCCC CCAAACTCTCATCTATATACTAATAATCAGCGGC CCTCAGGGGTCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTCTGTG CAACATTGATGACAGCCTGAATGCTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCTCAGGTC AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTC</p> <p>SEQ ID NO: 603</p>
				<p>CAGATGCAGGTGGTGCGAGTCTGGGCTGAGGTG AAGAAGCCTGGGCCTCAGTGAAAGTCTCCTGC AAGGCTTCCGGATACACCTTCAACCGGCTACTAT ATGCATTGGTGCGACAGGCCCTGGACAAAGG CTTGAGTGGATGGATGGATGATCAACCTAACAGT GGTGGCACAACCTATGCACAGAAATTCAGGGC AGGTCAACATGACACAGGACACGTCCTCAGT ACAGCTACATGAGAGCTGACGAGGCTGAGGTCT GACGACACGGCGGTGATTACTGTGCGAGAGGG GGGATTACGTTTGGGGGACTTATCGGCCTCAC TACTACTACGGTATGGACGCTCTGGGGCCAAAGG</p> <p>SEQ ID NO: 603</p>

A-2124-WO-PCT

	<p>GCCCTCCTCTGAGGAGCTTCAAGCCAAACAAGGC CACACTGGTGTCTCATAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCTGGAAAGGCAGATAG CAGCCCCGTCAAGCGGGAGTGGAGACCACAC ACCTCCAAACAAGCAACAACAAGTACGCGGC CAGCAGTATCTGAGCCTGACGCCCTGAGCAGTG GAACTCCACAGAAAGCTACAGCTGCCAGGTCAC GCATGAAGGAGCACCGTGGAGAAAGACAGTGG CCCCTACAGAAATGTTCA</p>	<p>ACCACGGTACCGTCTCCTCAGCCTCCACCAAG GGCCCATCGTCTTCCCCCTGGCACCTCTCTCCA AGACACCTCTGGGGGCACAGCGGCCCTGGGCT GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA CGGTGCTGTGAATCTCAGGGGCCCTGACCAGCG GCGTGACACCTTCCCCGGGTCTCTACAGTCTC AGGACTCTACTCCTCTCAGCAGCGTGGTGACCGT GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT CTGCAACGTGAATCAAGCCACGCAACACCAA GGTGACAAAGAAAGTTGAGCCCAATCTTGTGA CAAACTCACACATGCCACCGTGCCACGACC TGAACTCCTGGGGGACCGTCAGTCTTCTCTTC CCCCCAAACCCAAAGGACACCTCATGATCTCC CGGACCCCTGAGGTCACATGCGTGGTGGTGAC GTGAGCCACGAAGACCTGAGGTCAAGTTC AAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCC AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG CACGTACCGTTGTGACGCTCTCACCGTCTCTG CACCAGGACTGGCTGAATGGCAAGGAGTACAA GTGCAAGGTCTCCAAACAAAGCCCTCCCAGCCC CATCGAGAAACCATCTCTCAAAGCCAAAGGGCA GCCCCGAGAACACAGGTGTACACCTGCCCCC ATCCCGGAGGAGATGACCAAGAACCAAGGTCA GCTTGACCTGCCCTGGTCAAAGGCTTCTATCCCA GCGACATCGCCGTGGAGTGGGAGAGCAATGGG CAGCCGAGAACAACTACAGACCAACGCTCCC GTGCTGGACTCCGACGGCTCTTCTTCTCTATA GCAAGCTCACCGTGGACAAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAAACCACTACACGCAAGAGAGC CTCTCCCTGTCTCCGGTAAA</p>
	<p>SEQ ID NO: 2017</p>	<p>SEQ ID NO: 2174</p>
AA	<p>QSVLTQPPSASGTPGQRVTISCSGSSNIGSNTVNW YQHLPGTAPKLLIYTNNQRPSGVDPDRFSGSKSGTS ASLAISGLQSEDEADYFCAIFDDSLNAPVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD</p>	<p>QMQVVQSGAEVKKPGASVKVSKKASGYTFTGYY MHWVVRQAPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLSDDTAVYYCARG GDYVWVGTYRPHYYYGMDVWVGQGTITVTVSSAST</p>

A-2124-WO-PCT

			FYPGAVTVAWKADSSPVKAGVETTTTPSKQSNKYY AASSYLSLTPEQWKSHRYSQCVTHEGSTVEKTV APTECS	KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSLTVLHQDWLNGKEYKCKVSNK ALPAIEKTIKAKGPQREPQVYVTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LDSGSEFLYSKLTVDKSRWQQGNVVFSCSVMHEA LHNHYTQKSLSLSPGK
			SEQ ID NO: 447	SEQ ID NO: 604
			CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCCGGGCAGAGGGTCACCACTCTCTTGT CTGGAAGTAGCTCCAACATCGGAAGTAATACTG TAAACTGGTACCAAGCACTCCCAAGAACGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTCTGTG CAACATTTCGATAGCAGCCTGAATGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCTCAGTGC AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTC GCCCCTCTCTGAGGAGCTTCAAGCCCAACAAGGC CACACTGGTGTGTCTCATAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCCTGGAAAGGCAGATAG CAGCCCCGTCAAGCGGGAGTGGAGACCAACCAC ACCC'TCCAAACAAGCAACAACAAGTACGGGGC CAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG GAAGTCCACACAGAAAGCTACAGCTGCCAGGTAC GCATGAAGGGAGCACCCGTGGAGAGACAGTGG CCCCACAGATGTTCA	CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAGTCTCCTGTC AAGGCTCCGGATACACCTTCAACCGGCTACTAT ATGCAATTGGTGCAGACGGCCCTGGACAAAGGG CTTGAGTGGATGGATGGATCAACCTTAACAGT GGTGGCACAACTATGCACAGAAATTTTCAGGGC AGGTCAACATGACACGGGACACGTCCATCAGT ACAGCTACATGAGGTGAGCAGGCTGAGGTCT GACGACACGGCGTGTATTACTGTGCGAGAGGG GGGATTACGTTTGGGGGACTTATCGGCCTCAC TACTACTACGATATGGACGTCTGGGGCCAAAGG ACCAGGTCAACGTCTCCTCAGCCTCCACCAAG GGCCCATCGGTCTTCCCCCTGGCACCCCTCCCA AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA CGGTGTCGTGGAACCTCAGGGGCCCTGACCAAGC GCGTGACACACCTTCCCCGGCTGTCTACAGTCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT GCCCCCAGCAGCTTGGGCAACCCAGACCTACAT CTGCAACGTGAATCAAGCCCAAGCAACACCAA GGTGGACAAGAAAGTTGAGCCCAATCTTGTGA CAAACCTCACACATGCCACCGTGGCCAGCAC TGAACTCCTGGGGGACCGTCAGTCTTCTCTTC CCCCCAAACCAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTACATGCGTGGTGGTGGAC
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				GTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCC AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG CACGTACCGTTGTGTCAAGCGTCTCACCGTCTCTG CACCAGGACTGGCTGAATGGCAAGGAGTACAA GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCC CATCGAGAAAACCATCTCCAAGCCAAGGGCA GCCCCGAGAACACAGGTGTACACCTGCCCCC ATCCCGGAGGAGATGACCAAGAACACAGGTCA GCCTGACCTGCCCTGGTCAAAGGCTTCTATCCCA GCGACATCGCCGTGGAGTGGGAGAGCAATGGG CAGCCGGAGAACAACTACAAGACCACGCTCCC GTGCTGGACTCCGACGGCTCCTTCTTCTCTATA GCAAGCTCACCGTGGAACAAGACAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACCACTACACGCAAGAAGC CTCTCCCTGTCTCCGGTAAA	
				SEQ ID NO: 2018	SEQ ID NO: 2175
				QSVLTQPPSASGTPGQRVITISCGSSNIGSNTVNW YQHLPGTAPKLLIYTNNQRPSPGVDPDRFSGSKSGTS ASLAISGLOSEADYFCAITFDSSLNPGPVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTTPSKQSNKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS	QMQVVQSGAEVKKPGASVKVSKASGYTFTGYV MHWVVRQAPQGQLEWGMWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLSDDTAVYYCARG GDYVWGTYPHYYYGMDVWVGQGTITVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LSDSGSFFLYSKLTVDKSRWQQGNVVFSCSVMHEA LHNHYTQKLSLSLSPGK
	AA			SEQ ID NO: 448	SEQ ID NO: 605
				CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCCGGGCAGAGGTCACCATCTCTTGT CTGGAAGTAGCTCCAACATCGGAAGTAATTATG	CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGCGCTCAGTGAAGGTCTCCTGC AAGGCTTCGGGATACACCTTCACCGGCTACTAT
			NA	PS:3 6147 202. 005.0	

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TAAACTGGTACCAGCACCTCCAGGAACGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTCTGTG CAACATTTCGATAGCAGCCTGAATGCTCCGGTAT TCGGCGGAGGGACCAGCTGACCGTCTCAGGTC AGCCCAAGGTGCCCCCTCGGTCACTCTGTTCCTC GCCCCTCCTGAGGAGCTTCAAGCCAAACAAAGGC CACACTGGTGTCTCATAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCTGGAAAGGCAGATAG CAGCCCCGTCAGCGGGAGTGGAGACCAACCAC ACCC'TCCAAACAAAGCAACACAAAGTACGGCGC CAGCAGCTATCTGAGCCTGACGCCCTGAGCAGTG GAAGTCCACAGAAAGCTACAGCTGCCAGGTCAC GCATGAAGGGAGCACCGTGGAGAAAGACAGTGG CCCCACAGATGTTCA	ATGCATTGGGTGCGACAGGCCCTGGACAAAGGG CTTGAGTGGATGGATGGATCAACCTTAACAGT GGTGGCACAACTATGCACAGAAATTTTCAGGGC AGGTCAACATGACCAGGACACGTCCATCAGT ACAGCCTACATGAGCTGAGCAGGCTGAGGTCT GACGACACGGCGGTGATTACTGTGCGAGAGGG GGGATTACGTTGGGGGACTTATCGGCCCTCAC TACTACTACGATATGGACGTCTGGGGCCAAAGG ACCAGGTCAACGCTCTCCTCAGCCTCCACCAAAG GGCCCATCGGTCTTCCCCCTGGCACCTCTCTCCA AGACACCTCTGGGGGCACAGCGGCCCTGGGCT GCC'TGGTCAAGGACTACTTCCCCGAACCGGTGA CGGTGCTGTGGAAC'TCAGGGGCCCTGACCAAGC GCGTGCACACCTTCCCCGGCTGTCTACAGTCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT GCC'TCCAGCAGCTTGGGCACCCAGACCTACAT CTGCAACGTGAATCACAAGCCACGCAACACCAA GGTGGACAAGAAAGTTGAGCCCAATCTTGTGA CAA'AACTCACACATGCCACCGTGGCCAGCAC TGAACTCCTGGGGGACCGTCAGTCTTCTCTTC CCCCAAAACCAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTACATGCCGTGGTGGTGAC GTGAGCCACGAAGACCCCTGAGGTCAAGTTC AAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCC AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG CACGTACCGTGTGTGACGCTCCACCGTCTCTG CACCAGGACTGGCTGAATGGCAAGGAGTACAA GTGCAAGGTCTCCAAACAAAGCCCTCCAGCCCC CATCGAGAAACCATCTTCCAAAGCCAAAGGGCA GCCCCGAGAACACAGGTGTACACCTGCCCCC ATCCCGGGAGGAGATGACCAAGAACAGGTCA GCTTGACCTGCCCTGGTCAAAGGCTTCTATCCCC GCGACATCGCCGTGGAGTGGGAGAGCAATGGG CAGCCGGAGAACAACTACAGACCAACGCTCCC GTGCTGGACTCCGACGGCTCTTCTTCTCTATA GCAAGCTCACCGTGGACAAAGAGCAGGTGGCAG
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			SEQ ID NO: 2019 QSVLTQPPSASGTPGQVVTISCGSSSNIGSNYVNVW YQHLPGTAPKLLIYTNNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATDFDSSLNAPVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTPPSKQSNKKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS		CAGGGAAAGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACCACTACACGCAGAAGAGC CTCTCCCTGTCTCCGGGTAAA
	AA		SEQ ID NO: 449 CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG GGACCCCCGGGCAGAGGCTCACCATCTCTTTGTT CTGGAAGTAGCTCCAAACATCGGAAGTAATTATG TAAACTGGTACCAAGCACCTCCCAGGAAGGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACTCAGCCTCCCTTGCCATCAGTGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATAGCAGCCTGAATGCTCCGGTAT TCGGCGGAGGACCAGCTGACCGTCCCTAGGTC AGCCCCAAGGTCGCCCTCCGGTCACTCTGTTCCC GCCCTCCTCTGAGGAGCTTCAAGGCCAACAAAGGC CACACTGGTGTGTTCTCATAAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCTGGAAGGCAGATAG CAGCCCCGTCAAAGCGGGGAGTGGAGACCACCAC ACCCTCCAAACAAGCAACAACAAGTACGCGGC CAGCAGCTATCTGAGCCTGACGCTGAGCAGTG	NA	SEQ ID NO: 2176 QMQVVQSGAEVKKPGASVKVSKASGYTFTGYY MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFPQ GRV/TMTRDTSISTAYMELSLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWVGQGTITVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDNLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYVTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPV LDSGGSFFLYSKLTVDKSRWQQGNVVFSCSVMHEA LHNHYTQKSLSLSPGK
IPs:361478	2C2,005,013		SEQ ID NO: 606 CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCGGATACACCTTCACCGGCTACTAT ATGCAATTGGTGCAGACAGGCCCTGGACAAAGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGCAAAACTATGCACAGAAAGTTTCAGGGC AGGTCACCATGACCAAGGACACGTCCATCAGT ACAGCCTACATGGAGCTGAGCAGCCTGAGGTCT GACGACACGGCGTGTATTACTGTGCGAGAGGG GGGATTACGTTTTTCGGGACTTATCGGCCCTCACT ACTACTACGGTATGGAGCTGTGGGGCCAAAGGGA CCACGGTACCGTCTCTCTCAGCCTCCACCAAGG GCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAA GAGCACCTCTGGGGGCACAGCGGCCCTGGGCTG CCTGGTCAAGGACTACTTCCCCGAACCGGTGAC GGTGTGTGGAACCTCAGCGGCCCTGACCAAGCGG CGTGCAACACCTTCCCGGCTCTCCTACAGTCTCA		SEQ ID NO: 606 CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCGGATACACCTTCACCGGCTACTAT ATGCAATTGGTGCAGACAGGCCCTGGACAAAGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGCAAAACTATGCACAGAAAGTTTCAGGGC AGGTCACCATGACCAAGGACACGTCCATCAGT ACAGCCTACATGGAGCTGAGCAGCCTGAGGTCT GACGACACGGCGTGTATTACTGTGCGAGAGGG GGGATTACGTTTTTCGGGACTTATCGGCCCTCACT ACTACTACGGTATGGAGCTGTGGGGCCAAAGGGA CCACGGTACCGTCTCTCTCAGCCTCCACCAAGG GCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAA GAGCACCTCTGGGGGCACAGCGGCCCTGGGCTG CCTGGTCAAGGACTACTTCCCCGAACCGGTGAC GGTGTGTGGAACCTCAGCGGCCCTGACCAAGCGG CGTGCAACACCTTCCCGGCTCTCCTACAGTCTCA

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		<p>GAAGTCCACAGAAAGCTACAGCTGCCAGGTAC GCATGAAGGGAGCACCGTGGAGAAAGACAGTGG CCCCACAGAAATGTTCA</p>	<p>GGACTCTACTCCCTCAGCAGCGTGGTGACCGTG CCCTCCAGCAGCTTGGGCACCCAGACCTACATC TGCAACGTGAATCACAAGCCACGCAACACCAAG GTGGACAAAGAAAGTTGAGCCCAATCTTGTGAC AAACTCACACATGCCACCGTGCCAGCACCT GAATCTCTGGGGGACCGTCAGTCTTCTCTTCC CCCCAAACCCAAAGACACCCCTCATGATCTCC GGACCCCTGAGGTACATGCGTGGTGGTGACG TGAGCCACGAAGACCCCTGAGGTCAAAGTTCAA GGTACGTGGACCGCGTGGAGGTGCATAATGCCA AGACAAAGCCGTGTGAGGAGCAGTACGGCAGC ACGTACCGTTGTGTGACGCTCTCACCGTCTG ACCAGGACTGGCTGAATGGCAAGGAGTACAAGT GCAAGGCTCCCAACAAAGCCCTCCAGCCCCCA TCGAGAAACCATCTCCAAAGCCAAAGGCGAGC CCCGAGAACCAAGGTGTACACCTGCCCCCAT CCCGGAGGAGATGACCAAGAACCCAGGTGAGC CTGACCTGCTGGTCAAAGGCTTCTATCCCAGC GACATCGCGTGGAGTGGAGAGCAATGGGCA GCCGGAGAACAACTACAAAGACCACGCTCCCGT GCTGGACTCCGACGGCTCTTCTTCTCTATAGC AAGCTCACCGTGGACAAAGCAGGTGGCAGCA GGGGAACGTCTTCTCATGCTCCGTGATGCATGA GGCTCTGCACAACCACTACACGCAAGAGCCT CTCCCTGTCTCCGGGTA</p>
		<p>SEQ ID NO: 2020</p> <p>QSVLTQPPSASGTPGQRTVISCSSSSNIGSNYVNW YQHLPGTAPKLLIYTNNQRPSGVDPDRFSGSKSGTS ASLAISGLQSEDEADYFCAITFDSSLNAPVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTTPSKQSNKKY AASSYLSLTPEQWKSHRYSQCVTHEGSTVEKTV APTECS</p>	<p>SEQ ID NO: 2177</p> <p>QMQVVQSGAEVKKPGASVKVSKASGYTFTGY MHWVVRQAPQGQGLEWMGWNPNSGGTNYAQKFQ GRVTMTTRDTSISTAYMELSSLRSDDTAVVYCARG GDYVFGTYRPHYYYGMDVWVGQGTTVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS SLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKA</p>
	AA		

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				<p>LPAPIEKTISKAKGQPREPQVYVTLPPSREEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFELYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK</p>
				<p>SEQ ID NO: 450</p> <p>CAGTCTGTGCTGACTAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGGTCAACCATCTCTTGT CTGGAAGTAGCTCCAAACATCGGAAGTCAAACTG TAAACTGGTACCAAGCAACCTCCCAAGAAACGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTCTGTG CAACATTCTGATGAAAGCCTGAGTGGTCCGGTAT TCGGGGAGGGACCAAGCTGACCGTCTCAGGTC AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCTC GCCCCTCTCTGAGGAGCTTCAAGCCAAACAAGGC CACACTGGTGTCTCATAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCTGGAAAGGCAGATAG CAGCCCCGTCAAGCGGGAGTGGAGACCAACAC ACCTCCAAACAAGCAACAACAAGTACGCGGC CAGCAGCTATCTGAGCCTGACGCTGAGCAGTG GAAGTCCACAGAAAGCTACAGCTGCCAGGTCA GCATGAAGGGAGCACCGTGGAGAGACAGTGG CCCCACAGATGTTCA</p>
				<p>SEQ ID NO: 607</p> <p>CAGATCAGGTGCTGTCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAGTCTCCTGC AAGCTTCCGGATACACCTTCAACCGGCTACTAT ATGCAATTGGTGCACAGGCCCTGGACAAAGGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGGCACAACTATGCACAGAAATTTCAAGGC AGGTCAACATGACCAAGGACACGTCCATCAGT ACAGCCTACATGAGGCTGAGCAGGCTGAGGTCT GACGACACGGCGTGTATTACTGTGCGAGAGGG GGGATTACGTTTTCGGGACTTATCGGCCCTCACT ACTACTACGGTATGACGCTCTGGGGCCAAAGGA CCACGGTCAACGCTCTCCTCAGCCTCCACCAAGG GCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAA GAGCACCTCTGGGGGCACAGCGGCCCTGGGTG CCTGTCAAGGACTACTTCCCCGAACCGGTGAC GGTGTCTGGAACCTCAGCGCCCTGACCAAGCG CGTGCAACCTTCCCCGGCTGTCTACAGTCTCA GGACTCTACTCCCTCAGCAGCGTGGTGACCGTG CCCTCCAGCAGCTTGGGCACCCAGACCTACATC TGCAACGTGAATCACAAGCCCAAGCAACACCAAG GTGGACAAAGAAAGTTGAGCCCCAATCTTGTGAC AAACTCACACATGCCACCCGTGCCAGCACCT GAACCTCTGGGGGACCGTCACTTCTCTTCC CCCCAAACCAAGGACACCCCTCATGATCTCCC GGACCCCTGAGGTACATGCGTGGTGGTGGACG TGAGCCACGAAGACCCCTGAGGTCAAGTTCAACT GGTACGTGGACCGCGTGGAGGTGATAATGCCA AGACAAAGCCGTGTGAGGAGCAAGTACGGCAGC ACGTACCGTTGTGTACGCGTCTCACCGTCTGC ACCAAGGACTGGCTGAATGGCAAGGAGTACAAGT GCAAGGTCTCCCAACAAGGCCCTCCAGCCCCCA</p>

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			TCGAGAAAACCATCTCCAAAGCCAAAGGCAGC CCCGAGAACACAGGTGTACACCTGCCCCCAT CCCGGAGGAGATGACCAAGAACCCAGGTCAGC CTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC GACATCGCCGTGGAGTGGAGAGCAATGGGCA GCCGGAGAACAACTACAAAGACCACGCCTCCCGT GCTGGACTCCGACGGCTCTTCTTCCCTCTATAGC AAGCTCACCGTGGACAAGAGCAGGTGGCAGCA GGGGAACGTCTTCTCATGCTCCGTGATGCATGA GGCTCTGCACAACCACTACACGCAGAAAGGCCT CTCCCTGTCTCCGGTAA
		SEQ ID NO: 2021	SEQ ID NO: 2178
	AA	QSVLTQPPSASGTPGQRVTISCSGSSNIGSQTVNW YQHLPGTAPKLLIYTNNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCA TFDESLSGPVFGGGTK LTVLGGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGA VTVAWKADSSPVKAGVETTTTPSKQSNKKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS	QMQVVQSGAEVKKPGASVKVSKASGYTFTGY MHWVVRQAPGQGLEWMGWNPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLSDDTA VYYCARG GDYVFGTYRPHYYYGMDVWVGQGTTVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS SLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTIISKAKGQPREPQVYTLPPSREEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKLSLSLSPGK
		SEQ ID NO: 451	SEQ ID NO: 608
IPS:361845	18F2.013	NA	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTTCAGTAACCTTTGGCA TGC ACTGGGTCCGCCAGGCCCAAGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTACCATCTCCAGAGACAATTCCAAGAAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATA

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	GGGACCAAAGTGGATATCAACGAACGGTGGCT GCACCATCTGTCTTTCATCTTCCCGCCATCTGATG AGCAGTTGAATCTGGAACCTGCCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCCAGAGAGGCCA AAGTACAGTGGAAAGGTGGATAACGCCCTCCAAAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCCGAAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	GGACGATCTTTGGAGTGGTCTTTGGGGGACTACT GGGGCAGGGAACCCCTGGTCACCGTCTCCTCAG CTCCACCAAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGCTGCCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGC CCTGACCAAGCGGCTGCACACCTTCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGGCTTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACAC GTGCCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAAACCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAAGGACTGGCTGAATGG CAAGGAGTACAAAGTGCAAGGTCTCCACAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCATCCCGGAGGAGATGACCA AGAACAGGTGACCTGACCTGCCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGACAACATACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTA
	SEQ ID NO: 2022	SEQ ID NO: 2179
AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YQQKPGKAPKRLIYGASSLQSGVPSRFSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDI	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAWIYDASNENYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR

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			KRTVAAPSFIFFPSDEQLKSGTASVCLLNFFPR EAKVQWKVDNALQSGNSQESVTEQDSKDSYSL STLTLKADYEKHKVYACEVTHQGLSSPVTKSFN RGE	TIFGVVLGDYWGQGLTVTVSSASTKGPSVFP LAPSKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDRLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTKISK AKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFNCSVMHEALHNHYTQKS LSLSPGK
			SEQ ID NO: 452 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGATCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACCAAGGGAAGCCCTA AGCCCTGATCTATGGTGATCCAGTTTGCAAA GTGGGTCCCTTCAAGGTTCAAGCGGCAGTGGAT CTGGGACAGAAATCACTCTCACAAATCAGCAGCC TGACGCCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAAATAATTACCCCTTCACTTCGGCCAA GGGACCAAGTGGATATCAACGAACGGTGGCT GCACCATCTGTCTTCACTTCCCGCCATCTGATG AGCAGTTGAATCTGGAACTGCCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAA CGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCAAAAGAGCTTCAACA GGGAGAGTGT	SEQ ID NO: 609 CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAAGCTCTGGATTCAACCTTCAGTTACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCAACCATCTCCAGAGACAATTCAGAAACA CGCTGATCTGCAAAATGAACAGCCTGAGAGCCG AGGACAGGCTGTGTATTACTGTGCGCGAGATA GGACGATTTTGGAGTGTCTTTGGGGGACTACT GGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCTGGGTGCCGTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTGTCACACCTTCCCGGTGT CCTGACCAAGCGGTGTGTCACACCTTCCCGGTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTTGACCGTGGCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACATCAACATGCCACAC GTGCCACGACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAAACCCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG

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			<p>CGTGGTGGGACGTGAGCCACGAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCAATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTGAGCGT CCTCACCGTCTGCACCAAGACTGGCTGAATGG CAAGGAGTACAAAGTGCAAGGTCTCCAAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACAGGTGAGCCTGACCTGCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGAGAGACAACATACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTAAA</p> <p>SEQ ID NO: 2180</p>
			<p>QVQLVESGGGVVQPGRSRLRSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIYDASNKYAYADA VKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLLGDYWGQGTLLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPGK</p> <p>SEQ ID NO: 610</p>
		AA	<p>DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTEFT LTISLQPEDFATYYCLQHNNYPFTFGQGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSYSTSLSS TLTL SKADYEEKHKVYACEVTHQGLSSPVTKSFNR GEC</p> <p>SEQ ID NO: 2023</p>
			<p>SEQ ID NO: 453</p>

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IP5:361855	2C2.005.015	NA	<p>CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCCGGGAGAGGGTCACCATCTCTTGTT CTGGAAGTAGCTCCAAACATCGGAAGTAATACTG TAAACTGGTACCAGCAACTCCCAGGAACGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTCTGTG CAACATTTCGATAGCAGCCTGAGTGGTCCGGTAT TCGGCGGAGGGACCAGCTGACCGTCCTAGGTC AGCCCAAGGTGCCCCCTCGGTCACTCTGTTCCTC GCCCCTCCTGAGGAGCTTCAAGCCAAACAAGGC CACACTGGTGTCTCATAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCTGGAAAGGCAGATAG CAGCCCCGTCAGCGGGAGTGGAGACCACCAC ACCTTCCAAACAAGCAACAACAAGTACGGCGC CAGCAGCTATCTGAGCCTGACGCCCTGAGCAGTG GAAGTCCCACAGAAAGCTACAGTGCCAGGTCAC GCATGAAGGGAGCACCGTGGAGAAAGACAGTGG CCCCACAGATGTTCA</p> <p>CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCTGGGGCTCAGTGAAAGGTCTCCTGC AAGGTTCCGGATACACCTTCAACCGGCTACTAT ATGCATTGGTGCAGACGGCCCCCTGGACAAAGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGGCACAACTATGCACAGAAAGTTTCAGGGC AGGTCAACATGACAGGACACGTCATCAGT ACAGCCTACATGAGCTGAGCAGGCTGAGGTCT GACGACACGGCGTGTATTACTGTGCGAGAGGG GGGGATTACGTTGGGGGACTTATCGGCCCTCAC TACTACTACGATATGGACGCTGGGGCCAAAGG ACCAGGTCAACGCTCTCCTCAGCCTCCACCAA GGCCCATCGTCTTCCCCCTGGCACCCCTCCTCCA AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT GCCGTGTCAGGACTACTTCCCCGAACCGGTGA CGGTGCTGTGGAACTCAGGGGCCCTGACCAGCG GCGTGACACCTTCCCCGGGTGCTCTACAGTCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT CTGCAACGTGAATCAAGCCCAAGCAACACCAA GGTGGACAAGAAAGTTGAGCCCCAATCTTGTGA CAAACTCACACATGCCCCACCGTGCCCCAGCAC TGAACTCCTGGGGGACCGTCAGTCTTCTCTTC CCCCCAAACCCAAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTACATGCGTGGTGGTGGAC GTGAGCCACGAAGACCTGAGGTCAAGTTC AAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCC AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG CACGTACCGTTGTGTCAGCGTCTCACCGTCTCTG CACCAGGACTGGCTGAATGGCAAGGAGTACAA GTGCAAGGTCTCCAAACAAGCCCTCCCAGCCCC CATCGAGAAACCATCTCTCCAAGCCAAAGGGCA GCCCCGAGAACACAGGTGTACACCTGCCCCC ATCCCGGAGGAGATGACCAAGAACACAGGTCA GCCGTGACCTGCCCTGGTCAAGGCTTCTATCCCCA GCGACATCGCCGTGGAGTGGGAGAGCAATGGG</p>
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					CAGCCGAGAACAACTACAAGACCACGCCTCCC GTGCTGGACTCCGACGGCTCCTTCTTCTCTATA GCAAGCTCACCGTGGACAAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCCGTGATGCAT GAGGCTCTGCACAACCACTACACGCAAGAGAGC CTCTCCCTGTCTCCGGGTAAA
				SEQ ID NO: 2024	SEQ ID NO: 2181
				QSVLTQPPSASGTPGQRVITISCGSSSNIIGSNTVNW YQQLPGTAPKLLIYTNNQRPSGVDPDRFSGSKSGTS ASLAISGLQSEDEADYFCAITFDSSLGPFVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTTPSKQSNKRY AASSYLSLTPEQWKSHRYSYSCQVTHEGSTVEKTV APTECS	QMQVVQSGAEVKKPGASVKVSKASGYTFTGYY MHWVVRQAPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLSDDTA VYYCARG GDYVWGTYPHYYYGMDVWVGQGTITVTVSSAST KGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPV VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSLTVLHQDWLNGKEYKCKVSNK ALPAIEKTIKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LSDSGSFELYSKLTVDKSRWQQGNVVFCSVMHEA LHNHYTQKLSLSPGK
			AA	SEQ ID NO: 454	SEQ ID NO: 611
				GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCACTCTGTAGGAGACAGAGTCACTATACATT GCCGGGCAAGTCAGACCAATTAGCAGGTTTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCCGTG AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG TGGGTCCCATCAAAGATTGAGTGGCAGTGGTTC TGGGACAGATTTCACTCTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCTGATCAGTTTTTGCCCA GGGACCAAGCTGGAGATCACACGAACGGTGG CTGCACCATCTGTCTTCACTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCCTCTGTTGT GTGCTGTGTAATAACTTCTATCCCAAGAGAGGC CAAAAGTACAGTGAAGGTGGATAACGCCCTCCA	CAGGTGCAGTTGGTGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT ACAGCGTCTGGATTCACTTTCAGTAGCTATGGC ATACACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGGA AGTAATAAGTTCCATGCAGACTCCGTGAAGGGC CGATTACCATCTCCAGAGACAATTCCAAGAAC ACGCTGATCTGCAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC TGGGGCCAAAGGACAAAGGTCAACCGTCTCTTCA GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTG GCACCTCTCTCAAGAGACACCTCTGGGGGCACA GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC
IPS:336067	5G12.006	NA			

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	<p>ATCGGGTAACTCCAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCCTGACGCTGAGCAAGCAGACTACGAGA AACACAAAGTCTACGCCCTGCGAAGTCAACCCATC AGGCCCTGAGCTCGCCCCGTACAAAGAGCTTCA ACAGGGGAGAGTGT</p>	<p>CCCGAACCCGGTGACGGTGTCTGTGGAACCTCAGGC GCCCTGACCAGCGGCGTGACACCTTCCCGGCT GTCCTACAGTCCTCAGGACTCTACTCCCTCAGCA GCGTGTGACCGTGCCCTCCAGCAGCTTGGGCA CCCAGACCTACATCTGCAACGTGAATCACAAGC CCAGCAACACCAAGGTGGACAAGAAAGTTGAG CCCAATCTTGTGACAAACTCACACATGCCCCA CCGTGCCAGCACCTGAACCTCTGGGGGACCG TCAGTCTTCTCTTCCCCCAAAACCCAAAGACA CCCTCATGATCTCCCGGACCCCTGAGGTCACAT GCGTGGTGGTGGACGTGAGCCACGAAGACCCCTG AGTCAAGTTCAACTGGTACGTGGACGGCGTGG AGTGCATAATGCCAAGACAAGGCCGTGTGAGG AGCAGTACGGCAGCACGTACCGTTGTGTACGCG TCCTCACCGTCTGACCAAGGACTGGCTGAATG GCAAGGAGTACAAGTGC AAGTCTCCAAACAAA GCCCTCCAGCCCCCATCGAGAAAACCATCTCC AAAGCCAAAGGCAGCCCCCGAGAACACACAGGT GTACACCTGCCCCCATCCCGGAGGAGATGAC CAAGAACACAGGTACGCTGACCTGCCTGGTCAA AGCTTCTATCCAGCGACATCGCCGTGGAGTG GGAGAGCAATGGGCAGCCGGAACAACA AGACCACGCTCCCGTGTGCTGGACTCCGACGGCT CCTTCTTCTCTATAGCAAGCTCACCGTGGACAA GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATG CTCCGTGATGCATGAGGCTCTGCACAACCACTA CAGGCAGAAAGACCTCTCCCTGTCTCCGGGTAA A</p>
AA	<p>SEQ ID NO: 2025</p> <p>DIQLTQSPSSLSASVGDVRVTITCRASQTSRFLNWX QQKPGKAPPELLIYVASSLQSGVPSRFSGSGTDFD LTISSLQPEDFATYYCQQSYSTLISFGQGTGLEITRT VAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSYSTLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC</p>	<p>SEQ ID NO: 2182</p> <p>QVQLVESGGGVVQPRSLRLSCTASGFTFSSYGIH WVRQAPGKGLEWVAWIYDGSNKFHADSVKGRF TISRDNSKNTLYLQMNSLRAEDSAMYFCARGKVA GMPEAFEIWGQGTKVTVSSASTKGPSVFPLAPSSK STSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVN HKPSNTKVDKKEPKSCDKTHTCTPCPPAPELLGGP</p>

A-2124-WO-PCT

				SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVFSQSVMHREALHNHYTQKSLSL SPGK
			SEQ ID NO: 455	SEQ ID NO: 612
			CAGTCTGTGTGACGCAGCCGCCCTCAGTGTCTG CGGCCCCAGGACAGAGGTACCACTCTCCTGCT CTGGAAGCAGCTCCAACATTGGAAATAATTATG TATCCTGGTATGAGCAGTTCCCAAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTACGCCACCTGGGCATCACCCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGTGTGT ATTCGGCGGAGGGACCAAACTGACCCGTCTAGG TCAGCCCCAAGGCTGCCCTCGGTCACTCTGTTC CCGCCCTCCTGAGGAGCTTCAAGCCAACAAG GCCACACTGGTGTCTCATAAGTGACTTCTACC CGGGAGCCGTGACAGTGGCTGGAGGCCAGAT AGCAGCCCCGTCAAGCGGGGAGTGGAGACCAC CACACCTCCAACAAGCAACAACAAGTACGC GGCCAGCAGCTATCTGAGCCTGACGCCGTAGCA GTGGAGTCCACAGAAAGCTACAGCTGCCAGGT CACGCATGAAGGGAGCACCCGTGGAGAAAGACAG TGGCCCCCTACAGAATGTTCA	CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCAGTTATGAT ATCAACTGGTGCACAGGCCACTGGACAAGGG CTTGAGTGGATGGATGGATGAACCTAACAGT GGTAACACAGGCTATGCACAGAAATTCCAGGGC AGAGTCACATGACAGGGACACCTCCACATAAGC ACAGCCTACATGAGCTGAGCAGCCTGAGATCT CAGGACACGGCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGAGTTATCGTCCCTACT ACTACTACTAGGTATGGACGCTCTGGGGCCAAAG GGACCACGGTCAACGCTCTCCTCAGCCTCCACCA AGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTC CAAGAGCACCTCTGGGGGCAAGCGGGCCCTGGG CTGCTGGTCAAGGACTACTTCCCCGAACCCGGT GACGGTGTGTGGAACCTCAGGGCCCTGACCCAG CGCGTGCACACCTTCCCGGCTGTCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCACAAGCCCCAGCAACACC AAGGTGGACAAGAAAGTTGAGCCCCAAATCTGT GACAAAATCACAACATGCCACCCGTGCCAGCA CCTGAACCTCTGGGGGACCCGTCACTTCTCCTCT TCCCCCAAAACCAAGGACACCCCTCATGATCT CCCGGACCCCTGAGGTCAATGCGTGGTGGTG ACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCA ACTGGTACGTGGACGGCGTGGAGGTGCATAATG CCAAGACAAGCCCGTGTGAGGAGCAGTACGGC
IPS:336169	17B11.002	NA		

