

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

FIELD OF THE INVENTION

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

BACKGROUND OF THE INVENTION

[0002] Glucose-dependent 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.

[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).

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

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

[0006] Glucagon-like peptide-1 (“GLP-1”) is a 31-amino acid peptide derived from the proglucagon gene. It is secreted by intestinal L-cells and released in response to food ingestion to induce insulin secretion from pancreatic β - cells (Diabetes 2004, 53:S3, 205-214). In addition to the incretin effects, GLP-1 also decreases glucagon secretion, delays gastric emptying and reduces caloric intake (Diabetes Care, 2003, 26(10): 2929-2940). GLP-1 exerts its effects by activation of the GLP-1 receptor, which belongs to a class B G-protein-coupled receptor (Endocrinology. 1993, 133(4):1907-10). The function of GLP-1 is limited by rapid degradation by the DPP-IV enzyme, resulting in a half-life of approximately 2 minutes. Recently, long-lasting GLP-1 receptor agonists such as exenatide, liraglutide, dulaglutide have been developed and are now being used clinically to improve glycemic control in patients with type 2 diabetes. Furthermore, GLP-1 receptor agonists also promote body weight reduction as well as reduction in blood pressure and plasma cholesterol levels in patients (Bioorg. Med. Chem.Lett 2013, 23:4011-4018).

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

SUMMARY OF THE INVENTION

[0007a] In one aspect, the present invention provides an isolated antigen binding protein that specifically binds to a human gastric inhibitory peptide receptor (GIPR) polypeptide, wherein said antigen binding protein is an antibody or a fragment thereof, and wherein said antibody comprises a CDRL1, a CDRL2, a CDRL3, a CDRH1, a CDRH2, and a CDRH3, wherein said CDRL1 comprises SEQ ID NO: 702 ; said CDRL2 comprises SEQ ID NO: 859; said CDRL3 comprises SEQ ID NO: 1016; said CDRH1 comprises SEQ ID NO: 1173; said CDRH2 comprises SEQ ID NO: 1330; and said CDRH3 comprises SEQ ID NO: 1487.

[0007b] In another aspect, the present invention provides a pharmaceutical composition comprising at least one antibody or fragment thereof as disclosed herein, and pharmaceutically acceptable excipient.

[0008] Disclosed is a method of treating a subject with a metabolic disorder, the method comprising administering to the subject a therapeutically effective amount of an antigen binding protein that specifically binds to a protein having an amino acid sequence having at least 90% amino acid sequence identity to an amino acid sequence of a GIPR. Also disclosed is a method of treating a subject with a metabolic disorder, the method comprising administering to the subject a therapeutically effective amount of a GLP-1 receptor agonist and a therapeutically effective amount of a GIPR antagonist that specifically binds to a protein having an amino acid sequence having at least 90% amino acid sequence identity to an amino acid sequence of a GIPR. In one 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 antigen binding protein reduces body weight in an obese subject. In another example, administering the antigen binding protein reduces body weight gain in an obese subject. In another example, administering the antigen binding protein reduces fat mass in an obese subject. In another example, the glucose metabolism disorder comprises insulin resistance and administering the antigen binding protein reduces insulin resistance in an obese subject. In another example, administering the antigen binding protein reduces liver steatosis in an obese subject having increased liver steatosis. In another example, administering the antigen binding protein reduces liver fat content in an obese subject having increased liver fat content.

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

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

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

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

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

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

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

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

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

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

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

[0019] 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; 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); and Gly^{8,36},Glu²²,Asn³⁴-GLP-1(7-

36) (SEQ ID NO: 3202).

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

[0021] Also disclosed is an antigen binding protein that specifically binds to a human GIPR polypeptide and inhibits activation of GIPR by GIP ligand. In one example, the antigen binding protein inhibits GIP ligand binding to GIPR. In another example, the antigen binding protein is a human antigen binding protein. In another example, the antigen binding protein is a human antibody. In another example, the antigen binding protein is a monoclonal antibody.

[0022] Also disclosed is a pharmaceutical composition comprising at least one antigen binding protein according to any one of the foregoing examples.

[0023] Also disclosed is a nucleic acid molecule encoding an antigen binding protein according to any one of the foregoing examples.

[0024] Also disclosed is a vector comprising a nucleic acid molecule encoding an antigen binding protein according to any one of the foregoing examples.

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

[0026] Also disclosed is a method of making an antigen binding protein according to any one of the foregoing examples, the method comprising expressing the antigen binding protein in a host cell that secretes the antigen binding protein, and then purifying the antigen binding protein from the cell culture media. Also disclosed is an antigen binding protein that specifically binds to a human GIPR polypeptide purified from the host cell.

[0027] Also disclosed is an antigen binding protein of any one of the foregoing examples or a pharmaceutical composition of any one of the foregoing examples for use in therapy.

BRIEF DESCRIPTION OF THE DRAWINGS

[0028] Figure 1. Mouse Pharmacodynamic Assay To Test GIPR Antibodies - Study Design

[0029] Figure 2. GIPR Antibody 2.63.1 Antagonized GIP Induced Insulin Secretion

[0030] Figure 3. Chronic Treatment Of Diet Induced Obese Mice With GIPR Antibody 2.63.1 - Study Design

[0031] Figure 4. GIPR Antibody 2.63.1 Results In Reduced Body Weight Gain

[0032] Figure 5. GIPR Antibody 2.63.1 Results In Lower Fat Mass

[0033] Figure 6. GIPR Antibody 2.63.1 Results In Lower Epididymal White Adipose Tissue Weights

[0034] Figure 7. GIPR Antibody 2.63.1 Results In Lower Fasting Glucose Levels

[0035] Figure 8. GIPR Antibody 2.63.1 Results In Lower Insulin Levels

[0036] Figure 9. GIPR Antibody 2.63.1 Results In Improved Glucose Tolerance

[0037] Figure 10. GIPR Antibody 2.63.1 Results In Lower Serum Total Cholesterol And Triglycerides

[0038] Figure 11. GIPR Antibody 2.63.1 Results In A Reduction In Hepatocyte Microvesicular Change And Corresponding Lipid Accumulation

[0039] Figure 12. GIPR Antibody 2.63.1 Results In Reduced Liver Weight And Triglyceride Content

[0040] Figure 13. Reduced Inflammation And Reduced Infiltrating Macrophages Cells Surrounding Adipocytes In Epididymal White Adipose Tissue With GIPR Antibody 2.63.1 Treatment

[0041] Figures 14A-14Q. The graphs summarize the measured dissociation rate constant (1/s) for the tested samples binding with huGIPR ECD as well as IC₆₀ values for inhibition of GIP binding to huGIPR ECD.

[0042] Figure 15. 16H1 Family Binding to huGIPR ECD. 200nM huGIPR ECD binding to goat anti-huFc antibody captured anti-huGIPR antibody 6H1 family.