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				AGCACGTACCGTTGTGTCAAGCGTCTCACCGTCC TGCACCAAGGACTGGCTGAATGGCAAGGAGTACA AGTGCAAGGTCTCCAACAAAGCCCTCCAGCCC CCATCGAGAAAACCATCTCCAAGCCAAAGGGC AGCCCCGAGAACACAGGTGTACACCTGCCCC CATCCCGGAGGAGATGACCAAGAACCAAGGTC AGCTGACCTGCCTGGTCAAAGGCTTCTATCCC AGCGACATCGCCGTGGAGTGGGAGAGCAATGG GCAGCGGAGAACAACTACAAGACCACGCCCTCC CGTGTGGACTCCGACGGCTCTTCTTCTCTCTAT AGCAAAGCTCACCGTGGACAAGAGCAGGTGGCA GCAGGGGAACGTCTTCTCATGCTCCGTGATGCA TGAGGCTCTGCACAACCACTACACGCAGAGAAG CCTCTCCCTGCTCCGGGTAAA	
				SEQ ID NO: 2026	SEQ ID NO: 2183
			AA	QSVLTQPPSVSAAPGQKVITISCSGSSNIGNNYVS WYEQFPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTS ATLGITGLQTGDEADYYCGTWDSSLSAVVFGGGT KLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLIS DFYPGAVTVAWKADSSPVKAGVETTTPSKQSNK YAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKT VAPTECS	QMLVQSGAEVKKPGASVKVSKASGYTFTSYDI NWVRQATGQGLEWMGWMNPNSGNTGYAQKFQ GRVTMTRDTSISTAYMELSSLSRQDТАVYYCARG GDYVWGSYRPPYYYGMDVWVGQGTTVTVSSAS TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTP SSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTH TCPPCPAPPELLGGPSVFLFPPKPKDТLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LSDSGSFFLYSKLTVDKSRWQQGNVFSCSVMHЕA LHNHYTQKSLSLSPGK
				SEQ ID NO: 456	SEQ ID NO: 613
	5G12.006.001	!PS:361127	NA	GACATCCAGCTGACCCAGTCTCCAТCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTG AGCTCCTGATCTATGTTGCAТCСAGTTTGCAAG TGGGGTCCCATCAAGATTCAGTGGCAGTGГTTC	CAGGTGCAGTTGTGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTCAGTAGCTATGGC ATACACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGТATGATGCA AGTAAТАAGTTCCATGCAGACGCCGTGAAGGGC

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TGGGACAGATTTCACTCTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGATCAGTTTGGCCA GGGACCAAGCTGGAGATCAACGAACGGTGG CTGCACCATCTGTCTTCACTCTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCCTCTGTTGT GTGCTGCTGAATAACTTCTATCCCAGAGAGGC CAAAGTACAGTGGAGGTGGATAACGCCCTCCA ATCGGGTAATCCCCAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCCTGACGCTGAGCAAGCAGACTACGAGA AACACAAAGTCTACGCCCTGCGAAGTCAACCCATC AGGCCCTGAGCTCGCCCCGTACAAAGAGCTTCA ACAGGGGAGAGTGT	CGATTACCATCTCCAGAGACAATTCCAAGAAC ACGCTGATCTGCAAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCTGAAGCTTTTGAATC TGGGGCCAAGGACAAAGGTCAACCGTCTCTTCA GCCCTCCACCAAGGCCCATCGGTCTTCCCCCTG GCACCTCTCCAAAGACACCTCTGGGGGCACA GCGGCCCTGGGCTGCCCTGGTCAAGGACTACTTC CCGAAACCGGTGACGGTGTCTGTGGAACCTCAGGC GCCCTGACCAGCGGCGTGCACACCTTCCCCGGCT GTCTACAGTCTCTCAGGACTCTACTCCCTCAGCA GCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA CCCAGACCTACATCTGCAACGTGAATCACAAGC CCAGCAACACCAAGGTGGACAAGAAAGTTGAG CCCAATCTTGTGACAAACTCACACATGCCCA CCGTGCCAGCACCTGAACCTCTGGGGGACCG TCAGTCTTCTCTTCCCCCAAAACCAAGGACA CCCTCATGATCTCCCGACCCCTGAGGTCACAT GCGTGGTGGTGAGCTGAGCCACGAAGACCTG AGTCAAGTTCAACTGGTACGTGGACGGCGTGG AGTGCATATATGCCAAGACAAGCCGTGTGAGG AGCAGTACGGCAGCACGTACCGTTGTGTACGG TCCTCACCGTCTGCACCAGGACTGGCTGAATG GCAAGGAGTACAAGTGCAGGTCTCCAACAAA GCCCTCCAGCCCCCATCGAGAAAACCATCTCC AAAGCCAAGGGCAGCCCCGAGAACCCACAGGT GTACACCTGCCCCCATCCCGGAGGAGATGAC CAAGAACAGGTCAAGCTGACCTGCCCTGGTCAA AGCTTCTATCCAGCGACATCGCCGTGGAGTG GGAGAGCAATGGGCAGCCGGAACAACATA AGACCACGCCCTCCGTGTGGACTCCGACGGCT CCTTCTTCTCTATAGCAAGCTCACCCTGGACAA GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATG CTCCGTGATGCATGAGGCTCTGCACAACCACTA CACGCAGAAAGACCCTCTCCCTGTCTCCGGGTAA
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		SEQ ID NO: 2027	SEQ ID NO: 2184
	AA	DIQLTQSPSSLSASVGDRTVITCRASQTISRFLNWWY QQKPGKAPELLIYVASSLQSGVPSRFSGSGSDFT LTISSLQPEDFATYCCQSYSTLISFGQGTKEIKRT VAAPSVFIPPSDEQLKSGTASVCLLNFFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSITYLSST LTLKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC	QVQLVESGGGVVQGRSLRLSCAASGFTSSYGIH WVRQAPGKGLEWVAWIYDASNKFHADAVKGR FTISRDNSKNTLYLQMNSLRAEDSAMFYFCARGKV AGMPEAFEIWGQGTKVTVSSASTKGPSVFPLAPSS KSTSGGTAAALGCLVKDYFPEPTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCTPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDSDGSEFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
IPS:361136	5G12.006.002	SEQ ID NO: 457	SEQ ID NO: 614
	NA	GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA ATTGGTATCAGAGAAACCTGGGAAAGCCCCGTG AGCTCTGATCTATGTTGCATCCAGTTTGCAAAG TGGGTCCCATCAAGATTTCAGTGGCAGTGGTTC TGGACAGATTTCACCTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGATCAGTTTGGCCA GGGACCAAGCTGGAGATCAACGAAACGTTGG CTGCACCATCTGTCTTCACTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACCTGCCTCTGTTGT GTGCTGCTGAATAACTTCTATCCAGAGAGGC CAAAGTACAGTGAAGGTGGATAACGCCCTCCA ATCGGGTAACCTCCAGGAGAGTGTCAAGAGCA GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCTGACGCTGAGCAAGCAGACTACGAGA AACACAAAAGTCTACGCTGCGAAGTCAACCCATC AGGGCTGAGCTCGCCCGTCAACAAAGAGCTTCA ACAGGGGAGAGTGT	CAGTGCAAGTTGGTGAGTCTGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT ACAGGCTCTGGATTCACTTCAAGTATGCTATGGC ATACACTGGTCCCGCAGGCTCCAGGCAAGGGG CTGGAGTGGTGCGAGTTATATGGTATGATGCA AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC CGATTCAACATCTCCAGAGACAATTCCAAGAAC ACGCTGATCTGCAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC TGGGGCCAAGGGACAAGGTCAACCGTCTCTTCA GCCTCCACCAAGGCCCATCGGTCTTCCCGCTG GCACCTCTCCAAAGAGCACCTCTGGGGGCA GCGGCCCTGGCTGCCTGGTCAAGGACTACTTC CCCGAACCGGTGACGGTGTGTGGAACCTCAGGC GCCCTGACCAAGCGGTGTCAACCTTCCCGGCT GTCTACAGTCTCAGGACTCTACTCCCTCAGCA GCGTGGTGACCGTGCCTCCAGCAGCTTGGGCA CCCAGACCTACATCTGCAACGTGAATCAACAGC CCAGCAACACCAAGGTGGACAAGAAAGTTGAG

A-2124-WO-PCT

			<p>CCCAATCTTTGTGACAAAACTCACACATGCCCCA CCGTGCCAGCACCTGAACCTCCTGGGGGACCG TCAGTCTTCTCTTCCCCCAAAACCAAGGACA CCCTCATGATCTCCCGGACCCCTGAGGTCACAT GCGTGGTGGTGGACGTGAGCCACGAAGACCCCTG AGTCAAGTTCAACTGGTACGTGGACGGCGTGG AGTGCATAATGCCAAGACAAAGCCGTGTGAGG AGCAGTACGGCAGCACGTACCGTTGTGTACGG TCCTCACCGTCTGACACAGGACTGGCTGAATG GCAAGGAGTACAAGTGAAGTCTCCAACAAA GCCCCTCCAGCCCCATCGAGAAAACCATCTCC AAAGCCAAAGGCGAGCCCCGAGAACACAGGT GTACACCTGCCCCCATCCCGGAGGAGATGAC CAAGAACAGGTACAGCTGACCTGCCTGGTCAA AGCTTCTATCCAGCGACATCGCCGTGGAGTG GGAGAGCAATGGGCGAGCCGGAACAACATA AGACCACGCTCCCTGCTGGACTCCGACGGCT CCTTCTCTCTATAGCAAGCTCACCGTGGACAA GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATG CTCCGTGATGATGAGGCTCTGCACAACCACTA CAGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAA A</p>
		<p>SEQ ID NO: 2028</p> <p>DIQLTQSPSSLASVGDVRVTITCRASQTISRFLNWW QQKPGKAPPELLIYVASSLQSGVPSRFSGSGSDFT LTISSLQPEDFATYYCQOSYSTLISFGQGTKEIKRT VAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSYSTLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC</p>	<p>SEQ ID NO: 2185</p> <p>QVQLVESGGGVVQPGRSLRLSCTASGFTFSSYGIH WVRQAPGKGLEWVAWIYDASNKFHADAVKGR FTISRDNSKNTLYLQMNSLRAEDSAMFYFCARGKV AGMPEAFEIWGQGTKVTVSSASTKGPSVFPLAPSS KSTSGGTAAALGCLVKDYFPEPTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKEPKSCDKTHCTCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSK</p>
	AA		

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				LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
				SEQ ID NO: 615
				CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTCAGTAGCTATGGC ATACACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGATCTGCAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCTGAAGCTTTTGAATC TGGGGCCAAGGACAAGGTCAACCGTCTCTTCA GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTG GCACCTCTCCAAAGACACCTCTGGGGGCACA GCGGCCCTGGGTGCTGGTCAAGGACTACTTC CCCGAACCGGTGACGGTGTCTGGAACTCAGGC GCCCTGACCAGCGGCGTGACACCTTCCCCGGCT GTCTACAGTCTCAGGACTCTACTCCCTCAGCA GCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA CCCAGACCTACATCTGCAACGTGAATCACAAGC CCAGCAACACCAAGGTGGACAAGAAAGTTGAG CCCAATCTTGTGACAAACTCACACATGCCCCA CCGTGCCAGCACCTGAACCTCTGGGGGACCG TCAGTCTCTCTTCCCCCAAAACCCAAAGACA CCCTCATGATCTCCCGGACCCCTGAGGTCACAT GCGTGGTGGTGACGTGAGCCACGAAGACCCCTG AGGTCAAGTTCAACTGGTACGTGGACGGCGTGG AGGTGCATAATGCCAAGACAAAGCCGTGTGAGG AGCAGTACGGCAGCACGTACCGTTGTGTACGCG TCCTCACCGTCTGCACCCAGGACTGGCTGAATG GCAAGGAGTACAAGTGAAGGTCTCCCAACAAA GCCCTCCAGCCCCCATCGAGAAAACCATCTCC
				SEQ ID NO: 458
				GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGGCAAGTCAGACCATAGCAGGTTTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTG AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG TGGGTCCCATCAAGATTCAAGTGGCAGTGGTTC TGGGACAGATTTCACTCTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCTGATCAGTTTTGGCCA GGGACCAAGCTGGAGATCACACGAACGGTGG CTGCACCATCTGTCTTCACTTCCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCCTCTGTTGT GTGCTGCTGAATAACTTCTATCCAGAGAGGC CAAAGTACAGTGAAGGTGGATAACGCCCTCCA ATCGGGTAACTCCAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCTGACGCTGAGCAAGCAGACTACGAGA AACACAAAGTCTACGCTGCGAAGTCAACCCATC AGGGCCTGAGCTCGCCCCGTACAAAGAGCTTCA ACAGGGGAGAGTGT
			NA	
		5G12.006.003		
		IPS:361140		

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			<p>AAAGCCAAAGGGCAGCCCCGAGAACACAGGT GTACACCCCTGCCCCCATCCCGGAGAGATGAC CAAGAACAGGTACAGCTGACCTGCCTGGTCAA AGGCTTCTATCCAGCGACATCGCCGTGGAGTG GGAGAGCAATGGGCAGCCGGAACAACA AGACCACGCCCTCCCTGCTGGACTCCGACGGCT CCTTCTCCTCTATAGCAAGCTCACCGTGGACAA GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATG CTCCGTGATGCATGAGGCTCTGCACAACCACTA CAGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAA A</p>
			<p>SEQ ID NO: 2029</p> <p>DIQLTQSPSSLASVGDRTVTITCRASQTISRFLNWY QQKPGKAPPELLIYVASSLQSGVPSRFSGSGTDFT LTISSLQPEDFATYYCQQSYSTLISFGQGTCKLEITRT VAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSITYLSST LTLISKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC</p>
		AA	<p>SEQ ID NO: 2186</p> <p>QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGIH WVRQAPGKGLEWVAWIYDASNKFHADAVKGR FTISRDNSKNTLYLQMNSLRAEDSAMFYFCARGKV AGMPEAFEIWGGQGTKVTVSSASTKGPSVFPLAPSS KSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKEPKSCDKTHCTCPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKA KGPQREPVVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK</p>
		NA	<p>SEQ ID NO: 459</p> <p>GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCAATCTGTAGGAGACAGAGTCACTATACATT GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCCCTA AGCTCCTGATCTATGTTGCATCCAGTTTGCAAG TGGGTCCCATCAAGATTTCAGTGGCAGTGGTTC TGGGACAGATTTCACCTCTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGATCAGTTTTTGCCCA</p>
!PS:35919	5G12.006.004		<p>SEQ ID NO: 616</p> <p>CAGGTGCAGTTGGTGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCAACCTTCAGTAGCTATGGC ATACACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGCGAGTTATATGGTATGATGCA AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC CGATTACCATCTCCAGAGACAATTCCAAAGAAC ACGCTGATCTGCAAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA</p>

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	GGGACCAAGCTGGAGATCAAAACGAACGGTGG CTGCACCATCTGTCTTTCATCTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCCTCTGTTGT GTGCTGCTGAATAACTTCTATCCACAGAGGC CAAAGTACAGTGAAGGTGGATAACGCCCTCCA ATCGGGTAATCCCCAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCTGACGCTGAGCAAGCAGACTACGAGA AACACAAAGTCTACGCCCTGCGAAGTCAACCATC AGGCCCTGAGCTCGCCCCGTACAAAGAGCTTCA ACAGGGGAGAGTGT	AAAGTGGCTGGTATGCCTGAAGCTTTTGAATC TGGGCCAAGGACATTTGTCACCGTCTCTTCA GCTCCACCAAGGCCCATCGGTCTTCCCCCTG GCACCTCTCCAAAGACACCTCTGGGGCACA GCGGCCCTGGGCTGCCCTGGTCAAGGACTACTTC CCGAACCGGTGACGGTGTCTGTGGAACCTCAGGC GCCCTGACCAGCGGCGTGCACACCTTCCCGGCT GTCTACAGTCTCAGGACTCTACTCCCTCAGCA GCGTGTGACCGTGCCCTCCAGCAGCTTGGGCA CCCAGACCTACATCTGCAACGTGAATCACAAGC CCAGCAACACCAAGGTGGACAAGAAAGTTGAG CCCAATCTTGTGACAAACTCACACATGCCCA CCGTGCCAGCACCTGAACTCCTGGGGGACCG TCAGTCTTCTCTTCCCCCAAAACCAAGGACA CCCTCATGATCTCCCGGACCCCTGAGGTCACAT GCGTGGTGGTGGACGTGAGCCACGAAGACCTG AGTCAAGTTCAACTGGTACGTGGACGGCGTGG AGTGCATAATGCCAAGACAAGGCCGTGTGAGG AGCAGTACGGCAGCACGTACCGTTGTGTACGCG TCCTCACCGTCTGCACAGGACTGGCTGAATG GCAAGGAGTACAAGTGCAGGTCTCCAACAAA GCCCTCCAGCCCCCATCGAGAAAACCATCTCC AAAGCCAAGGGCAGCCCCCGAGAACACAGGT GTACACCTGCCCCCATCCCCGGAGGAGATGAC CAAGAACAGGTACGCTGACCTGCCCTGGTCAA AGGCTTCTATCCAGCGACATCGCCGTGGAGTG GGAGAGCAATGGGCAGCCGGAACAACATA AGACCAGCCTCCCGTGTGGACTCCGACGGCT CCTTCTTCTCTATAGCAAGCTCACCGTGGACAA GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATG CTCCGTGATGCATGAGGCTCTGCACAACCACTA CAGGCAGAAAGACCTCTCCCTGTCTCCGGGTAA A
	SEQ ID NO: 2030	SEQ ID NO: 2187
AA	DIQLTQSPSSLSASVGDRTVTITCRASQTSRFLNWWY QQKPGKAPKLLIYVASSLSQSGVPSRFSGSGTGDF	QVQLVESGGGVVQPRSLRLSCAASGFTSSYGIH WVRQAPGKGLEWVAWIYDASNKFHADAVKGR

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			TLTISSLQPEDFATYYCQSYSTLISFGQGTKEIKR TVAAAPSVFIPPSDEQLKSGTASVCLLNFFYPREA KVQWKVDNALQSGNSQESVTEQDSKSDSTYLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC	SEQ ID NO: 460	FTISRDNKNTLYLQMNSLRAEDSAMFYFCARGKV AGMPEAFEIWGGQTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHCTCPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEVESNGQPENNYKTTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
IPS:361144	5G12.006.005	NA	GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACATACACTT GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTG AGCTCTGATCTATGTTGCATCCAGTTTGCAAAG TGGGTCCCATCAAGATTCAAGTGGCAGTGGTTC TGGGACAGATTTCACCTTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGATCAGTTTGGCCA GGGACCAAGCTGGAGATCAACGAAACGTTGG CTGCACCATCTGTCTTCTATCTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCCTCTGTTGT GTGCTGTCTGAATAACTTCTATCCCAGAGAGGC CAAGTACAGTGGAAAGGTGGATAACGCCCTCCA ATCGGTAACCTCCAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACTACAGCCTCAGCA GCACCTGACGCTGAGCAAGAGCAGACTACGAGA AACACAAAGTCTACGCCCTGCGAAGTCAACCATC AGGGCTGAGCTCGCCCGTCAACAAAGAGCTTCA ACAGGGGAGAGTGT	SEQ ID NO: 617	CAGTGCAGTTGGTGAGTCTGGGGGAGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCAACCTTCAAGTATGCTATGGC ATACACTGGTCCGACGGTCCAGGCAAGGGG CTGAGTGGTGGCAGTTATATGATATGATGCA AGTAATAAGTTCCATGCAGACTCCGTGAAGGCG CGATTACCATCTCCAGAGACAATTCCAAGAAC ACGCTGATCTGCAATGAAACAGCTGAGAGGCC GAGGACTCGGCTATGTAATCTTGTGCGAGAGGA AAAGTGGTGGTATGCTGTAAGCTTTTGAAATC TGGGGCCAAGGACAAAGGTCAACCGTCTCTTCA GCCCTCCACCAAGGCCCATCGGTCTTCCCCCTG GCACCTCTCCAGAGCACTCTGGGGGCACA GCGGCCCTGGGCTGCTGGTCAAGGACTACTTC CCCGAACCGGTGACGGTGTGTGGAACCTCAGGC GCCCTGACCAAGCGGTGTGCAACCTTCCCGGCT GTCTACAGTCTCAGGACTCTACTCCCTCAGCA GCGTGGTGACCGTGGCTCCAGCAGCTTGGGCA CCCAGACCTACATCTGCAACGTGAATCACAAGC CCAGCAACACCAAGGTGGACAAGAAAGTTGAG CCCAATCTTGTGACAATACTCACACATGCCCA CCGTGCCCAAGCAGTGAACCTCTGGGGGACCG TCAGTCTTCTCTTCCCCCAAAACCCCAAGGACA

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			CCCTCATGATCTCCCGGACCCCTGAGGTCACAT GCGTGGTGGTGGACGTGAGCCACGAAGACCCCTG AGTCAAGTTCAACTGGTACGTGGACGGCGTGG AGTGCATATGCCAAGACAAAGCCGTGTGAGG AGCAGTACGGCAGCACGTACCGTTGTGTACGG TCCTCACCGTCTGACACAGGACTGGCTGAATG GCAAGGAGTACAAGTGAAGTCTCCAAACAA GCCCTCCAGCCCCCATCGAGAAACCATCTCC AAAGCCAAAGGCAGCCCCGAGAACACAGGT GTACACCTGCCCCCATCCCGGAGAGATGAC CAAGAACAGGTACAGCTGACCTGCCTGGTCAA AGCTTCTATCCAGCGACATCGCCGTGGAGTG GGAGAGCAATGGGCAGCCGAGAACACTACA AGACCAGCCTCCGTGCTGGACTCCGACGGCT CCTTCTCCTCTATAGCAAGCTCACCGTGGACAA GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATG CTCCGTGATGATGAGGCTCTGCACAAACCACTA CAGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAA A
	SEQ ID NO: 2031	SEQ ID NO: 2188	
	DIQLTQSPSSLASVGDRTVTITCRASQTISRFLNWW QQKPGKAPPELLIYVASSLQSGVPSRFSGSGTDF LTISSLQPEDFATYYCQQSYSTLISFGQGTGLEIKRT VAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSYSTLSST LTLKADYEEKHKVYACEVTHQGLSSPVTKSFNRG EC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGIH WVRQAPGKGLEWVAWIYDASNKFHADSVKGRF TISRDNSKNTLYLQMNSLRAEDSAMYFCARGKVA GMPEAFEIWGQGTQKVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVVFSCSVMHEALHNHYTQKSLSL SPGK	
	AA		
	SEQ ID NO: 461	SEQ ID NO: 618	

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IP:361151	5G12.006.006	NA	<p>GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTG AGCTCTGATCTATGTTGCATCCAGTTTGCAAAG TGGGTCCCATCAAGATTCAAGTGGCAGTGGTTC TGGACAGATTTCACTCTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGATCAGTTTTTGGCCA GGGACCAAGCTGGAGATCAACGAACGGTGG CTGCACCATCTGTCTTCACTTCCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCCTCTGTTGT GTGCTGCTGAATAACTTCTATCCCAGAGAGGC CAAGTACAGTGAAGGTGGATAACGCCCTCCA ATCGGGTAACTCCAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACTACAGCCTCAGCA GCACCCTGACGCTGAGCAAGCAGACTACGAGA AACACAAAGTCTACGCCCTGCGAAGTCAACCATC AGGCCCTGAGCTCGCCCCGTACAAAGAGCTTCA ACAGGGGAGAGTGT</p> <p>CAGTGCAAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCAACCTTCACTAGTATGGC ATACACTGGTCCGACGGTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGGA AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGATCTGCAAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGATGCCTGAAGCTTTTGAATC TGGGGCCAAAGGACAAAGGTCAACCTCTGGGGCACA GCCCTCCACCAAGGCCCATCGGTCTTCCCCCTG GCACCTCTCCAAAGACACCTCTGGGGGCACA GCGGCCCTGGGCTGCCCTGGTCAAGGACTACTTC CCGAAACCGGTGACGGTGTCTGTGGAACTCAGGC GCCCTGACCAGCGGCGTGCACACCTTCCCCGGCT GTCTACAGTCTCAGGACTCTACTCCCTCAGCA GCGTGTGACCGTGCCCTCCAGCAGCTTGGGCA CCCAGACCTACATCTGCAACGTGAATCACAAGC CCAGCAACACCAAGGTGGACAAGAAAGTTGAG CCCAAATCTTGTGACAAACTCACACATGCCCA CCGTGCCAGCACCTGAACCTCTGGGGGACCG TCAGTCTTCTCTTCCCCCAAAACCAAGGACA CCCTCATGATCTCCCGGACCCCTGAGGTCACAT GCGTGGTGGTGGACGTGAGCCACGAAGACCCTG AGGTCAAAGTTCAACTGGTACGTGGACGGCGTGG AGGTGCATAATGCCAAGACAAGCCGTGTGAGG AGCAGTACGGCAGCACGTACCGTTGTGTACGG TCCTCACCGTCTGCACCAGGACTGGCTGAATG GCAAGGAGTACAAGTGAAGGTCTCCAACAAA GCCCTCCAGCCCCCATCGAGAAAACCATCTCC AAAGCCAAGGGCAGCCCCGAGAACACAGGT GTACACCTGCCCCCATCCCCGGGAGGAGATGAC CAAGAACCAAGGTACGCTGACCTGCCTGGTCAA AGGCTTCTATCCCAGGACATCGCCGTGGAGTG GGAGAGCAATGGGCAGCCGGAGAACACTACA</p>
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				<p>AGACCACGCCTCCCCTGCTGGACTCCGACGGCT CCTTCTCCTCTATAGCAAGCTCACCGTGGACAA GAGCAGGTGGCAGCAGGGAACGTCTTCTCATG CTCCGTGATGCATGAGGCTCTGCACAACCACTA CAGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAA A</p>
				<p>SEQ ID NO: 2032</p> <p>DIQLTQSPSSLSASVGDRTVTITCRASQTSRFLNWW QQKPGKAPPELLIYVASSLQSGVPSRFSGSGTDFT LTISSLQPEDFATYQCQSYSTLISFGQGTKEIKRT VAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSITYLSST LTLKADYEEKHKVYACEVTHQGLSSPVTKSFNRG EC</p>
			AA	<p>SEQ ID NO: 2189</p> <p>QVQLVESGGGVVQGRSLRLSCAASGFTFSYGIH WVRQAPGKGLEWVAWIYDGSNKFHADAVKGR FTISRDNSKNTLYLQMNSLRAEDSAMFYFCARGKV AGMPEAFEIWGQGTKVTVSSASTKGPSVFPLAPSS KSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKEPKSCDKTHCTCPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEVESNGQPENNYKTTTPPVLDSGDSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK</p>
				<p>SEQ ID NO: 462</p> <p>CAGTCTGTGTGACGCAGCCGCCCTCAGTGTCTG CGGCCCGCAGACAGAGGTACCACTCTCCTGCT CTGGAAGCAGCTCCACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTACGCCACCTGGGCATCACCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGTGTGGT ATTCCGGCGGAGGGACCAAACTGACCGTCTTAGG TCAGCCCAAGGCTGCCCTCGGTCACTCTGTTC CCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAG GCCACACTGGTGTCTCATAAGTGACTTCTACC CGGGAGCCGTGACAGTGGCCTGGAAGGCAGAT</p>
		17B11.002.001	NA	<p>SEQ ID NO: 619</p> <p>CAATGCAGCTGGTGCGAGTCTGGGGCTGAGGTG AAGAAGCCTGGGCCCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCAAGTTATGAT ATCAACTGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGATGGATGAACCTAACACAGT GGTGGCACAGGCTATGCACAGAAAGTTCCAGGGC AGAGTCAACATGACACAGGACACCTCCATAAGC ACAGCCTACATGAGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGGAGTTATCGTCCCTACT ACTACTACTAGGTATGGACGTCTGGGGCCCAAG GGACCACGGTCAACGTCTCCTCAGCCTCCACCA AGGGCCCAATCGGTCTTCCCCCTGGCACCCCTCCTC CAAGAGCACCTCTGGGGGCACAGCGGCCCTGGG</p>
IPS:361491	17B11.002.001	NA		

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	<p>AGCAGCCCCGTCAAAGGCGGGAGTGGAGACCCAC CACACCCCTCCAAACAAGCAACAACAAGTACGC GGCCAGCAGCTATCTGAGCCTGACGCCGTGAGCA GTGGAAGTCCACAGAAGCTACAGCTGCCAGGT CACGCATGAAGGGAGCACCGTGGAGAAGACAG TGGCCCCCTACAGAATGTTCA</p>	<p>CTGCCTGGTCAAGGACTACTTCCCCGAACCGGT GACGGTGTGTGGAACTCAGGCGCCCTGACCAG CGCGTGCACACCTTCCCCGGTGTCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCACAAGCCCAAGCAACACC AAGTGGACAAAGAAAGTTGAGCCCAAAATCTTGT GACAAAATCACAACATGCCACCCGTGCCACGCA CCTGAACCTCTGGGGGACCGTCAGTCTTCCCTCT TCCCCCAAAACCAAGGACACCCCTCATGATCT CCCGGACCCCTGAGTCAATGCGTGGTGGTGG ACGTGAGCCACGAAGACCTGAGGTCAAAGTTCA ACTGTACGTGGACGGCGTGGAGGTGCATAATG CCAAGACAAGCCGTGTGAGGAGCAGTACGGC AGCACGTACCGTTGTGTCAGCGTCTCACCCTCC TGCACCAGGACTGGCTGAATGGCAAGGAGTACA AGTGCAAGGTCTCCACAAAGCCCTCCCAAGCCC CCATCGAGAAACCATCTCCAAAGCCAAAGGGC AGCCCCGAGAACCACAGGTGTACACCCTGCCCC CATCCCGGAGGAGATGACCAAGAACCAAGGTC AGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC AGCGACATCGCCGTGGAGTGGGAGAGCAATGG GCAGCCGGAGAAACAATAACAAGACACGCCCTCC CGTGTGACTCCGACGGCTCCTTCTTCCCTCTAT AGCAAGCTCACCGTGGACAAGAGCAGGTGGCA GCAGGGGAACGTCTTCTCATGCTCCGTGATGCA TGAGGCTCTGCACAACCACTACACGCAGAAAGAG CCTCTCCCTGTCTCCGGGTAAA</p>
	<p>SEQ ID NO: 2033</p> <p>QSVLTQPPSVSAAPGQKVITISCSGSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLGITGLQTGDEADYYCGTWDSSLASVVFSGG TKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLL SDFYPGAVTVAWKADSSPVKAGVETTPSKQSN KYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS</p>	<p>SEQ ID NO: 2190</p> <p>QMLVQSGAEVKPGASVKVSKASGYTFTSYDI NWVRQATGQGLEWMGWMPNPSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDQTAIVYFCARG GDYVWGSYRPIYYGYMDVWVGQGTITVTVSSAS TKGPSVFPPLAPSSKSTSGGTAAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH</p>

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				<p>TCPPCPAPELLGGPSVFLFPPKPKDITLMISRTPEVT CVVVDVSHEDPEVKFNWYVVDGVEVHNATKPCPE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LDSGSEFLYSKLTVDKSRWQQGNVVFSCSVMHEA LHNHYTQKSLSLSPGK</p>
				<p>SEQ ID NO: 463</p> <p>CAGTCTGTGTGACGCAGCCGCCCTCAGTGTCTG CGGCCCAAGACAGAGGTACCACTCTCCTGCT CTGGAAGCAGCTCCAACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCAGCTCAGCCACCCTGGGCATCACCCG ACTCCAGACTGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGTGTGT ATTCGGCGGAGGGACCAAACTGACCCCTCCTAGG TCAGCCCAAGGCTGCCCTCGGTCACTCTGTTC CCGCCCTCCTGAGGAGCTTCAAGCCAACAAG GCCACACTGGTGTCTCATAAGTGACTTCTACC CGGAGCCGTGACAGTGGCTGGAGGCAAGAT AGCAGCCCGTCAAGCGGGAGTGGAGACCAC CACACCTCCAACAAGCAACAACAAGTACGC GGCCAGCAGCTATCTGAGCCTGACGCTGAGCA GTGGAAGTCCACAGAAAGCTACAGCTGCCAGGT CACGCATGAAGGAGCACCCGTGGAGAAAGACAG TGGCCCCCTACAGAATGTTCA</p>
				<p>SEQ ID NO: 620</p> <p>CAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCTGGGGCTCAGTGAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCAAGTTATGAT ATCAACTGGTGCAGACGCCACTGGACAAAGGG CTTGAGTGGATGGATGGATGAACCTAACAGT GGTAACACAGGCTATGCACAGAAAGTTCCAGGGC AGATCACCATGACAGGGACACCTCCACATAAGC ACAGCTACATGAGCTGAGCAGCCTGAGATCT CAGGACACGGCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTGGGGAGTTATCGTCCCTACT ACTACTACTAGGTATGGACGCTCTGGGGCCAAAG GGACACGTCACCGTCTCCTCAGCCTCCACCA AGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTC CAAGAGCACCTCTGGGGGCAAGCGGGCCCTGGG CTGCTGGTCAAGGACTACTTCCCGCAACCCGGT GACGGTGTGTGGAACCTCAGCGGCCCTGACCCAG CGCGTGCACACCTTCCCGGCTGTCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCACAAGCCCAAGCAACACC AAGGTGGACAAGAAAGTTGAGCCCAAACTTGT GACAAAATCACAACATGCCACCCGTGCCAGCA CCTGAACCTCTGGGGGACCGTCACTTCTCCTCT TCCCCCAAAACCAAGGACACCCCTCATGATCT CCCGGACCCCTGAGGTCAATGCGTGGTGGTGG ACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCA ACTGTTACGTGGACGGCGTGGAGGTGCATAATG CCAAGACAAGCCGTGTGAGGAGCAGTACGGC</p>

IPS:361499

17B11.002.002

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				AGCACGTACCGTTGTGTACGGCTCCTCACCGTCC TGACACGAGACTGGCTGAATGGCAAGGAGTACA AGTGCAAGGTCTCCACAAAGCCCTCCAGGCC CCATCGAGAAACCATCTCCAAAGCCAAAGGGC AGCCCCGAGAACACAGGTGTACACCCCTGCCCC CATCCCGGAGGAGATGACCAAGAACCAAGGTC AGCTGACCTGCCTGGTCAAAGGCTTCTATCCC AGCGACATCGCCGTGGAGTGGGAGAGCAATGG GCAGCCGGAGAACAACTACAAAGACACGCCCTCC CGTGTGACTCCGACGGCTCCTTCTTCTCTAT AGCAAGCTCACCGTGGACAAGACAGGTGGCA GCAGGGGAACGTCTTCTCATGCTCCGTGATGCA TGAGGCTCTGCACAAACCACTACACGCAGAAAGAG CCTCTCCCTGCTCCGGGTAAA
				SEQ ID NO: 2191
				QMLVQSGAEVKPGASVKVCKASGYTFTSYDI NWVRQATGQGLEWMGWMPNPSNGTGYAQKFQ GRVTMRDTSISTAYMELSSLSQDQAVVYCARG GDYVWGSYPYVYYGMDVWVWQQGTTVTVSSAS TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LDSGGSFFLYSKLTVDKSRWQQGNVVFSCVMHEA LHNHYTQKLSLSPGK
				SEQ ID NO: 621
				CAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGCCTCAGTGAAAGGTCTCCTGC AAGGCTTCTGGATACACCTTTCACCAAGTTATGAT ATCAACTGGGTGCACAGGCCACTGGACAAGGG CTTGAGTGGATGGGATGGATGAACCCCTAACAGT GGTGGCACAGGCTATGCACAGAAAGTTCCAGGGC
				SEQ ID NO: 2034
				QSVLTQPPSVSAAPGQKVITISCSGSSNIGNNYYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLGITGLQTGDEADYYCGTWDSSL SAVVFGGG TKLTVLGGQPKAAPSVTLFPPSSEELQANKATLVCLI SDFYPGAVTVAWKADSSPVKAGVETTTTPSKQSNIN KYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS
			AA	
				SEQ ID NO: 464
				CAGTCTGTGTGACGCAGCCGCCCTCAGTGTCTG CGGCCCGCAGCAGAGGTACCATCTCCTGCT CTGGAAGCAGCTCCACACATTGGAAATAATTATG TATCCTGGTATGAGCAGTTCACAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCTGACCGGATTCTCTGGCTCCAA
			NA	
			3	
			17B11.002.00	
			IPS:361503	

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GTCTGGCAGTCAGCCACCCTGGGCATCACCGG ACTCCAGACTGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGCTGTGGT ATTGCGCGGAGGGACCAAACTGACCGTCCTAGG TCAGCCCCAAGGCTGCCCCCTCGTCACTCTGTTT CCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAG GCCACACTGGTGTCTCATAGTGACTTCTACC CGGAGCCGTGACAGTGGCCTGGAAGGCAGAT AGCAGCCCCGTCAAGCGGGGAGTGGAGACCCAC CACACCTCCAAACAAGCAACAACAAGTACGC GGCCAGCAGCTATCTGAGCCTGACGCCGTAGCA GTGGAAGTCCACAGAAGCTACAGCTGCCAGGT CACGCATGAAGGAGCACCGTGGAGAAAGACAG TGGCCCCCTACAGAAATGTTCA	AGAGTCACCATGACCAGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCAAAG GGACCACGGTCACCGTCTCCTCAGCCTCCACCA AGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTC CAAGAGCACCTCTGGGGGACACAGGGCCCTGGG CTGCCTGGTCAAGGACTACTTCCCCGAACCCGGT GACGGTGTCTGGAACTCAGGGGCCCTGACCAG CGCGTGCACACCTTCCCCGGCTGTCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCACAAGCCCCAGCAACACC AAGGTGGACAAAGAAAGTTGAGCCCCAAATCTGT GACAAAATCACAACATGCCCACCGTGCCCCAGCA CCTGAACCTCTGGGGGACCGTCAGTCTTCCCTCT TCCCCCAAACCCCAAGCACACCTCATGATCT CCCGGACCCCTGAGTCAATGCGTGGTGGTGG ACGTGAGCCACGAAGACCTGAGGTCAAAGTTCA ACTGTACGTGGACGGCGTGGAGGTGCATAATG CCAAGACAAGCCGTGTAGGAGCAGTACGGC AGCACGTACCGTTGTGTCAAGCTCCTCACCGTCC TGCACCAAGACTGGCTGAATGGCAAGGAGTACA AGTGCAAGGTCTCCAACAAGCCCTCCAGCCC CCATCGAGAAACCATCTCCAAGCCAAAGGGC AGCCCCGAGAACCACAGGTGTACACCTGCCCC CATCCCGGAGGAGATGACCAAGAACCAAGGTC AGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC AGCGACATCGCGTGGAGTGGGAGAGCAATGG GCAGCCGGAGAAACAATAACAAGACCCGCTCC CGTGTGACTCCGACGGCTCCTTCTTCTCTAT AGCAAGCTCACCGTGGACAAAGCAGGTGGCA GCAGGGGAACGTCTTCTCATGTCTCCGTGATGCA TGAGGCTCTGCACAACCACTACACGCAGAAAGAG CCTCTCCCTGTCTCCGGGTAAA
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			SEQ ID NO: 2035	QSVLTQPPSVSAAPGQKVITISCSGSSNIGNNYVS WYEQFPGTAPKLLIYDNNKRPSPGIPDRFSGSKSGTS ATLGITGLQTGDEADYYCGTWDSSL SAVVFGGGT KLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLIS DFYPGA VTVAWKADSSPVKAGVETTTPSKQSNK YAASSYLSTPEQWKSHRSYSCQVTHEGSTVEKT VAPTECS	SEQ ID NO: 2192	QMLVQSGAEVKPGASVKVCKASGYTFTSYDI NWVRQATGQGLEWMGWMPNPSGGTGYAQKFQ GRVTMRDTSISTAYMELSSLRSDTA VYYCARG GDYVWGSYPYYYYGMDVWVGQGT TVTVSSAS TKGPSVFLPAPSSKSTSGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTP SSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTH TCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNATKPCPE EQYGSTYRCVSLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LDSGGSFELYSKLTVDKSRWQQGNVFSQSVMHEA LHNHYTQKSLSLSPGK
		AA	SEQ ID NO: 465	CAGTCTGTGTGACGACGCCGCCCTCAGTGTCTG CGGCCCAAGACAGAGGTACCACTCTCCTGCT CTGGAAGCAGCTCCAACATTGGAATAATTATG TATCCTGGTATCAGCAGCTCCAGGAACAGCCC CCAAACTCCTCAATTTATGACAATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTCAGCCACCCTGGCCATCACCGG ACTCCAGACTGGGACGAGGCCGATTATTACTG CGGAACATTGCAAGCAGCCTGAGTGTGTGT ATTCCGGCGGAGGACCAAACTGACCGTCTAGG TCAGCCCAAGGCTGCCCTCGGTCACTCTGTTC CCGCCCTCCTTGAGGAGCTTCAAGCCAACAAG GCCACACTGGTGTCTCATAAGTGACTTCTACC CGGGAGCCGTGACAGTGGCTGGAAGGCAGAT AGCAGCCCGTCAAGCGGGAGTGGAGACCAC CACACCTCCAACAAGCAACAACAAGTACGC GGCCAGCAGCTATCTGAGCCTGACGCTGAGCA GTGGAAGTCCACAGAAAGCTACAGCTGCCAGGT CACGCATGAAGGAGCACCGCTGGAGAAGACAG TGGCCCCCTACAGAATGTTCA	SEQ ID NO: 622	CAATGCAGCTGGTGCGAGTCTGGGGCTGAGGTG AAGAAGCTGGGGCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCAAGTTATGAT ATCAACTGGTGCACAGGCCCTGGACAAAGGG CTTGAGTGGATGGATGGATGAACCTAACAGT GGTGGCACAGGCTATGCACAGAAAGTTCCAGGGC AGAGTCACCATGACAGGACACCTCCATAAGC ACAGCCTACATGAGAGCTGAGCAGCCTGAGATCT GACGACAGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGAGTTATCGTCCCTACT ACTACTACTAGGTATGACAGCTCTGGGGCCAAAG GGACACGCTACCGTCTCCTCAGCCTCCACCA AGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTC CAAGAGCACCTCTGGGGGACAGCGGGCCCTGGG CTGCTGGTCAAGGACTACTTCCCCGAACCGGT GACGGTGTGTGGAACCTCAGCGGCCCTGACCCAG CGCGGTGCAACCTTCCCGGCTGTCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGACCCAGACCTAC ATCTGCAACGTGAATCACAAGCCCCAGCAACACC
IPS:361507	17B11.002.004	NA				

		<p>AAAGTGGACAAAGAAAGTTGAGCCCCAAATCTTGT GACAAAACTCACACATGCCACCGTGCCCCAGCA CCTGAACCTCTGGGGGACCGTCAGTCTTCCTCT TCCCCCAAAAACCAAGGACACCCCTCATGATCT CCCGACCCCTGAGGTCACATGCGTGGTGGTGG ACGTGAGCCACGAAGACCCCTGAGGTCAAAGTTCA ACTGTAAGTGGACGGCGTGAGGTGCATAATG CCAAGACAAAGCCGTGTGAGGAGCAGTACGGC AGCACGTACCGTTGTGTGACAGCTCTCACCGTCC TGCACAGGACTGGCTGAATGGCAAGGAGTACA AGTCAAGGTCTCCAACAAAGCCCTCCCAGCCC CCATCGAGAAACCATCTCCAAGCCAAGGGC AGCCCCGAGAACACAGGTGTACACCCCTGCCCC CATCCCCGGAGGAGATGACCAAGAACCAAGGTC AGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC AGCGACATCGCCGTGGAGTGGGAGAGCAATGG GCAGCCGGAACAACATAAGACACGCTCC CGTGTGGACTCCGACGGCTCTTCTTCCTCTAT AGCAAGCTCACCGTGGACAAGAGCAAGGTGGCA GCAGGGGAACGTCTTCTCATGTCTCCGTGATGCA TGAGGCTCTGCAACCAACCTACACGCAGAAAGAG CCTCTCCCTGTCTCCGGGTAA</p>
	AA	<p>SEQ ID NO: 2036</p> <p>QSVLTQPPSVSAAPGQKVITISCGSSSNIINNYYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLAITGLQTGDEADYYCGTFESSLSAVVFGGGT KLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLIS DFYPGAVTVAWKADSSPVKAGVETTTTPSKQSNK YAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKT VAPTECS</p>

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					LSDSGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK		
				SEQ ID NO: 466	SEQ ID NO: 623		
				CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG CGGCCCAGGACAGAAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAATAATTATG TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTACGCCACCTGGCCATCACCGG ACTCCAGACTGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGTGTGGT ATTGCGCGGAGGGACCAAACTGACCGTCTAGG TCAGCCCAAGGCTGCCCTCGGTCACTCTGTTC CCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAG GCCACACTGGTGTCTCATAAGTGACTTCTACC CGGGAGCCGTGACAGTGGCCTGGAAGGCAGAT AGCAGCCCCGTCAAGCGGGAGTGGAGACCAC CACACCCCTCCAACAACAAGCAACAACAAGTACGC GGCCAGCAGCTATCTGAGCCTGACGCCGTAGCA GTGGAAGTCCACAGAAAGCTACAGCTGCCAGGT CACGCATGAAGGGAGCACCGTGGAGAAGACAG TGGCCCCCTACAGAATGTTCA	NA	17B11.002.005	!PS:361514
				CAAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCAGTTATGAT ATCAACTGGTGCAGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGATGGATGAACCTTAACAGT GGTGGCACAGGCTATGCACAGAAAGTTCCAGGGC AGAGTACCATGACCAAGGACACCTCCATAAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGGAGTTATCGTCCCTACT ACTACTACTACGTATGACACGTCTGGGGCCAAAG GGACCACGGTACCGTCTCTCTCAAGCCTCCACCA AGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTC CAAGAGCACCTCTGGGGGACAGCGGCCCTGGG CTGCCCTGGTCAAGGACTACTTCCCCGAAACCGGT GACGGTGTGTGGAACTCAGGGCGCCCTGACCCAG CGGCGTGACACACCTTCCCGGCTGTCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCAAAAGCCCAAGCAACACC AAGTGGACAAGAAAGTTGAGCCCCAAATCTTGT GACAAACTCACACATGCCCCACCGTGCCCAAGCA CCTGAACCTCCTGGGGGACCGTCAGTCTTCTCT TCCCCCAAAACCCAAGGACACCCCTCATGATCT CCCGGACCCCTGAGGTCACATGCGTGGTGGTGG ACGTGAGCCACGAAAGACCTGAGGTCAAGTTCA ACTGTTACGTGGACGGCGTGGAGGTGCATAATG CCAAAGACAAAGCCGTGTGAGGAGCAGTACGGC AGCACGTACCGTTGTGTCAGCGTCTCCTCACCGTCC TGCAACGAGACTGGCTGAATGGCAAGGAGTACA AGTGCAAGGTCTCCAACAAGGCCCTCCAGGCC CCATCGAGAAACCATCTCCAAGCCAAAGGGC AGCCCCGAGAACACAGGTGTACACCCCTGCCCC			

A-2124-WO-PCT

				<p>CATCCCGGAGGAGATGACCAAGAACCAGGTC AGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC AGGACATCGCCGTGGAGTGGGAGACAATGG GCAGCCGGAGAACAACTACAAGACCACGCCTCC CGTGCTGACTCCGACGGCTCCTTCTTCTCTAT AGCAAGCTCACCGTGGACAAGACGAGGTGGCA GCAGGGGAACGTCTTCTCATGCTCCGTGATGCA TGAGGCTCTGCACAACCACTACACGCAGAAAGAG CCTCTCCCTGCTCCGGGTAAA</p> <p>SEQ ID NO: 2194</p>
			AA	<p>QSVLTQPPSVSAAPGQKVITISCSGSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLAITGLQTGDEADYYCGTWDSSL SAVVFGGG TKLTVLGGPKAAPSVTLFPPSSSEELQANKATLVCLI SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNIN KYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS</p> <p>SEQ ID NO: 2037</p>
			NA	<p>CAGTCTGTGTGACGCAGCCGCCCTCAGTGTCTG CGGCCCGCAGACAGAAGGTACCAATCTCCTGCT CTGGAAGCAGCTCCACATTTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTACGCCACCTGGCCATCACCCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGTGTGGT ATTCGGCGGAGGGACCAAACTGACCGTCTCCTAGG TCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTC</p> <p>SEQ ID NO: 467</p>
!PS:360582	17B11.002.006			<p>CAAATGCAGCTGGTGCACTGTGGGGCTGAGGTG AAGAAGCCTGGGCCCTCAGTGAAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCAAGTTATGAT ATCAACTGGGTGCGACAGGCCCTGGACAAGGG CTTGAGTGGATGGGATGGATGAACCTAACAGT GGTAACACAGGCTATGCACAGAAAGTTCCAGGGC AGAGTCACCATGACACAGGACACCTCCATAAGC ACAGCCTACATGAGCTGAGCAGCCTGAGATCT GACGACAGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGCTCTGGGGCCAAAG</p> <p>SEQ ID NO: 624</p>

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	CCGCCCTCCTCTGAGGAGCTTCAAGCCAAACAAG GCCACACTGGTGTCTCATAGTGACTTCTTACC CGGAGCCGTGACAGTGGCTTGGAGGACAGAT AGCAGCCCGGTCAAGGCGGAGTGGAGACCCAC CACACCTCCAACAAGCAACAACAAGTACGC GGCAGCAGCTATCTGAGCCTGACGCTGAGCA GTGGAAGTCCACAGAAGCTACAGCTGCCAGGT CACGCATGAAGGAGCACCGTGGAGAAAGACAG TGGCCCTACAGAATGTTCA	GGACCACGGTCACCGTCTCCTCAGCCTCCACCA AGGGCCATCGGTCTTCCCCCTGGCACCCCTCCTC CAAGAGCACCTCTGGGGGACACAGGGCCCTGGG CTGCTGGTCAAGGACTACTTCCCCGAACCCGGT GACGGTGTGTGGAACCTCAGGGCCCTGACCAG CGCGTGCACACCTTCCCCGTGTCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCCTCAGCAGCTTGGGACCCAGACCTAC ATCTGCAACGTGAATCACAAGCCCAAGCAACACC AAGTGGACAAAGAAAGTTGAGCCCAATCTTGT GACAAACTCACACATGCCACCGTGCCACGCA CCTGAACCTCTGGGGGACCGTCAGTCTTCTCT TCCCCCAAAACCAAGGACACCTCATGATCT CCCGGACCCCTGAGTCAATGCGTGGTGGTGG ACGTGAGCCACGAAGACCTGAGGTCAAAGTTCA ACTGTACGTGGACGGCGTGGAGGTGCATAATG CCAAGACAAGCCGTGTAGGAGCAGTACGGC AGCACGTACCGTTGTGTCAGCGTCTCACCGTCC TGCACGAGACTGGCTGAATGGCAAGGAGTACA AGTGCAAGGTCTCCACAAAGCCCTCCACGCCC CCATCGAGAAACCATCTCCAAGCCAAAGGGC AGCCCCGAGAACACAGGTGTACACCTGCCCC CATCCCGGAGGAGATGACCAAGAACCAAGGTC AGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC AGCGACATCGCCGTGGAGTGGGAGAGCAATGG GCAGCCGGAGAACAACTACAAGACACGCCCTCC CGTGTGACTCCGACGGCTCCTTCTTCTCTAT AGCAAGCTCACCGTGGACAAAGCAGGTGGCA GCAGGGGAACGTCTTCTCATGCTCCGTGATGCA TGAGGCTCTGCACAACCACTACACGCAAGAG CCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 2038	SEQ ID NO: 2195
AA	QSVLTQPPSVSAAPGQKVITISCSGSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLAITGLQTGDEADYYCGTWDSSLASVVFSGG TKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLLI	QMLVQSGAEVKKPGASVKVSKASGYTFTSYDI NWVRAQPGQGLEWGMWNPNSGNTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDDTAVVYCARG GDYVWGSYRPPYYYYGMDVWVGQGTITVTVSSAS

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			SDFYPGAVTVAWKADSSPVKAGVETTTTPSKQSN KYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS	TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSQVHTFPAVLQSSGLYSLSSVVTVP SSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTH TCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYVTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LDSGSEFLYSKLTVDKSRWQQGNVVFSCSVMHEA LHNHYTQKSLSLSPGK
			SEQ ID NO: 468	SEQ ID NO: 625
			CAGTCTGTGTGACGCAGCCGCCCTCAGTGTCTG CGGCCCAAGACAGAGGTACCACTCTCCTGCT CTGGAAGCAGCTCCAACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTACGCCACCCTGGGCATCACCCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGTGTGT ATTCGGCGGAGGGACCAAACTGACCGTCTAGG TCAGCCCAAGGCTGCCCTCGGTCACTCTGTTC CCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAG GCCACACTGGTGTCTCATAAGTGACTTCTACC CGGGAGCCGTGACAGTGGCTGGAAAGGCAGAT AGCAGCCCGTCAAGCGGGAGTGGAGACCAC CACACCTCCAACAAGCAACAACAAGTACGC GGCCAGCAGCTATCTGAGCCTGACGCTGAGCA GTGGAAGTCCACAGAAAGCTACAGCTGCCAGGT CACGCATGAAGGGAGCACCGTGGAGAAAGACAG TGGCCCCCTACAGAAATGTTCA	CAATGCAGCTGGTGCACTCTGGGCTGAGGTG AAGAAGCTGGGGCTCAGTGAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCAAGTTATGAT ATCAACTGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGATGGATGAACCTAACAGT GGTGGCACAGGCTATGCACAGAAATTCACAGGGC AGAGTCAACATGACCAAGGACACCTCCATAAGC ACAGCTACATGAGAGCTGAGCAGCCTGAGATCT CAGGACACGGCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTTCGGGAGTTATCGTCCCTACT ACTACTACTAGGTATGGACGTCTGGGGCCAAAG GGACCACGTCACCGTCTCCTCAGCCTCCACCA AGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTC CAAGAGCACCTCTGGGGGCAAGGGGCCCTGGG CTGCTGGTCAAGGACTACTTCCCCGAACCCGGT GACGGTGTGTGGAACCTCAGGCGCCCTGACCCAG CGCGTGCACACCTTCCCGGTGTCTACAGTCC TCAGGACTCTACTCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCACAAGCCCAAGCAACACC AAGGTGGACAAGAAAGTTGAGCCCAAAATCTGT GACAAAACCTACACATGCCACCCGTGCCAGCA CCTGAACCTCTGGGGGACCGTCAGTCTTCTCT TCCCCCAAAACCAAGGACACCCCTCATGATCT CCCGGACCCCTGAGGTCAATGCGTGGTGGTGG
IPS:361518	17B11.002.007	NA		

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			<p>ACGTGAGCCACGAAGACCCCTGAGGTCAAAGTTCA ACTGGTACGTGGACGGCGTGGAGGTGCATAATG CCAAAGACAAGCCGTGTGAGGAGCAGTACGGC AGCACGTACCGTTGTGTGTCAGCGTCTCACCCTCC TGCACCAGGACTGGCTGAATGGCAAGGAGTACA AGTGCAAGGTCTCCACAAAGCCCTCCCAAGCCC CCATCGAGAAAACCATCTCCAAGCCAAAGGGC AGCCCCGAGAACACAGGTGTACACCCCTGCCCC CATCCCGGAGGAGATGACCAAGAACCAAGGTC AGCTGACCTGCCTGGTCAAAGGCTTCTATCCC AGCGACATCGCCGTGGAGTGGGAGAGCAATGG GCAGCCGGAGAACAACTACAAGACACGCCCTCC CGTGTGACTCCGACGGCTCCTTCTTCTCTAT AGCAAGCTCACCGTGGACAAAGACAGGTGGCA GCAGGGGAACGTCTTCTCATGCTCCGTGATGCA TGAGGCTCTGCACAACCACTACACGCAGAAAGAG CCTCTCCCTGCTCCCGGTAAA</p>
		SEQ ID NO: 2039	SEQ ID NO: 2196
	AA	<p>QSVLTQPPSVSAAPGQKVITISCSGSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLGITGLQTGDEADYYCGTWDSSLASVVFSGG TKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI SDFYPGAVTVAWKADSSPVKAGVETTTTPSKQSN KYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS</p>	<p>QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQATQGLEWMGWMPNPNSSGGTGYAQKFKQ GRVTMTRDTSISTAYMELSSLRSDQTAIVYCARG GDYVFGSYRPYYYYGMDVWGQGTITVTVSSAST KGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPV VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LDSGGSFFLYSKLTVDKSRWQQGNVVFSCSVMHEA LHNHYTQKLSLSPGK</p>
		SEQ ID NO: 469	SEQ ID NO: 626

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IPS:360570	17B11.002.008	NA	<p>CAGTCTGTGTGACGCAGCCGCCCTCAGTGTCTG CGCCCCCAGGACAGAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTACGCCACCCTGGCCATCACCCGG ACTCCAGACTGGGACGAGGCCGATTATTACTG CGGAACATTTCGAAAGCAGCCTGAGTGCTGGT ATTCCGGCGGAGGACCAAACTGACCCTCCTAGG TCAGCCCCAAGGCTGCCCTCGGTCACTCTGTTC CCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAG GCCACACTGGTGTCTCATAGTGACTTCTACC CGGAGCCGTGACAGTGGCTGGAAGGCAGAT AGCAGCCCCGTCAAGCGGGAGTGGAGACCCAC CACACCTCCAAACAAGCAACAACAAGTACGC GGCCAGCAGCTATCTGAGCCTGACGCTGAGCA GTGGAAGTCCACAGAAGCTACAGCTGCCAGGT CACGCATGAAGGAGCACCGTGGAGAAAGACAG TGGCCCCCTACAGAAATGTTCA</p>
			<p>CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAAGTTATGAT ATCAACTGGTGCACAGGCCCTTGACAAAGGG CTTGAGTGGATGGATGGATGAACCTAACAGT GGTGGCACAGGCTATGCACAGAAAGTTCCAGGGC AGAGTCACCATGACCAGGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTTCGGGAGTTATCGTCCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCAAAG GGACCACGGTCACCGTCTCCTCAGCCTCCACCA AGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTC CAAGAGCACCTCTGGGGGACAGCGGCCCTGGG CTGCCTGGTCAAGGACTACTTCCCCGAACCCGGT GACGGTGTCTGGAACTCAGGGCCCTGACCAAG CGCGTGCACACCTTCCCCGGTGTCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCACAAGCCCCAGCAACACC AAGTGGACAAAGAAAGTTGAGCCCCAAATCTTGT GACAAAACCTCACACATGCCACCCGTGCCCAGCA CCTGAACCTCTGGGGGACCGTCAGTCTTCCCTCT TCCCCCCTCAACCCAGGACACCCCTCATGATCT CCCGGACCCCTGAGGTACATGCGTGGTGGTGG ACGTGAGCCACGAAGACCTGAGGTCAAAGTTCA ACTGTAAGTGGACGGCGTGGAGGTGCATAATG CCAAGACAAGCCGTGTGAGGAGCAGTACGGC AGCACGTACCGTTGTGTGAGCCTCACCCTCC TGCACCAAGACTGGCTGAATGGCAAGGAGTACA AGTGCAAGGTCTCCACAAAGCCCTCCCCAGCCC CCATCGAGAAACCATCTCCAAGCCAAAGGGC AGCCCCGAGAACCACAGGTGTACACCTGCCCC CATCCCCGGAGGAGATGACCAAGAACCAAGGTC AGCCTGACCTGCCTGGTCAAGGCTTCTATCCC AGCGACATCGCCGTGGAGTGGGAGAGCAATGG</p>

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				GCAGCCGGAGAACTACAAGACCACGCCTCC CGTGCTGGACTCCGACGGCTCCTCTTCTCCTCTAT AGCAAGCTCACCGTGGACAAGACGAGGTGGCA GCAGGGGAACGTCTTCTCATGCTCCGTGATGCA TGAGGCTCTGCACAACCACTACACGCAGAAAGAG CCTCTCCCTGCTCCGGGTAAA
			SEQ ID NO: 2040	SEQ ID NO: 2197
			QSVLTQPPSVSAAPGQKVITISCSGSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLAITGLQTGDEADYYCGTFESSLSA VVFGGGT KLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLIS DFYPGA VTVAWKADSSPVKAGVETTTPSKQSNK YAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKT VAPTECS	QMLVQSGAEVKKPGASVKVCKASGYTFTSYDI NWVRQAPGGGLEWMGMWNPNSGGTGYAQKFQ GRVTMRDTSISTAYMELSSLRSDDTAVYYCARG GDYVFGSYRPYYYYGMDVWVGQGTTVTVSSAST KGPSVFPLAPSSKSTSGGTAAAGCLVKDYFPEPV VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LDSGGSFELYSKLTVDKSRWQQGNVVFCSVMHEA LHNHYTQKLSLSPGK
		AA	SEQ ID NO: 470	SEQ ID NO: 627
			GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCA TCTGTAGGAGACAGAGTCACTATACATT GCCGGGCAAGTCAGACCAATTAGCAGGTTTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCCA AGCTCCTGATCTATGTTGCATCCAGTTTGCAAG TGGGTCCCATCAAGATTGAGTGGCAGTGGTTC TGGGACAGATTTCACTCTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCTGCTCAGTTTTGGCCA GGGACCAAGCTGGAGATCAAAACGAACGGTGG CTGCACCATCTGCTTCTATCTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCCTCTGTTGT GTGCTGTGTAATAACTTCTATCCACAGAGAGGC CAAAAGTACAGTGAAGGTGGATAACGCCCTCCA	CAGGTGCAGTTGGTGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAGCTATGGC ATACACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC CGATTACCATCTCCAGAGACAATTCCAAGAAC ACGCTGATCTGCAAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGGAGAGGA AAAGTGGTGGTATGCCTGAAGCTTTTGAATC TGGGGCCAAAGGACATTTGGTACCGCTCTCTTCA GCCCTCCACCAGGGCCCATCGGTCTTCCCCCTG GCACCTCTCTCAAGAGACACCTCTGGGGGCACA GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC
IPS:362051	5G12.005.001	NA		

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	<p>ATCGGGTAACTCCAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCCTGACGCTGAGCAAGCAGACTACGAGA AACACAAAGTCTACGCCCTGCGAAGTCAACCCATC AGGCCCTGAGCTCGCCCCGTACAAAGAGCTTCA ACAGGGGAGAGTGT</p>	<p>CCCGAACCCGGTGACGGTGTCTGTGGAACCTCAGGC GCCCTGACCAGCGGCGTGACACCTTCCCGGCT GTCCTACAGTCCCTCAGGACTCTACTCCCTCAGCA GCGTGTGACCGTGCCCTCCAGCAGCTTGGGCA CCCAGACCTACATCTGCAACGTGAATCACAAGC CCAGCAACACCAAGGTGGACAAGAAAGTTGAG CCCAATCTTGTGACAAACTCACACATGCCCA CCGTGCCAGCACCTGAACCTCTGGGGGACCG TCAGTCTTCTCTTCCCCCAAAACCCAAAGACA CCCTCATGATCTCCCGGACCCCTGAGGTCACAT GCGTGGTGGTGGACGTGAGCCACGAAGACCCCTG AGTCAAGTTCAACTGGTACGTGGACGGCGTGG AGTGCATAATGCCAAGACAAGGCCGTGTGAGG AGCAGTACGGCAGCACGTACCGTTGTGTACGCG TCCTCACCGTCTGCAACAGGACTGGCTGAATG GCAAGGAGTACAAGTGCAGGTCTCCAACAAA GCCCTCCAGCCCCCATCGAGAAACCATCTCC AAAGCCAAAGGCAGCCCCCGAGAACACAGGT GTACACCTGCCCCCATCCCGGAGGAGATGAC CAAGAACAGGTACAGCTGACCTGCCTGGTCAA AGCTTCTATCCAGCGACATCGCCGTGGAGTG GGAGAGCAATGGGCAGCCGGAACAACATA AGACCACGCTCCCGTGTGCTGGACTCCGACGGCT CCTTCTTCTCTATAGCAAGCTCACCGTGGACAA GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATG CTCCGTGATGCATGAGGCTCTGCACAACCACTA CAGGCAGAAAGACCTCTCCCTGTCTCCGGGTAA A</p>
	<p>SEQ ID NO: 2041</p> <p>DIQLTQSPSSLASVGDVRVTITCRASQTSRFLNWY QQKPGKAPKLLIYVASSLQSGVPSRFSGSGTDF TLTISSLQPEDFATYYCQQSYSTLLSFGQGTLEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLS TLTLTKADYEEKHKVYACEVTHQGLSPVTKSFNR GEC</p>	<p>SEQ ID NO: 2198</p> <p>QVQLVESGGGVVQPRSLRLSCAASGFTSSYGIH WVRQAPGKGLEWVAWIYDASNKFHADAVKGR FTISRDNSKNTLYLQMNSLRAEDSAMFYFCARGKV AGMPEAFEIWQGQGLVTVSSASTKGPSVFP LAPSS KSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNV NHKPSNTKVDKKEPKSCDKTHHTCPPCPAPELLG</p>

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					GPSVFLFPPKPKDTLMISRTPEVTCVVVVDVSHEDPE VKFNWYVVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLS LSPGK
				SEQ ID NO: 471	SEQ ID NO: 628

[0207] In one embodiment the antibody or fragment thereof comprises a light chain variable region comprising a sequence selected from the group consisting of SEQ ID NOs: 1-157 and a heavy chain variable region comprising a sequence selected from the group consisting of SEQ ID NOs: 158-314, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid substitution at one or more conjugation site(s) selected from the group consisting of D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455, E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612.

[0208] In one embodiment the antibody or fragment thereof comprises a combination of light chain variable region and a heavy chain variable region selected from the group consisting of a light chain variable region comprising SEQ ID NO: 1 and a heavy chain variable region comprising SEQ ID NO: 158; a light chain variable region comprising SEQ ID NO: 2 and a heavy chain variable region comprising SEQ ID NO: 159; a light chain variable region comprising SEQ ID NO: 3 and a heavy chain variable region comprising SEQ ID NO: 160; a light chain variable region comprising SEQ ID NO: 4 and a heavy chain variable region comprising SEQ ID NO: 161; a light chain variable region comprising SEQ ID NO: 5 and a heavy chain variable region comprising SEQ ID NO: 162; a light chain variable region comprising SEQ ID NO: 6 and a heavy chain variable region comprising SEQ ID NO: 163; a light chain variable region comprising SEQ ID NO: 7 and a heavy chain variable region comprising SEQ ID NO: 164; a light chain variable region comprising SEQ ID NO: 8 and a heavy chain variable region comprising SEQ ID NO: 165; a light chain variable region comprising SEQ ID NO: 9 and a heavy chain variable region comprising SEQ ID NO: 166; a light chain variable region comprising SEQ ID NO: 10 and a heavy chain variable region comprising SEQ ID NO: 167; a light chain variable region comprising SEQ ID NO: 11 and a heavy chain variable region comprising SEQ ID NO: 168; a light chain variable region comprising SEQ ID NO: 12 and a heavy chain variable region comprising SEQ ID NO: 169; a light chain variable region comprising SEQ ID NO: 13 and a heavy chain variable region comprising SEQ ID NO: 170; a light chain variable region comprising SEQ ID NO: 14 and a heavy chain variable region comprising SEQ ID NO: 171; a light chain variable region comprising SEQ ID NO: 15 and a heavy chain variable region comprising SEQ ID NO: 172; a light chain variable region comprising SEQ ID NO: 16 and a heavy chain variable region comprising SEQ ID NO: 173; a light chain variable region comprising SEQ ID NO: 17 and a heavy chain variable region comprising SEQ ID NO: 174; a light chain variable region

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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, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455, E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612.

In one embodiment the antibody or fragment thereof comprises a light chain variable region encoded by a polynucleotide sequence selected from the group consisting of SEQ ID NOs: 1571-1727 and a heavy chain variable region encoded by a polynucleotide sequence selected from the group consisting of SEQ ID NOs: 1728-1884, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455, E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612.

In one embodiment the antibody or fragment thereof comprises a combination of light chain variable region and a heavy chain variable region selected from the group consisting of a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO:

1571 and a heavy chain variable region encoded by a polynucleotide sequence comprising
SEQ ID NO: 1728; a light chain variable region encoded by a polynucleotide sequence
comprising SEQ ID NO: 1572 and a heavy chain variable region encoded by a polynucleotide
sequence comprising SEQ ID NO: 1729; a light chain variable region encoded by a
5 polynucleotide sequence comprising SEQ ID NO: 1573 and a heavy chain variable region
encoded by a polynucleotide sequence comprising SEQ ID NO: 1730; a light chain variable
region encoded by a polynucleotide sequence comprising SEQ ID NO: 1574 and a heavy
chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1731; a
light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO:
10 1575 and a heavy chain variable region encoded by a polynucleotide sequence comprising
SEQ ID NO: 1732; a light chain variable region encoded by a polynucleotide sequence
comprising SEQ ID NO: 1576 and a heavy chain variable region encoded by a polynucleotide
sequence comprising SEQ ID NO: 1733; a light chain variable region encoded by a
polynucleotide sequence comprising SEQ ID NO: 1577 and a heavy chain variable region
15 encoded by a polynucleotide sequence comprising SEQ ID NO: 1734; a light chain variable
region encoded by a polynucleotide sequence comprising SEQ ID NO: 1578 and a heavy
chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1735; a
light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO:
1579 and a heavy chain variable region encoded by a polynucleotide sequence comprising
20 SEQ ID NO: 1736; a light chain variable region encoded by a polynucleotide sequence
comprising SEQ ID NO: 1580 and a heavy chain variable region encoded by a polynucleotide
sequence comprising SEQ ID NO: 1737; a light chain variable region encoded by a
polynucleotide sequence comprising SEQ ID NO: 1581 and a heavy chain variable region
encoded by a polynucleotide sequence comprising SEQ ID NO: 1738; a light chain variable
25 region encoded by a polynucleotide sequence comprising SEQ ID NO: 1582 and a heavy
chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1739; a
light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO:
1583 and a heavy chain variable region encoded by a polynucleotide sequence comprising
SEQ ID NO: 1740; a light chain variable region encoded by a polynucleotide sequence
30 comprising SEQ ID NO: 1584 and a heavy chain variable region encoded by a polynucleotide
sequence comprising SEQ ID NO: 1741; a light chain variable region encoded by a
polynucleotide sequence comprising SEQ ID NO: 1585 and a heavy chain variable region
encoded by a polynucleotide sequence comprising SEQ ID NO: 1742; a light chain variable
region encoded by a polynucleotide sequence comprising SEQ ID NO: 1586 and a heavy

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region encoded by a polynucleotide sequence comprising SEQ ID NO: 1662 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1819; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1663 and a heavy chain variable region encoded by a polynucleotide sequence comprising

5 SEQ ID NO: 1820; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1664 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1821; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1665 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1822; a light chain variable

10 region encoded by a polynucleotide sequence comprising SEQ ID NO: 1666 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1823; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1667 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1824; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1668 and a heavy chain variable region encoded by a polynucleotide

15 sequence comprising SEQ ID NO: 1825; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1669 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1826; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1670 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1827; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1671 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1828; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1672 and a heavy chain variable region encoded by a polynucleotide

20 sequence comprising SEQ ID NO: 1829; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1673 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1830; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1674 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1831; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1675 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1832; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1676 and a heavy chain variable region encoded by a polynucleotide

25 sequence comprising SEQ ID NO: 1833; a light chain variable region encoded by a

30

polynucleotide sequence comprising SEQ ID NO: 1677 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1834; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1678 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1835; a
5 light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1679 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1836; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1680 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1837; a light chain variable region encoded by a
10 polynucleotide sequence comprising SEQ ID NO: 1681 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1838; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1682 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1839; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO:
15 1683 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1840; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1684 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1841; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1685 and a heavy chain variable region
20 encoded by a polynucleotide sequence comprising SEQ ID NO: 1842; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1686 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1843; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1687 and a heavy chain variable region encoded by a polynucleotide sequence comprising
25 SEQ ID NO: 1844; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1688 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1845; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1689 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1846; a light chain variable
30 region encoded by a polynucleotide sequence comprising SEQ ID NO: 1690 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1847; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1691 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1848; a light chain variable region encoded by a polynucleotide sequence

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chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1879; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1723 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1880; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1724 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1881; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1725 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1882; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1726 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1883; and a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1727 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1884, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid substitution at one or more conjugation site(s) selected from the group consisting of D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455, E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612.