[0043] Figure 16. Mouse Pharmacodynamic Assay To Test GIPR Antibodies - Study Design

[0044] Figure 17. GIPR Antibody 5G12.006 Antagonized GIP Induced Insulin Secretion

[0045] Figure 18. Chronic Treatment Of Diet Induced Obese Mice With GIPR Antibody 5G12.006 - Study Design

[0046] Figure 19. GIPR Antibody 5G12.006 Results In Reduced Body Weight Gain

[0047] Figure 20. GIPR Antibody 5G12.006 Results In Improved Glucose Tolerance

[0048] Figure 21. GIPR Antibody 5G12.006 Results In Lower Glucose and Insulin Levels

- [0049] Figure 22. GIPR Antibody 5G12.006 Results In Lower Liver Weights
- [0050] Figure 23. GIPR Antibody 5G12.006 Results In Lower Total Cholesterol Levels
- [0051] Figure 24. Treatment Of Mice With Anti-GIPR 2.63.1 In Combination With Liraglutide - Study Design
- [0052] Figure 25. Body Weight Loss In Mice Treated With Anti-GIPR 2.63.1 In Combination With Liraglutide
- [0053] Figure 26. Significant Fat Mass Loss In Mice Treated With Anti-GIPR 2.63.1 In Combination With Liraglutide
- [0054] Figure 27. Food Intake In Mice Treated With Anti-GIPR 2.63.1 In Combination With Liraglutide
- [0055] Figure 28. Liver, Epididymal Fat And Inguinal Fat Weight In Mice Treated With Anti-GIPR 2.63.1 In Combination With Liraglutide
- [0056] Figure 29. Glucose Tolerance In Mice Treated With Anti-GIPR 2.63.1 In Combination With Liraglutide
- [0057] Figure 30. Blood Glucose Levels In Mice Treated With Anti-GIPR 2.63.1 In Combination With Liraglutide
- [0058] Figure 31. Plasma Insulin Levels In Mice Treated With Anti-GIPR 2.63.1 In Combination With Liraglutide
- [0059] Figure 32. Serum Total Cholesterol Levels In Mice Treated With Anti-GIPR 2.63.1 In Combination With Liraglutide
- [0060] Figure 33. Serum Leptin Level In Mice Treated With Anti-GIPR 2.63.1 In Combination With Liraglutide
- [0061] Figure 34. Serum Triglyceride In Mice Treated With Anti-GIPR 2.63.1 In Combination With Liraglutide
- [0062] Figure 35. Study In Mice Treated With Anti-GIPR 2.63.1 In Combination with Liraglutide, Dulaglutide Or Exendin IV
- [0063] Figure 36. Body Weight Loss In Mice Treated With Anti-GIPR 2.63.1 In Combination With Liraglutide, Dulaglutide Or Exendin IV
- [0064] Figure 37. Fat and Lean Mass In Mice Treated With Anti-GIPR 2.63.1 In Combination With Liraglutide, Dulaglutide Or Exendin IV
- [0065] Figure 38. Food Intake In Mice Treated With Anti-GIPR 2.63.1 In Combination With Liraglutide, Dulaglutide Or Exendin IV
- [0066] Figure 39. Insulin, Glucose And Glucose Tolerance In Mice Treated With Anti-GIPR 2.63.1 In Combination With Liraglutide, Dulaglutide Or Exendin IV

[0067] Figure 40. Serum Total Cholesterol And Triglyceride In Mice Treated With Anti-GIPR 2.63.1 In Combination With Liraglutide, Dulaglutide Or Exendin IV

[0068] Figure 41. Anti-GIPR Treatment In Mice Pre-treated with A GLP-1 Analog – Study Design. Diet-induced Obese (DIO) mice dosed with combination of 1) daily saline or Liraglutide (Lira), and 2) weekly vehicle or the GIPR Antibody (Ab). An overview of the study divided into 2 phases: Phase 1 consisted of two doses of Liraglutide. Phase 2 consisted of the GIPR Ab in addition to Liraglutide dosed mice from Phase 1. During Phase 1 and 2, a group of mice were simultaneously dosed with Liraglutide and GIPR Ab to establish the maximal percent weight loss.

[0069] Figures 42. (A) Body Weights – Combined Graphs and (B) Body Weights – Separated Graphs. Diet-induced Obese (DIO) mice dosed with combination of 1) daily saline or Liraglutide (Lira), and 2) weekly vehicle or the GIPR Antibody (Ab) and daily percent body weight change was calculated. The study was divided into 2 phases: Phase 1 established percent body weight change in response to two doses of Liraglutide. Phase 2 established percent body weight change of the GIPR Ab in addition to Liraglutide dosed mice from Phase 1. During Phase 1 and 2, a group of mice were simultaneously dosed with Liraglutide and GIPR Ab to establish the maximal percent weight loss.

[0070] Figure 43. Food Intake. Diet-induced Obese (DIO) mice dosed with combination of 1) daily saline or Liraglutide (Lira), and 2) weekly vehicle or the GIPR Antibody (Ab) and food intake was measured for 3 separate periods. The study was divided into 2 phases: Phase 1 established food intake changes at initiation of two doses of Liraglutide. Phase 2 established food intake changes at initiation and conclusion of the GIPR Ab in addition to Liraglutide dosed mice from Phase 1. During Phase 1 and 2, a group of mice were simultaneously dosed with Liraglutide and GIPR Ab to establish the maximal percent weight loss.

[0071] Figure 44. Insulin. Diet-induced Obese (DIO) mice dosed with combination of 1) daily saline or Liraglutide (Lira), and 2) weekly vehicle or the GIPR Antibody (Ab) and insulin was measured for 3 separate periods. The study was divided into 2 phases: Phase 1 established insulin levels prior to two doses of Liraglutide. Phase 2 established insulin levels prior to the GIPR Ab in addition to Liraglutide dosed mice from Phase 1 and at the conclusion of Phase 2. During Phase 1 and 2, a group of mice were simultaneously dosed with Liraglutide and GIPR Ab to establish the maximal percent weight loss.

[0072] Figure 45. (A) Clinical Chemistry – Liver Enzymes. (B) Clinical Chemistry – Cholesterol and Triglycerides. (C) Clinical Chemistry – NEFA and Glucose. Diet-induced

Obese (DIO) mice dosed with combination of 1) daily saline or Liraglutide (Lira), and 2) weekly vehicle or the GIPR Antibody (Ab) and liver enzymes, lipid levels, glucose and non-essential fatty acids were measured for 3 separate periods. The study was divided into 2 phases: Phase 1 established clinical chemistry levels prior to two doses of Liraglutide. Phase 2 established clinical chemistry levels prior to the GIPR Ab in addition to Liraglutide dosed mice from Phase 1 and at the conclusion of Phase 2. During Phase 1 and 2, a group of mice were simultaneously dosed with Liraglutide and GIPR Ab to establish the maximal percent weight loss.

[0073] Figure 46. Tissue Weights. Diet-induced Obese (DIO) mice dosed with combination of 1) daily saline or Liraglutide (Lira), and 2) weekly vehicle or the GIPR Antibody (Ab) and tissues were weighted at terminal tissue collection. The study was divided into 2 phases: Phase 1 consisted of two doses of Liraglutide. Phase 2 consisted of GIPR Ab in addition to Liraglutide dosed mice from Phase 1 and at the conclusion of Phase 2. During Phase 1 and 2, a group of mice were simultaneously dosed with Liraglutide and GIPR Ab to establish the maximal percent weight loss.

[0074] Figure 47. (A) Plasma Hormones. (B) Plasma Hormones (cont.). Diet-induced Obese (DIO) mice dosed with combination of 1) daily saline or Liraglutide (Lira), and 2) weekly vehicle or the GIPR Antibody (Ab) and mouse hormone levels were measured from the terminal blood collection. The study was divided into 2 phases: Phase 1 consisted of two doses of Liraglutide. Phase 2 consisted of the GIPR Ab in addition to Liraglutide dosed mice from Phase 1 and at the conclusion of Phase 2. During Phase 1 and 2, a group of mice were simultaneously dosed with Liraglutide and GIPR Ab to establish the maximal percent weight loss.

[0075] Figure 48. GIPR Ab chronic study design in spontaneously obese cynomolgus monkeys.

[0076] Figure 49. 2G10 causes body weight reduction in spontaneous obese cynomolgus monkeys with or without dulaglutide.

[0077] Figure 50. 2G10 alone causes body weight reduction in spontaneously obese cynomolgus monkeys (baseline reinitiated at day 15 prior starting 2G10 treatment).

[0078] Figure 51. 2G10 prevents increase in insulin and reduces triglycerides levels with or without Dulaglutide in overnight fasted spontaneously obese cynomolgus monkeys (% change from baseline).

[0079] Figure 52. 2G10 prevents increase in insulin levels and reduces triglycerides levels with or without Dulaglutide in overnight fasted spontaneously obese cynomolgus monkeys (raw data) post treatment phase (day 45).

[0080] Figure 53. 2G10 did not worsen OGTT in overnight fasted spontaneously obese cynomolgus monkeys with or without Dulaglutide post treatment phase (day 49).

[0081] Figure 54. 2G10 had no effects on total cholesterol, LDL-C and HDL-C levels in overnight fasted spontaneously obese cynomolgus monkeys post treatment phase (day 45).

[0082] Figure 55. 2G10 had no effects on glucose levels in overnight fasted normoglycemic obese cynomolgus monkeys post treatment phase (day 45).

[0083] Figure 56. 2G10 had no effects on liver enzymes in overnight fasted spontaneously obese cynomolgus monkeys post treatment phase (day 45).

[0084] Figure 57. Overall structure of the huGIPR-Fab 2G10 complex. A). The two pairs of complexes are packed against each within the asymmetric unit. The Fab 2G10 molecules are shown in cartoon representation and colored in white and cyan or wheat and dark green for their respective light chain and heavy chain combination. The huGIPR domain is shown in magenta and orange cartoon respectively. B). Close-up view of one huGIPR-Fab 2G10 complex. The molecules are colored as in panel A.

[0085] Figure 58. Binding interface. A). Close-up view of the binding interface highlighting the CDR loops of Fab 2G10. The heavy chain and light chain of Fab 2G10 are shown in cyan and white cartoon. The CDR loops for heavy chain and light chain are colored in the following order: CDR1: red (HC) or light red (LC); CDR2: green (HC) or light green (LC); and CDR3: blue (HC) or light blue (LC). The huGIPR is shown in magenta cartoon. B). Close-up view of the binding interface highlighting the huGIPR residues. huGIPR is shown in magenta cartoon and the residues that interact with Fab 2G10 are colored in blue.

[0086] Figure 59 Overall structure of the huGIPR-Fab 2C2 complex. A). The two pairs of complexes adopt an anti-parallel conformation in the asymmetric unit. The Fab 2C2 molecules are shown in cartoon representation and colored in white and cyan or wheat and dark green for their respective light chain and heavy chain combination. The huGIPR domain is shown in magenta and orange cartoon. B). Close-up view of one huGIPR-Fab 2C2 complex. The molecules are colored as in panel A.

[0087] Figure 60. Binding interface. A). Close-up view of the binding interface highlighting the CDR loops of Fab 2C2. The heavy chain and light chain of Fab 2C2 are shown in cyan and white cartoon. The CDR loops for heavy chain and light chain are colored in the

following order: CDR1: red (HC) or light red (LC); CDR2: green (HC) or light green (LC); and CDR3: blue (HC) or light blue (LC). The huGIPR is shown in magenta cartoon. B). Close-up view of the binding interface highlighting the huGIPR residues. huGIPR is shown in magenta cartoon and the residues that interact with Fab 2C2 are colored in blue.

[0088] Figure 61 Overall structure of the huGIPR-Fab 6H1 complex. The Fab molecule is shown in cartoon representation and colored in white and cyan for light chain and heavy chain combination. The huGIPR domain is shown in magenta.

[0089] Figure 62. Binding interface. A). Close-up view of the binding interface highlighting the CDR loops of Fab 6H1. The heavy chain and light chain of Fab 6H1 are shown in cyan and white cartoon. The CDR loops for heavy chain and light chain are colored in the following order: CDR1: red (HC) or light red (LC); CDR2: green (HC) or light green (LC); and CDR3: blue (HC) or light blue (LC). The huGIPR is shown in magenta cartoon. B). Close-up view of the binding interface highlighting the huGIPR residues. huGIPR is shown in magenta cartoon and the residues that interact with Fab 6H1 are colored in blue.

[0090] Figure 63 Overall structure of the huGIPR-Fab 17H11 complex. The Fab molecule is shown in cartoon representation and colored in white and cyan for light chain and heavy chain combination. The huGIPR domain is shown in magenta.

[0091] Figure 64. Binding interface. A). Close-up view of the binding interface highlighting the CDR loops of Fab 17H11. The heavy chain and light chain of Fab 17H11 are shown in cyan and white cartoon. The CDR loops for heavy chain and light chain are colored in the following order: CDR1: red (HC) or light red (LC); CDR2: green (HC) or light green (LC); and CDR3: blue (HC) or light blue (LC). The huGIPR is shown in magenta cartoon. B). Close-up view of the binding interface highlighting the huGIPR residues. huGIPR is shown in magenta cartoon and the residues that interact with Fab 17H11 are colored in blue.

[0092] Figure 65. Surface representation of antibody epitope. The GIPR ECD domain is shown in pink surface representation. The epitope for the four antibodies, A) 2G10, B) 2C2, C) 6H1 and D) 17H11, are highlighted in blue, green, cyan and orange respectively. Epitope for the Gipg013 (PDB: 4JH0) is highlighted in red in panel E.

DETAILED DESCRIPTION OF THE INVENTION

[0093] The present disclosure provides a method of treating a metabolic disorder, such as a disorder of glucose metabolism (e.g. Type 2 diabetes, elevated glucose levels, elevated insulin levels, dyslipidemia, metabolic syndrome (Syndrome X or insulin resistance syndrome), glucosuria, metabolic acidosis, Type 1 diabetes, obesity and conditions exacerbated by obesity) by blocking or interfering with the biological activity of GIP. In one embodiment, a therapeutically effective amount of an isolated human GIPR binding protein is administered to a subject in need thereof. Methods of administration and delivery are also provided.

[0094] 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.

[0095] The section headings used herein are for organizational purposes only and are not to be construed as limiting the subject matter described.