[0209] The present invention relates to a composition comprising an anti-GIPR antigen binding protein having at least one conjugation site. The conjugation site must be amenable to conjugation of an additional functional moiety (e.g., a GLP-1 receptor agonist) by a defined conjugation chemistry through the side chain of an amino acid residue at the conjugation site. Achieving highly selective, site-specific conjugation to the anti-GIPR antigen binding protein, in accordance with the present invention, requires consideration of a diverse variety of design criteria. First, a preferred conjugation or coupling chemistry must be defined or predetermined. Functional moieties such as, GLP-1 receptor agonists, can be conjugated or coupled to the selected conjugation site of the anti-GIPR antigen binding protein through an assortment of different conjugation chemistries known in the art. For example, a maleimide-activated conjugation partner targeting an accessible cysteine thiol on the anti-GIPR antigen binding protein is one embodiment, but numerous conjugation or coupling chemistries targeting the side chains of either canonical or non-canonical, e.g., unnatural amino acids in the anti-GIPR antigen binding protein sequence, can be employed in accordance with the present invention.

[0210] Chemistries for the chemoselective conjugation include: copper(I)-catalyzed azide-alkyne [3+2] dipolar cycloadditions, Staudinger ligation, other acyl transfers processes ($S \rightarrow N$; $X \rightarrow N$), oximations, hydrazone bonding formation and other suitable organic chemistry reactions such as cross-couplings using water-soluble palladium catalysts. (E.g., Bong et al., Chemoselective Pd(0)-

catalyzed peptide coupling in water, *Organic Letters* 3(16):2509-11 (2001); Dibowski et al., Bioconjugation of peptides by palladium-catalyzed C-C cross-coupling in water, *Angew. Chem. Int. Ed.* 37(4):476-78 (1998); DeVasher et al., Aqueous-phase, palladium-catalyzed cross-coupling of aryl bromides under mild conditions, using water-soluble, sterically demanding alkylphosphines, *J. Org. Chem.* 69:7919-27 (2004); Shaugnessy et al., *J. Org. Chem.*, 2003, 68, 6767-6774; Prescher, JA and Bertozzi CR, Chemistry in living system, *Nature Chemical Biology* 1(1); 13-21 (2005)).

[0211] As mentioned above, the conjugation (or covalent binding) to the anti-GIPR antigen binding protein is through the side chain of an amino acid residue at the conjugation site, for example, but not limited to, a cysteinyl residue. The amino acid residue, for example, a cysteinyl residue, at the internal conjugation site that is selected can be one that occupies the same amino acid residue position in a native Fc domain sequence, or the amino acid residue can be engineered into the Fc domain sequence by substitution or insertion. .

[0212] Other examples of unnatural amino acid residues that can be particularly useful as the conjugation site in some embodiments of the inventive processes and compositions of matter include: azido-containing amino acid residues, e.g., azidohomoalanine, p-azido-phenylalanine; keto-containing amino acid residues, e.g., p-acetyl-phenylalanine; alkyne- containing amino acid residues, e.g., p-ethynylphenylalanine, homopropargylglycine, p-(prop-2-ynyl)-tyrosine; alkene-containing amino acid residues e.g., homoallylglycine; aryl halide- containing amino acid residues e.g. p-iodophenylalanine, p-bromophenylalanine; and 1,2-aminothiol containing amino acid residues.

[0213] The non-canonical amino acid residues can be incorporated by amino acid substitution or insertion. Non-canonical amino acid residues can be incorporated into the peptide by chemical peptide synthesis rather than by synthesis in biological systems, such as recombinantly expressing cells, or alternatively the skilled artisan can employ known techniques of protein engineering that use recombinantly expressing cells. (See, e.g., Link et al., Non-canonical amino acids in protein engineering, *Current Opinion in Biotechnology*, 14(6):603-609 (2003); Schultz et al., In vivo incorporation of unnatural amino acids, U.S. Patent No. 7,045,337).

[0214] The selection of the placement of the conjugation site in the overall anti-GIPR antigen binding protein is another important facet of selecting an internal conjugation site in accordance with the present invention. Any of the exposed amino acid residues on the anti-GIPR antigen binding protein can be potentially useful conjugation sites and can be mutated to cysteine or some other reactive amino acid for site-selective coupling, if not already present at the selected conjugation site of the anti-GIPR antigen binding protein sequence. However, this approach does not take into account potential steric constraints that may perturb the activity of the conjugated partner or limit the reactivity of the engineered mutation.

[0215] In one embodiment, the anti-GIPR antigen binding protein is an antibody or functional fragment thereof. In one embodiment, the anti-GIPR antibody or functional fragment thereof

comprises a cysteine or non-canonical amino acid substitution at one or more conjugation site(s). The conjugation site(s) can be essentially on any residue of the antigen binding protein. In certain embodiments the conjugation site is located within the CL, CH1, CH2 or CH3 region of an antibody or functional fragment thereof. In certain embodiments the conjugation site(s) are selected from the group consisting of D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455; E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612; and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612. For sake of clarity, "D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455" is the same substitution site as AHo position D88 of the light chain of antibody 5G12.006 and Kabat position D70 of the light chain of antibody 5G12.006; "E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612" is the same substitution site as AHo position E384 of the heavy chain of antibody 5G12.006 and Kabat position E285 of the heavy chain of antibody 5G12.006; and "T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612" is the same substitution site as AHo position T487 of the heavy chain of antibody 5G12.006 and Kabat position T382 of the heavy chain of antibody 5G12.006.

[0216] Some antigen binding proteins comprise a variable light domain and a variable heavy domain as listed in one of the rows for one of the antibodies listed in TABLE 3. In some instances, the antigen binding protein comprises two identical variable light domains and two identical variable heavy domains from one of the antibodies listed in TABLE 3. Some antigen binding proteins that are provided comprise a variable light domain and a variable heavy domain as listed in one of the rows for one of the antibodies listed in TABLE 3, except that one or both of the domains differs from the sequence specified in the table at only 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15 amino acid residues, wherein each such sequence difference is independently either a single amino acid deletion, insertion or substitution, with the deletions, insertions and/or substitutions resulting in no more than 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15 amino acid changes relative to the variable domain sequences specified in TABLE 3. In one embodiment, the antigen binding protein comprises a variable region sequence from Table 3, but with the N-terminal methionine deleted. Other antigen binding proteins also comprise a variable light domain and a variable heavy domain as listed in one of the rows for one of the antibodies listed in TABLE 3, except that one or both of the domains differs from the sequence specified in the table in that the heavy chain variable domain and/or light chain variable domain comprises or consists of a sequence of amino acids that has at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% sequence

identity to the amino acid sequences of the heavy chain variable domain or light chain variable domain sequences as specified in TABLE 3.

[0217] In another aspect, the antigen binding protein consists just of a variable light or variable heavy domain from an antibody listed in TABLE 3. In still another aspect, the antigen binding protein comprises two or more of the same variable heavy domains or two or more of the same variable light domains from those listed in TABLE 3. Such domain antibodies can be fused together or joined via a linker as described in greater detail below. The domain antibodies can also be fused or linked to one or more molecules to extend the half-life (e.g., PEG or albumin).

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

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

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

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

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

identity to the amino acid sequences of one or more of the CDRs presented in TABLES 4A and 4B. These CDRs use the system described by Kabat et al. as noted above.

[0223] The structure and properties of CDRs within a naturally occurring antibody has been described, *supra*. Briefly, in a traditional antibody, the CDRs are embedded within a framework in the heavy and light chain variable region where they constitute the regions responsible for antigen binding and recognition. A variable region comprises at least three heavy or light chain CDRs, *see, supra* (Kabat *et al.*, 1991, *Sequences of Proteins of Immunological Interest*, Public Health Service N.I.H., Bethesda, MD; *see also* Chothia and Lesk, 1987, *J. Mol. Biol.* 196:901-917; Chothia *et al.*, 1989, *Nature* 342: 877-883), within a framework region (designated framework regions 1-4, FR1, FR2, FR3, and FR4, by Kabat *et al.*, 1991, *supra*; *see also* Chothia and Lesk, 1987, *supra*). The CDRs provided herein, however, may not only be used to define the antigen binding domain of a traditional antibody structure, but may be embedded in a variety of other polypeptide structures, as described herein.

[0224] In one embodiment the antibody or fragment thereof comprises a CDRL1, a CDRL2, a CDRL3, a CDRH1, a CDRH2, and a CDRH3, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid substitution at one or more conjugation site(s) selected from the group consisting of D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455, E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612. In one embodiment the antibody or fragment thereof comprises a CDRL1, a CDRL2, a CDRL3, a CDRH1, a CDRH2, and a CDRH3, wherein each CDRL1, CDRL2, CDRL3, CDRH1, CDRH2, and CDRH3, respectively, comprises a sequence selected from the group consisting of SEQ ID NO: 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

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ID NO: 1081, SEQ ID NO: 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: 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 ID NO: 1248, SEQ ID NO: 1405, and SEQ ID NO: 1562; SEQ ID NO: 778, SEQ ID NO: 935, SEQ ID NO: 1092, SEQ ID NO: 1249, SEQ ID NO: 1406, and SEQ ID NO: 1563; SEQ ID NO: 779, SEQ ID NO: 936, SEQ ID NO: 1093, SEQ ID NO: 1250, SEQ ID NO: 1407, and SEQ ID NO: 1564; 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: 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 NO: 1570, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455, E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612.

[0225] In one embodiment the antibody or fragment thereof comprises a CDRL1, a CDRL2, a CDRL3, a CDRH1, a CDRH2, and a CDRH3, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of D70 of the antibody light chain

relative to reference sequence SEQ ID NO: 455, E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, encoded by a polynucleotide. In one embodiment the antibody or fragment thereof comprises a CDRL1, a CDRL2, a CDRL3, a CDRH1, a CDRH2, and a CDRH3, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455, E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, wherein each CDRL1, CDRL2, CDRL3, CDRH1, CDRH2, and CDRH3, respectively, is encoded by a sequence selected from the group consisting of SEQ ID NO: 2199, SEQ ID NO: 2356, SEQ ID NO: 2513, SEQ ID NO: 2670, SEQ ID NO: 2827, and SEQ ID NO: 2984 ; SEQ ID NO: 2200, SEQ ID NO: 2357, SEQ ID NO: 2514, SEQ ID NO: 2671, SEQ ID NO: 2828, and SEQ ID NO: 2985 ; SEQ ID NO: 2201, SEQ ID NO: 2358, SEQ ID NO: 2515, SEQ ID NO: 2672, SEQ ID NO: 2829, and SEQ ID NO: 2986 ; SEQ ID NO: 2202, SEQ ID NO: 2359, SEQ ID NO: 2516, SEQ ID NO: 2673, SEQ ID NO: 2830, and SEQ ID NO: 2987 ; SEQ ID NO: 2203, SEQ ID NO: 2360, SEQ ID NO: 2517, SEQ ID NO: 2674, SEQ ID NO: 2831, and SEQ ID NO: 2988 ; SEQ ID NO: 2204, SEQ ID NO: 2361, SEQ ID NO: 2518, SEQ ID NO: 2675, SEQ ID NO: 2832, and SEQ ID NO: 2989 ; SEQ ID NO: 2205, SEQ ID NO: 2362, SEQ ID NO: 2519, SEQ ID NO: 2676, SEQ ID NO: 2833, and SEQ ID NO: 2990 ; SEQ ID NO: 2206, SEQ ID NO: 2363, SEQ ID NO: 2520, SEQ ID NO: 2677, SEQ ID NO: 2834, and SEQ ID NO: 2991 ; SEQ ID NO: 2207, SEQ ID NO: 2364, SEQ ID NO: 2521, SEQ ID NO: 2678, SEQ ID NO: 2835, and SEQ ID NO: 2992 ; SEQ ID NO: 2208, SEQ ID NO: 2365, SEQ ID NO: 2522, SEQ ID NO: 2679, SEQ ID NO: 2836, and SEQ ID NO: 2993 ; SEQ ID NO: 2209, SEQ ID NO: 2366, SEQ ID NO: 2523, SEQ ID NO: 2680, SEQ ID NO: 2837, and SEQ ID NO: 2994 ; SEQ ID NO: 2210, SEQ ID NO: 2367, SEQ ID NO: 2524, SEQ ID NO: 2681, SEQ ID NO: 2838, and SEQ ID NO: 2995 ; SEQ ID NO: 2211, SEQ ID NO: 2368, SEQ ID NO: 2525, SEQ ID NO: 2682, SEQ ID NO: 2839, and SEQ ID NO: 2996 ; SEQ ID NO: 2212, SEQ ID NO: 2369, SEQ ID NO: 2526, SEQ ID NO: 2683, SEQ ID NO: 2840, and SEQ ID NO: 2997 ; SEQ ID NO: 2213, SEQ ID NO: 2370, SEQ ID NO: 2527, SEQ ID NO: 2684, SEQ ID NO: 2841, and SEQ ID NO: 2998 ; SEQ ID NO: 2214, SEQ ID NO: 2371, SEQ ID NO: 2528, SEQ ID NO: 2685, SEQ ID NO: 2842, and SEQ ID NO: 2999 ; SEQ ID NO: 2215, SEQ ID NO: 2372, SEQ ID NO: 2529, SEQ ID NO: 2686, SEQ ID NO: 2843, and SEQ ID NO: 3000 ; SEQ ID NO: 2216, SEQ ID

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NO: 2439, SEQ ID NO: 2596, SEQ ID NO: 2753, SEQ ID NO: 2910, and SEQ ID NO: 3067
; SEQ ID NO: 2283, SEQ ID NO: 2440, SEQ ID NO: 2597, SEQ ID NO: 2754, SEQ ID NO:
2911, and SEQ ID NO: 3068 ; SEQ ID NO: 2284, SEQ ID NO: 2441, SEQ ID NO: 2598,
SEQ ID NO: 2755, SEQ ID NO: 2912, and SEQ ID NO: 3069 ; SEQ ID NO: 2285, SEQ ID
25 NO: 2442, SEQ ID NO: 2599, SEQ ID NO: 2756, SEQ ID NO: 2913, and SEQ ID NO: 3070
; SEQ ID NO: 2286, SEQ ID NO: 2443, SEQ ID NO: 2600, SEQ ID NO: 2757, SEQ ID NO:
2914, and SEQ ID NO: 3071 ; SEQ ID NO: 2287, SEQ ID NO: 2444, SEQ ID NO: 2601,
SEQ ID NO: 2758, SEQ ID NO: 2915, and SEQ ID NO: 3072 ; SEQ ID NO: 2288, SEQ ID
NO: 2445, SEQ ID NO: 2602, SEQ ID NO: 2759, SEQ ID NO: 2916, and SEQ ID NO: 3073
30 ; SEQ ID NO: 2289, SEQ ID NO: 2446, SEQ ID NO: 2603, SEQ ID NO: 2760, SEQ ID NO:
2917, and SEQ ID NO: 3074 ; SEQ ID NO: 2290, SEQ ID NO: 2447, SEQ ID NO: 2604,
SEQ ID NO: 2761, SEQ ID NO: 2918, and SEQ ID NO: 3075 ; SEQ ID NO: 2291, SEQ ID
NO: 2448, SEQ ID NO: 2605, SEQ ID NO: 2762, SEQ ID NO: 2919, and SEQ ID NO: 3076
; SEQ ID NO: 2292, SEQ ID NO: 2449, SEQ ID NO: 2606, SEQ ID NO: 2763, SEQ ID NO:

2920, and SEQ ID NO: 3077 ; SEQ ID NO: 2293, SEQ ID NO: 2450, SEQ ID NO: 2607,
SEQ ID NO: 2764, SEQ ID NO: 2921, and SEQ ID NO: 3078 ; SEQ ID NO: 2294, SEQ ID
NO: 2451, SEQ ID NO: 2608, SEQ ID NO: 2765, SEQ ID NO: 2922, and SEQ ID NO: 3079
; SEQ ID NO: 2295, SEQ ID NO: 2452, SEQ ID NO: 2609, SEQ ID NO: 2766, SEQ ID NO:
5 2923, and SEQ ID NO: 3080 ; SEQ ID NO: 2296, SEQ ID NO: 2453, SEQ ID NO: 2610,
SEQ ID NO: 2767, SEQ ID NO: 2924, and SEQ ID NO: 3081 ; SEQ ID NO: 2297, SEQ ID
NO: 2454, SEQ ID NO: 2611, SEQ ID NO: 2768, SEQ ID NO: 2925, and SEQ ID NO: 3082
; SEQ ID NO: 2298, SEQ ID NO: 2455, SEQ ID NO: 2612, SEQ ID NO: 2769, SEQ ID NO:
2926, and SEQ ID NO: 3083 ; SEQ ID NO: 2299, SEQ ID NO: 2456, SEQ ID NO: 2613,
10 SEQ ID NO: 2770, SEQ ID NO: 2927, and SEQ ID NO: 3084 ; SEQ ID NO: 2300, SEQ ID
NO: 2457, SEQ ID NO: 2614, SEQ ID NO: 2771, SEQ ID NO: 2928, and SEQ ID NO: 3085
; SEQ ID NO: 2301, SEQ ID NO: 2458, SEQ ID NO: 2615, SEQ ID NO: 2772, SEQ ID NO:
2929, and SEQ ID NO: 3086 ; SEQ ID NO: 2302, SEQ ID NO: 2459, SEQ ID NO: 2616,
SEQ ID NO: 2773, SEQ ID NO: 2930, and SEQ ID NO: 3087 ; SEQ ID NO: 2303, SEQ ID
15 NO: 2460, SEQ ID NO: 2617, SEQ ID NO: 2774, SEQ ID NO: 2931, and SEQ ID NO: 3088
; SEQ ID NO: 2304, SEQ ID NO: 2461, SEQ ID NO: 2618, SEQ ID NO: 2775, SEQ ID NO:
2932, and SEQ ID NO: 3089 ; SEQ ID NO: 2305, SEQ ID NO: 2462, SEQ ID NO: 2619,
SEQ ID NO: 2776, SEQ ID NO: 2933, and SEQ ID NO: 3090 ; SEQ ID NO: 2306, SEQ ID
NO: 2463, SEQ ID NO: 2620, SEQ ID NO: 2777, SEQ ID NO: 2934, and SEQ ID NO: 3091
20 ; SEQ ID NO: 2307, SEQ ID NO: 2464, SEQ ID NO: 2621, SEQ ID NO: 2778, SEQ ID NO:
2935, and SEQ ID NO: 3092 ; SEQ ID NO: 2308, SEQ ID NO: 2465, SEQ ID NO: 2622,
SEQ ID NO: 2779, SEQ ID NO: 2936, and SEQ ID NO: 3093 ; SEQ ID NO: 2309, SEQ ID
NO: 2466, SEQ ID NO: 2623, SEQ ID NO: 2780, SEQ ID NO: 2937, and SEQ ID NO: 3094
; SEQ ID NO: 2310, SEQ ID NO: 2467, SEQ ID NO: 2624, SEQ ID NO: 2781, SEQ ID NO:
25 2938, and SEQ ID NO: 3095 ; SEQ ID NO: 2311, SEQ ID NO: 2468, SEQ ID NO: 2625,
SEQ ID NO: 2782, SEQ ID NO: 2939, and SEQ ID NO: 3096 ; SEQ ID NO: 2312, SEQ ID
NO: 2469, SEQ ID NO: 2626, SEQ ID NO: 2783, SEQ ID NO: 2940, and SEQ ID NO: 3097
; SEQ ID NO: 2313, SEQ ID NO: 2470, SEQ ID NO: 2627, SEQ ID NO: 2784, SEQ ID NO:
2941, and SEQ ID NO: 3098 ; SEQ ID NO: 2314, SEQ ID NO: 2471, SEQ ID NO: 2628,
30 SEQ ID NO: 2785, SEQ ID NO: 2942, and SEQ ID NO: 3099 ; SEQ ID NO: 2315, SEQ ID
NO: 2472, SEQ ID NO: 2629, SEQ ID NO: 2786, SEQ ID NO: 2943, and SEQ ID NO: 3100
; SEQ ID NO: 2316, SEQ ID NO: 2473, SEQ ID NO: 2630, SEQ ID NO: 2787, SEQ ID NO:
2944, and SEQ ID NO: 3101 ; SEQ ID NO: 2317, SEQ ID NO: 2474, SEQ ID NO: 2631,
SEQ ID NO: 2788, SEQ ID NO: 2945, and SEQ ID NO: 3102 ; SEQ ID NO: 2318, SEQ ID

NO: 2475, SEQ ID NO: 2632, SEQ ID NO: 2789, SEQ ID NO: 2946, and SEQ ID NO: 3103
; SEQ ID NO: 2319, SEQ ID NO: 2476, SEQ ID NO: 2633, SEQ ID NO: 2790, SEQ ID NO:
2947, and SEQ ID NO: 3104 ; SEQ ID NO: 2320, SEQ ID NO: 2477, SEQ ID NO: 2634,
SEQ ID NO: 2791, SEQ ID NO: 2948, and SEQ ID NO: 3105 ; SEQ ID NO: 2321, SEQ ID
5 NO: 2478, SEQ ID NO: 2635, SEQ ID NO: 2792, SEQ ID NO: 2949, and SEQ ID NO: 3106
; SEQ ID NO: 2322, SEQ ID NO: 2479, SEQ ID NO: 2636, SEQ ID NO: 2793, SEQ ID NO:
2950, and SEQ ID NO: 3107 ; SEQ ID NO: 2323, SEQ ID NO: 2480, SEQ ID NO: 2637,
SEQ ID NO: 2794, SEQ ID NO: 2951, and SEQ ID NO: 3108 ; SEQ ID NO: 2324, SEQ ID
NO: 2481, SEQ ID NO: 2638, SEQ ID NO: 2795, SEQ ID NO: 2952, and SEQ ID NO: 3109
10 ; SEQ ID NO: 2325, SEQ ID NO: 2482, SEQ ID NO: 2639, SEQ ID NO: 2796, SEQ ID NO:
2953, and SEQ ID NO: 3110 ; SEQ ID NO: 2326, SEQ ID NO: 2483, SEQ ID NO: 2640,
SEQ ID NO: 2797, SEQ ID NO: 2954, and SEQ ID NO: 3111 ; SEQ ID NO: 2327, SEQ ID
NO: 2484, SEQ ID NO: 2641, SEQ ID NO: 2798, SEQ ID NO: 2955, and SEQ ID NO: 3112
; SEQ ID NO: 2328, SEQ ID NO: 2485, SEQ ID NO: 2642, SEQ ID NO: 2799, SEQ ID NO:
15 2956, and SEQ ID NO: 3113 ; SEQ ID NO: 2329, SEQ ID NO: 2486, SEQ ID NO: 2643,
SEQ ID NO: 2800, SEQ ID NO: 2957, and SEQ ID NO: 3114 ; SEQ ID NO: 2330, SEQ ID
NO: 2487, SEQ ID NO: 2644, SEQ ID NO: 2801, SEQ ID NO: 2958, and SEQ ID NO: 3115
; SEQ ID NO: 2331, SEQ ID NO: 2488, SEQ ID NO: 2645, SEQ ID NO: 2802, SEQ ID NO:
2959, and SEQ ID NO: 3116 ; SEQ ID NO: 2332, SEQ ID NO: 2489, SEQ ID NO: 2646,
20 SEQ ID NO: 2803, SEQ ID NO: 2960, and SEQ ID NO: 3117 ; SEQ ID NO: 2333, SEQ ID
NO: 2490, SEQ ID NO: 2647, SEQ ID NO: 2804, SEQ ID NO: 2961, and SEQ ID NO: 3118
; SEQ ID NO: 2334, SEQ ID NO: 2491, SEQ ID NO: 2648, SEQ ID NO: 2805, SEQ ID NO:
2962, and SEQ ID NO: 3119 ; SEQ ID NO: 2335, SEQ ID NO: 2492, SEQ ID NO: 2649,
SEQ ID NO: 2806, SEQ ID NO: 2963, and SEQ ID NO: 3120 ; SEQ ID NO: 2336, SEQ ID
25 NO: 2493, SEQ ID NO: 2650, SEQ ID NO: 2807, SEQ ID NO: 2964, and SEQ ID NO: 3121
; SEQ ID NO: 2337, SEQ ID NO: 2494, SEQ ID NO: 2651, SEQ ID NO: 2808, SEQ ID NO:
2965, and SEQ ID NO: 3122 ; SEQ ID NO: 2338, SEQ ID NO: 2495, SEQ ID NO: 2652,
SEQ ID NO: 2809, SEQ ID NO: 2966, and SEQ ID NO: 3123 ; SEQ ID NO: 2339, SEQ ID
NO: 2496, SEQ ID NO: 2653, SEQ ID NO: 2810, SEQ ID NO: 2967, and SEQ ID NO: 3124
30 ; SEQ ID NO: 2340, SEQ ID NO: 2497, SEQ ID NO: 2654, SEQ ID NO: 2811, SEQ ID NO:
2968, and SEQ ID NO: 3125 ; SEQ ID NO: 2341, SEQ ID NO: 2498, SEQ ID NO: 2655,
SEQ ID NO: 2812, SEQ ID NO: 2969, and SEQ ID NO: 3126 ; SEQ ID NO: 2342, SEQ ID
NO: 2499, SEQ ID NO: 2656, SEQ ID NO: 2813, SEQ ID NO: 2970, and SEQ ID NO: 3127
; SEQ ID NO: 2343, SEQ ID NO: 2500, SEQ ID NO: 2657, SEQ ID NO: 2814, SEQ ID NO:

2971, and SEQ ID NO: 3128 ; SEQ ID NO: 2344, SEQ ID NO: 2501, SEQ ID NO: 2658,
 SEQ ID NO: 2815, SEQ ID NO: 2972, and SEQ ID NO: 3129 ; SEQ ID NO: 2345, SEQ ID
 NO: 2502, SEQ ID NO: 2659, SEQ ID NO: 2816, SEQ ID NO: 2973, and SEQ ID NO: 3130
 ; SEQ ID NO: 2346, SEQ ID NO: 2503, SEQ ID NO: 2660, SEQ ID NO: 2817, SEQ ID NO:
 5 2974, and SEQ ID NO: 3131 ; SEQ ID NO: 2347, SEQ ID NO: 2504, SEQ ID NO: 2661,
 SEQ ID NO: 2818, SEQ ID NO: 2975, and SEQ ID NO: 3132 ; SEQ ID NO: 2348, SEQ ID
 NO: 2505, SEQ ID NO: 2662, SEQ ID NO: 2819, SEQ ID NO: 2976, and SEQ ID NO: 3133
 ; SEQ ID NO: 2349, SEQ ID NO: 2506, SEQ ID NO: 2663, SEQ ID NO: 2820, SEQ ID NO:
 2977, and SEQ ID NO: 3134 ; SEQ ID NO: 2350, SEQ ID NO: 2507, SEQ ID NO: 2664,
 10 SEQ ID NO: 2821, SEQ ID NO: 2978, and SEQ ID NO: 3135 ; SEQ ID NO: 2351, SEQ ID
 NO: 2508, SEQ ID NO: 2665, SEQ ID NO: 2822, SEQ ID NO: 2979, and SEQ ID NO: 3136
 ; SEQ ID NO: 2352, SEQ ID NO: 2509, SEQ ID NO: 2666, SEQ ID NO: 2823, SEQ ID NO:
 2980, and SEQ ID NO: 3137 ; SEQ ID NO: 2353, SEQ ID NO: 2510, SEQ ID NO: 2667,
 SEQ ID NO: 2824, SEQ ID NO: 2981, and SEQ ID NO: 3138 ; SEQ ID NO: 2354, SEQ ID
 15 NO: 2511, SEQ ID NO: 2668, SEQ ID NO: 2825, SEQ ID NO: 2982, and SEQ ID NO: 3139
 ; and SEQ ID NO: 2355, SEQ ID NO: 2512, SEQ ID NO: 2669, SEQ ID NO: 2826, SEQ ID
 NO: 2983, and SEQ ID NO: 3140.

[0226] In another aspect, an antigen binding protein includes 1, 2, 3, 4, 5, or 6 variant forms
 of the CDRs listed in TABLES 4A and 4B, each having at least 80%, 85%, 90%, 95% , 96%,
 20 97%, 98%, or 99% sequence identity to a CDR sequence listed in TABLES 4A and 4B. Some
 antigen binding proteins include 1, 2, 3, 4, 5, or 6 of the CDRs listed in TABLES 4A and 4B,
 each or collectively differing by no more than 1, 2, 3, 4 or 5 amino acids from the CDRs
 listed in this table.

[0227] In various other embodiments, the antigen binding protein is derived from such
 25 antibodies. For instance, in one aspect, the antigen binding protein comprises 1, 2, 3, 4, 5 or
 all 6 of the CDRs listed in one of the rows for any particular antibody listed in TABLES 4A
 and 4B. In another aspect, an antigen binding protein includes 1, 2, 3, 4, 5, or 6 variant forms
 of the CDRs listed in one of the rows for an antibody in TABLES 4A and 4B, each CDR
 having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% sequence identity to a CDR
 30 sequence listed in TABLES 4A and 4B. Some antigen binding proteins include 1, 2, 3, 4, 5,
 or 6 of the CDRs listed in one of the rows of TABLES 4A and 4B, each differing by no more
 than 1, 2, 3, 4 or 5 amino acids from the CDRs listed in these tables. In another aspect, the
 antigen binding protein comprises all 6 of the CDRS listed in a row of TABLES 4A and 4B

and the total number of amino acid changes to the CDRs collectively is no more than 1, 2, 3, 4, or 5 amino acids.

[0228] In one embodiment the antibody or fragment thereof comprises a light chain comprising a sequence selected from the group consisting of SEQ ID NOs: 472-628 and a heavy chain comprising a sequence selected from the group consisting of SEQ ID NOs: 472-628, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455, E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612. In one embodiment the antibody or fragment thereof comprises a combination of a light chain and a heavy chain selected from the group consisting of a light chain comprising SEQ ID NO: 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

[illegible]

[illegible]

[illegible]

and a heavy chain comprising SEQ ID NO: 596; a light chain comprising SEQ ID NO: 440
and a heavy chain comprising SEQ ID NO: 597; a light chain comprising SEQ ID NO: 441
and a heavy chain comprising SEQ ID NO: 598; a light chain comprising SEQ ID NO: 442
and a heavy chain comprising SEQ ID NO: 599; a light chain comprising SEQ ID NO: 443
5 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
10 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
15 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
20 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
25 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
30 and a heavy chain comprising SEQ ID NO: 625; a light chain comprising SEQ ID NO: 469
and a heavy chain comprising SEQ ID NO: 626; a light chain comprising SEQ ID NO: 470
and a heavy chain comprising SEQ ID NO: 627; and a light chain comprising SEQ ID NO:
471 and a heavy chain comprising SEQ ID NO: 628, wherein the antibody or functional
fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at

one or more conjugation site(s) selected from the group consisting of D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455, E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612.

- 5 [0229] In one embodiment the antibody or fragment thereof comprises a light chain encoded by a polynucleotide sequence selected from the group consisting of SEQ ID NOs: 1885-2014 and a heavy chain comprising a sequence selected from the group consisting of SEQ ID NOs: 2042-2198, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from
- 10 the group consisting of D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455, E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612. In one embodiment the antibody or fragment thereof comprises a combination of a light chain and a heavy chain, wherein the antibody or functional fragment thereof comprises a cysteine or
- 15 non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455, E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, selected from the group consisting of a light chain encoded by a polynucleotide
- 20 sequence comprising SEQ ID NO: 1885 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2042; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1886 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2043; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1887 and a heavy chain encoded by a polynucleotide sequence
- 25 comprising SEQ ID NO: 2044; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1888 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2045; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1889 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2046; a light chain encoded by a polynucleotide sequence
- 30 comprising SEQ ID NO: 1890 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2047; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1891 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2048; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1892 and a heavy chain encoded by a polynucleotide sequence

comprising SEQ ID NO: 2049; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1893 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2050; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1894 and a heavy chain encoded by a polynucleotide sequence
5 comprising SEQ ID NO: 2051; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1895 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2052; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1896 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2053; a light chain encoded by a polynucleotide sequence
10 comprising SEQ ID NO: 1897 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2054; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1898 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2055; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1899 and a heavy chain encoded by a polynucleotide sequence
15 comprising SEQ ID NO: 2056; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1900 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2057; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1901 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2058; a light chain encoded by a polynucleotide sequence
20 comprising SEQ ID NO: 1902 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2059; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1903 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2060; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1904 and a heavy chain encoded by a polynucleotide sequence
25 comprising SEQ ID NO: 2061; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1905 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2062; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1906 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2063; a light chain encoded by a polynucleotide sequence
30 comprising SEQ ID NO: 1907 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2064; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1908 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2065; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1909 and a heavy chain encoded by a polynucleotide sequence

comprising SEQ ID NO: 2066; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1910 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2067; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1911 and a heavy chain encoded by a polynucleotide sequence
5 comprising SEQ ID NO: 2068; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1912 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2069; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1913 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2070; a light chain encoded by a polynucleotide sequence
10 comprising SEQ ID NO: 1914 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2071; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1915 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2072; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1916 and a heavy chain encoded by a polynucleotide sequence
15 comprising SEQ ID NO: 2073; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1917 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2074; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1918 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2075; a light chain encoded by a polynucleotide sequence
20 comprising SEQ ID NO: 1919 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2076; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1920 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2077; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1921 and a heavy chain encoded by a polynucleotide sequence
25 comprising SEQ ID NO: 2078; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1922 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2079; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1923 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2080; a light chain encoded by a polynucleotide sequence
30 comprising SEQ ID NO: 1924 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2081; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1925 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2082; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1926 and a heavy chain encoded by a polynucleotide sequence

comprising SEQ ID NO: 2083; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1927 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2084; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1928 and a heavy chain encoded by a polynucleotide sequence
5 comprising SEQ ID NO: 2085; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1929 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2086; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1930 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2087; a light chain encoded by a polynucleotide sequence
10 comprising SEQ ID NO: 1931 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2088; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1932 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2089; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1933 and a heavy chain encoded by a polynucleotide sequence
15 comprising SEQ ID NO: 2090; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1934 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2091; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1935 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2092; a light chain encoded by a polynucleotide sequence
20 comprising SEQ ID NO: 1936 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2093; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1937 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2094; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1938 and a heavy chain encoded by a polynucleotide sequence
25 comprising SEQ ID NO: 2095; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1939 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2096; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1940 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2097; a light chain encoded by a polynucleotide sequence
30 comprising SEQ ID NO: 1941 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2098; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1942 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2099; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1943 and a heavy chain encoded by a polynucleotide sequence

comprising SEQ ID NO: 2100; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1944 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2101; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1945 and a heavy chain encoded by a polynucleotide sequence
5 comprising SEQ ID NO: 2102; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1946 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2103; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1947 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2104; a light chain encoded by a polynucleotide sequence
10 comprising SEQ ID NO: 1948 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2105; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1949 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2106; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1950 and a heavy chain encoded by a polynucleotide sequence
15 comprising SEQ ID NO: 2107; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1951 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2108; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1952 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2109; a light chain encoded by a polynucleotide sequence
20 comprising SEQ ID NO: 1953 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2110; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1954 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2111; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1955 and a heavy chain encoded by a polynucleotide sequence
25 comprising SEQ ID NO: 2112; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1956 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2113; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1957 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2114; a light chain encoded by a polynucleotide sequence
30 comprising SEQ ID NO: 1958 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2115; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1959 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2116; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1960 and a heavy chain encoded by a polynucleotide sequence

comprising SEQ ID NO: 2117; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1961 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2118; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1962 and a heavy chain encoded by a polynucleotide sequence
5 comprising SEQ ID NO: 2119; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1963 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2120; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1964 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2121; a light chain encoded by a polynucleotide sequence
10 comprising SEQ ID NO: 1965 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2122; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1966 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2123; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1967 and a heavy chain encoded by a polynucleotide sequence
15 comprising SEQ ID NO: 2124; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1968 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2125; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1969 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2126; a light chain encoded by a polynucleotide sequence
20 comprising SEQ ID NO: 1970 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2127; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1971 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2128; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1972 and a heavy chain encoded by a polynucleotide sequence
25 comprising SEQ ID NO: 2129; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1973 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2130; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1974 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2131; a light chain encoded by a polynucleotide sequence
30 comprising SEQ ID NO: 1975 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2132; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1976 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2133; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1977 and a heavy chain encoded by a polynucleotide sequence

comprising SEQ ID NO: 2134; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1978 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2135; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1979 and a heavy chain encoded by a polynucleotide sequence
5 comprising SEQ ID NO: 2136; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1980 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2137; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1981 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2138; a light chain encoded by a polynucleotide sequence
10 comprising SEQ ID NO: 1982 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2139; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1983 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2140; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1984 and a heavy chain encoded by a polynucleotide sequence
15 comprising SEQ ID NO: 2141; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1985 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2142; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1986 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2143; a light chain encoded by a polynucleotide sequence
20 comprising SEQ ID NO: 1987 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2144; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1988 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2145; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1989 and a heavy chain encoded by a polynucleotide sequence
25 comprising SEQ ID NO: 2146; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1990 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2147; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1991 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2148; a light chain encoded by a polynucleotide sequence
30 comprising SEQ ID NO: 1992 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2149; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1993 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2150; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1994 and a heavy chain encoded by a polynucleotide sequence

comprising SEQ ID NO: 2151; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1995 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2152; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1996 and a heavy chain encoded by a polynucleotide sequence
5 comprising SEQ ID NO: 2153; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1997 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2154; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 1998 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2155; a light chain encoded by a polynucleotide sequence
10 comprising SEQ ID NO: 1999 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2156; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2000 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2157; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2001 and a heavy chain encoded by a polynucleotide sequence
15 comprising SEQ ID NO: 2158; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2002 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2159; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2003 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2160; a light chain encoded by a polynucleotide sequence
20 comprising SEQ ID NO: 2004 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2161; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2005 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2162; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2006 and a heavy chain encoded by a polynucleotide sequence
25 comprising SEQ ID NO: 2163; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2007 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2164; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2008 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2165; a light chain encoded by a polynucleotide sequence
30 comprising SEQ ID NO: 2009 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2166; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2010 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2167; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2011 and a heavy chain encoded by a polynucleotide sequence

comprising SEQ ID NO: 2168; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2012 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2169; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2013 and a heavy chain encoded by a polynucleotide sequence
5 comprising SEQ ID NO: 2170; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2014 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2171; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2015 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2172; a light chain encoded by a polynucleotide sequence
10 comprising SEQ ID NO: 2016 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2173; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2017 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2174; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2018 and a heavy chain encoded by a polynucleotide sequence
15 comprising SEQ ID NO: 2175; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2019 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2176; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2020 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2177; a light chain encoded by a polynucleotide sequence
20 comprising SEQ ID NO: 2021 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2178; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2022 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2179; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2023 and a heavy chain encoded by a polynucleotide sequence
25 comprising SEQ ID NO: 2180; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2024 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2181; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2025 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2182; a light chain encoded by a polynucleotide sequence
30 comprising SEQ ID NO: 2026 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2183; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2027 and a heavy chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2184; a light chain encoded by a polynucleotide sequence
comprising SEQ ID NO: 2028 and a heavy chain encoded by a polynucleotide sequence

comprising SEQ ID NO: 2185; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2029 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2186; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2030 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2187; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2031 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2188; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2032 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2189; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2033 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2190; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2034 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2191; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2035 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2192; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2036 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2193; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2037 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2194; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2038 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2195; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2039 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2196; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2040 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2197; and a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2041 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2198.