[0096] 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.

[0097] Generally, nomenclatures used in connection with, and techniques of, cell and tissue culture, molecular biology, immunology, microbiology, genetics and protein and nucleic acid chemistry and hybridization described herein are those well-known and commonly used in the art. The methods and techniques of the present application are generally performed according to conventional methods well known in the art and as described in various general and more specific references that are cited and discussed throughout the present specification unless otherwise indicated. See, e.g., Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 3rd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (2001), Ausubel et al., *Current Protocols in Molecular Biology*, Greene Publishing Associates (1992), and Harlow and Lane *Antibodies: A Laboratory Manual* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1990), which are incorporated herein by reference. Enzymatic reactions and purification techniques are performed according to manufacturer's specifications, as commonly accomplished in the art or as described herein. The terminology

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

[0098] It should be understood that this invention is not limited to the particular methodology, protocols, and reagents, etc., described herein and as such may vary. The terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the disclosed, which is defined solely by the claims.

[0099] 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 $\pm 1\%$.

[0100] Following convention, as used herein “a” and “an” mean “one or more” unless specifically indicated otherwise.

[0101] As used herein, the terms “amino acid” and “residue” are interchangeable and, when used in the context of a peptide or polypeptide, refer to both naturally occurring and synthetic amino acids, as well as amino acid analogs, amino acid mimetics and non-naturally occurring amino acids that are chemically similar to the naturally occurring amino acids.

[0102] A “naturally occurring amino acid” is an amino acid that is encoded by the genetic code, as well as those amino acids that are encoded by the genetic code that are modified after synthesis, e.g., hydroxyproline, γ -carboxyglutamate, and O-phosphoserine. An amino acid analog is a compound that has the same basic chemical structure as a naturally occurring amino acid, i.e., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs can have modified R groups (e.g., norleucine) or modified peptide backbones, but will retain the same basic chemical structure as a naturally occurring amino acid.

[0103] An “amino acid mimetic” is a chemical compound that has a structure that is different from the general chemical structure of an amino acid, but that functions in a manner similar to a naturally occurring amino acid. Examples include a methacryloyl or acryloyl derivative of an amide, β -, γ -, δ -amino acids (such as piperidine-4-carboxylic acid) and the like.

[0104] 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 (IgI), para-iodophenylalanine (pI-Phe), para-aminophenylalanine (4AmP or 4-Amino-Phe), 4-guanidino phenylalanine (Guf), glycyllsine (abbreviated “K(N ϵ -glycyl)” or “K(glycyl)” or “K(gly)”), nitrophenylalanine (nitrophe), aminophenylalanine (aminophe or Amino-Phe), 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), acetylgarginine (acetylarg), α , β -diaminopropionic acid (Dpr), α , γ -diaminobutyric acid (Dab), diaminopropionic acid (Dap), cyclohexylalanine (Cha), 4-methyl-phenylalanine (MePhe), β , β -diphenyl-alanine (BiPhA), aminobutyric acid (Abu), 4-phenyl-phenylalanine (or biphenylalanine; 4Bip), α -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.

[0105] 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.

[0106] 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.

[0107] The term “encoding” refers to a polynucleotide sequence encoding one or more amino acids. The term does not require a start or stop codon.

[0108] The terms “identical” and percent “identity,” in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same. “Percent identity” means the percent of identical residues between the amino acids or nucleotides in the compared molecules and is calculated based on the size of the smallest of the molecules being compared. For these calculations, gaps in alignments (if any) can be addressed by a particular mathematical model or computer program (i.e., an “algorithm”). Methods that can be used to calculate the identity of the aligned nucleic acids or polypeptides include those described in Computational Molecular Biology, (Lesk, A. M., ed.), (1988) New York: Oxford University Press; Biocomputing Informatics and Genome Projects, (Smith, D. W., ed.), 1993, New York: Academic Press; Computer Analysis of Sequence Data, Part I, (Griffin, A. M., and Griffin, H. G., eds.), 1994, New Jersey: Humana Press; von Heinje, G., (1987) Sequence Analysis in Molecular Biology, New York: Academic Press; Sequence

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

[0109] In calculating percent identity, the sequences being compared are aligned in a way that gives the largest match between the sequences. The computer program used to determine percent identity is the GCG program package, which includes GAP (Devereux et al., (1984) Nucl. Acid Res. 12:387; Genetics Computer Group, University of Wisconsin, Madison, WI). The computer algorithm GAP is used to align the two polypeptides or polynucleotides for which the percent sequence identity is to be determined. The sequences are aligned for optimal matching of their respective amino acid or nucleotide (the “matched span”, as determined by the algorithm). A gap opening penalty (which is calculated as 3x the average diagonal, wherein the “average diagonal” is the average of the diagonal of the comparison matrix being used; the “diagonal” is the score or number assigned to each perfect amino acid match by the particular comparison matrix) and a gap extension penalty (which is usually 1/10 times the gap opening penalty), as well as a comparison matrix such as PAM 250 or BLOSUM 62 are used in conjunction with the algorithm. In certain embodiments, a standard comparison matrix (see, Dayhoff et al., (1978) Atlas of Protein Sequence and Structure 5:345-352 for the PAM 250 comparison matrix; Henikoff et al., (1992) Proc. Natl. Acad. Sci. U.S.A. 89:10915-10919 for the BLOSUM 62 comparison matrix) is also used by the algorithm.

[0110] Recommended parameters for determining percent identity for polypeptides or nucleotide sequences using the GAP program are the following:

[0111] Algorithm: Needleman et al., 1970, J. Mol. Biol. 48:443-453;

[0112] Comparison matrix: BLOSUM 62 from Henikoff et al., 1992, supra;

[0113] Gap Penalty: 12 (but with no penalty for end gaps)

[0114] Gap Length Penalty: 4

[0115] Threshold of Similarity: 0

[0116] 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.

[0117] 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 acid 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 acid residues and which is encoded by the nucleic acid sequence of SEQ ID NO: 3150.

[0118] 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.

[0119] In various embodiments, a GIPR polypeptide comprises an amino acid sequence that is at least about 85 percent identical to a naturally-occurring GIPR polypeptide (e.g., SEQ ID NOs: 3141, 3143 or 3145). In other embodiments, a GIPR polypeptide comprises an amino acid sequence that is at least about 90 percent, or about 95, 96, 97, 98, or 99 percent identical 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.

[0120] 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).

[0121] 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).

[0122] The terms “GIP”, “Gastric inhibitory polypeptide”, “glucose-dependent insulintropic peptide” and “GIP ligand” are used interchangeably and mean a naturally-occurring wild-type polypeptide expressed in a mammal, such as a human or a mouse, and includes naturally occurring alleles (e.g., naturally occurring allelic forms of human GIP protein). For purposes of this disclosure, the term “GIP” can be used interchangeably to refer to any mature GIP polypeptide.