[0230] In another aspect, the antigen binding protein comprises a full length light chain and a full length heavy chain as listed in one of the rows for one of the antibodies listed in TABLE 5. Some antigen binding proteins that are provided comprise a full length light chain and a full length heavy chain as listed in one of the rows for one of the antibodies listed in TABLE 5, except that one or both of the chains differs from the sequence specified in the table at only 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15 amino acid residues, wherein each such sequence difference is independently either a single amino acid deletion, insertion or

substitution, with the deletions, insertions and/or substitutions resulting in no more than 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15 amino acid changes relative to the full length sequences specified in TABLE 5. In one embodiment the antigen binding protein comprises a full length light chain and/or a full length heavy chain from Table 5 with the N-terminal methionine deleted. In one embodiment the antigen binding protein comprises a full length light chain and/or a full length heavy chain from Table 5 with the C-terminal lysine deleted. Other antigen binding proteins also comprise a full length light chain and a full length heavy chain as listed in one of the rows for one of the antibodies listed in TABLE 5, except that one or both of the chains differs from the sequence specified in the table in that the light chain and/or heavy chain comprises or consists of a sequence of amino acids that has at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequences of the light chain or heavy chain sequences as specified in TABLE 5.

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

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

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

[0234] In another embodiment, antigen binding proteins are provided that compete with one of the exemplified antibodies or functional fragments described above for specific binding to a human GIPR (e.g., SEQ ID NO: 3141). Such antigen binding proteins may bind to the same epitope as one of the antigen binding proteins described herein, or to an overlapping epitope. Antigen binding proteins and fragments that compete with the exemplified antigen binding proteins are expected to show similar functional properties. The exemplified antigen binding proteins and fragments include those described above, including those with heavy and light chains, variable region domains and CDRs included in TABLES 3, 4A, 4B, and 5. Thus, as a specific example, the antigen binding proteins that are provided include those that compete with an antibody having:

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

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

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

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

[0239] In some instances, a hybridoma cell line is produced by immunizing an animal (e.g., a transgenic animal having human immunoglobulin sequences) with a GIPR immunogen;

20 harvesting spleen cells from the immunized animal; fusing the harvested spleen cells to a myeloma cell line, thereby generating hybridoma cells; establishing hybridoma cell lines from the hybridoma cells, and identifying a hybridoma cell line that produces an antibody that binds a GIPR polypeptide. Such hybridoma cell lines, and anti-GIPR monoclonal antibodies produced by them, are aspects of the present application.

25 [0240] Monoclonal antibodies secreted by a hybridoma cell line can be purified using any technique known in the art. Hybridomas or mAbs may be further screened to identify mAbs with particular properties, such as the ability to increase GIPR activity.

[0241] Chimeric and humanized antibodies based upon the foregoing sequences are also provided. Monoclonal antibodies for use as therapeutic agents may be modified in various
30 ways prior to use. One example is a chimeric antibody, which is an antibody composed of protein segments from different antibodies that are covalently joined to produce functional immunoglobulin light or heavy chains or immunologically functional portions thereof.

Generally, a portion of the heavy chain and/or light chain is identical with or homologous to a corresponding sequence in antibodies derived from a particular species or belonging to a

particular antibody class or subclass, while the remainder of the chain(s) is/are identical with or homologous to a corresponding sequence in antibodies derived from another species or belonging to another antibody class or subclass. For methods relating to chimeric antibodies, *see*, for example, United States Patent No. 4,816,567; and Morrison *et al.*, 1985, *Proc. Natl. Acad. Sci. USA* 81:6851-6855, which are hereby incorporated by reference. CDR grafting is described, for example, in United States Patent No. 6,180,370, No. 5,693,762, No. 5,693,761, No. 5,585,089, and No. 5,530,101.

[0242] Generally, the goal of making a chimeric antibody is to create a chimera in which the number of amino acids from the intended patient species is maximized. One example is the “CDR-grafted” antibody, in which the antibody comprises one or more complementarity determining regions (CDRs) from a particular species or belonging to a particular antibody class or subclass, while the remainder of the antibody chain(s) is/are identical with or homologous to a corresponding sequence in antibodies derived from another species or belonging to another antibody class or subclass. For use in humans, the variable region or selected CDRs from a rodent antibody often are grafted into a human antibody, replacing the naturally-occurring variable regions or CDRs of the human antibody.

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

[0244] In one aspect, the CDRs of the light and heavy chain variable regions of the antibodies provided herein are grafted to framework regions (FRs) from antibodies from the same, or a different, phylogenetic species. For example, the CDRs of the heavy and light chain variable regions V_{H1}, V_{H2}, V_{H3}, V_{H4}, V_{H5}, V_{H6}, V_{H7}, V_{H8}, V_{H9}, V_{H10}, V_{H11}, V_{H12} and/or V_{L1}, and V_{L2} can be grafted to consensus human FRs. To create consensus human FRs, FRs from several human heavy chain or light chain amino acid sequences may be aligned to identify a consensus amino acid sequence. In other embodiments, the FRs of a heavy chain or light chain disclosed herein are replaced with the FRs from a different heavy chain or light chain. In one aspect, rare amino acids in the FRs of the heavy and light chains

of GIPR antibodies are not replaced, while the rest of the FR amino acids are replaced. A "rare amino acid" is a specific amino acid that is in a position in which this particular amino acid is not usually found in an FR. Alternatively, the grafted variable regions from the one heavy or light chain may be used with a constant region that is different from the constant region of that particular heavy or light chain as disclosed herein. In other embodiments, the grafted variable regions are part of a single chain Fv antibody.

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

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

[0247] Fully human antibodies can be produced by immunizing transgenic animals (usually mice) that are capable of producing a repertoire of human antibodies in the absence of endogenous immunoglobulin production. Antigens for this purpose typically have six or more contiguous amino acids, and optionally are conjugated to a carrier, such as a hapten. *See, e.g., Jakobovits et al., 1993, Proc. Natl. Acad. Sci. USA 90:2551-2555; Jakobovits et al., 1993, Nature 362:255-258; and Bruggermann et al., 1993, Year in Immunol. 7:33.* In one example of such a method, transgenic animals are produced by incapacitating the endogenous mouse immunoglobulin loci encoding the mouse heavy and light immunoglobulin chains therein, and inserting into the mouse genome large fragments of human genome DNA containing loci that encode human heavy and light chain proteins. Partially modified animals, which have less than the full complement of human immunoglobulin loci, are then cross-bred to obtain an animal having all of the desired immune system modifications. When administered an immunogen, these transgenic animals produce antibodies that are immunospecific for the immunogen but have human rather than murine amino acid sequences, including the variable regions. For further details of such methods, *see, for example, WO96/33735 and WO94/02602.* Additional methods relating to transgenic mice for making human antibodies are described in United States Patent No. 5,545,807; No. 6,713,610; No. 6,673,986;

No. 6,162,963; No. 5,545,807; No. 6,300,129; No. 6,255,458; No. 5,877,397; No. 5,874,299 and No. 5,545,806; in PCT publications WO91/10741, WO90/04036, and in EP 546073B1 and EP 546073A1.

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

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

[0250] Fully human antibodies can also be derived from phage-display libraries (as disclosed in Hoogenboom *et al.*, 1991, *J. Mol. Biol.* 227:381; and Marks *et al.*, 1991, *J. Mol. Biol.* 222:581). Phage display techniques mimic immune selection through the display of antibody repertoires on the surface of filamentous bacteriophage, and subsequent selection of phage by their binding to an antigen of choice. One such technique is described in PCT Publication No. WO 99/10494 (hereby incorporated by reference).

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

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

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

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

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

[0256] 3) acidic: Asp, Glu;

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

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

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

[0260] Conservative amino acid substitutions may involve exchange of a member of one of these classes with another member of the same class. Conservative amino acid substitutions may encompass non-naturally occurring amino acid residues, which are typically

incorporated by chemical peptide synthesis rather than by synthesis in biological systems. These include peptidomimetics and other reversed or inverted forms of amino acid moieties.

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

[0262] In making such changes, according to certain embodiments, the hydropathic index of amino acids may be considered. The hydropathic profile of a protein is calculated by assigning each amino acid a numerical value ("hydropathy index") and then repetitively averaging these values along the peptide chain. Each amino acid has been assigned a

hydropathic index on the basis of its hydrophobicity and charge characteristics. They are: isoleucine (+4.5); valine (+4.2); leucine (+3.8); phenylalanine (+2.8); cysteine/cystine (+2.5); methionine (+1.9); alanine (+1.8); glycine (-0.4); threonine (-0.7); serine (-0.8); tryptophan (-0.9); tyrosine (-1.3); proline (-1.6); histidine (-3.2); glutamate (-3.5); glutamine (-3.5);
 5 aspartate (-3.5); asparagine (-3.5); lysine (-3.9); and arginine (-4.5).

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

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

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

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

Table 8: Conservative Amino Acid Substitutions

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

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

[0268] Additionally, one skilled in the art can review structure-function studies identifying residues in similar polypeptides that are important for activity or structure. In view of such a comparison, one can predict the importance of amino acid residues in a protein that correspond to amino acid residues important for activity or structure in similar proteins. One

skilled in the art may opt for chemically similar amino acid substitutions for such predicted important amino acid residues.

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

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

[0271] Additional methods of predicting secondary structure include "threading" (Jones, 1997, *Curr. Opin. Struct. Biol.* 7:377-387; Sippl *et al.*, 1996, *Structure* 4:15-19), "profile analysis" (Bowie *et al.*, 1991, *Science* 253:164-170; Gribskov *et al.*, 1990, *Meth. Enzym.* 183:146-159; Gribskov *et al.*, 1987, *Proc. Nat. Acad. Sci.* 84:4355-4358), and "evolutionary linkage" (See, Holm, 1999, *supra*; and Brenner, 1997, *supra*).

[0272] In some embodiments, amino acid substitutions are made that: (1) reduce susceptibility to proteolysis, (2) reduce susceptibility to oxidation, (3) alter binding affinity for forming protein complexes, (4) alter ligand or antigen binding affinities, and/or (4) confer or modify other physicochemical or functional properties on such polypeptides. For example, single or multiple amino acid substitutions (in certain embodiments, conservative amino acid substitutions) may be made in the naturally-occurring sequence. Substitutions can be made in that portion of the antibody that lies outside the domain(s) forming intermolecular contacts).

In such embodiments, conservative amino acid substitutions can be used that do not substantially change the structural characteristics of the parent sequence (e.g., one or more replacement amino acids that do not disrupt the secondary structure that characterizes the parent or native antigen binding protein). Examples of art-recognized polypeptide secondary and tertiary structures are described in *Proteins, Structures and Molecular Principles* (Creighton, Ed.), 1984, W. H. New York: Freeman and Company; *Introduction to Protein Structure* (Branden and Tooze, eds.), 1991, New York: Garland Publishing; and Thornton *et al.*, 1991, *Nature* 354:105, which are each incorporated herein by reference.

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

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

[0275] Mimetics (e.g., “peptide mimetics” or “peptidomimetics”) based upon the variable region domains and CDRs that are described herein are also provided. These analogs can be peptides, non-peptides or combinations of peptide and non-peptide regions. Fauchere, 1986, *Adv. Drug Res.* 15:29; Veber and Freidinger, 1985, *TINS* p. 392; and Evans *et al.*, 1987, *J. Med. Chem.* 30:1229, which are incorporated herein by reference for any purpose. Peptide

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

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

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

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

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

[0280] In general, labels fall into a variety of classes, depending on the assay in which they are to be detected: a) isotopic labels, which may be radioactive or heavy isotopes; b)

magnetic labels (*e.g.*, magnetic particles); c) redox active moieties; d) optical dyes; enzymatic groups (*e.g.* horseradish peroxidase, β -galactosidase, luciferase, alkaline phosphatase); e) biotinylated groups; and f) predetermined polypeptide epitopes recognized by a secondary reporter (*e.g.*, leucine zipper pair sequences, binding sites for secondary antibodies, metal binding domains, epitope tags, etc.). In some embodiments, the labeling group is coupled to the antigen binding protein *via* spacer arms of various lengths to reduce potential steric hindrance. Various methods for labeling proteins are known in the art.

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

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

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

[0284] Nucleic acids that encode for the antigen binding proteins described herein, or portions thereof, are also provided, including nucleic acids encoding one or both chains of an

antibody, or a fragment, derivative, mutein, or variant thereof, polynucleotides encoding heavy chain variable regions or only CDRs, polynucleotides sufficient for use as hybridization probes, PCR primers or sequencing primers for identifying, analyzing, mutating or amplifying a polynucleotide encoding a polypeptide, anti-sense nucleic acids for inhibiting expression of a polynucleotide, and complementary sequences of the foregoing. The nucleic acids can be any length. They can be, for example, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 75, 100, 125, 150, 175, 200, 250, 300, 350, 400, 450, 500, 750, 1,000, 1,500, 3,000, 5,000 or more nucleotides in length, and/or can comprise one or more additional sequences, for example, regulatory sequences, and/or be part of a larger nucleic acid, for example, a vector.

The nucleic acids can be single-stranded or double-stranded and can comprise RNA and/or DNA nucleotides, and artificial variants thereof (e.g., peptide nucleic acids). Any variable region provided herein may be attached to these constant regions to form complete heavy and light chain sequences. However, it should be understood that these constant regions sequences are provided as specific examples only. In some embodiments, the variable region sequences are joined to other constant region sequences that are known in the art.

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

[0286] An aspect further provides nucleic acids that hybridize to other nucleic acids under particular hybridization conditions. Methods for hybridizing nucleic acids are well-known in the art. *See, e.g.*, Current Protocols in Molecular Biology, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. As defined herein, a moderately stringent hybridization condition uses a prewashing solution containing 5x sodium chloride/sodium citrate (SSC), 0.5% SDS, 1.0 mM EDTA (pH 8.0), hybridization buffer of about 50% formamide, 6x SSC, and a hybridization temperature of 55°C (or other similar hybridization solutions, such as one containing about 50% formamide, with a hybridization temperature of 42°C), and washing conditions of 60°C, in 0.5x SSC, 0.1% SDS. A stringent hybridization condition hybridizes in 6x SSC

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

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

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

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

[0290] Another aspect provides nucleic acid molecules that are suitable for use as primers or hybridization probes for the detection of nucleic acid sequences. A nucleic acid molecule can comprise only a portion of a nucleic acid sequence encoding a full-length polypeptide, for

example, a fragment that can be used as a probe or primer or a fragment encoding an active portion of a polypeptide.

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

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

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

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

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

[0295] The antigen binding proteins provided herein may be prepared by any of a number of conventional techniques. For example, GIPR antigen binding proteins may be produced by recombinant expression systems, using any technique known in the art. *See, e.g.*, Monoclonal Antibodies, Hybridomas: A New Dimension in Biological Analyses, Kennet et al. (eds.) Plenum Press, New York (1980); and Antibodies: A Laboratory Manual, Harlow and Lane (eds.), Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1988).

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

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

[0297] Recombinant expression constructs typically comprise a nucleic acid molecule encoding a polypeptide comprising one or more of the following: one or more CDRs provided herein; a light chain constant region; a light chain variable region; a heavy chain constant region (*e.g.*, CH1, CH2 and/or CH3); and/or another scaffold portion of a GIPR

antigen binding protein. These nucleic acid sequences are inserted into an appropriate expression vector using standard ligation techniques. In one embodiment, the heavy or light chain constant region is appended to the C-terminus of the anti-GIPR specific heavy or light chain variable region and is ligated into an expression vector. The vector is typically selected to be functional in the particular host cell employed (*i.e.*, the vector is compatible with the host cell machinery, permitting amplification and/or expression of the gene can occur). In some embodiments, vectors are used that employ protein-fragment complementation assays using protein reporters, such as dihydrofolate reductase (*see*, for example, U.S. Pat. No. 6,270,964, which is hereby incorporated by reference). Suitable expression vectors can be purchased, for example, from Invitrogen Life Technologies or BD Biosciences (formerly "Clontech"). Other useful vectors for cloning and expressing the antibodies and fragments include those described in Bianchi and McGrew, 2003, *Biotech. Biotechnol. Bioeng.* 84:439-44, which is hereby incorporated by reference. Additional suitable expression vectors are discussed, for example, in *Methods Enzymol.*, vol. 185 (D. V. Goeddel, ed.), 1990, New York: Academic Press.

[0298] Typically, expression vectors used in any of the host cells will contain sequences for plasmid maintenance and for cloning and expression of exogenous nucleotide sequences. Such sequences, collectively referred to as "flanking sequences" in certain embodiments will typically include one or more of the following nucleotide sequences: a promoter, one or more enhancer sequences, an origin of replication, a transcriptional termination sequence, a complete intron sequence containing a donor and acceptor splice site, a sequence encoding a leader sequence for polypeptide secretion, a ribosome binding site, a polyadenylation sequence, a polylinker region for inserting the nucleic acid encoding the polypeptide to be expressed, and a selectable marker element. Each of these sequences is discussed below.

[0299] Optionally, the vector may contain a "tag"-encoding sequence, *i.e.*, an oligonucleotide molecule located at the 5' or 3' end of the GIPR antigen binding protein coding sequence; the oligonucleotide sequence encodes polyHis (such as hexaHis), or another "tag" such as FLAG[®], HA (hemagglutinin influenza virus), or myc, for which commercially available antibodies exist. This tag is typically fused to the polypeptide upon expression of the polypeptide, and can serve as a means for affinity purification or detection of the GIPR antigen binding protein from the host cell. Affinity purification can be accomplished, for example, by column chromatography using antibodies against the tag as an affinity matrix. Optionally, the tag can subsequently be removed from the purified GIPR antigen binding protein by various means such as using certain peptidases for cleavage.

[0300] Flanking sequences may be homologous (*i.e.*, from the same species and/or strain as the host cell), heterologous (*i.e.*, from a species other than the host cell species or strain), hybrid (*i.e.*, a combination of flanking sequences from more than one source), synthetic or native. As such, the source of a flanking sequence may be any prokaryotic or eukaryotic
5 organism, any vertebrate or invertebrate organism, or any plant, provided that the flanking sequence is functional in, and can be activated by, the host cell machinery.

[0301] Flanking sequences useful in the vectors may be obtained by any of several methods well known in the art. Typically, flanking sequences useful herein will have been previously identified by mapping and/or by restriction endonuclease digestion and can thus be isolated
10 from the proper tissue source using the appropriate restriction endonucleases. In some cases, the full nucleotide sequence of a flanking sequence may be known. Here, the flanking sequence may be synthesized using the methods described herein for nucleic acid synthesis or cloning.

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

[0303] An origin of replication is typically a part of those prokaryotic expression vectors
25 purchased commercially, and the origin aids in the amplification of the vector in a host cell. If the vector of choice does not contain an origin of replication site, one may be chemically synthesized based on a known sequence, and ligated into the vector. For example, the origin of replication from the plasmid pBR322 (New England Biolabs, Beverly, MA) is suitable for most gram-negative bacteria, and various viral origins (*e.g.*, SV40, polyoma, adenovirus,
30 vesicular stomatitis virus (VSV), or papillomaviruses such as HPV or BPV) are useful for cloning vectors in mammalian cells. Generally, the origin of replication component is not needed for mammalian expression vectors (for example, the SV40 origin is often used only because it also contains the virus early promoter).

[0304] A transcription termination sequence is typically located 3' to the end of a polypeptide coding region and serves to terminate transcription. Usually, a transcription termination sequence in prokaryotic cells is a G-C rich fragment followed by a poly-T sequence. While the sequence is easily cloned from a library or even purchased commercially as part of a vector, it can also be readily synthesized using methods for nucleic acid synthesis such as those described herein.

[0305] A selectable marker gene encodes a protein necessary for the survival and growth of a host cell grown in a selective culture medium. Typical selection marker genes encode proteins that (a) confer resistance to antibiotics or other toxins, *e.g.*, ampicillin, tetracycline, or kanamycin for prokaryotic host cells; (b) complement auxotrophic deficiencies of the cell; or (c) supply critical nutrients not available from complex or defined media. Specific selectable markers are the kanamycin resistance gene, the ampicillin resistance gene, and the tetracycline resistance gene. Advantageously, a neomycin resistance gene may also be used for selection in both prokaryotic and eukaryotic host cells.

[0306] Other selectable genes may be used to amplify the gene that will be expressed. Amplification is the process wherein genes that are required for production of a protein critical for growth or cell survival are reiterated in tandem within the chromosomes of successive generations of recombinant cells. Examples of suitable selectable markers for mammalian cells include dihydrofolate reductase (DHFR) and promoterless thymidine kinase genes. Mammalian cell transformants are placed under selection pressure wherein only the transformants are uniquely adapted to survive by virtue of the selectable gene present in the vector. Selection pressure is imposed by culturing the transformed cells under conditions in which the concentration of selection agent in the medium is successively increased, thereby leading to the amplification of both the selectable gene and the DNA that encodes another gene, such as an antigen binding protein that binds GIPR polypeptide. As a result, increased quantities of a polypeptide such as an antigen binding protein are synthesized from the amplified DNA.

[0307] A ribosome-binding site is usually necessary for translation initiation of mRNA and is characterized by a Shine-Dalgarno sequence (prokaryotes) or a Kozak sequence (eukaryotes). The element is typically located 3' to the promoter and 5' to the coding sequence of the polypeptide to be expressed.

[0308] In some cases, such as where glycosylation is desired in a eukaryotic host cell expression system, one may manipulate the various pre- or pro-sequences to improve glycosylation or yield. For example, one may alter the peptidase cleavage site of a particular

signal peptide, or add prosequences, which also may affect glycosylation. The final protein product may have, in the -1 position (relative to the first amino acid of the mature protein), one or more additional amino acids incident to expression, which may not have been totally removed. For example, the final protein product may have one or two amino acid residues found in the peptidase cleavage site, attached to the amino-terminus. Alternatively, use of some enzyme cleavage sites may result in a slightly truncated form of the desired polypeptide, if the enzyme cuts at such area within the mature polypeptide.

[0309] Expression and cloning will typically contain a promoter that is recognized by the host organism and operably linked to the molecule encoding the GIPR antigen binding protein. Promoters are untranscribed sequences located upstream (*i.e.*, 5') to the start codon of a structural gene (generally within about 100 to 1000 bp) that control transcription of the structural gene. Promoters are conventionally grouped into one of two classes: inducible promoters and constitutive promoters. Inducible promoters initiate increased levels of transcription from DNA under their control in response to some change in culture conditions, such as the presence or absence of a nutrient or a change in temperature. Constitutive promoters, on the other hand, uniformly transcribe a gene to which they are operably linked, that is, with little or no control over gene expression. A large number of promoters, recognized by a variety of potential host cells, are well known. A suitable promoter is operably linked to the DNA encoding heavy chain or light chain comprising a GIPR antigen binding protein by removing the promoter from the source DNA by restriction enzyme digestion and inserting the desired promoter sequence into the vector.

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

[0311] An enhancer sequence may be inserted into the vector to increase transcription of DNA encoding light chain or heavy chain comprising a GIPR antigen binding protein by higher eukaryotes. Enhancers are cis-acting elements of DNA, usually about 10-300 bp in length, that act on the promoter to increase transcription. Enhancers are relatively orientation and position independent, having been found at positions both 5' and 3' to the transcription

unit. Several enhancer sequences available from mammalian genes are known (*e.g.*, globin, elastase, albumin, alpha-feto-protein and insulin). Typically, however, an enhancer from a virus is used. The SV40 enhancer, the cytomegalovirus early promoter enhancer, the polyoma enhancer, and adenovirus enhancers known in the art are exemplary enhancing elements for the activation of eukaryotic promoters. While an enhancer may be positioned in the vector either 5' or 3' to a coding sequence, it is typically located at a site 5' from the promoter. A sequence encoding an appropriate native or heterologous signal sequence (leader sequence or signal peptide) can be incorporated into an expression vector, to promote extracellular secretion of the antibody. The choice of signal peptide or leader depends on the type of host cells in which the antibody is to be produced, and a heterologous signal sequence can replace the native signal sequence. Examples of signal peptides that are functional in mammalian host cells include the following: the signal sequence for interleukin-7 (IL-7) described in US Patent No. 4,965,195; the signal sequence for interleukin-2 receptor described in Cosman *et al.*, 1984, *Nature* 312:768; the interleukin-4 receptor signal peptide described in EP Patent No. 0367 566; the type I interleukin-1 receptor signal peptide described in U.S. Patent No. 4,968,607; the type II interleukin-1 receptor signal peptide described in EP Patent No. 0 460 846.

[0312] In one embodiment the leader sequence comprises SEQ ID NO: 3157 (MDMRVPAQLL GLLLLWLRGA RC) which is encoded by SEQ ID NO: 3158 (atggacatga

gagtgcctgc acagctgctg ggctgctgc tgcctgtggct gagaggcgcc agatgc).

In another embodiment the leader sequence comprises SEQ ID NO: 3159 (MAWALLLLTL LTQGTGSWA) which is encoded by SEQ ID NO: 3160 (atggcctggg ctctgctgct cctcaccctc ctactcagg gcacagggtc ctgggcc).

[0313] The expression vectors that are provided may be constructed from a starting vector such as a commercially available vector. Such vectors may or may not contain all of the desired flanking sequences. Where one or more of the flanking sequences described herein are not already present in the vector, they may be individually obtained and ligated into the vector. Methods used for obtaining each of the flanking sequences are well known to one skilled in the art.

[0314] After the vector has been constructed and a nucleic acid molecule encoding light chain, a heavy chain, or a light chain and a heavy chain comprising a GIPR antigen binding sequence has been inserted into the proper site of the vector, the completed vector may be inserted into a suitable host cell for amplification and/or polypeptide expression. The transformation of an expression vector for an antigen-binding protein into a selected host cell

may be accomplished by well-known methods including transfection, infection, calcium phosphate co-precipitation, electroporation, microinjection, lipofection, DEAE-dextran mediated transfection, or other known techniques. The method selected will in part be a function of the type of host cell to be used. These methods and other suitable methods are well known to the skilled artisan, and are set forth, for example, in Sambrook *et al.*, 2001, *supra*.

[0315] A host cell, when cultured under appropriate conditions, synthesizes an antigen binding protein that can subsequently be collected from the culture medium (if the host cell secretes it into the medium) or directly from the host cell producing it (if it is not secreted).

The selection of an appropriate host cell will depend upon various factors, such as desired expression levels, polypeptide modifications that are desirable or necessary for activity (such as glycosylation or phosphorylation) and ease of folding into a biologically active molecule.

[0316] Mammalian cell lines available as hosts for expression are well known in the art and include, but are not limited to, immortalized cell lines available from the American Type Culture Collection (ATCC), including but not limited to Chinese hamster ovary (CHO) cells, HeLa cells, baby hamster kidney (BHK) cells, monkey kidney cells (COS), human hepatocellular carcinoma cells (*e.g.*, Hep G2), and a number of other cell lines. In certain embodiments, cell lines may be selected through determining which cell lines have high expression levels and constitutively produce antigen binding proteins with GIPR binding properties. In another embodiment, a cell line from the B cell lineage that does not make its own antibody but has a capacity to make and secrete a heterologous antibody can be selected.

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

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

[0319] Pharmaceutical compositions that comprise a GIPR antigen binding protein are also provided and can be utilized in any of the preventive and therapeutic methods disclosed herein. In an embodiment, a therapeutically effective amount of one or a plurality of the antigen binding proteins and a pharmaceutically acceptable diluent, carrier, solubilizer, emulsifier, preservative, and/or adjuvant are also provided. Acceptable formulation materials are nontoxic to recipients at the dosages and concentrations employed.

[0320] In certain embodiments, the pharmaceutical composition may contain formulation materials for modifying, maintaining or preserving, for example, the pH, osmolarity,

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

[0321] In certain embodiments, the optimal pharmaceutical composition will be determined by one skilled in the art depending upon, for example, the intended route of administration, delivery format and desired dosage. *See*, for example, REMINGTON'S PHARMACEUTICAL SCIENCES, *supra*. In certain embodiments, such compositions may influence the physical state, stability, rate of *in vivo* release and rate of *in vivo* clearance of the antigen binding proteins disclosed. In certain embodiments, the primary vehicle or carrier in a pharmaceutical composition may be either aqueous or non-aqueous in nature. For example, a suitable vehicle or carrier may be water for injection or physiological saline solution. In certain embodiments, GIPR antigen binding protein compositions may be prepared for storage by mixing the selected composition having the desired degree of purity with optional formulation agents (REMINGTON'S PHARMACEUTICAL SCIENCES,

supra) in the form of a lyophilized cake or an aqueous solution. Further, in certain embodiments, the GIPR antigen binding protein may be formulated as a lyophilizate using appropriate excipients such as sucrose.

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

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

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

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

[0325] Certain pharmaceutical compositions are formulated for inhalation. In some
25 embodiments, GIPR antigen binding proteins are formulated as a dry, inhalable powder. In specific embodiments, GIPR antigen binding protein inhalation solutions may also be formulated with a propellant for aerosol delivery. In certain embodiments, solutions may be nebulized. Pulmonary administration and formulation methods therefore are further described in International Patent Application No. PCT/US94/001875, which is incorporated by
30 reference and describes pulmonary delivery of chemically modified proteins. Some formulations can be administered orally. GIPR antigen binding proteins that are administered in this fashion can be formulated with or without carriers customarily used in the compounding of solid dosage forms such as tablets and capsules. In certain embodiments, a capsule may be designed to release the active portion of the formulation at the point in the

gastrointestinal tract when bioavailability is maximized and pre-systemic degradation is minimized. Additional agents can be included to facilitate absorption of the GIPR antigen binding protein. Diluents, flavorings, low melting point waxes, vegetable oils, lubricants, suspending agents, tablet disintegrating agents, and binders may also be employed.

5 [0326] Some pharmaceutical compositions comprise an effective quantity of one or a plurality of GIPR antigen binding proteins in a mixture with non-toxic excipients that are suitable for the manufacture of tablets. By dissolving the tablets in sterile water, or another appropriate vehicle, solutions may be prepared in unit-dose form. Suitable excipients include, but are not limited to, inert diluents, such as calcium carbonate, sodium carbonate or
10 bicarbonate, lactose, or calcium phosphate; or binding agents, such as starch, gelatin, or acacia; or lubricating agents such as magnesium stearate, stearic acid, or talc.

[0327] Additional pharmaceutical compositions will be evident to those skilled in the art, including formulations involving GIPR binding proteins in sustained- or controlled-delivery formulations. Techniques for formulating a variety of other sustained- or controlled-delivery
15 means, such as liposome carriers, bio-erodible microparticles or porous beads and depot injections, are also known to those skilled in the art. *See*, for example, International Patent Application No. PCT/US93/00829, which is incorporated by reference and describes controlled release of porous polymeric microparticles for delivery of pharmaceutical compositions. Sustained-release preparations may include semipermeable polymer matrices
20 in the form of shaped articles, *e.g.*, films, or microcapsules. Sustained release matrices may include polyesters, hydrogels, polylactides (as disclosed in U.S. Patent No. 3,773,919 and European Patent Application Publication No. EP 058481, each of which is incorporated by reference), copolymers of L-glutamic acid and gamma ethyl-L-glutamate (Sidman *et al.*, 1983, *Biopolymers* 2:547-556), poly (2-hydroxyethyl-inethacrylate) (Langer *et al.*, 1981, *J. Biomed. Mater. Res.* 15:167-277 and Langer, 1982, *Chem. Tech.* 12:98-105), ethylene vinyl
25 acetate (Langer *et al.*, 1981, *supra*) or poly-D(-)-3-hydroxybutyric acid (European Patent Application Publication No. EP 133,988). Sustained release compositions may also include liposomes that can be prepared by any of several methods known in the art. *See, e.g.*, Epstein *et al.*, 1985, *Proc. Natl. Acad. Sci. U.S.A.* 82:3688-3692; European Patent
30 Application Publication Nos. EP 036,676; EP 088,046 and EP 143,949, incorporated by reference.

[0328] Pharmaceutical compositions used for *in vivo* administration are typically provided as sterile preparations. Sterilization can be accomplished by filtration through sterile filtration membranes. When the composition is lyophilized, sterilization using this method may be

conducted either prior to or following lyophilization and reconstitution. Compositions for parenteral administration can be stored in lyophilized form or in a solution. Parenteral compositions generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection
5 needle.