[0123] The 42 amino acid sequence of mature human GIP is:

[0124] Y A E G T F I S D Y S I A M D K I H Q Q D F V N W L L A Q K G K K N D W K H N I T Q (SEQ ID NO: 3151)

[0125] and is encoded by the DNA sequence:

[0126] t a t g c g g a a g g c a c c t t t a t t a g c g a t t a t a g c a t t g c g a t g g a t a a a a t
t c a t c a g c a g g a t t t t g t g a a c t g g c t g c t g g c g c a g a a a g g c a a a a a a a
a c g a t t g g a a a c a t a a c a t t a c c c a g (SEQ ID NO: 3152).

[0127] The 42 amino acid sequence of mature murine GIP is:

[0128] Y A E G T F I S D Y S I A M D K I R Q Q D F V N W L L A Q R G K K S D W K H N I T Q (SEQ ID NO: 3153)

[0129] and is encoded by the DNA sequence:

[0130] t a t g c g g a a g g c a c c t t t a t t a g c g a t t a t a g c a t t g c g a t g g a t a a a a t
t c g c c a g c a g g a t t t t g t g a a c t g g c t g c t g g c g c a g c g c g g c a a a a a a a
g c g a t t g g a a a c a t a a c a t t a c c c a g (SEQ ID NO: 3154).

[0131] The 42 amino acid sequence of mature rat GIP is:

[0132] Y A E G T F I S D Y S I A M D K I R Q Q D F V N W L L A Q K G K K N D W K H N L T Q (SEQ ID NO: 3155)

[0133] and is encoded by the DNA sequence:

[0134] tatgcggaag gcacctttat tagcgattat agcattgcga tggataaaat
tcgccagcag gattttgtga actggctgctg gcgcagaaag gcaaaaaaaaa
cgattggaaa cataacctga cccag (SEQ ID NO: 3156).

[0135] An “antigen binding protein” as used herein means any protein that specifically binds a specified target antigen, such as a GIPR polypeptide (e.g., a human GIPR polypeptide such as provided in SEQ ID NOS: 3141, 3143 or 3145). The term encompasses intact antibodies that comprise at least two full-length heavy chains and two full-length light chains, as well as derivatives, variants, fragments, and mutations thereof. Examples of antibody fragments include Fab, Fab', F(ab')₂, and Fv fragments. An antigen binding protein also includes domain antibodies such as nanobodies and scFvs as described further below.

[0136] In general, a GIPR antigen binding protein is said to “specifically bind” its target antigen GIPR when the antigen binding protein exhibits essentially background binding to non-GIPR molecules. An antigen binding protein that specifically binds GIPR may, however, cross-react with GIPR polypeptides from different species. Typically, a GIPR antigen binding protein specifically binds human GIPR when the dissociation constant (KD) is $\leq 10^{-7}$ M as measured via a surface plasma resonance technique (e.g., BIAcore, GE-Healthcare Uppsala, Sweden) or Kinetic Exclusion Assay (KinExA, Sapidyn, Boise, Idaho). A GIPR antigen binding protein specifically binds human GIPR with “high affinity” when the KD is $\leq 5 \times 10^{-9}$ M, and with “very high affinity” when the KD is $\leq 5 \times 10^{-10}$ M, as measured using methods described.

[0137] “Antigen binding region” means a protein, or a portion of a protein, that specifically binds a specified antigen. For example, that portion of an antigen binding protein that contains the amino acid residues that interact with an antigen and confer on the antigen binding protein its specificity and affinity for the antigen is referred to as “antigen binding region.” An antigen binding region typically includes one or more “complementary binding regions” (“CDRs”) of an immunoglobulin, single-chain immunoglobulin, or camelid antibody. Certain antigen binding regions also include one or more “framework” regions. A “CDR” is an amino acid sequence that contributes to antigen binding specificity and affinity. “Framework” regions can aid in maintaining the proper conformation of the CDRs to promote binding between the antigen binding region and an antigen.

[0138] 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.

[0139] The term “antibody” refers to an intact immunoglobulin of any isotype, or a fragment thereof that can compete with the intact antibody for specific binding to the target antigen, and includes, for instance, chimeric, humanized, fully human, and bispecific antibodies. An “antibody” as such is a species of an antigen binding protein. An intact antibody generally will comprise at least two full-length heavy chains and two full-length light chains. Antibodies may be derived solely from a single source, or may be “chimeric,” that is, different portions of the antibody may be derived from two different antibodies as described further below. The antigen binding proteins, antibodies, or binding fragments may be produced in hybridomas, by recombinant DNA techniques, or by enzymatic or chemical cleavage of intact antibodies.

[0140] 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.

[0141] 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.

[0142] 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.

[0143] 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.

[0144] In another embodiment, Fvs, domain antibodies and scFvs, and may be derived from an antibody of the present invention.

[0145] 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.

[0146] 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.

[0147] 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.

[0148] 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.

[0149] 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.

[0150] The “Fv region” comprises the variable regions from both the heavy and light chains, but lacks the constant regions.

[0151] “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.

[0152] 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.

[0153] 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*.

[0154] A multispecific antigen binding protein” or “multispecific antibody” is one that targets more than one antigen or epitope.

[0155] 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.

[0156] The term “compete” when used in the context of antigen binding proteins (e.g., antibodies) means competition between antigen binding proteins is determined by an assay in which the antigen binding protein (e.g., antibody or immunologically functional fragment thereof) under test prevents or inhibits specific binding of a reference antigen binding protein to a common antigen (e.g., GIPR or a fragment thereof). Numerous types of competitive binding assays can be used, for example: solid phase direct or indirect radioimmunoassay (RIA), solid phase direct or indirect enzyme immunoassay (EIA), sandwich competition assay (see, e.g., Stahli et al., 1983, *Methods in Enzymology* 9:242-253); solid phase direct biotin-avidin EIA (see, e.g., Kirkland et al., 1986, *J. Immunol.* 137:3614-3619) solid phase direct labeled assay, solid phase direct labeled sandwich assay (see, e.g., Harlow and Lane, 1988, *Antibodies, A Laboratory Manual*, Cold Spring Harbor Press); solid phase direct label RIA using I-125 label (see, e.g., Morel et al., 1988, *Molec. Immunol.* 25:7-15); solid phase direct biotin-avidin EIA (see, e.g., Cheung, et al., 1990, *Virology* 176:546-552); and direct labeled RIA (Moldenhauer et al., 1990, *Scand. J. Immunol.* 32:77-82). Typically, such an assay involves the use of purified antigen bound to a solid surface or cells bearing either of these, an unlabeled test antigen binding protein and a labeled reference antigen binding

protein. Competitive inhibition is measured by determining the amount of label bound to the solid surface or cells in the presence of the test antigen binding protein. Usually the test antigen binding protein is present in excess. Additional details regarding methods for determining competitive binding are provided in the examples herein. Usually, when a competing antigen binding protein is present in excess, it will inhibit specific binding of a reference antigen binding protein to a common antigen by at least 40%, 45%, 50%, 55%, 60%, 65%, 70% or 75%. In some instances, binding is inhibited by at least 80%, 85%, 90%, 95%, or 97% or more.

[0157] 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.

[0158] 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.

[0159] 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.

[0160] 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.

[0161] An “effective amount” is generally an amount sufficient to reduce the severity and/or frequency of symptoms, eliminate the symptoms and/or underlying cause, prevent the occurrence of symptoms and/or their underlying cause, and/or improve or remediate the damage that results from or is associated with the disease state (e.g., diabetes, obesity, dyslipidemia, elevated glucose levels, elevated insulin levels or diabetic nephropathy). In some embodiments, the effective amount is a therapeutically effective amount or a prophylactically effective amount. A “therapeutically effective amount” is an amount sufficient to remedy a disease state (e.g. atherosclerosis) or symptoms, particularly a state or symptoms associated with the disease state, or otherwise prevent, hinder, retard or reverse the progression of the disease state or any other undesirable symptom associated with the disease in any way whatsoever. A “prophylactically effective amount” is an amount of a pharmaceutical composition that, when administered to a subject, will have the intended prophylactic effect, e.g., preventing or delaying the onset (or reoccurrence) of the disease state, or reducing the likelihood of the onset (or reoccurrence) of the disease state or associated symptoms. The full therapeutic or prophylactic effect does not necessarily occur by administration of one dose, and may occur only after administration of a series of doses.

Thus, a therapeutically or prophylactically effective amount may be administered in one or more administrations.

[0162] 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.

[0163] 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.

[0164] 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.

[0165] 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.

[0166] 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."

[0167] 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.

[0168] 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.

[0169] 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.

[0170] 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.

[0171] 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.

[0172] 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.

[0173] 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.

[0174] 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.

[0175] 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.

[0176] 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.

[0177] A “subject” or “patient” as used herein can be any mammal. In a typical embodiment, the subject or patient is a human.

[0178] 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.

[0179] 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.

[0180] The 466 amino acid sequence of human GIPR is (Volz et al., FEBS Lett. 373:23-29 (1995); NCBI Reference Sequence: NP_0001555):

[0181] MTTSPILQLL LRLSLCGLLL QRAETGSKGQ TAGELYQRWE RYRRECQETL
 AAAPPSGLA CNGSFDMYVC WDYAAPNATA RASCPWYLPW HHHVAAGFVL
 RQCGSDGQWG LWRDHTQCEN PEKNEAFLDQ RLILERLQVM YTVGYSLSLA
 TLLLALLILS LFRRLHCTRN YIHINLFTSF MLRAAAILSR DRLLPRPGPY
 LGDQALALWN QALAACRTAQ IVTQYCVGAN YTWLLVEGVY LHSLLVLVGG
 SEEGHFRYYL LLGWGAPALF VIPWVIVRYL YENTQCWERN EVKAIWWIIR

TPILMTILIN FLIFIRILGI LLSKLRTRQM RCRDYRLRLA RSTLTLVPLL
 GVHEVVFAPV TEEQARGALR FAKLGFEIFL SSFQGFLVSV LYCFINKEVQ
 SEIRRGWHHC RLRRSLGEEQ RQLPERAFRA LPSGSGPGEV PTSRGLSSGT
 LPGPGNEASR ELESYC (SEQ ID NO: 3141)

[0182] and is encoded by the DNA sequence (NCBI Reference Sequence: NM_000164):

[0183] ggcagcggtg gcaggggctg caggagcaag tgaccaggag caggactggg
 gacaggcctg atcgcccctg cacgaaccag acccttcgcc gccctcacga
 tgactacctc tccgatactg cagctgctgc tgcggctctc actgtgcggg
 ctgctgctcc agagggcgga gacaggctct aaggggcaga cggcggggga
 gctgtaccag cgctgggaac ggtaccgcag ggagtgccag gagaccttg
 cagccgcgga accgccttca ggcctcgcct gtaacgggtc cttcgatatg
 tacgtctgct gggactatgc tgcacccaat gccactgcc gtgcgtcctg
 cccctggtac ctgccctggc accaccatgt ggctgcaggt ttcgtcctcc
 gccagtgtgg cagtgatggc caatggggac tttggagaga ccatacacia
 tgtgagaacc cagagaagaa tgaggccttt ctggaccaa ggctcatctt
 ggagcggttg caggatcatgt aactgtcgg ctactccctg tctctcgcca
 cactgctgct agccctgctc atcttgagtt tgttcaggcg gctacattgc
 actagaaact atatccacat caacctgttc acgtctttca tgctgcgagc
 tgcggccatt ctcagccgag accgtctgct acctcgacct ggcccctacc
 ttggggacca ggcccttgcg ctgtggaacc aggcctcgc tcctgcccgc
 acggcccaga tcgtgaccca gtactgcgtg ggtgccaact acacgtggct
 gctggtggag ggcgtctacc tgcacagtct cctggtgctc gtgggaggct
 ccgaggaggg ccacttccgc tactacctgc tcctcggtg gggggcccc
 gcgcttttctg tcattccctg ggtgatcgtc aggtacctgt acgagaacac
 gcagtgtggt gagcgcaacg aagtcaaggc cttttggtgg attatacga
 cccccatcct catgaccatc ttgattaatt tcctcatttt tatccgcatt
 cttggcattc tcctgtccaa gctgaggaca cggcaaattgc gctgccggga
 ttaccggctg aggctggctc gctccacgct gacgctggtg cccctgctgg
 gtgtccacga ggtggtgttt gctcccgtga cagaggaaca ggcccggggc
 gccctgcgct tcgccaagct cggctttgag atcttcctca gtccttcca
 gggcttcctg gtcagcgtcc tctactgctt catcaacaag gaggtgcagt
 cggagatccg ccgtggctgg caccactgcc gcctgcgccg cagcctgggc
 gaggagcaac gccagctccc ggagcgcgcc ttccggggcc tgccctccgg
 ctccggcccc ggcgaggctc ccaccagccg cggcttgtcc tcggggaccc
 tcccagggcc tgggaatgag gccagccggg agttggaaag ttactgctag
 ggggcgggat ccccggtgtc gttcagttag catggattta ttgagtcca
 actgcgtgcc aggccagta cggaggacgc tggggaaatg gtgaaggaaa
 cagaaaaaag gtccctgccc ttctggagat gacaactgag tggggaaaac

agaccgtgaa cacaaaacat caagttccac acacgctatg gaatggttat
gaaggggaagc gagaaggggg cctaggggtgg tctgggaggc gtctccaagg
aggtgacact taagccatcc ccgaaagagg tgaaagagat cactttgggg
agagctggag aacaggattc taggcggaag cgatagcata ggcaaaggcc
cttgggcagg aaggcgctca gccttggtg gagtagaatt aagtcagagc
caacaggtgg ggagagacag agaagtgggc aggggcaccc aagttgggat
ttcatttcag gtgcattgga gattcttagg agtgtctctt gggggtaata
ttttatTTTT taaaaaatga ggat (SEQ ID NO: 3142).