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

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

[0331] Dosing frequency will depend upon the pharmacokinetic parameters of the particular GIPR antigen binding protein in the formulation used. Typically, a clinician administers the composition until a dosage is reached that achieves the desired effect. The composition may

therefore be administered as a single dose, or as two or more doses (which may or may not contain the same amount of the desired molecule) over time, or as a continuous infusion *via* an implantation device or catheter. Appropriate dosages may be ascertained through use of appropriate dose-response data. In certain embodiments, the antigen binding proteins can be administered to patients throughout an extended time period. In certain embodiments, the antigen binding protein is dosed every two weeks, every month, every two months, every three months, every four months, every five months, or every six months.

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

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

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

[0335] A physician will be able to select an appropriate treatment indication and target lipid levels depending on the individual profile of a particular patient. One well-accepted standard for guiding treatment of hyperlipidemia is the Third Report of the National Cholesterol Education Program (NCEP) Expert Panel on Detection, Evaluation, and Treatment of the High Blood Cholesterol in Adults (Adult Treatment Panel III) Final Report, National Institutes of Health, NIH Publication No. 02-5215 (2002), the printed publication of which is hereby incorporated by reference in its entirety.

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

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

[0338] In one aspect the present invention is directed to a method of treating a subject with a metabolic disorder, the method comprising administering to the subject a composition comprising a GIPR antagonist that inhibits GIPR function and a GLP-1 receptor agonist, wherein the GLP-1 receptor agonist is conjugated to the GIPR antagonist. In one embodiment the GIPR antagonist inhibits GIP binding to GIPR.

[0339] In one aspect the present invention is directed to a method of treating a subject with a metabolic disorder, the method comprising administering to the subject a composition comprising an antibody or functional fragment thereof that specifically binds to human GIPR, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s); and a GLP-1 receptor agonist, wherein the GLP-1 receptor agonist is conjugated to the antibody or functional fragment thereof through the side-chain of the cysteine residue or non-canonical amino acid residue substituted at the one or more conjugation site(s).

[0340] In one aspect the present invention is directed to a method of treating a subject with a metabolic disorder, the method comprising administering to the subject a therapeutically effective amount of a GLP-1 receptor agonist and a therapeutically effective amount of a GIPR antagonist that specifically binds to a protein having an amino acid sequence having at least 90% amino acid sequence identity to an amino acid sequence of a GIPR, wherein the GIPR antagonist is conjugated to the GLP-1 receptor agonist. Such conjugated molecules can be referred to as “anti-GIPR/GLP-1R bispecific conjugate”, “anti-GIPR/GLP-1R peptide conjugate”, “anti-GIPR/GLP-1R conjugate”, or even “bispecific conjugate”.

[0341] In one aspect the present invention is directed to a method of promoting GIPR and GLP-1R internalization into the cell upon which they are co-expressed by administering a GIPR antagonist conjugated to a GLP-1 receptor agonist to the cell. In one embodiment, the GIPR and GLP-1R are co-localized while being internalized.

[0342] In one aspect the present invention is directed to a method of stimulating calcium flux in a cell by administering a GIPR antagonist conjugated to a GLP-1 receptor agonist to the cell.

5 [0343] In one aspect the present invention is directed to a method of promoting beta-arrestin recruitment in a cell by administering a GIPR antagonist conjugated to a GLP-1 receptor agonist to the cell.

[0344] In one aspect the present invention is directed to a method of stimulating insulin secretion from a cell by administering a GIPR antagonist conjugated to a GLP-1 receptor agonist to the cell. In one embodiment the cell is a human pancreatic microislet.

10 [0345] A “GLP-1 receptor agonist” refers to compounds having GLP-1 receptor activity. Such exemplary compounds include exendins, exendin analogs, exendin agonists, GLP-1(7-37), GLP-1(7-37) analogs, GLP-1(7-37) agonists, and the like. The GLP-1 receptor agonist compounds may optionally be amidated. The terms “GLP-1 receptor agonist” and “GLP-1 receptor agonist compound” have the same meaning.

15 [0346] The term “exendin” includes naturally occurring (or synthetic versions of naturally occurring) exendin peptides that are found in the salivary secretions of the Gila monster. Exendins of particular interest include exendin-3 and exendin-4. The exendins, exendin analogs, and exendin agonists for use in the methods described herein may optionally be amidated, and may also be in an acid form, pharmaceutically acceptable salt form, or any
20 other physiologically active form of the molecule.

[0347] In one embodiment, the GLP-1 receptor agonist is GLP-1(7-37) or a GLP-1(7-37) analog.

[0348] In one embodiment, the GLP-1 receptor agonist is selected from the group consisting of exenatide, liraglutide, lixisenatide, albiglutide, dulaglutide, semaglutide, and taspoglutide.

25 [0349] In one aspect the present invention is directed to a method of treatment comprising administering to a subject a therapeutically effective amount of at least one GLP-1 receptor agonist in combination with administration of at least one GIPR antagonist, wherein the GIPR antagonist is conjugated to the GLP-1 receptor agonist, which upon administration to a subject with symptoms of a metabolic disorder provides sustained beneficial effects.

30 [0350] In one embodiment, administration of at least one GLP-1 receptor agonist in combination with administration of at least one GIPR antagonist provides sustained beneficial effects of at least one symptom of a metabolic disorder.

[0351] In one embodiment, the therapeutically effective amounts of the GLP-1 receptor agonist and the GIPR antagonist are combined prior to administration to the subject.

[0352] In one embodiment, the therapeutically effective amounts of the GLP-1 receptor agonist and the GIPR antagonist are administered to the subject sequentially.

[0353] In one embodiment, the therapeutically effective amounts of a GLP-1 receptor agonist and a GIPR antagonist are synergistically effective amounts.

5 [0354] Exendin-4 (HGEFTFTSDLSKQMEEEEAVRLFIEWLKNGGPSSGAPPPS-NH₂ (SEQ ID NO: 3163)) is a peptide found in the saliva of the Gila monster, *Heloderma suspectum*; and exendin-3 (HSDGTFTSDLSKQMEEEEAVRLFIEWLKNGGPSSGAPPPS-NH₂ (SEQ ID NO: 3164)) is a peptide found in the saliva of the beaded lizard, *Heloderma horridum*.

10 Exendins have some amino acid sequence similarity to some members of the glucagon-like peptide (GLP) family. For example, exendin-4 has about 53% sequence identity with glucagon-like peptide-1(GLP-1)(7-37) (HAEGTFTSDVSSYLEGQAAKEFIAWLVKGRG (SEQ ID NO: 3184)). However, exendin-4 is transcribed from a distinct gene, not the Gila monster homolog of the mammalian proglucagon gene from which GLP-1 is expressed. Additionally, exendin-4 is not an analog of GLP-1(7-37) because the structure of synthetic
15 exendin-4 peptide was not created by sequential modification of the structure of GLP-1. Nielsen et al., *Current Opinion in Investigational Drugs*, 4(4):401-405 (2003).

[0355] Synthetic exendin-4, also known as exenatide, is commercially available as BYETTA® (Amylin Pharmaceuticals, Inc. and Eli Lilly and Company). A once weekly formulation of exenatide is described in WO 2005/102293, the disclosure of which is
20 incorporated by reference herein.

[0356] “Exendin analog” refers to peptides which elicit a biological activity of an exendin reference peptide, preferably having a potency equal to or better than the exendin reference peptide (e.g., exendin-4), or within five orders of magnitude (plus or minus) of potency compared to the exendin reference peptide, when evaluated by art-known measures such as
25 receptor binding and/or competition studies as described, e.g., by Hargrove et al., *Regulatory Peptides*, 141:113-119 (2007), the disclosure of which is incorporated by reference herein. Preferably, the exendin analogs will bind in such assays with an affinity of less than 1 μM, and more preferably with an affinity of less than 3 nM, less than 1 nM, or less than 0.1 nM. The term “exendin analog” may also be referred to as “exendin agonist”. In a preferred
30 embodiment, the exendin analog is an exendin-4 analog.

[0357] Exendin analogs also include the peptides described herein which have been chemically derivatized or altered, for example, peptides with non-natural amino acid residues (e.g., taurine, β-amino acid residues, γ-amino acid residues, and D-amino acid residues), C-terminal functional group modifications, such as amides, esters, and C-terminal ketone

modifications and N-terminal functional group modifications, such as acylated amines, Schiff bases, or cyclization, as found, for example, in the amino acid pyroglutamic acid. Exendin analogs may also contain other chemical moieties, such as peptide mimetics.

[0358] Exemplary exendins and exendin analogs 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); 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); octylGly¹⁴,Gln²⁸-exendin-4 (SEQ ID NO: 3178); Leu¹⁴,Gln²⁸,octylGly³⁴-exendin-4 (SEQ ID NO: 3179); 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); Val¹¹,Ile¹³,Leu¹⁴,Ala¹⁶,Lys²¹,Phe²⁵-exendin-4 (SEQ ID NO: 3182); exendin-4-Lys⁴⁰ (SEQ ID NO: 3183); lixisenatide (Sanofi-Aventis/Zealand Pharma); CJC-1134 (ConjuChem, Inc.); [N^ε-(17-carboxyheptadecanoic acid)Lys²⁰]exendin-4-NH₂ (SEQ ID NO: 3208); [N^ε-(17-carboxyhepta-decanoyl)Lys³²]exendin-4-NH₂ (SEQ ID NO: 3209); [desamino-His¹,N^ε-(17-carboxyheptadecanoyl)Lys²⁰]exendin-4-NH₂ (SEQ ID NO: 3210); [Arg^{12,27},NLe¹⁴,N^ε-(17-carboxy-heptadecanoyl)Lys³²]exendin-4-NH₂ (SEQ ID NO: 3211); [N^ε-(19-carboxy-nonadecanoylamino)Lys²⁰]-exendin-4-NH₂ (SEQ ID NO: 3212); [N^ε-(15-carboxypentadecanoylamino)Lys²⁰]-exendin-4-NH₂ (SEQ ID NO: 3213); [N^ε-(13-carboxytridecanoylamino)Lys²⁰]exendin-4-NH₂ (SEQ ID NO: 3214); [N^ε-(11-carboxyundecanoyl-amino)Lys²⁰]exendin-4-NH₂ (SEQ ID NO: 3215); exendin-4-Lys⁴⁰(e-MPA)-NH₂ (SEQ ID NO: 3216); exendin-4-Lys⁴⁰(e-AEEA-AEEA-MPA)-NH₂ (SEQ ID NO: 3217); exendin-4-Lys⁴⁰(e-AEEA-MPA)-NH₂ (SEQ ID NO: 3218); exendin-4-Lys⁴⁰(e-MPA)-albumin (SEQ ID NO: 3219); exendin-4-Lys⁴⁰(e-AEEA-AEEA-MPA)-albumin (SEQ ID NO: 3220); exendin-4-Lys⁴⁰(e-AEEA-MPA)-albumin (SEQ ID NO: 3221); and the like. AEEA refers to [2-(2-amino)ethoxy]acetic acid. EDA refers to ethylenediamine. MPA refers to maleimidopropionic acid. The exendins and exendin analogs may optionally be amidated.

[0359] In one embodiment, the GLP-1 receptor agonist compound is an exendin-4 analog that has at least 80% sequence identity to exendin-4 (SEQ ID NO: 3163); at least 85% sequence identity to exendin-4 (SEQ ID NO: 3163); at least 90% sequence identity to

exendin-4 (SEQ ID NO: 3163); or at least 95% sequence identity to exendin-4 (SEQ ID NO: 3163).

[0360] Other exendins and exendin analogs useful in the methods described herein include those described in WO 98/05351; WO 99/07404; WO 99/25727; WO 99/25728; WO 99/40788; WO 00/41546; WO 00/41548; WO 00/73331; WO 01/51078; WO 03/099314; U.S. Pat. No. 6,956,026; U.S. Pat. No. 6,506,724; U.S. Pat. No. 6,703,359; U.S. Pat. No. 6,858,576; U.S. Pat. No. 6,872,700; U.S. Pat. No. 6,902,744; U.S. Pat. No. 7,157,555; U.S. Pat. No. 7,223,725; U.S. Pat. No. 7,220,721; US Publication No. 2003/0036504; and US Publication No. 2006/0094652, the disclosures of which are incorporated by reference herein in their entirety.

[0361] "GLP-1(7-37) analogs" refers to peptides which elicit a biological activity similar to that of GLP-1(7-37), when evaluated by art-known measures such as receptor binding assays or in vivo blood glucose assays as described, e.g., by Hargrove et al., *Regulatory Peptides*, 141:113-119 (2007), the disclosure of which is incorporated by reference herein. In one embodiment, the term "GLP-1(7-37) analog" refers to a peptide that has an amino acid sequence with 1, 2, 3, 4, 5, 6, 7 or 8 amino acid substitutions, insertions, deletions, or a combination of two or more thereof, when compared to the amino acid sequence of GLP-1(7-37). In one embodiment, the GLP-1(7-37) analog is GLP-1(7-36)-NH₂. GLP-1(7-37) analogs include the amidated forms, the acid form, the pharmaceutically acceptable salt form, and any other physiologically active form of the molecule. In some embodiments a simple nomenclature is used to describe the GLP-1 receptor agonist, e.g., [Aib⁸] GLP-1(7-37) designates an analogue of GLP-1(7-37) wherein the naturally occurring Ala in position 8 has been substituted with Aib.

[0362] Exemplary GLP-1(7-37) and GLP-1(7-37) analogs include GLP-1(7-37) (SEQ ID NO: 3184); GLP-1(7-36)-NH₂ (SEQ ID NO: 3185); liraglutide (VICTOZA® from Novo Nordisk); albiglutide (SYNCRIA® from GlaxoSmithKline); taspoglutide (Hoffman La-Roche); dulaglutide (also known LY2189265; Eli Lilly and Company); LY2428757 (Eli Lilly and Company); desamino-His⁷,Arg²⁶,Lys³⁴(N^ε-(γ-Glu(N-α-hexadecanoyl)))-GLP-1(7-37) (core peptide disclosed as SEQ ID NO: 3222); desamino-His⁷,Arg²⁶,Lys³⁴(N^ε-octanoyl)-GLP-1(7-37) (SEQ ID NO: 3223); Arg^{26,34},Lys³⁸(N^ε-(ω-carboxypentadecanoyl))-GLP-1(7-38) (SEQ ID NO: 3224); Arg^{26,34},Lys³⁶(N^ε-(γ-Glu(N-α-hexadecanoyl)))-GLP-1(7-36) (core peptide disclosed as SEQ ID NO: 3225); Aib^{8,35},Arg^{26,34},Phe³¹-GLP-1(7-36)) (SEQ ID NO: 3186); HXaa₈EGTFTSDVSSYLEXaa₂₂Xaa₂₃AAKEFIXaa₃₀WLXaa₃₃Xaa₃₄G Xaa₃₆Xaa₃₇; wherein Xaa₃ is A, V, or G; Xaa₂₂ is G, K, or E; Xaa₂₃ is Q or K; Xaa₃₀ is A or E; Xaa₃₃ is V

or K; Xaa₃₄ is K, N, or R; Xaa₃₆ is R or G; and Xaa₃₇ is G, H, P, or absent (SEQ ID NO: 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); 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); Val⁸,Glu²²,Gly³⁶Pro³⁷-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); 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). Each of the GLP-1(7-37) and GLP-1(7-37) analogs may optionally be amidated.

[0363] The GLP-1 receptor agonists of the inventive composition of matter can also be chemically derivatized at one or more amino acid residues by known organic chemistry techniques. “Chemical derivative” or “chemically derivatized” refers to a subject peptide having one or more residues chemically derivatized by reaction of a functional side group. Such derivatized molecules include, for example, those molecules in which free amino groups have been derivatized to form amine hydrochlorides, p-toluene sulfonyl groups, carbobenzoxy groups, t-butyloxycarbonyl groups, chloroacetyl groups or formyl groups. Free carboxyl groups may be derivatized to form salts, methyl and ethyl esters or other types of esters or hydrazides. Free hydroxyl groups may be derivatized to form O-acyl or O-alkyl derivatives. The imidazole nitrogen of histidine may be derivatized to form N-im-benzylhistidine. Also included as chemical derivatives are those peptides which contain one or more naturally occurring amino acid derivatives of the twenty canonical amino acids, whether in L- or D- form. For example, 4-hydroxyproline may be substituted for proline; 5-hydroxylysine may be substituted for lysine; 3-methylhistidine may be substituted for histidine; homoserine may be substituted for serine; and ornithine may be substituted for lysine.

[0364] Useful derivatizations include, in some embodiments, those in which the amino terminal of the peptide is chemically blocked so that conjugation with the vehicle will be prevented from taking place at an N-terminal free amino group. There may also be other beneficial effects of such a modification, for example a reduction in the toxin peptide analog’s susceptibility to enzymatic proteolysis. The N-terminus can be acylated or modified to a substituted amine, or derivatized with another functional group, such as an aromatic

moiety (e.g., an indole acid, benzyl (Bzl or Bn), dibenzyl (DiBzl or Bn₂), or benzyloxycarbonyl (Cbz or Z)), *N,N*-dimethylglycine or creatine. For example, in some embodiments, an acyl moiety, such as, but not limited to, a formyl, acetyl (Ac), propanoyl, butanyl, heptanyl, hexanoyl, octanoyl, or nonanoyl, can be covalently linked to the N-terminal end of the peptide, which can prevent undesired side reactions during conjugation of the vehicle to the peptide. Other exemplary N-terminal derivative groups include -NRR¹ (other than -NH₂), -NRC(O)R¹, -NRC(O)OR¹, -NRS(O)₂R¹, -NHC(O)NHR¹, succinimide, or benzyloxycarbonyl-NH- (Cbz-NH-), wherein R and R¹ are each independently hydrogen or lower alkyl and wherein the phenyl ring may be substituted with 1 to 3 substituents selected from C₁-C₄ alkyl, C₁-C₄ alkoxy, chloro, and bromo.

[0365] In some embodiments, one or more peptidyl [-C(O)NR-] linkages (bonds) between amino acid residues can be replaced by a non-peptidyl linkage. Exemplary non-peptidyl linkages are -CH₂-carbamate [-CH₂-OC(O)NR-], phosphonate, -CH₂-sulfonamide [-CH₂-S(O)₂NR-], urea [-NHC(O)NH-], -CH₂-secondary amine, and alkylated peptide [-C(O)NR⁶- wherein R⁶ is lower alkyl].

[0366] In some embodiments, one or more individual amino acid residues can be derivatized. Various derivatizing agents are known to react specifically with selected sidechains or terminal residues, as described in detail below by way of example.

[0367] Lysiny residues and amino terminal residues may be reacted with succinic or other carboxylic acid anhydrides, which reverse the charge of the lysiny residues. Other suitable reagents for derivatizing alpha-amino-containing residues include imidoesters such as methyl picolinimidate; pyridoxal phosphate; pyridoxal; chloroborohydride; trinitrobenzenesulfonic acid; O-methylisourea; 2,4 pentanedione; and transaminase-catalyzed reaction with glyoxylate.

[0368] Arginy residues may be modified by reaction with any one or combination of several conventional reagents, including phenylglyoxal, 2,3-butanedione, 1,2-cyclohexanedione, and ninhydrin. Derivatization of arginy residues requires that the reaction be performed in alkaline conditions because of the high pK_a of the guanidine functional group. Furthermore, these reagents may react with the groups of lysine as well as the arginine epsilon-amino group.

[0369] Specific modification of tyrosyl residues has been studied extensively, with particular interest in introducing spectral labels into tyrosyl residues by reaction with aromatic diazonium compounds or tetranitromethane. Most commonly, N-acetylimidazole and

tetranitromethane are used to form O-acetyl tyrosyl species and 3-nitro derivatives, respectively.

[0370] Carboxyl sidechain groups (aspartyl or glutamyl) may be selectively modified by reaction with carbodiimides ($R'-N=C=N-R'$) such as 1-cyclohexyl-3-(2-morpholinyl-(4-ethyl) carbodiimide or 1-ethyl-3-(4-azonia-4,4-dimethylpentyl) carbodiimide. Furthermore, aspartyl and glutamyl residues may be converted to asparaginyl and glutaminyl residues by reaction with ammonium ions.

[0371] Glutaminyl and asparaginyl residues may be deamidated to the corresponding glutamyl and aspartyl residues. Alternatively, these residues are deamidated under mildly acidic conditions. Either form of these residues falls within the scope of this invention.

[0372] Cysteinyl residues can be replaced by amino acid residues or other moieties either to eliminate disulfide bonding or, conversely, to stabilize cross-linking. (See, e.g., Bhatnagar et al., J. Med. Chem., 39:3814-3819 (1996)).

[0373] Other possible modifications include hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, oxidation of the sulfur atom in Cys, methylation of the alpha-amino groups of lysine, arginine, and histidine side chains. Creighton, Proteins: Structure and Molecule Properties (W. H. Freeman & Co., San Francisco), 79-86 (1983).

[0374] The above examples of derivatizations are not intended to be an exhaustive treatment, but merely illustrative

[0375] In one embodiment, the GLP-1(7-37) or GLP-1(7-37) analogs are covalently linked (directly or by a linking group) to an Fc portion of an immunoglobulin (e.g., IgG, IgE, IgG, and the like). For example, any one of SEQ ID NOs:25-40 may be covalently linked to the Fc portion of an immunoglobulin comprising the sequence of:

25 AESKYGPPCPPCPAPX_{Aa16}X_{Aa17}X_{Aa18}GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVDSQ
EDPEVQFNWYVDGVEVHNAKTKPREEQFX_{Aa80}STYRVVSVLTVLHQDWLNGKEYK
CKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHN
HYTQKSLSLSLGX_{Aa230}; wherein X_{Aa16} is P or E; X_{Aa17} is F, V or A; X_{Aa18} is L, E or A;
30 X_{Aa80} is N or A; and X_{Aa230} is K or absent (SEQ ID NO: 3203). The linking group may be any chemical moiety (e.g., amino acids and/or chemical groups). In one embodiment, the linking group is (-GGGGS-)_x (SEQ ID NO: 3204) where x is 1, 2, 3, 4, 5 or 6; preferably 2, 3 or 4; more preferably 3. In one embodiment, the GLP-1(7-37) analog covalently linked to the Fc portion of an immunoglobulin comprises the amino acid sequence:

HGEGTFTSDVSSYLEEQAAKEFIAWLVKGGGGGGSGGGGSGGGGSAESKYGPPCP
 PCPAPEAAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEV
 HNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKG
 QPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVL
 5 DSDGSFFLYSR LTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLGLG (SEQ ID
 NO: 3205).

[0376] In another embodiment, the GLP-1(7-37) or GLP-1(7-37) analog may be covalently
 linked (directly or through a linking group) to one or two polyethylene glycol molecules. For
 example, a GLP-1(7-37) analog may comprise the amino acid sequence: HXaa8EGTFTSDVS
 10 SYLEXaa22QAAKEFIAWLXaa33KGGPSSGAPPPC₄₅C₄₆-Z, wherein Xaa8 is: D-Ala, G, V,
 L, I, S or T; Xaa22 is G, E, D or K; Xaa33 is: V or I; and Z is OH or NH₂, (SEQ ID NO: 3206),
 and, optionally, wherein (i) one polyethylene glycol moiety is covalently attached to C₄₅, (ii)
 one polyethylene glycol moiety is covalently attached to C₄₆, or (iii) one polyethylene glycol
 moiety is attached to C₄₅ and one polyethylene glycol moiety is attached to C₄₆. In one
 15 embodiment, the GLP-1(7-37) analog is HVEGTFTSDVSSYLEEQAAKEFI
 AWLIKGGPSSGAPPPC₄₅C₄₆-NH₂ (SEQ ID NO: 3207) and, optionally, wherein (i) one
 polyethylene glycol moiety is covalently attached to C₄, (ii) one polyethylene glycol moiety is
 covalently attached to C₄₆, or (iii) one polyethylene glycol moiety is attached to C₄₅ and one
 polyethylene glycol moiety is attached to C₄₆.

[00549] GLP-1 receptor agonist amino acid residues that can provide a primary amine
 moiety for conjugation include residues of lysine, homolysine, ornithine, α , β -
 diaminopropionic acid (Dap), α , β -diaminopropionic acid (Dpr), and α , γ -diaminobutyric
 acid (Dab), aminobutyric acid (Abu), and α -amino-isobutyric acid (Aib). The polypeptide N-
 terminus also provides a useful α -amino group for conjugation as does an amidated
 25 polypeptide C-terminus. In certain embodiments, the GLP-1(7-37) or GLP-1(7-37) analog is
 conjugated to the antibody or fragment thereof at a residue that corresponds to K26 (position
 20 of SEQ ID NO: 3184), K34 (position 28 of SEQ ID NO: 3184), K36 (position 30 of SEQ
 ID NO: 3184; *e.g.*, via a R36K mutation), K37 (position 31 of SEQ ID NO: 3184; *e.g.*, via a
 G37K mutation), K39 (*e.g.*, via addition of two amino acids to the GLP-1(7-37) or GLP-1(7-
 30 37) analog with lysine at position 39) or a C-terminal amine group of said analog. Amino
 acid residues that can provide a secondary amine moiety include ϵ -N-alkyl lysine, α -N-alkyl
 lysine, δ -N-alkyl ornithine, α -N-alkyl ornithine, or an N-terminal proline, where the alkyl is
 C₁ to C₆.

[00550] A “linker moiety” as used herein refers to a biologically acceptable peptidyl or non-peptidyl organic group that is covalently bound to an amino acid residue of a toxin peptide analog or other polypeptide chain (e.g., an immunoglobulin HC or LC or immunoglobulin Fc domain) contained in the inventive composition, which linker moiety covalently joins or conjugates the toxin peptide analog or other polypeptide chain to another peptide or polypeptide chain in the composition, or to a half-life extending moiety. In some embodiments of the composition, a half-life extending moiety, as described herein, is conjugated, i.e., covalently bound directly to an amino acid residue of the toxin peptide analog itself, or optionally, to a peptidyl or non-peptidyl linker moiety (including but not limited to aromatic or aryl linkers) that is covalently bound to an amino acid residue of the toxin peptide analog. The presence of any linker moiety is optional. When present, its chemical structure is not critical, since it serves primarily as a spacer to position, join, connect, or optimize presentation or position of one functional moiety in relation to one or more other functional moieties of a molecule of the inventive composition. The presence of a linker moiety can be useful in optimizing pharmacological activity of some embodiments of the inventive composition. The linker, if present, can be made up of amino acids linked together by peptide bonds. The linker moiety, if present, can be independently the same or different from any other linker, or linkers, that may be present in the inventive composition. In some embodiments the linker can be a multivalent linker that facilitates multivalent display of toxin peptide analogs of the present invention; multivalent display of such biologically active compounds can increase binding affinity and/or potency through avidity. The in vivo properties of a therapeutic can be altered (i.e., specific targeting, half-life extension, distribution profile, etc.) through conjugation to a polymer or protein.

[00551] Peptidyl linkers. As stated above, the linker moiety, if present (whether within the primary amino acid sequence of the toxin peptide analog, or as a linker for attaching a half-life extending moiety to the toxin peptide analog), can be “peptidyl” in nature (i.e., made up of amino acids linked together by peptide bonds) and made up in length, preferably, of from 1 up to about 40 amino acid residues, more preferably, of from 1 up to about 20 amino acid residues, and most preferably of from 1 to about 10 amino acid residues. Preferably, but not necessarily, the amino acid residues in the linker are from among the twenty canonical amino acids, more preferably, cysteine, glycine, alanine, proline, asparagine, glutamine, and /or serine. Even more preferably, a peptidyl linker is made up of a majority of amino acids that are sterically unhindered, such as glycine, serine, and alanine linked by a peptide bond. It is

also desirable that, if present, a peptidyl linker be selected that avoids rapid proteolytic turnover in circulation *in vivo*. Some of these amino acids may be glycosylated, as is well understood by those in the art. For example, a useful linker sequence constituting a sialylation site is X₁X₂NX₄X₅G (SEQ ID NO: 3250), wherein X₁, X₂, X₄ and X₅ are each independently
 5 any amino acid residue.

[00552] In other embodiments, the 1 to 40 amino acids of the peptidyl linker moiety are selected from glycine, alanine, proline, asparagine, glutamine, and lysine. Preferably, a linker is made up of a majority of amino acids that are sterically unhindered, such as glycine and alanine. Thus, preferred linkers include polyglycines, polyserines, and polyalanines, or
 10 combinations of any of these. Some exemplary peptidyl linkers are poly(Gly)₁₋₈, particularly (Gly)₃ (SEQ ID NO:3251), (Gly)₄ (SEQ ID NO:480), (Gly)₅ (SEQ ID NO:3251) and (Gly)₇ (SEQ ID NO:3252), as well as, GlySer and poly(Gly)₄Ser, such as “L15” (GGGGSGGGSGGGGS; SEQ ID NO:3253), poly(Gly-Ala)₂₋₄ and poly(Ala)₁₋₈. Other specific examples of peptidyl linkers include (Gly)₅Lys (SEQ ID NO:3254), and
 15 (Gly)₅LysArg (SEQ ID NO:3255). Other examples of useful peptidyl linkers are: Other examples of useful peptidyl linkers are:

[0001] (Gly)₃Lys(Gly)₄ (SEQ ID NO:3256);
[0002] (Gly)₃AsnGlySer(Gly)₂ (SEQ ID NO:3257);
[0003] (Gly)₃Cys(Gly)₄ (SEQ ID NO:3258); and
 20 **[0004]** GlyProAsnGlyGly (SEQ ID NO:3259).
[0005]
[0006] To explain the above nomenclature, for example, (Gly)₃Lys(Gly)₄ means Gly-Gly-Gly-Lys-Gly-Gly-Gly-Gly (SEQ ID NO:3260). Other combinations of Gly and Ala are also useful.
 25 **[0007]**
[00553] Other preferred linkers are those identified herein as “L5” (GGGGS; or “G4S”; SEQ ID NO:3261), “L10” (GGGGSGGGGS; SEQ ID NO:3262); “L20” (GGGGSGGGSGGGSGGGGS; SEQ ID NO:3263); “L25” (GGGGSGGGSGGGSGGGSGGGGS; SEQ ID NO:3264) and any linkers used in the
 30 working examples hereinafter.

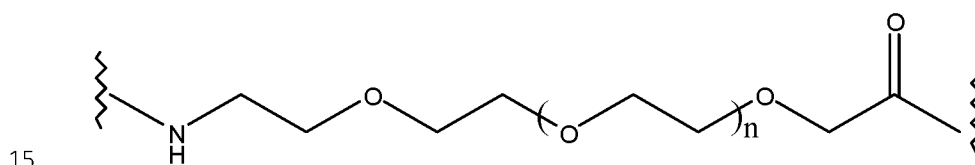
[00554] In some embodiments of the compositions of this invention, which comprise a peptide linker moiety, acidic residues, for example, glutamate or aspartate residues, are

placed in the amino acid sequence of the linker moiety. Examples include the following peptide linker sequences:

- [0008] GGEGGG (SEQ ID NO:3265);
- [0009] GGEEEGGG (SEQ ID NO:3266);
- 5 [0010] GEEEG (SEQ ID NO:3267);
- [0011] GEEE (SEQ ID NO:3268);
- [0012] GGDGGG (SEQ ID NO:3269);
- [0013] GGDDDGG (SEQ ID NO:3270);
- [0014] GDDDG (SEQ ID NO:3271);
- 10 [0015] GDDD (SEQ ID NO:3272);
- [0016] GGGGSDDSDEGSDGEDGGGGS (SEQ ID NO:3273);
- [0017] WEWEW (SEQ ID NO:3274);
- [0018] FEFEF (SEQ ID NO:3275);
- [0019] EEEWW (SEQ ID NO:3276);
- 15 [0020] EEEFFF (SEQ ID NO:3277);
- [0021] WEEEEWW (SEQ ID NO:3278); or
- [0022] FFEEEFF (SEQ ID NO:3279).
- [00555] In other embodiments, the linker constitutes a phosphorylation site, e.g.,
 $X_1X_2YX_4X_5G$ (SEQ ID NO:3280), wherein X_1 , X_2 , X_4 , and X_5 are each independently any
 20 amino acid residue; $X_1X_2SX_4X_5G$ (SEQ ID NO:3281), wherein X_1 , X_2 , X_4 and X_5 are each
 independently any amino acid residue; or $X_1X_2TX_4X_5G$ (SEQ ID NO:3282), wherein X_1 , X_2 ,
 X_4 and X_5 are each independently any amino acid residue.
- [00556] The linkers shown here are exemplary; peptidyl linkers within the scope of this
 invention may be much longer and may include other residues. A peptidyl linker can contain,
 25 e.g., a cysteine, another thiol, or nucleophile for conjugation with a half-life extending
 moiety. In another embodiment, the linker contains a cysteine or homocysteine residue, or
 other 2-amino-ethanethiol or 3-amino-propanethiol moiety for conjugation to maleimide,
 iodoacetaamide or thioester, functionalized half-life extending moiety.
- [00557] Another useful peptidyl linker is a large, flexible linker comprising a random
 30 Gly/Ser/Thr sequence, for example: GSGSATGGSGSTASSGSGSATH (SEQ ID NO:3283)
 or HGSGSATGGSGSTASSGSGSAT (SEQ ID NO:3284), that is estimated to be about the
 size of a 1 kDa PEG molecule. Alternatively, a useful peptidyl linker may be comprised of

amino acid sequences known in the art to form rigid helical structures (e.g., Rigid linker: -AEAAAKEAAAKEAAAKAGG-// SEQ ID NO:3285). Additionally, a peptidyl linker can also comprise a non-peptidyl segment such as a 6 carbon aliphatic molecule of the formula -CH₂-CH₂-CH₂-CH₂-CH₂-CH₂-. The peptidyl linkers can be altered to form derivatives as
 5 described herein.

[00558] Non-peptidyl linkers. Optionally, a non-peptidyl linker moiety is also useful for conjugating the half-life extending moiety to the peptide portion of the half-life extending moiety-conjugated toxin peptide analog. For example, alkyl linkers such as -NH-(CH₂)_s-C(O)-, wherein s = 2-20 can be used. These alkyl linkers may further be substituted by any
 10 non-sterically hindering group such as lower alkyl (e.g., C₁-C₆) lower acyl, halogen (e.g., Cl, Br), CN, NH₂, phenyl, *etc.* Exemplary non-peptidyl linkers are PEG linkers (e.g., shown below):



[0023] wherein n is such that the linker has a molecular weight of about 100 to about 5000 Daltons (Da), preferably about 100 to about 500 Da.

20 **[0024]**

[00559] In one embodiment, the non-peptidyl linker is aryl. The linkers may be altered to form derivatives in the same manner as described herein. “Aryl” is phenyl or phenyl vicinally-fused with a saturated, partially-saturated, or unsaturated 3-, 4-, or 5 membered carbon bridge, the phenyl or bridge being substituted by 0, 1, 2 or 3 substituents selected
 25 from C₁₋₈ alkyl, C₁₋₄ haloalkyl or halo. “Heteroaryl” is an unsaturated 5, 6 or 7 membered monocyclic or partially-saturated or unsaturated 6-, 7-, 8-, 9-, 10- or 11 membered bicyclic ring, wherein at least one ring is unsaturated, the monocyclic and the bicyclic rings

containing 1, 2, 3 or 4 atoms selected from N, O and S, wherein the ring is substituted by 0, 1, 2 or 3 substituents selected from C₁₋₈ alkyl, C₁₋₄ haloalkyl and halo.

[00560] Non-peptide portions of the inventive composition of matter, such as non-peptidyl linkers or non-peptide half-life extending moieties can be synthesized by conventional organic chemistry reactions.

[00561] Other embodiments of the multivalent linker comprise a rigid polyheterocyclic core of controlled length. The linkers are chemically differentiated on either end to accommodate orthogonal coupling chemistries (i.e. azide “Click”, amide coupling, thioether formation by alkylation with maleimide or haloacetamide, oxime formation, reductive amination, etc.).

[00562] The above is merely illustrative and not an exhaustive treatment of the kinds of linkers that can optionally be employed in accordance with the present invention.

[0377] In one embodiment, the GLP-1 receptor agonist compound is a peptide that has at least 80% sequence identity to GLP-1(7-37) (SEQ ID NO: 3184); at least 85% sequence identity to GLP-1(7-37) (SEQ ID NO: 3184); at least 90% sequence identity to GLP-1(7-37) (SEQ ID NO: 3184); or at least 95% sequence identity to GLP-1(7-37) (SEQ ID NO: 3184).