[0184] A 430 amino acid isoform of human GIPR (isoform X1), predicted by automated computational analysis, has the sequence (NCBI Reference Sequence XP_005258790):

[0185] MTTSPILQLL LRLSLCGLLL QRAETGSKGQ TAGELYQRWE RYRRECQETL
AAAEPPSVAA GFVLRQCGSD GQWGLWRDHT QCENPEKNEA FLDQRLILER
LQVMYTVGYS LSLATLLLAL LILSLFRRRLH CTRNYIHINL FTSFMLRAAA
ILSRDRLLP PGPYLGDAQAL ALWNQALAAC RTAQIVTQYC VGANYTWLLV
EGVYLHSLLV LVGGSEEGHF RYLLLLGWGA PALFVIPWVI VRYLYENTQC
WERNEVKAIW WIIRTPILMT ILINFLIFIR ILGILLSKLR TRQMRCRDYR
LRLARSTLTL VPLLGVHEVV FAPVTEEQAR GALRFAKLGF EIFLSSFQGF
LVSVLYCFIN KEVQSEIRRG WHHCRLRRSL GEEQRQLPER AFRALPSGSG
PGEVPTSRGL SSGTLPGPGN EASRELESYC (SEQ ID NO: 3143)

[0186] and is encoded by the DNA sequence:

[0187] atgaccacca gcccgattct gcagctgctg ctgcgcctga gcctgtgcgg
cctgctgctg cagcgcgcgg aaaccggcag caaaggccag accgcgggcg
aactgtatca gcgctgggaa cgctatcgcc gcgaatgcca ggaaaccctg
gcggcgggcg aaccgccgag cgtggcgggc ggctttgtgc tgcgccagtg
cggcagcgat ggccagtggg gcctgtggcg cgatcatacc cagtgcgaaa
acccggaaaa aaacgaagcg tttctggatc agcgctgat tctggaacgc
ctgcaggtga tgtataccgt gggctatagc ctgagcctgg cgaccctgct
gctggcgctg ctgattctga gctgtttcg ccgcctgcat tgcaccgcga
actatattca tattaacctg tttaccagct ttatgctgcg cgcggcgggc
attctgagcc gcgatcgct gctgccgcgc ccgggcccgt atctggggcg
tcaggcgctg gcgctgtgga accaggcgct ggcggcgtgc cgcaccgcgc
agattgtgac ccagtattgc gtgggcgcga actataacctg gctgctggtg
gaaggcggtg atctgcatag cctgctggtg ctggtggggc gcagcgaaga
aggccatttt cgctattatc tgctgctggg ctggggcgcg ccggcgctgt
ttgtgattcc gtgggtgatt gtgcgctatc tgtatgaaaa caccagtg
tggaacgcga acgaagtga agcgatttgg tggattatc gcaccccgat
tctgatgacc attctgatta actttctgat ttttatcgc attctgggca
ttctgctgag caaactgcgc acccgccaga tgcgctgccg cgattatcgc

ctgcgcctgg cgcgccagcac cctgaccctg gtgccgctgc tgggcgtgca
 tgaagtgggtg tttgcgccgg tgaccgaaga acaggcgcg gcgcgcgtgc
 gctttgcgaa actgggcttt gaaatttttc tgagcagctt tcagggcttt
 ctgggtgagcg tgctgtattg ctttattaac aaagaagtgc agagcgaaat
 tcgccgcggc tggcatcatt gccgcctgcg ccgcagcctg ggccaagaac
 agcggcagct gccggaacgc gcgttttcg cgctgccgag cggcagcggc
 ccgggcgaag tgccgaccag ccgcggcctg agcagcggca ccctgccggg
 cccgggcaac gaagcgagcc gcgaactgga aagctattgc (SEQ ID NO: 3144).

[0188] 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):

[0189] MTTSPILQLL LRLSLCGLLL QRAETGSKGQ TAGELYQRWE RYRRECQETL
 AAAPPSGLA CNGSFDMYVC WDYAAPNATA RASCPWYLPW HHHVAAGFVL
 RQCGSDGQWG LWRDHTQCEN PEKNEAFLDQ RLILERLQVM YTVGYSLSLA
 TLLLALLILS LFRRLHCTRN YIHINLFTSF MLRAAAILSR DRLLPRPGPY
 LGDQALALWN QALAACRTAQ IVTQYCVGAN YTWLLVEGVY LHSLLVLVGG
 SEEGHFRYYL LLGWGAPALF VIPWVIVRYL YENTQCWERN EVKAIWWIIR
 TPILMTILIN FLIFIRILGI LLSKLRTRQM RCRDYRLRLA RSTLTLLVPLL
 GVHEVVFAPV TEEQARGALR FAKLGFEIFL SSFQGFVSV LYCFINKEVG
 RDPAAAPALW RRRGTAPPLS AIVSQVQSEI RRGWHHCRLR RSLGEEQRQL
 PERAFRALPS GSGPGEVPTS RGLSSGTLPG PGNEASRELE SYC (SEQ ID NO: 3145)

[0190] and is encoded by the DNA sequence:

[0191] atgaccacca gcccgattct gcagctgctg ctgcgcctga gcctgtgcgg
 cctgctgctg cagcgcgcg aaaccggcag caaaggccag accgcggggc
 aactgtatca gcgctgggaa cgctatcgcc gcgaatgcc a ggaaaccctg
 gcggcgggcg aaaccggcag cggcctggcg tgcaacggca gctttgatat
 gtatgtgtgc tgggattatg cggcgccgaa cgcgaccg cgcgcgagct
 gcccgaggta tctgccgtgg catcatcatg tggcgggggg ctttgtgctg
 cgccagtgcg gcagcgatgg ccagtggggc ctgtggcgcg atcataccca
 gtgcgaaaac ccggaaaaaa acgaagcgtt tctggatcag cgctgattc
 tggaacgcct gcaggtgatg tataccgtgg gctatagcct gagcctggcg
 accctgctgc tggcgctgct gattctgagc ctgtttcgcc gcctgcattg
 caccgcgaac tatattcata ttaacctgtt taccagcttt atgctgcgcg
 cggcgggcgat tctgagccgc gatcgccctgc tgccgcgccc gggcccgat
 ctggggcgatc aggcgctggc gctgtggaac caggcgctgg cggcgtgccg
 caccgcgcag attgtgacct agtattgcgt gggcgcgaaac tatacctggc
 tgctgggtgga aggcgtgtat ctgcatagcc tgctgggtgct ggtgggcggc
 agcgaagaag gccattttcg ctattatctg ctgctgggct ggggcgcgcc

ggcgctgttt gtgattccgt ggggtgattgt gcgctatctg tatgaaaaca
 cccagtgtctg ggaacgcaac gaagtgaag cgatttggtg gattattcgc
 accccgattc tgatgaccat tctgattaac tttctgattt ttattcgc
 tctgggcatt ctgctgagca aactgcgcac ccgccagatg cgctgccgcg
 attatcgctt gcgcctggcg cgcagcacc tgaccctggt gccgctgctg
 ggcgtgcatg aagtgggtgtt tgcgccggtg accgaagaac aggcgcgcg
 cgcgctgcgc tttgcgaaac tgggctttga aatttttctg agcagctttc
 agggctttct ggtgagcgtg ctgtattgct ttattaacaa agaagtgggc
 cgcgatccgg cggcgccgcg ggcgctgtgg cgccgccgcg gcaccgcgc
 gccgctgagc gcgattgtga gccaggtgca gagcgaaatt cgccgcggct
 ggcatcattg ccgcctgcgc cgcagcctgg gcgaagaaca gcgccagctg
 ccggaacgcg cgtttcgcgc gctgccgagc ggcagcggcc cgggcgaagt
 gccgaccagc cgcggcctga gcagcggcac cctgccgggc cggggcaacg
 aagcgagccg cgaactggaa agctattgct aa (SEQ ID NO: 3146)

[0192] The 460 amino acid sequence of murine GIPR is (NCBI Reference Sequence: NP_001074284; uniprotKB/Swiss-Prot Q0P543-1); see Vassilatis et al., PNAS USA 2003, 100:4903-4908.