[0378] GLP-1 receptor agonist compounds may be prepared by processes well known in the art, e.g., peptide purification as described in Eng et al., *J. Biol. Chem.*, 265:20259-62 (1990); standard solid-phase peptide synthesis techniques as described in Raufman et al., *J. Biol. Chem.*, 267:21432-37 (1992); recombinant DNA techniques as described in Sambrook et al., *Molecular Cloning: A Laboratory Manual, 2d Ed.*, Cold Spring Harbor (1989); and the like.

[0379] Table 7. Examples of GLP-1 receptor agonist Sequences

SEQ ID NO:	Sequence	Description
3163	HGEGTFTSDLSKQMEEEAVRLFIEWLKN GGPSSGAPPPS	Exendin-4
3164	HSDGTFTSDLSKQMEEEAVRLFIEWLKN GGPSSGAPPPS	Exendin-3
3165	HGEGTFTSDLSKQLEEEAVRLFIEWLKN GGPSSGAPPPS	Leu ¹⁴ -exendin-4
3166	HGEGTFTSDLSKQLEEEAVRLFIEFLKN GGPSSGAPPPS	Leu ¹⁴ ,Phe ²⁵ -exendin-4
3167	HGEGTFTSDLSKQLEEEAARLFIEFLKN GGPSSGAPPPS	Leu ¹⁴ ,Ala ¹⁹ ,Phe ²⁵ -exendin-4

3168	HGEGTFTSDLSKQMEEEEAVRLFIEWLKN GG	exendin-4(1-30)
3169	HGEGTFTSDLSKQLEEEAVRLFIEWLKN GG	Leu ¹⁴ -exendin-4(1-30)
3170	HGEGTFTSDLSKQLEEEAVRLFIEFLKN GG	Leu ¹⁴ ,Phe ²⁵ -exendin-4(1-30)
3171	HGEGTFTSDLSKQLEEEAARLFIEFLKN GG	Leu ¹⁴ ,Ala ¹⁹ ,Phe ²⁵ -exendin-4(1-30)
3172	HGEGTFTSDLSKQMEEEEAVRLFIEWLKN	exendin-4(1-28)
3173	HGEGTFTSDLSKQLEEEAVRLFIEWLKN	Leu ¹⁴ -exendin-4(1-28)
3174	HGEGTFTSDLSKQLEEEAVRLFIEFLKN	Leu ¹⁴ ,Phe ²⁵ -exendin-4(1-28)
3175	HGEGTFTSDLSKQLEEEAARLFIEFLKN	Leu ¹⁴ ,Ala ¹⁹ ,Phe ²⁵ -exendin-4 (1-28)
3176	HGEGTFTSDLSKQLEEKAAKEFIEFLKQ GGPSSGAPPPS	Leu ¹⁴ ,Lys ^{17,20} ,Ala ¹⁹ ,Glu ²¹ ,Phe ²⁵ ,Gln ²⁸ -exendin-4
3177	HGEGTFTSDLSKQLEEKAAKEFIEWLKQ GGPSSGAPPPS	Leu ¹⁴ ,Lys ^{17,20} ,Ala ¹⁹ ,Glu ²¹ ,Gln ²⁸ -exendin-4
3178	HGEGTFTSDLSKQ(octylG)EEEAVRLFIEWLKQGGPSSGAPPPS	octylGly ¹⁴ ,Gln ²⁸ -exendin-4
3179	HGEGTFTSDLSKQLEEEAVRLFIEWLKQGGPSS(octylG)APPPS	Leu ¹⁴ ,Gln ²⁸ ,octylGly ³⁴ -exendin-4
3180	HGEFTFTSDLSKQLEEEAVRLFIEWLKQGGPSKEIIS	Phe ⁴ ,Leu ¹⁴ ,Gln ²⁸ ,Lys ³³ ,Glu ³⁴ ,Ile ^{35,36} ,Ser ³⁷ -exendin-4(1-37)
3181	HGEFTFTSDLSKQLEEKAAKEFIEWLKQGGPSSGAPPPS	Phe ⁴ ,Leu ¹⁴ ,Lys ^{17,20} ,Ala ¹⁹ ,Glu ²¹ ,Gln ²⁸ -exendin-4
3182	HGEGTFTSDLVKILEAEAVRKFIIEFLKNGGPSSGAPPPS	Val ¹¹ ,Ile ¹³ ,Leu ¹⁴ ,Ala ¹⁶ ,Lys ²¹ ,Phe ²⁵ -exendin-4
3183	HGEGTFTSDLSKQMEEEEAVRLFIEWLKNGGPSSGAPPPSK	exendin-4-Lys ⁴⁰
3184	HAEGTFTSDVSSYLEGQAAKEFIAWLVGGRG	GLP-1(7-37)
3185	HAEGTFTSDVSSYLEGQAAKEFIAWLVGGR	GLP-1(7-36)-NH ₂
3186	H(Aib)EGTFTSDVSSYLEGQAAREFIAFLVR(Aib)R	Aib ^{8,35} ,Arg ^{26,34} ,Phe ³¹ -GLP-1(7-36))
3187	HXaa ₈ EGTFTSDVSSYLEXaa ₂₂ Xaa ₂₃ AAKEFI Xaa ₃₀ WLXaa ₃₃ Xaa ₃₄ GXaa ₃₆ Xaa ₃₇ wherein Xaa ₈ is A, V, or G Xaa ₂₂ is G, K, or E Xaa ₂₃ is Q or K Xaa ₃₀ is A or E Xaa ₃₃ is V or K Xaa ₃₄ is K, N, or R Xaa ₃₆ is R or G and Xaa ₃₇ is G, H, P, or absent	HXaa ₈ EGTFTSDVSSYLEXaa ₂₂ Xaa ₂₃ AAKEFIXaa ₃₀ WLXaa ₃₃ Xaa ₃₄ G Xaa ₃₆ Xaa ₃₇ wherein Xaa ₈ is A, V, or G Xaa ₂₂ is G, K, or E Xaa ₂₃ is Q or K Xaa ₃₀ is A or E Xaa ₃₃ is V or K Xaa ₃₄ is K, N, or R Xaa ₃₆ is R or G and Xaa ₃₇ is G, H, P, or absent
3188	HAEGTFTSDVSSYLEGQAAKEFIAWLVRGRG	Arg ³⁴ -GLP-1(7-37)
3189	HAEGTFTSDVSSYLEGQAAKEFIEWLVKGRG	Glu ³⁰ -GLP-1(7-37)
3190	HAEGTFTSDVSSYLEKQAAKEFIAWLVRGRG	Lys ²² -GLP-1(7-37)

3191	HGEGTFTSDVSSYLEEQAAKEFIAWLKVG GGG	Gly ^{8,36} , Glu ²² -GLP-1(7-37)
3192	HVEGTFTSDVSSYLEEQAAKEFIAWLKVG GGG	Val ⁸ , Glu ²² , Gly ³⁶ -GLP-1(7-37)
3193	HGEGTFTSDVSSYLEEQAAKEFIAWLKVG GGG	Gly ^{8,36} , Glu ²² , Lys ³³ , Asn ³⁴ -GLP-1(7-37)
3194	HVEGTFTSDVSSYLEEQAAKEFIAWLKVG GGG	Val ⁸ , Glu ²² , Lys ³³ , Asn ³⁴ , Gly ³⁶ -GLP-1(7-37)
3195	HGEGTFTSDVSSYLEEQAAKEFIAWLKVG GGP	Gly ^{8,36} , Glu ²² , Pro ³⁷ -GLP-1(7-37)
3196	HVEGTFTSDVSSYLEEQAAKEFIAWLKVG GGP	Val ⁸ , Glu ²² , Gly ³⁶ , Pro ³⁷ -GLP-1(7-37)
3197	HGEGTFTSDVSSYLEEQAAKEFIAWLKVG GGP	Gly ^{8,36} , Glu ²² , Lys ³³ , Asn ³⁴ , Pro ³⁷ -GLP-1(7-37)
3198	HVEGTFTSDVSSYLEEQAAKEFIAWLKVG GGP	Val ⁸ , Glu ²² , Lys ³³ , Asn ³⁴ , Gly ³⁶ , Pro ³⁷ -GLP-1(7-37)
3199	HGEGTFTSDVSSYLEEQAAKEFIAWLKVG GG	Gly ^{8,36} , Glu ²² -GLP-1(7-36)
3200	HVEGTFTSDVSSYLEEQAAKEFIAWLKVG GG	Val ⁸ , Glu ²² , Gly ³⁶ -GLP-1(7-36)
3201	HVEGTFTSDVSSYLEEQAAKEFIAWLKVG GG	Val ⁸ , Glu ²² , Asn ³⁴ , Gly ³⁶ -GLP-1(7-36)
3202	HGEGTFTSDVSSYLEEQAAKEFIAWLKVG GG	Gly ^{8,36} , Glu ²² , Asn ³⁴ -GLP-1(7-36)
3203	AESKYGPPCPPCPAPXaa ₁₆ Xaa ₁₇ Xaa ₁₈ G GPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKTKPR EEQFXaa ₈₀ STYRVVSVLTVLHQDWLNGK EYKCKVSNKGLPSSIEKTISKAKGQPRE PQVYTLPPSQEEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLGLXaa ₂₃₀ wherein Xaa ₁₆ is P or E Xaa ₁₇ is F, V or A Xaa ₁₈ is L, E or A Xaa ₈₀ is N or A and Xaa ₂₃₀ is K or absent	Fc portion of an immunoglobulin
3204	(-GGGS-) _x where x is 1, 2, 3, 4, 5 or 6	Linker
3205	HGEGTFTSDVSSYLEEQAAKEFIAWLKVG GGGGGGSGGGSGGGGSAESKYGPPCP PCPAPEAAGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSQEDPEVQFNWYVDGVE VHNAKTKPREEQFNSTYRVVSVLTVLHQ DWLNGKEYKCKVSNKGLPSSIEKTISKA KGQPREPQVYTLPPSQEEMTKNQVSLTCL LVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSR LTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLGL	Fc portion of an immunoglobulin
3206	HXaa ₈ EGTFTSDVS SYLEXaa ₂₂ QAAKEFIAWLXaa ₃₃ KGGPSS GAPPPC ₄₅ C ₄₆ -Z, wherein Xaa ₈ is: D-Ala, G, V, L, I, S or T	GLP-1 analog

	Xaa ₂₂ is G, E, D or K Xaa ₃₃ is: V or I and Z is OH or NH ₂ and, optionally, wherein (i) one polyethylene glycol moiety is covalently attached to C ₄₅ , (ii) one polyethylene glycol moiety is covalently attached to C ₄₆ , or (iii) one polyethylene glycol moiety is attached to C ₄₅ and one polyethylene glycol moiety is attached to C ₄₆ .	
3207	HVEGTFTSDVSSYLEEQAAKEFIWLIK GGPSSGAPPPC ₄₅ C ₄₆ -NH ₂ and, optionally, wherein (i) one polyethylene glycol moiety is covalently attached to C ₄ , (ii) one polyethylene glycol moiety is covalently attached to C ₄₆ , or (iii) one polyethylene glycol moiety is attached to C ₄₅ and one polyethylene glycol moiety is attached to C ₄₆ .	GLP-1 analog
3208	HGEGTFTSDLSKQMEEEEAVKLFIEWLKN GGPSSGAPPPS	[N ^ε -(17-carboxyheptadecanoic acid)Lys ²⁰]exendin-4-NH ₂
3209	HGEGTFTSDLSKQMEEEEAVRLFIEWLKN GGPKSGAPPPS	[N ^ε -(17-carboxyhepta- decanoyl)Lys ³²]exendin-4-NH ₂
3210	GEGTFTSDLSKQMEEEEAVKLFIEWLKN GPSSGAPPPS	[desamino-His ¹ ,N ^ε -(17- carboxyheptadecanoyl)Lys ²⁰]exen- din-4-NH ₂
3211	HGEGTFTSDLSRQNorLeEEEAVRLFIE WLRNGGPKSGAPPPS	[Arg ^{12,27} ,NLe ¹⁴ ,N ^ε -(17-carboxy- heptadecanoyl)Lys ³²]exendin-4- NH ₂
3212	HGEGTFTSDLSKQMEEEEAVKLFIEWLKN GGPSSGAPPPS	[N ^ε -(19-carboxy- nonadecanoylamino)Lys ²⁰]- exendin-4-NH ₂
3213	HGEGTFTSDLSKQMEEEEAVKLFIEWLKN GGPSSGAPPPS	[N ^ε -(15- carboxypentadecanoylamino)Lys ²⁰]- exendin-4-NH ₂
3214	HGEGTFTSDLSKQMEEEEAVKLFIEWLKN GGPSSGAPPPS	[N ^ε -(13- carboxytridecanoylamino)Lys ²⁰]ex- endin-4-NH ₂
3215	HGEGTFTSDLSKQMEEEEAVKLFIEWLKN GGPSSGAPPPS	[N ^ε -(11-carboxy-undecanoyl)- amino)Lys ²⁰]exendin-4-NH ₂
3216	HGEGTFTSDLSKQMEEEEAVRLFIEWLKN GGPSSGAPPPSK	exendin-4-Lys ⁴⁰ (e-MPA)-NH ₂
3217	HGEGTFTSDLSKQMEEEEAVRLFIEWLKN GGPSSGAPPPSK	exendin-4-Lys ⁴⁰ (e-AEEA-AEEA- MPA)-NH ₂
3218	HGEGTFTSDLSKQMEEEEAVRLFIEWLKN GGPSSGAPPPSK	exendin-4-Lys ⁴⁰ (e-AEEA-MPA)- NH ₂

3219	HGEGTFTSDLSKQMEEEEAVRLFIEWLKN GGPSSGAPPPSK	exendin-4-Lys ⁴⁰ (e-MPA)-albumin
3220	HGEGTFTSDLSKQMEEEEAVRLFIEWLKN GGPSSGAPPPSK	exendin-4-Lys ⁴⁰ (e-AEEA-AEEA- MPA)-albumin
3221	HGEGTFTSDLSKQMEEEEAVRLFIEWLKN GGPSSGAPPPSK	exendin-4-Lys ⁴⁰ (e-AEEA-MPA)- albumin
3222	AEGTFTSDVSSYLEGQAAREFIAWLKVG RG	desamino-His ⁷ ,Arg ²⁶ ,Lys ³⁴ (N ^ε -(γ- Glu(N-α-hexadecanoyl)))-GLP- 1(7-37) (core peptide disclosed as SEQ ID NO: 3222)
3223	AEGTFTSDVSSYLEGQAAREFIAWLKVG RG	desamino-His ⁷ ,Arg ²⁶ ,Lys ³⁴ (N ^ε - octanoyl)-GLP-1(7-37)
3224	HAEGTFTSDVSSYLEGQAAREFIAWLVR GRGK	Arg ^{26,34} ,Lys ³⁸ (N ^ε -(ω- carboxypentadecanoyl))-GLP-1(7- 38)
3225	HAEGTFTSDVSSYLEGQAAREFIAWLVR GRGK	Arg ^{26,34} ,Lys ³⁶ (N ^ε -(γ-Glu(N-α- hexadecanoyl)))-GLP-1(7-36) (core peptide disclosed as SEQ ID NO: 3225)
3226	H [Aib] EGTFTSDVSSYLEGQAAKEFIA WLKGRK	[Aib ⁸ ,Lys ³⁷]GLP-1_(7-37)
3227	H [Aib] EGTFTSDVSSYLEGQAAKEFIA WLKGGK	[Aib ⁸ , Lys ³⁶]GLP-1_(7-37)
3228	H [Aib] EGTFTSDVSSYLE [Aib] QAAK EFIAWLKGGK	[Aib ^{8,22} ,Lys ³⁶]GLP-1(7-36)- Amide
3229	H [Aib] EGTFTSDVSSYLE [Aib] QAAK EFIAW [BLeu] VKGK	[Aib ^{8,22} ,BLeu ³² ,Lys ³⁶]GLP-1(7- 36)-Amide
3230	H [Aib] EGTFTSDVSSYLE [Aib] QAAK EFIAWLKGRK	[Aib ^{8,22} ,Lys ³⁷]GLP-1(7-37)- Amide
3231	H [Aib] EGTFTSDVSSYLE [Aib] QAAK EFIAW [BLeu] VKGRK	[Aib ^{8,22} ,BLeu ³² ,Lys ³⁷]GLP-1(7- 37)-Amide
3232	H [Aib] EGTFTSDVSSYLE [Aib] QAAK EFIAW [aMeLeu] VKGRK	[Aib ^{8,22} ,aMeLeu ³² ,Lys ³⁷]GLP-1(7- 37)-Amide
3233	H [Aib] EGT [AMEF] TSDVSSYLE [Aib]] QAAKEFIAWLKGRK	[Aib ^{8,22} ,AMEF ¹² ,Lys ³⁷]GLP-1(7- 37)-Amide
3234	H [Aib] EGTFTSD [BLeu] SSYLE [Aib]] QAAKEFIAWLKGRK	[Aib ^{8,22} ,BLeu ¹⁶ ,Lys ³⁷]GLP-1(7- 37)-Amide
3235	H [Aib] EGTFTSDVSSYLE [Aib] QAAK EFIAWLKGGK	[Aib ^{8,22} ,Gly ³⁶ ,Lys ³⁷]GLP-1(7-37)- Amide
3236	H [Aib] EGTFTSDVSSYLE [Aib] QAAK EFIAWLKNGGK	[Aib ^{8,22} ,Lys ^{33,37} ,Asn ³⁴ ,Gly ³⁶]GLP- 1(7-37)-Amide
3237	H [Aib] EGTFTSDVSSYLE [Aib] QAAK EFIAWLKNGG [Aeea]	[Aib ^{8,22} ,Lys ³³ ,Asn ³⁴ ,Gly ³⁶ ,Aeea ³⁷] GLP-1(7-37)-Aeea-Lys-Amide
3238	H [Aib] EGTFTSDVSSYLE [Aib] QAAK EFIAWLKGGG	[Aib ^{8,22} ,Gly ³⁶]GLP-1(7-37)
3239	H [Aib] EGTFTSDVSSYLEGEAAKKFIA WLKGGG	cyclo[E ²³ -K ²⁷][Aib ⁸ ,Gly ³⁶]GLP- 1(7-37)
3240	H [Aib] EGTFTSDVSSYLEEQAAKEKFI AWLVKGGK	cyclo[E ²² - K ²⁶][Aib ⁸ ,Gly ³⁶ ,Lys ³⁷]GLP-1(7- 37)-Amide

3241	H [Aib] EGTFTSDVSSYLE [Aib] EAVR LFIEWLKNNGPSSGAPPPS	[Aib ^{8,22}]-GLP-1(7-22)-Ex4(17-39)
3242	HGEGTFTSDVSSYLEEQAAKEFIAWLK GGG	[Gly ^{8,36} ;Glu ²²]GLP-1(7-37)
3243	H [Aib] EGTFTSDVSSYLEEQAAKEFIA WLVKGGG	[Aib ⁸ ;Glu ²² ;Gly ³⁶]GLP-1(7-37)- Amide
3244	H [Aib] EGTFTSDYSSYLEEQAAKEFIA WLVKGGG	[Aib ⁸ ;Tyr ¹⁶ ;Glu ²² ;Gly ³⁶]GLP- 1 (7-37)
3245	H [Aib] EGTFTSDVSKYLEEEEAVRLFIE WLKNNGG	[Aib ⁸ ;Lys ^{18,33} ;Glu ^{22,23,30} ;Val ²⁵ ;Arg 26;Leu ²⁷ ;Asn ³⁴ ;Gly ³⁶]GLP-1(7-37)
3246	H [Aib] EGTFTSDVSKYLEEEAAKLFIE WLKNNGG	[Aib ⁸ ;Lys ^{18,33} ;Glu ^{22,23,30} ;Leu ²⁷ ;Asn 34;Gly ³⁶]GLP-1(7-37)
3247	H [Aib] EGTFTSDVSKYLEEEAAKLFIE WLVKGGG	[Aib ⁸ ;Lys ¹⁸ ;Glu ^{22,23,30} ;Leu ²⁷ ;Gly ³⁶] GLP-1(7-37)
3248	H [Aib] IGTFTSDVSSYLE [Aib] QAAK EFIAWLVKGG	[Aib ^{8,22} ;Ile ⁹ ;Gly ³⁶]GLP-1_(7-36)
3249	H [Aib] EGTFTSEVSSYLE [Aib] QAAK EFIAWLVKGG	[Aib ^{8,22} ;Glu ¹⁵ ;Gly ³⁶]GLP-1_(7-36)
3286	{H2}H [Aib] EGTFTSDVSSYLE [Aib] QAAKEFIAWLKNNG [Aeea] [Aeea] K{ CONH2}	
3287	{H2}H [Aib] EGTFTSDVSSYLE [Aib] QAAKEFIAWLVKGGG	
3288	{H2}H [Aib] EGTFTSDVSSYLEGEAAK KFIAWLVKGGG	
3289	{H2}H [Aib] EGTFTSDVSSYLEEQAAK EFIAWLVKGGK{ CONH2}	
3290	{H2}H [Aib] EGTFTSDVSSYLE [Aib] EAVRLFIEWLKNNGPSSGAPPPS	
3291	{H2}HGEGTFTSDVSSYLEEQAAKEFIA WLVKGGG	
3292	{H2}H [Aib] EGTFTSDVSSYLEEQAAK EFIAWLVKGGG	
3293	{H2}H [Aib] EGTFTSDYSSYLEEQAAK EFIAWLVKGGG	
3294	{H2}H [Aib] EGTFTSDVSKYLEEEEAVR LFIEWLKNNGG	
3295	{H2}H [Aib] EGTFTSDVSKYLEEEAAK LFIEWLKNNGG	
3296	{H2}H [Aib] EGTFTSDVSKYLEEEAAK LFIEWLVKGGG	
3297	{H2}H [Aib] IGTFTSDVSSYLE [Aib] QAAKEFIAWLVKGG	
3298	{H2}H [Aib] EGTFTSEVSSYLE [Aib] QAAKEFIAWLVKGG	
3299	{H2}H [Aib] AGTFTSDVSSYLE [Aib] QAAKEFIAWLVKGG	
3300	{H2}H [Aib] EGTFTSDVSSYLE [Aib] QAAKEFAAWLVKGG	
3301	{H2}H [Aib] EGTFTSDVSSYLE [Aib] QAAKEFIAALVKGG	
3302	{H2}H [Aib] TGTFTSDVSSYLE [Aib] QAAKEFIAWLVKGGG	

3303	{H2}H[Aib]EGTFTSEVSSYLE[Aib] QAAKEFIAALVKGGG	
3304	{H2}H[Aib]EGTFTSDVSSYLE[Aib] QAAKEFIAALVKGGG	
3305	{H2}H[Aib]EGTFTSDVSSYLEEEEAVR LFIEWLKNGGPSSGAPPPS	
3306	{H2}H[Aib]EGTFTSDYSSYLE[Aib] QAAKEFIAWLVKGGG	
3307	{H2}H[Aib]EGTFTSDVSSYLE[Aib] QAAKEFIAWLVKGGG{CONH2}	
3308	{Dmia}SQGTFTSDYSKYLDERRAKDFV QWLMNT	
3309	{H2}HGEFTFTSDLSKQMEEEAVRLFIE WLKNGGPSSGAPPPS	

[0380] AEEA refers to [2-(2-amino)ethoxy]acetic acid

[0381] EDA refers to ethylenediamine.

[0382] MPA refers to maleimidopropionic acid.

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[0383] The disclosure also provides pharmaceutical compositions comprising the GLP-1 receptor agonist compounds described herein and a pharmaceutically acceptable carrier. The GLP-1 receptor agonist compounds can be present in the pharmaceutical composition in a therapeutically effective amount and can be present in an amount to provide a minimum blood plasma level of the GLP-1 receptor agonist compound necessary for therapeutic efficacy. Such pharmaceutical compositions are known in the art and described, e.g., in U.S. Pat. No. 7,521,423; U.S. Pat. No. 7,456,254; WO 2000/037098; WO 2005/021022; WO 2005/102293; WO 2006/068910; WO 2006/125763; WO 2009/068910; US Publication No. 2004/0106547; and the like, the disclosures of which are incorporated herein by reference.

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[0384] Pharmaceutical compositions containing the GLP-1 receptor agonist compounds described herein may be provided for peripheral administration, such as parenteral (e.g., subcutaneous, intravenous, intramuscular), a continuous infusion (e.g., intravenous drip, intravenous bolus, intravenous infusion), topical, nasal, or oral administration. Suitable pharmaceutically acceptable carriers and their formulation are described in standard formulation treatises, such as Remington's Pharmaceutical Sciences by Martin; and Wang et al., *Journal of Parenteral Science and Technology*, Technical Report No. 10, Supp. 42:2S (1988). The GLP-1 receptor agonist compounds described herein can be provided in parenteral compositions for injection or infusion. They can, for example, be suspended in water; an inert oil, such as a vegetable oil (e.g., sesame, peanut, olive oil, and the like); or other pharmaceutically acceptable carrier. In one embodiment, the compounds are suspended

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in an aqueous carrier, for example, in an isotonic buffer solution at a pH of about 3.0 to 8.0, or about 3.0 to 5.0. The compositions may be sterilized by conventional sterilization techniques or may be sterile filtered. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions, such as pH buffering agents.

[0385] Useful buffers include for example, acetic acid buffers. A form of repository or “depot” slow release preparation may be used so that therapeutically effective amounts of the preparation are delivered into the bloodstream over many hours or days following subcutaneous injection, transdermal injection or other delivery method. The desired isotonicity may be accomplished using sodium chloride or other pharmaceutically acceptable agents such as dextrose, boric acid, sodium tartrate, propylene glycol, polyols (such as mannitol and sorbitol), or other inorganic or organic solutes. In one embodiment for intravenous infusion, the formulation may comprise (i) the GLP-1 receptor agonist compound, (2) sterile water, and, optionally (3) sodium chloride, dextrose, or a combination thereof.

[0386] Carriers or excipients can also be used to facilitate administration of the GLP-1 receptor agonist compounds. Examples of carriers and excipients include calcium carbonate, calcium phosphate, various sugars such as lactose, glucose, or sucrose, or types of starch, cellulose derivatives, gelatin, vegetable oils, polyethylene glycols and physiologically compatible solvents.

[0387] The GLP-1 receptor agonist compounds can also be formulated as pharmaceutically acceptable salts (e.g., acid addition salts) and/or complexes thereof. Pharmaceutically acceptable salts are non-toxic salts at the concentration at which they are administered. Pharmaceutically acceptable salts include acid addition salts such as those containing sulfate, hydrochloride, phosphate, sulfamate, acetate, citrate, lactate, tartrate, methanesulfonate, ethanesulfonate, benzenesulfonate, p-toluenesulfonate, cyclohexylsulfamate and quinate. Pharmaceutically acceptable salts can be obtained from acids such as hydrochloric acid, sulfuric acid, phosphoric acid, sulfamic acid, acetic acid, citric acid, lactic acid, tartaric acid, malonic acid, methanesulfonic acid, ethanesulfonic acid, benzenesulfonic acid, p-toluenesulfonic acid, cyclohexylsulfamic acid, and quinic acid. Such salts may be prepared by, for example, reacting the free acid or base forms of the product with one or more equivalents of the appropriate base or acid in a solvent or medium in which the salt is insoluble, or in a solvent such as water which is then removed in vacuo or by freeze-drying or by exchanging the ions of an existing salt for another ion on a suitable ion exchange resin.

[0388] Exemplary pharmaceutical formulations of GLP-1 receptor agonist compounds are described in U.S. Pat. No. 7,521,423, U.S. Pat. No. 7,456,254; US Publication No 2004/0106547, WO 2006/068910, WO 2006/125763, and the like, the disclosures of which are incorporated by reference herein.

5 [0389] The therapeutically effective amount of the GLP-1 receptor agonist compounds described herein for use in the methods described herein will typically be from about 0.01 µg to about 5 mg; about 0.1 µg to about 2.5 mg; about 1 µg to about 1 mg; about 1 µg to about 50 µg; or about 1 µg to about 25 µg. Alternatively, the therapeutically effective amount of the GLP-1 receptor agonist compounds may be from about 0.001 µg to about 100 µg based on
10 the weight of a 70 kg patient; or from about 0.01 µg to about 50 µg based on the weight of a 70 kg patient. These therapeutically effective doses may be administered once/day, twice/day, thrice/day, once/week, biweekly, or once/month, depending on the formulation. The exact dose to be administered is determined, for example, by the formulation, such as an immediate release formulation or an extended release formulation. For transdermal, nasal or oral dosage
15 forms, the dosage may be increased from about 5-fold to about 10-fold.

[0390] In certain embodiments the GLP-1 receptor agonist will be administered concurrently with the GIPR antigen binding protein. In one embodiment the GLP-1 receptor agonist will be administered after the GIPR antigen binding protein. In one embodiment the GLP-1 receptor agonist will be administered before the GIPR antigen binding protein. In certain
20 embodiments the subject or patient will already be being treated with a GLP-1 receptor agonist before being subjected to further treatment with a GIPR antigen binding protein.

[0391] The GIPR antigen binding proteins that are provided herein are useful for detecting GIPR in biological samples. For instance, the GIPR antigen binding proteins can be used in diagnostic assays, *e.g.*, binding assays to detect and/or quantify GIPR expressed in serum.

25 [0392] The antigen binding proteins of the described can be used for diagnostic purposes to detect, diagnose, or monitor diseases and/or conditions associated with GIPR. The disclosed antigen binding proteins provide a means for the detection of the presence of GIPR in a sample using classical immunohistological methods known to those of skill in the art (*e.g.*, Tijssen, 1993, *Practice and Theory of Enzyme Immunoassays*, Vol 15 (Eds R.H. Burdon and
30 P.H. van Knippenberg, Elsevier, Amsterdam); Zola, 1987, *Monoclonal Antibodies: A Manual of Techniques*, pp. 147-158 (CRC Press, Inc.); Jalkanen *et al.*, 1985, *J. Cell. Biol.* 101:976-985; Jalkanen *et al.*, 1987, *J. Cell Biol.* 105:3087-3096). The detection of GIPR can be performed *in vivo* or *in vitro*.

[0393] Diagnostic applications provided herein include use of the antigen binding proteins to detect expression of GIPR. Examples of methods useful in the detection of the presence of GIPR include immunoassays, such as the enzyme linked immunosorbent assay (ELISA) and the radioimmunoassay (RIA).

5 [0394] For diagnostic applications, the antigen binding protein typically will be labeled with a detectable labeling group. Suitable labeling groups include, but are not limited to, the following: radioisotopes or radionuclides (*e.g.*, ^3H , ^{14}C , ^{15}N , ^{35}S , ^{90}Y , ^{99}Tc , ^{111}In , ^{125}I , ^{131}I), fluorescent groups (*e.g.*, FITC, rhodamine, lanthanide phosphors), enzymatic groups (*e.g.*, horseradish peroxidase, β -galactosidase, luciferase, alkaline phosphatase), chemiluminescent
10 groups, biotinyl groups, or predetermined polypeptide epitopes recognized by a secondary reporter (*e.g.*, leucine zipper pair sequences, binding sites for secondary antibodies, metal binding domains, epitope tags). In some embodiments, the labeling group is coupled to the antigen binding protein *via* spacer arms of various lengths to reduce potential steric hindrance. Various methods for labeling proteins are known in the art and may be used.

15 [0395] In some embodiments, the GIPR antigen binding protein is isolated and measured using techniques known in the art. *See*, for example, *Harlow and Lane*, 1988, *Antibodies: A Laboratory Manual*, New York: Cold Spring Harbor (ed. 1991 and periodic supplements); *John E. Coligan, ed.*, 1993, *Current Protocols In Immunology* New York: John Wiley & Sons.

20 [0396] Another aspect of the disclosed provides for detecting the presence of a test molecule that competes for binding to GIPR with the antigen binding proteins provided. An example of one such assay would involve detecting the amount of free antigen binding protein in a solution containing an amount of GIPR in the presence or absence of the test molecule. An increase in the amount of free antigen binding protein (*i.e.*, the antigen binding protein not
25 bound to GIPR) would indicate that the test molecule is capable of competing for GIPR binding with the antigen binding protein. In one embodiment, the antigen binding protein is labeled with a labeling group. Alternatively, the test molecule is labeled and the amount of free test molecule is monitored in the presence and absence of an antigen binding protein.

[0397] GIPR binding proteins can be used to treat, diagnose or ameliorate, a metabolic
30 condition or disorder. In one embodiment, the metabolic disorder to be treated is diabetes, *e.g.*, type 2 diabetes. In another embodiment, the metabolic condition or disorder is obesity. In other embodiments the metabolic condition or disorder is dyslipidemia, elevated glucose levels, elevated insulin levels or diabetic nephropathy. For example, a metabolic condition or disorder that can be treated or ameliorated using a GIPR binding peptide includes a state in

which a human subject has a fasting blood glucose level of 125 mg/dL or greater, for example, 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190, 195, 200 or greater than 200 mg/dL. Blood glucose levels can be determined in the fed or fasted state, or at random. The metabolic condition or disorder can also comprise a condition in which a subject is at increased risk of developing a metabolic condition. For a human subject, such conditions include a fasting blood glucose level of 100 mg/dL. Conditions that can be treated using a pharmaceutical composition comprising a GIPR binding protein can also be found in the American Diabetes Association Standards of Medical Care in Diabetes Care-2011, American Diabetes Association, Diabetes Care Vol. 34, No. Supplement 1, S11-S61, 2010, incorporated herein by reference.

[0398] In application, a metabolic disorder or condition, such as Type 2 diabetes, elevated glucose levels, elevated insulin levels, dyslipidemia, obesity or diabetic nephropathy, can be treated by administering a therapeutically effective dose of a GIPR binding protein to a patient in need thereof. The administration can be performed as described herein, such as by IV injection, intraperitoneal (IP) injection, subcutaneous injection, intramuscular injection, or orally in the form of a tablet or liquid formation. In some situations, a therapeutically effective or preferred dose of a GIPR binding protein can be determined by a clinician. A therapeutically effective dose of GIPR binding protein will depend, *inter alia*, upon the administration schedule, the unit dose of agent administered, whether the GIPR binding protein is administered in combination with other therapeutic agents, the immune status and the health of the recipient. The term “therapeutically effective dose,” as used herein, means an amount of GIPR binding protein that elicits a biological or medicinal response in a tissue system, animal, or human being sought by a researcher, medical doctor, or other clinician, which includes alleviation or amelioration of the symptoms of the disease or disorder being treated, *i.e.*, an amount of a GIPR binding protein that supports an observable level of one or more desired biological or medicinal response, for example lowering blood glucose, insulin, triglyceride, or cholesterol levels; reducing body weight; or improving glucose tolerance, energy expenditure, or insulin sensitivity.

[0399] It is noted that a therapeutically effective dose of a GIPR binding protein can also vary with the desired result. Thus, for example, in situations in which a lower level of blood glucose is indicated a dose of GIPR binding protein will be correspondingly higher than a dose in which a comparatively lower level of blood glucose is desired. Conversely, in situations in which a higher level of blood glucose is indicated a dose of GIPR binding

protein will be correspondingly lower than a dose in which a comparatively higher level of blood glucose is desired.

[0400] In various embodiments, a subject is a human having a blood glucose level of 100 mg/dL or greater can be treated with a GIPR binding protein.

5 **[0401]** In one embodiment, a method of the instant disclosure comprises first measuring a baseline level of one or more metabolically-relevant compounds such as glucose, insulin, cholesterol, lipid in a subject. A pharmaceutical composition comprising a GIPR binding protein is then administered to the subject. After a desired period of time, the level of the one or more metabolically-relevant compounds (*e.g.*, blood glucose, insulin, cholesterol, lipid) in
10 the subject is again measured. The two levels can then be compared in order to determine the relative change in the metabolically-relevant compound in the subject. Depending on the outcome of that comparison another dose of the pharmaceutical composition comprising a GIPR binding protein can be administered to achieve a desired level of one or more metabolically-relevant compound.

15 **[0402]** It is noted that a pharmaceutical composition comprising a GIPR binding protein can be co-administered with another compound. The identity and properties of compound co-administered with the GIPR binding protein will depend on the nature of the condition to be treated or ameliorated. A non-limiting list of examples of compounds that can be administered in combination with a pharmaceutical composition comprising a GIPR binding
20 protein include rosiglitazone, pioglitazone, repaglinide, nateglinide, metformin, exenatide, sitagliptin, pramlintide, glipizide, glimepirideacarbose, and miglitol.

[0403] Also provided are kits for practicing the disclosed methods. Such kits can comprise a pharmaceutical composition such as those described herein, including nucleic acids encoding the peptides or proteins provided herein, vectors and cells comprising such nucleic acids, and
25 pharmaceutical compositions comprising such nucleic acid-containing compounds, which can be provided in a sterile container. Optionally, instructions on how to employ the provided pharmaceutical composition in the treatment of a metabolic disorder can also be included or be made available to a patient or a medical service provider.

[0404] In one aspect, a kit comprises (a) a pharmaceutical composition comprising a
30 therapeutically effective amount of a GIPR binding protein; and (b) one or more containers for the pharmaceutical composition. Such a kit can also comprise instructions for the use thereof; the instructions can be tailored to the precise metabolic disorder being treated. The instructions can describe the use and nature of the materials provided in the kit. In certain embodiments, kits include instructions for a patient to carry out administration to treat a

metabolic disorder, such as elevated glucose levels, elevated insulin levels, obesity, type 2 diabetes, dyslipidemia or diabetic nephropathy.

[0405] Instructions can be printed on a substrate, such as paper or plastic, etc, and can be present in the kits as a package insert, in the labeling of the container of the kit or
5 components thereof (e.g., associated with the packaging), etc. In other embodiments, the instructions are present as an electronic storage data file present on a suitable computer readable storage medium, e.g. CD-ROM, diskette, etc. In yet other embodiments, the actual instructions are not present in the kit, but means for obtaining the instructions from a remote source, such as over the internet, are provided. An example of this embodiment is a kit that
10 includes a web address where the instructions can be viewed and/or from which the instructions can be downloaded.

[0406] Often it will be desirable that some or all components of a kit are packaged in suitable packaging to maintain sterility. The components of a kit can be packaged in a kit containment element to make a single, easily handled unit, where the kit containment element, e.g., box or
15 analogous structure, may or may not be an airtight container, e.g., to further preserve the sterility of some or all of the components of the kit.

[0407] Example 1

[0408] **Generation of bis-cysteamine-capped anti-GIPR cys mAb (2 g scale)**

[0409] The reaction scheme for the generation of anti-GIPR/GLP-1 peptide conjugates is shown in Figure 1. Anti-GIPR monoclonal antibodies with specific cysteine mutation (anti-GIPR cys mAb, 2 g) was incubated with 800 mL solution of 2.5 mM cystamine and 2.5 mM cysteamine in 40 mM HEPES buffer, pH 7.5-8.5 for 15-20 h. The reaction mixture was filtered using 0.22 µm filter, and diluted in 1200 mL of 100 mM sodium acetate buffer pH 5.
25 Cation exchange chromatography was used to purify the bis-cysteamine-capped anti-GIPR cys mAb from the reaction mixture. First, 2 L of reaction mixture diluted in 100 mM sodium acetate buffer pH 5 was loaded onto 240 mL SP HP column at 20 mL/min. The column was washed with 2 column volumes of 100 mM sodium acetate pH 5, followed by a 0-20% gradient of 100 mM sodium acetate with 1.2 M NaCl pH 5. The main peak containing bis-
30 cysteamine-capped anti-GIPR cys mAb was collected and buffer exchanged to 10 mM sodium acetate with 9% sucrose pH 5.2 using tangential flow filtration.

[0410] Example 2

[0411] **Generation of anti-GIPR/GLP-1 peptide conjugates**

[0412] Bis-cysteamine-capped anti-GIPR cys mAb (6 mg/mL in 10 mM sodium acetate with 9% sucrose) was partially reduced using 3-4 equivalents of tris(2-carboxyethyl)phosphine (TCEP) at RT for 60-90 min. TCEP was removed, and partially reduced cys mAb was buffer exchanged to 50 mM sodium phosphate buffer containing 2 mM ethylenediaminetetraacetic acid (EDTA) pH 7.5. To the partially reduced cys mAb was added 6-10 equivalents of dehydroascorbic acid (DHAA), and oxidation was carried out at RT until only trace amount of partially reduced mAb species were observed (30-120 min). Without removing dhAA, 3-8 equivalents of bromoacetyl-GLP-1 peptides was added to the reaction mixture and incubated at RT for 15-20 h. All the reagents were removed, and the anti-GIPR/GLP-1 peptide conjugate product was buffer exchanged to final formulation using spin concentration or tangential flow filtration.

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Table 9. Anti-GIPR antagonist/GLP-1 receptor agonist bispecific conjugates constructs.

Conjugate#	Description	Peptide information	Site/linker	hGLP-1 IC ₅₀ (nM)	hGIPR IC ₅₀ (nM)
3159936#1	5G12-D88C-3156820	[Aib8, Lys26(SGGAcBr)]GLP-1 (7-37)	Lys26/SGG	0.167	81.9
1140-1	5G12-D88C-3156820	[Aib8, Lys26(SGGAcBr)]GLP-1 (7-37)	Lys26/SGG	0.059	101.6
1109-1	5G12-E384C- 3156820 DAR1	[Aib8, Lys26(SGGAcBr)]GLP-1 (7-37)	Lys26/SGG	0.622	44.9
1110-1	5G12-E384C- 3156820	[Aib8, Lys26(SGGAcBr)]GLP-1 (7-37)	Lys26/SGG	0.159	47.0
1118-1	5G12 SEFL2 D88C- 3156820 DAR1	[Aib8, Lys26(SGGAcBr)]GLP-1 (7-37)	Lys26/SGG	0.143	61.2
1135-1	5G12 T487C- 3156820	[Aib8, Lys26(SGGAcBr)]GLP-1 (7-37)	Lys26/SGG	0.065	50.6
1143-1	5G12-E384C- 3161655	[Aib8, 22; Gly36; Lys37(PEG11AcBr)]GLP-1(7-37)-Amide	Lys37/PEG11	0.047	37.0
1144-1	5G12-E384C- 3161021	[Aib8, 22; Lys36(SGGACBr)]GLP-1(7-36)-Amide	Lys36/SGG	0.036	37.9
1159-1	5G12-D88C-3166119	[Aib8, 22; Gly36]GLP-1(7-37)[GGGSGGGSGGGGSK(BrAc)]	C- term/(GGGGS)3	0.044	152.1
1160-1	5G12-E384C- 3166119	[Aib8, 22; Gly36]GLP-1(7-37)[GGGSGGGSGGGGSK(BrAc)]	C- term/(GGGGS)3	0.171	43.5
1161-1	5G12-T4874C- 3166119	[Aib8, 22; Gly36]GLP-1(7-37)[GGGSGGGSGGGGSK(BrAc)]	C- term/(GGGGS)3	0.032	41.3
1163-1	5G12-D88C-3157736	[Aib8; Glu22-Lys26; Gly36]GLP-1(7-37)[GGGSGGGSGGGGSK(BrAc)]	C- term/(GGGGS)3	0.01	275.5
1164-1	5G12-E384C- 3157736	[Aib8; Glu22-Lys26; Gly36]GLP-1(7-37)[GGGSGGGSGGGGSK(BrAc)]	C- term/(GGGGS)3	0.053	26.8
1165-1	5G12-T487C- 3157736	[Aib8; Glu22-Lys26; Gly36]GLP-1(7-37)[GGGSGGGSGGGGSK(BrAc)]	C- term/(GGGGS)3	0.014	34
1172-1	5G12-E384C- 3169019	cyclo[E22-K26][Aib8, Lys(NPeg11-BrAc)37]GLP-1(7-37)-Amide	Lys37/PEG11	0.044	50
1198-1	5G12-E384C- 3169018	[Aib8, 22; Gly36; Lys(NPeg27-BrAc)37]GLP-1(7-37)-Amide	Lys37/PEG27	0.0329	98.5

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1199-1	5G12-T487C-3169018	[Aib8,22;Gly36;Lys(NPeg27-BrAc)37][GLP-1(7-37)-Amide]	Lys37/PEG27	0.006	84
1200-1	5G12-E384C-3172563	[Aib8;Glu23-Lys27;Gly36][GLP-1(7-37)][GGGSGGGSGGGGSK(BrAc)]	C-term/(GGGGS)3	0.045	40.4
1201-1	5G12-T487C-3172563-DAR2	[Aib8;Glu23-Lys27;Gly36][GLP-1(7-37)][GGGSGGGSGGGGSK(BrAc)]	C-term/(GGGGS)3	0.011	35
1202-1	5G12-T487C-3172563-DAR1	[Aib8;Glu23-Lys27;Gly36][GLP-1(7-37)][GGGSGGGSGGGGSK(BrAc)]	C-term/(GGGGS)3	0.01	30
1203-1	5G12-T487C-3167736-DAR1	[Aib8;Glu22-Lys26;Gly36][GLP-1(7-37)][GGGSGGGSGGGGSK(BrAc)]	C-term/(GGGGS)3	0.0072	45.4
1227-1	5G12-E384C-3173043	[Aib8,22]-GLP-1(7-22)-Ex4(17-39)[GGGSGGGSGGGGSK(BrAc)]	C-term/(GGGGS)3	0.0236	96.5
1228-1	5G12-E384C-3173044	[Aib8,22;Gly36][GLP-1(7-37)-1K2015-Lys(BrAc)]	C-term/1Kmod	0.0306	103.8
1229-1	5G12-E384C-3340181	Exendin-4(1-39)[GGGSGGGSGGGGSK(BrAc)]	C-term/(GGGGS)3	0.013	84.9
1230-1	5G12-E384C-3340577	[Gly8,36;Glu22][GLP-1(7-37)][GGGSGGGSGGGGSK(BrAc)]	C-term/(GGGGS)3	0.0376	92.2
1231-1	5G12-E384C-3340578	[Aib8;Glu22;Gly36][GLP-1(7-37)][GGGSGGGSGGGGSK(BrAc)]	C-term/(GGGGS)3	0.0297	101.9
1233-1	aGIPR 5G12 E384C Ab-3342048	[Aib8,22;Glu15;Gly36;Lys][GLP-1(7-37)-(G4S)3K(BrAc)-amide]	C-term/(GGGGS)3	0.118	121
1234-1	aGIPR 5G12 E384C Ab-3341281	[Aib8,22;Gly36][GLP-1(7-37)-(G4S)2K(BrAc)-amide]	Lys37(C-term)/(GGGGS)2	0.0446	108
1235-1	aGIPR 5G12 E384C Ab-3341282	[Aib8,22;Gly36][GLP-1(7-37)-AS(AP)5GSK(BrAc)-amide]	C-term/AS(AP)5GS	0.0311	122
1237-1	aGIPR 5G12 SEFL2 E384C-3341284	[Aib8,22;Gly36][GLP-1(7-37)-Pro-Ser-Ser-Gly-Ala-Pro-Pro-Pro-Ser-(G4S)2K(AcBr)]	C-term/(GGGGS)2	0.0226	83.5
1238-1	aGIPR 5G12 SEFL2 E384C-3341285	[Aib8;Tyr16;Glu22;Gly36][GLP-1(7-37)-(G4S)3-K(AcBr)]	C-term/(GGGGS)3	0.0046	82.8
1239-1	aGIPR 6H1 SEFL2 E384C-3166119	[Aib8,22;Gly36][GLP-1(7-37)-G4S3-Lys(BrAc)]	C-term/(GGGGS)3	0.126	34.3
1240-1	aGIPR 5G12 SEFL2 E384C-3342047	[Aib8,22;Ile9;Gly36][GLP-1(7-36)-(G4S)3-K(AcBr)]	C-term/(GGGGS)3	0.0552	111

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1241-1	aGIPR 5G12 SEFL2 E384C-3342049	[Aib8,22;Ala9;Gly36]GLP-1_ (7-36)-(G4S)3-K(AcBr)	C- term/(GGGGGS)3	0.0549	92.3
1242-1	aGIPR 5G12 SEFL2 E384C-3342050	[Aib8,22;Ala29;Gly36]GLP-1_ (7-36)-(G4S)3-K(AcBr)	C- term/(GGGGGS)3	0.173	92.4
1243-1	aGIPR 5G12 SEFL2 E384C-3342051	[Aib8,22;Ala31;Gly36]GLP-1_ (7-36)-(G4S)3-K(AcBr)	C- term/(GGGGGS)3	1.147	75.9
1248-1	aGIPR 2G10 SEFL2 E384C-3166119	[Aib8,22;Gly36]GLP-1(7-37)[GGGGSGGGSGGGGS(BrAc)]	C- term/(GGGGGS)3	0.015	68.9
1250-1	aGIPR 5G12 SEFL2 E384C-3343106	[Aib8,22;Thr9;Gly36]GLP-1_ (7-37)-(G4S)3-K(AcBr)	C- term/(GGGGGS)3	0.069	85
1251-1	aGIPR 5G12 SEFL2 E384C-3343109	[Aib8,22;Glu15;Ala31;Gly36]GLP-1_ (7-37)-(G4S)3-K(AcBr)	C- term/(GGGGGS)3	0.32	85
1252-1	aGIPR 5G12 SEFL2 E384C-3343110	[Aib8,22;Ala31;Gly36]GLP-1_ (7-37)-(G4S)3-K(AcBr)	C- term/(GGGGGS)3	0.2	78.8
1253-1	aGIPR 5G12 SEFL2 E384C-3343906	[Aib8,22;LysG4S3G(AcBr)26;Gly36]GLP-1_ (7-37)	Lys26/(GGGGGS)3	0.0013	77.4
1253-2	aGIPR 5G12 SEFL2 E384C-3343906	[Aib8,22;LysG4S3G(AcBr)26;Gly36]GLP-1_ (7-37)	Lys26/(GGGGGS)3	0.0084	51.4
1254-1	aGIPR 5G12 SEFL2 E384C-3343905	[Aib8,22;Tyr16;Gly36]GLP-1_ (7-37)-(G4S)3-K(AcBr)	C- term/(GGGGGS)3	0.0058	73.8
1255-1	aGIPR 2G10 SEFL2 E384C-3341281	[Aib8,22;Gly36]GLP-1(7-37)-G4S2K(BrAc)	C- term/(GGGGGS)2	0.026	56.4
1256-1	aGIPR 2G10 SEFL2 E384C-3343106	[Aib8,22;Thr9;Gly36]GLP-1(7-37)-G4S2K(BrAc)	C- term/(GGGGGS)3	0.104	66
1257-1	aGIPR 2G10 SEFL2 E384C-3340578	[Aib8,22;Glu22;Gly36]GLP-1(7-37)-G4S3-K(BrAc)	C- term/(GGGGGS)3	0.011	66
1258-1	2G10 SEFL2 E384C- 3343109	[Aib8,22;Glu15;Ala31;Gly36]GLP-1_ (7-37)-(G4S)3-K(AcBr)	C- term/(GGGGGS)3	3.58	53.9
1261-1	2G10 SEFL2 E384C- 3343110	[Aib8,22;Ala31;Gly36]GLP-1_ (7-37)-(G4S)3-K(AcBr)	C- term/(GGGGGS)3	0.096	41.9
1262-1	aGIPR 2G10 SEFL2 E384C-3343905	[Aib8,22;Tyr16;Gly36]GLP-1_ (7-37)-(G4S)3-K(AcBr)	C- term/(GGGGGS)3	0.0347	52.9
1263-1	aGIPR 2G10 SEFL2 E384C-3343906	[Aib8,22;LysG4S3G(AcBr)26;Gly36]GLP-1_ (7-37)	Lys26/(GGGGGS)3	0.0143	48.7

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1264-1	2G10 SEFL2 E384C-3344713	[Aib8,22;Glu15;Gly36]GLP-1_(7-37)-(G4S)3-K(AcBr)	C-term/(GGGGS)3	0.0459	48.6
1264-2	2G10 SEFL2 E384C-3344713	[Aib8,22;Glu15;Gly36]GLP-1_(7-37)-(G4S)3-K(AcBr)	C-term/(GGGGS)3	0.112	40.3
1265-1	2G10 SEFL2 E384C-3344748	[Aib8,22;Tyr16;Gly36]GLP-1_(7-37)-(GGGGSGG)-K(AcBr)	C-term/(GGGGSGG)	0.0439	50.4
1265-2	2G10 SEFL2 E384C-3344748	[Aib8,22;Tyr16;Gly36]GLP-1_(7-37)-(GGGGSGG)-K(AcBr)	C-term/(GGGGSGG)	0.177	50.4
1267-1	aGIPR 2G10 SEFL2 E384C-3169019	cyclo[E22-K26][Aib8;(NPeg11-BrAc)37]GLP-1(7-37)-Amide	Lys37/PEG11	0.004	49.3
1269-1	aGIPR 5G12 SEFL2-E384C-3344713	[Aib8,22;Glu15;Gly36]GLP-1_(7-37)-(G4S)3-K(AcBr)	C-term/(GGGGS)3	0.0169	57.4
1270-1	aGIPR 5G12 SEFL2-E384C-3344748	[Aib8,22;Tyr16;Gly36]GLP-1_(7-37)-(GGGGSGG)-K(AcBr)	C-term/(GGGGS)3	0.0298	50.9
1272-1	aGIPR 2G10 SEFL2-E384C-3161655	[Aib8,22;Gly36]GLP-1_(7-37)-PEG11-AcBr	Lys37/PEG11	0.055	53
1273-1	aGIPR 2G10 SEFL2-E384C-3341285	[Aib8;Tyr16;Glu22;Gly36]GLP-1_(7-37)-(GGGGSGG)-K(AcBr)	C-term/(GGGGS)3	0.061	42.3
1274-1	aGIPR 2G10 SEFL2-E384C-3345837	[Aib8,22]-GLP-1(7-22)-Ex4(17-39)-(G4S)K-BrAc	C-term/(GGGGS)	0.199	36.4
1281-1	aGIPR 2G10 SEFL2-E384C-3345836	[Aib8,22]-GLP-1(7-22)-Ex4(17-39)-(G4S)2K-BrAc	C-term/(GGGGS)2	0.177	47.9
1282-1	aGIPR 2G10 SEFL2-E384C-3173043	[Aib8,22]-GLP-1(7-22)-Ex4(17-39)-(G4S)3K-BrAc	C-term/(GGGGS)3	0.094	43.9
1283-1	aGIPR 5G12 SEFL2-E384C-3345836	[Aib8,22]-GLP-1(7-22)-Ex4(17-39)-(G4S)2K-BrAc	C-term/(GGGGS)2	0.139	67.8
1284-1	aGIPR 5G12 SEFL2-E384C-3345837	[Aib8,22]-GLP-1(7-22)-Ex4(17-39)-(G4S)K-BrAc	C-term/(GGGGS)	0.154	63.8

[0413] Example 3

[0414] **Methods for In vitro and in vivo assay**

[0415] **GLP-1 receptor agonist activity**

[0416] CHOK1 cells stably expressing the human GLP-1R alone or both GLP-1R and GIPR
5 (M1) were used to measure peptide/conjugate-induced cAMP production in a homogeneous
time-resolved fluorescence (HTRF) assay (CISBIO, cat# 62AM4PEJ). Serial diluted
peptides/conjugates (3×10^{-7} M – 3×10^{-14} M) were incubated with 40,000 cells in assay buffer
(0.1% BSA, 500 uM IBMX in F12 media) for 15 min at 37°C. Cells were then lysed with
lysis buffer containing cAMP-d2 and cAMP cryptate (CISBIO) and incubated for 1 hour at
10 room temperature before measured in Evision plate reader (PerkinElmer). The cAMP levels
are expressed as a fluorescence ratio of 665/620 nm and shown in Figures 2A-2E and Figure
3.

[0417] Example 4

[0418] **GIPR antagonist activity**

15 [0419] HEK 293T cells stably expressing the human GIPR were used to measure
peptide/conjugate-induced cAMP generation in HTRF assay (Cisbio, cat# 62AM4PEJ).
Serial diluted conjugates or GIPR antibody (3×10^{-6} M – 1×10^{-11} M) were incubated with
30,000 cells in assay buffer (0.1% BSA, 500 uM IBMX in F12 media) for 30 min at 37°C
before being treated with GIP at final concentration of 0.05 nM. Cells were incubated for 30
20 min at 37°C and then lysed in lysis buffer containing cAMP-d2 and cAMP cryptate (CISBIO)
for 1 hour at room temperature. The fluorescence was measured in Evision plate reader
(PerkinElmer) and the cAMP levels are expressed as a ratio of 665/620 nm and shown in
Figures 2A-2E and Figure.

[0420] Example 5

25 [0421] **Materials and Methods for Bispecific-mouse *in vivo***

[0422] Diabetic mice were selected primarily to screen for GLP-1 activity of the bispecific
molecules. Molecules were selected based on their potential to reduce plasma glucose levels
at different time points post injection. In addition, body weight loss or inhibition of body
weight gain was also measured indicative of GLP-1 activity, GIPR inhibition, or a
30 combination of both, either from co-administration of each or from the bispecific molecule as
shown in Figures 4A-4I. Male db/db mice (#642) were obtained from Jackson Laboratories
(Bar Harbor, ME) and delivered at 8-9 weeks of age. Upon arrival, mice were group-housed
at four per cage and maintained in controlled environmental conditions with 12 hour light

(6:30 AM – 6:30 PM) and dark cycles (6:30 PM – 6:30 AM). Mice were fed a standard rodent chow diet (2020x Harlan Teklad) with free-access to drinking water.

[0423] In other studies, glucose tolerance test was used to rank the potency of GLP-1 analogs (Figures 5A-5C). C57Bl6 mice were acclimated to environment conditions for one to two weeks. Prior to dosing, mice were handled and body weight measurements were taken. One day prior to dosing, conscious mice were bled from the retro-orbital sinus for plasma glucose measurement using a handheld glucometer designed for rodent plasma. On the day of dosing, baseline plasma glucose and body weight measurements were taken. The cage mean for plasma glucose and body weight were used to stratify cages into treatment groups. Mice were maintained in their home cages. Following administration of test article, plasma glucose was measured at various time points at (1, 3, and 6hr) or (4hr) and plasma glucose and body weight measurements were taken every 24hrs thereafter. Plasma glucose levels were measured until levels returned to near baseline levels and body weight measurements were taken until the rate of body weight gain was similar to Vehicle-treated control group.

[0424] Diet-induced obese mice (DIO) were also used as a model to measure weight loss effects from treatment with different molecules as shown in Figure 6.

[0425] Male c57bl6 mice were obtained from Harlan Laboratories and delivered at 26 days of age. Mice were group-housed with littermates consisting between two to four mice per cage. Following one week of acclimation, mice were started on a feeding regimen of high-fat diet (HFD: D12492, Research Diets, New Brunswick, NJ) or continued on standard rodent diet (2020x, Harlan Laboratories). After 12 weeks of feeding, single-housed mice were acclimated to routine handling, food intake measurement, and daily saline injections (IP). Blood was collected from the retro orbital sinus of conscious DIO mice. A small volume of blood was immediately placed on a handheld glucometer designed for rodent plasma and the remaining blood was placed in EDTA filled collection tubes with a protease-inhibitor cocktail (Roche Diagnostics, Indianapolis, IN). Following centrifugation, plasma was stored at -80C. Mice were stratified into treatment groups based on body weight, and plasma glucose measurements. Mice were treated with Vehicle (Q3D), GIPR Ab (2.5 or 10 mg/kg, Q3D), GLP-1 Peptide (0.06 mg/kg, QD), Dulaglutide (1 mg/kg, Q3D), or bispecific conjugate (2.5 or 10 mg/kg, Q3D). 2 additional groups of mice received a combination treatment of GLP-1 and GIPR Ab with the above dosage and dose frequency (GIPR 2.5 mg/kg + GLP-1 Peptide and GIPR 2.5 mg/kg + Dulaglutide). Aside from the GLP-1 Peptide dosed groups, all other mice were injected with saline when not dosed with their respective test article. Body weight was measured daily and cumulative food intake over three days was averaged for a daily food intake value. Food intake

was measured between study days 0-3 and days 6-9. A blood collection was taken on study Day 9, 1 hour post injection and a terminal blood collection was taken on study Day 12, 1 or 3 days post the previous test article injection.

[0426] Plasma insulin was measured with a mouse ELISA kit following manufacturer's instructions (ALPCO, Salem, NH). Plasma glucose, cholesterol, triglyceride, non-esterified fatty acids, AST, and ALT were measured using an Olympus AU400e Chemistry Analyzer (Olympus America, Center Valley, PA).

[0427] Example 6

[0428] **Materials and Methods for Bispecific-cyno *in vivo***

10 [0429] Naive male spontaneously obese cynomolgus monkeys (age 9-14 years) were acclimated/trained to experimental procedures prior to study initiation and were sorted into 7 treatment groups with n=10 monkeys each with equal distribution among groups for all sorting parameters (body weight and blood chemistries). Monkeys were then injected once weekly for 6 weeks with vehicle or GLP-1R-GIPR conjugates (1264, 1273, 1248 or 1257). After the 6
15 week treatment period, monkeys went through a 4 week washout phase. During training/treatment/washout phases of study, total energy intake was monitored daily; body weight, blood chemistries and drug exposure were monitored weekly or every other week as shown in Figures 7-21.

[0430] Example 7

20 [0431] **Materials and Methods for GIP and GLP-1 Radioligand Competition Binding Assay**

[0432] Membranes were prepared from mammalian cell lines overexpressing hu GIPR and hu GLP-1R and were typically stored at -80°C in Assay Buffer: 50 mM HEPES (7.4), 5 mM MgCl₂, 1mM CaCl₂, 0.2% BSA and Protease Inhibitor Tablets "EDTA Free". Unlabeled GIP
25 and GLP-1 peptides were obtained from Phoenix Pharmaceuticals and Radiolabeled ¹²⁵I-GIP and ¹²⁵I-GLP-1 were ordered from Perkin Elmer. Primary reactions were conducted for 2h at room temperature with shaking in 96 well cell culture round bottom plates (Costar). Cell membrane concentration was fixed at 0.6 mg/mL and radioligands were used at a concentration of 0.1 nM. Test articles were titrated at six concentrations in duplicate. The primary plate was
30 harvested after two hours with ice cold 50 mM TRIS (pH 7.4) using a Filtermate Harvester (Perkin Elmer) and cell membranes were captured on PEI-treated GF/C UniFilter plates (Perkin Elmer). Plates were dried for 15 min using a vacuum oven and Microscint 20 was added to each well before counting in a Perkin Elmer TopCount NXT HTS instrument. Specific binding was determined by taking the difference of total and non-specific counts. Non-specific wells

contained 1 μ M cold ligand. Data was analyzed and plotted using GraphPad Prism 7 as shown in Figure 22.

[0433] Example 8

[0434] **Internalization assay**

5 [0435] GLP-1R and GIPR internalization were assessed in CHOK1 cells expressing both human GLP-1R and GIPR. Cells were plated at a density of 25,000 cells/well in 96 well plates and cultured overnight at 37°C, 5% CO₂. Cells were serum starved in F12 media (Thermo Fisher) with 0.1% BSA for 4 hours prior to treatment. Cells were treated with 20nM or dose titrations of GLP-1, GIP or bispecific conjugates for 30minutes or the specified time in the
10 respective figures. Cells were washed and fixed with 4% formaldehyde and permeabilized with 0.1% triton-X 100. To detect GIPR or GLP-1R, cells were first blocked with Odyssey blocking buffer (LiCor) for 1 hour at room temperature and incubated with 2 μ g/ml of mouse anti-human GLP-1R (R&D systems) or 5 μ g/ml of anti-human GIPR antibody (R&D Systems) at 4°C overnight followed by AlexaFluor-555 or Alexa-Fluor 647 conjugated anti-mouse secondary
15 antibody (Thermo Fisher) for GLP-1R or GIPR detection, respectively. Images (Figure 23) were captured using Operetta high content Imaging system (Perkin Elmer) and analyzed by using the Harmony software (Perkin Elmer) to quantify the intracellular GLP-1R content (total spot area) as the readout parameter for the degree of internalization (Figure 24).

[0436] Example 9

20 [0437] **GLP-1R, GIPR and bispecific conjugate are co-localized upon internalization**

[0438] U2OS cells expressing GIPR and SNAP-GLP-1R were plated at a density of 15,000 cells per well in 96 well plate and cultured overnight at 37°C with 5% CO₂. Prior to treatment, cells were starved for 3.5 hours in McCoy's 5A media (Thermo Fisher) with 0.1% BSA. Prior to treatment, GLP-1R on the surface of U2OS cells were labeled with Alexa-Fluor 564 by
25 incubating with SNAP-Surface Alexa-fluor 564 substrate (New England Biolabs) for 30 minutes. Cells were then washed to remove excess label and treated with 5nM bispecific conjugates for 30 minutes. After 3 washes, cells were fixed with 4% formaldehyde and permeabilized with 0.1% triton-X 100 in PBS. For GIPR detection, cells were first blocked with Odyssey blocking buffer (LiCor) for 1 hour at room temperature and then incubated with
30 5 μ g/ml of mouse anti-human GIPR (R&D Systems) at 4°C overnight followed by incubation with Alexa-Fluor 647 conjugated anti-mouse secondary antibody (Thermo Fisher) for 1 hour at room temperature. Bispecific conjugate was detected using Alexa-Fluor labeled anti-Human Fc antibody. Hoechst 33342 were used for nuclei detection (Thermo Fisher). Images were

captured using Operetta CLS high content Imaging system (Perkin Elmer) as shown in Figure 25.

[0439] Example 10

[0440] **GloSensor cAMP assay**

5 [0441] The GloSensor cAMP assay was conducted per manufacturer's protocol (Promega). In brief, CHO-K1 human GLP-1R/GIPR-expressing cells were seeded at 15,000 cells per well in a 96 well plate and incubated for 16 hours in a humidified 37°C, 5% CO₂ incubator. Cells were transiently transfected with 100 ng pGloSensor -22F cAMP plasmid using FuGENE HD for 24 hours. Cells were then equilibrated with 0.1% BSA, 2% GloSensor cAMP reagent in CO₂ independent media (Invitrogen) for 2 hours at room temperature. Cells were preincubated for 10 15 min with or without 0.43 M sucrose (Sigma). Basal luminescence measurements were taken for 10 minutes prior to addition of 1248 in conditions with or without sucrose. Immediately following addition of 1248, kinetic luminescence was measured using an integration time of 0.1-1 second every 60 seconds. Data were analyzed using GraphPad Prism software and presented in Figure 26.

[0442] Example 11

[0443] **FACS analysis**

[0444] CHOK1-GLP-1R H20, 293T-GIPR clone 10 and CHOK1-GLP-1R/GIPR cells were suspended at a density of 1×10^6 cells in 100ul of F12 assay media containing 1% FBS, 0.05% sodium azide and incubated with 10ug/ml of indicated antibodies or anti-GIPR/GLP-1R bispecific conjugates for 1 hr at 4°C. Cells were washed one time with assay buffer and then incubated with 10ug/ml of Alexa Fluor 647-goat anti-human Fc (Jackson) for 30min at 4°C. The Fluorescence was measured using BD LSR II Flow Cytometer (BD Biosciences) and shown in Figure 27.

25 [0445] Example 12

[0446] **Calcium flux assay**

[0447] CHOK1 cells expressing GIPR and GLP-1-R were plated at a density of 30,000 cells per well in 96 well black clear bottom plate and cultured overnight at 37°C with 5% CO₂. Cells were serum starved in F12 media (Thermo Fisher) with 20mM HEPES for 2 hours. Cells were then loaded with buffer containing the calcium-sensitive dye (BD Biosciences) and incubated 30 for 1 hour at room temperature before being treated with dose titrations of GLP-1 or bispecific conjugates. Changes in intracellular calcium content were monitored for using a FLIPR (Molecular Devices). Maximum peak height in each well was recorded as representing calcium influx as shown in Figure 28.

[0448] Example 13

[0449] **Beta- arrestin assay**

[0450] CHOK1 Pathhunter cells expressing ProLink™ tagged GLP-1R and GIPR from DiscoverX were transfected with un-tagged GIPR or GLP-1R, respectively. Cells were plated
5 at a density of 20,000 cells per well in assay media (F12/0.1%BSA) and incubated at 37°C overnight. Cells were treated with dose titrations of GLP-1, GIP or bispecific conjugates for 90 minutes. The working detection solution (DiscoverX) were then added to the cells and incubated for 60 min at room temp in the dark. Chemiluminescent signal representing beta-arrestin recruitments were measured using Envision and shown in Figure 29.

10 [0451] Example 14

[0452] **Human pancreatic islet microtissues glucose stimulated insulin secretion (GSIS) assay**

[0453] Human pancreatic islet microtissues were purchased from InSphero in 96 well format. Microtissues were incubated for 16 hours in InSphero assay media. They were then treated for
15 1 hour with fresh KREBS buffer (129 mM NaCl, 4.8 mM KCl, 1.2 mM KH₂PO₄, 1.2 mM MgSO₄-7H₂O, 10 mM HEPES, 1.3 mM CaCl₂, 0.5% BSA, pH 7.4) with 2.8 mM glucose. Following 2 KREBS buffer washes, they were then incubated with KREBS buffer alone, 2.8 mM or 11 mM glucose in KREBS buffer with or without GLP-1 (Phoenix Pharmaceuticals) and a dose response of 1248 for 16 hours. Supernatant was collected and analyzed for insulin
20 secretion according to manufacturer's protocol (Mercodia). Optical density was read at 450 nm on a TECAN microplate reader and shown in Figure 30.

CLAIMS

What is claimed is:

1. 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 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: 702, SEQ ID NO:
859, SEQ ID NO: 1016, SEQ ID NO: 1173, SEQ ID NO: 1330; and SEQ ID NO:
1487; and

the antibody or functional fragment thereof comprises a cysteine or non-
canonical amino acid amino acid substitution at one or more conjugation site(s)
selected from the group consisting of

D70 of the antibody light chain relative to reference sequence SEQ ID NO:
455,

E276 of the antibody heavy chain relative to reference sequence SEQ ID NO:
612, and

T363 of the antibody heavy chain relative to reference sequence SEQ ID NO:
612; and

b) a GLP-1 receptor agonist, wherein the GLP-1 receptor agonist comprises
[Aib⁸;Tyr¹⁶;Glu²²;Gly³⁶]GLP-1_(7-37) (SEQ ID NO: 3244) and is conjugated to
the antibody or functional fragment thereof through the side-chain of the cysteine
residue or non-canonical amino acid residue substituted at the one or more
conjugation site(s).

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
antibody, a chimeric antibody, or a multispecific antibody.

4. The composition of claim 3, wherein said antibody or functional fragment thereof is a human antibody.

5. The composition of claim 3, wherein said antibody or functional fragment thereof is a monoclonal antibody.

5 6. The composition of claim 3, wherein said antibody or functional fragment thereof is of the IgG1-, IgG2- IgG3- or IgG4-type.

7. The composition of claim 6, wherein said antibody or functional fragment thereof is of the IgG1- or the IgG2-type.

8. The composition of one of claim 3, wherein said antibody or functional
10 fragment thereof inhibits binding of GIP to the extracellular portion of human GIPR.

9. The composition of claim 3, wherein said antibody or functional fragment thereof comprises a light chain variable region comprising SEQ ID NO: 74 and a heavy chain variable region comprising SEQ ID NO: 231, wherein

the antibody or functional fragment thereof comprises a cysteine or non-canonical
15 amino acid amino acid substitution at E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612.

10. The composition of claim 3, wherein said antibody or functional fragment thereof comprises a light chain comprising SEQ ID NO: 388 and a heavy chain comprising
20 SEQ ID NO: 545, wherein

the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at

E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612.

25 11. The composition of claim 1, wherein the GLP-1 receptor agonist is conjugated to the antibody or functional fragment thereof at a C-terminal amine group of said agonist.

12. The composition of claim 1, wherein the GLP-1 receptor agonist if conjugated to the antibody or functional fragment thereof via a peptide linker comprising a sequence selected from the group consisting of (Gly₃Ser)₂, (Gly₄Ser)₂, (Gly₃Ser)₃, (Gly₄Ser)₃,
30 (Gly₃Ser)₄, (Gly₄Ser)₄, (Gly₃Ser)₅, (Gly₄Ser)₅, (Gly₃Ser)₆, and (Gly₄Ser)₆.

13. Use of a composition according to claim 1, in the manufacture of a medicament for treating a metabolic disorder, wherein the metabolic disorder is selected from the group consisting of hyperglycemia, hyperinsulinemia, glucose intolerance, insulin resistance, diabetes mellitus, Type 2 diabetes, dyslipidemia, metabolic syndrome (Syndrome X or insulin resistance syndrome), glucosuria, metabolic acidosis, diabetic neuropathy, diabetic nephropathy, diabetic retinopathy, diabetic cardiomyopathy, Type 1 diabetes, and obesity.