[0193] MPLRLLLLLL WLWGLQWAET DSEGQTTTGE LYQRWEHYGQ ECQKMLETTE
 PPSGLACNGS FDMYACWNYT AANTTARVSC PWYLPWFRQV SAGFVFRQCG
 SDGQWGSWRD HTQCENPEKN GAFQDQTLIL ERLQIMYTVG YSLSLTTLIL
 ALLILSLFRR LHCTRNYIHM NLFTSFMLRA AAILTRDQLL PPLGPYTGDO
 APTPNQALA 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
 GDEVLESYC (SEQ ID NO: 3147)

[0194] and is encoded by the DNA sequence (NCBI Reference Sequence: NM_001080815):

[0195] atgccgctgc gcctgctgct gctgctgctg tggctgtggg gcctgcagtg
 ggcggaaacc gatagcgaag gccagaccac caccggcgaa ctgtatcagc
 gctgggaaca ttatggccag gaatgccaga aaatgctgga aaccaccgaa
 ccgccgagcg gcctggcgtg caacggcagc tttgatattg atgcgtgctg
 gaactatacc gcggcgaaca ccaccgcgcg cgtgagctgc ccgtgggtatc
 tgccgtgggtt tcgccaggtg agcgcgggct ttgtgtttcg ccagtgcggc
 agcgatggcc agtggggcag ctggcgcgat catacccagt gcgaaaacc
 ggaaaaaac ggcgcgtttc aggatcagac cctgattctg gaacgcctgc
 agattatgta taccgtgggc tatagcctga gcctgaccac cctgctgctg
 gcgctgctga ttctgagcct gtttcgccgc ctgcattgca cccgcaacta

tattcatatg aacctgttta ccagctttat gctgcgcgcg gcggcgattc
 tgaccgcga tcagctgctg ccgccgctgg gcccgataac cggcgatcag
 gcgccgaccc cgtggaacca ggcgctggcg gcgtgccgca ccgcgcagat
 tatgaccag tattgctgg gcgcgaacta tacctggctg ctgggtggaag
 gcgtgtatct gcatcatctg ctgggtgattg tgggccgcag cgaaaaaggc
 cattttcgct gctatctgct gctgggctgg ggcgcgccgg cgctgtttgt
 gattccgtgg gtgattgtgc gctatctgcg cgaaaacacc cagtgtctggg
 aacgcaacga agtgaaagcg atttggtgga ttattcgac cccgattctg
 attaccattc tgattaactt tctgattttt attcgcattc tgggcattct
 ggtgagcaaa ctgcgacccc gccagatgcg ctgcccgat tatcgccctgc
 gcctggcgcg cagcaccctg accctgggtgc cgctgctggg cgtgcatgaa
 gtgggtgtttg cgccggtgac cgaagaacag gtggaaggca gcctgcgctt
 tgcgaaactg gcgtttgaaa tttttctgag cagctttcag ggctttctgg
 tgagcgtgct gtattgcttt attaacaaag aagtgcagag cgaaattcgc
 cagggctggc gccatcgccg cctgcgcctg agcctgcagg aacagcgccc
 gcgccgcat caggaactgg cgccgcgcgc ggtgccgctg agcagcgct
 gccgcgaagc ggcggtgggc aacgcgctgc cgagcggcat gctgcatgtg
 ccgggcatg aagtgtgga aagctattgc taa (SEQ ID NO: 3148)

[0196] 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):

[0197] MPLRLLLLLL WLWGLQWAET DSEGQTTTGE LYQRWEHYGQ ECQKMLETTE
 PPSGLACNGS FDMYACWNYT AANTTARVSC PWYLPWFRQV SAGFVFRQCG
 SDGQWGSWRD HTQCENPEKN GAFQDQTLIL ERLQIMYTVG YSLSLTLLLL
 ALLILSLFRR LHCTRNYIHM NLFTSFMLRA AAILTRDQLL PPLGPYTGDO
 APTPNQVLH RLLPGGTKTF PIYFRTFPHH (SEQ ID NO: 3149)

[0198] and is encoded by the DNA sequence:

[0199] 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 tcgccagggtg agcgcgggct ttgtgtttcg ccagtgcggc
 agcgtatggc agtggggcag ctggcgcgat cataccagc gcgaaaacc
 ggaaaaaac ggcgcgcttc aggatcagac cctgattctg gaacgcctgc
 agattatgta taccgtgggc tatagcctga gcctgaccac cctgctgctg
 gcgctgctga ttctgagcct gtttcgccgc ctgcattgca cccgcaacta
 tattcatatg aacctgttta ccagctttat gctgcgcgcg gcggcgattc

tgacccgcga tcagctgctg ccgccgctgg gcccgatatac cggcgatcag
 gcgccgaccc cgtggaacca ggtgctgcat cgctgctgc cgggcggcac
 caaaaccttt ccgatttatt ttcgcacctt tccgcatcat taa (SEQ ID NO: 3150).

[0200] As stated herein, the term “GIPR polypeptide” encompasses naturally occurring GIPR polypeptide sequences, e.g., human amino acid sequences SEQ ID NOs: 3141, 3143 or 3145. The term “GIPR polypeptide,” however, also encompasses polypeptides comprising an amino acid sequence that differs from the amino acid sequence of a naturally occurring GIPR polypeptide sequence, e.g., SEQ ID NOs: 3141, 3143 or 3145, by one or more amino acids, such that the sequence is at least 85% identical to SEQ ID NOs: 3141, 3143 or 3145. GIPR polypeptides can be generated by introducing one or more amino acid substitutions, either conservative or non-conservative and using naturally or non-naturally occurring amino acids, at particular positions of the GIPR polypeptide.

[0201] 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.

[0202] Naturally occurring residues can be divided into classes based on common side chain properties:

[0203] (1) hydrophobic: norleucine, Met, Ala, Val, Leu, Ile;

[0204] (2) neutral hydrophilic: Cys, Ser, Thr;

[0205] (3) acidic: Asp, Glu;

[0206] (4) basic: Asn, Gln, His, Lys, Arg;

[0207] (5) residues that influence chain orientation: Gly, Pro; and

[0208] (6) aromatic: Trp, Tyr, Phe.

[0209] Additional groups of amino acids can also be formulated using the principles described in, e.g., Creighton (1984) *PROTEINS: STRUCTURE AND MOLECULAR PROPERTIES* (2d Ed. 1993), W.H. Freeman and Company. In some instances it can be useful to further characterize substitutions based on two or more of such features (e.g., substitution with a “small polar” residue, such as a Thr residue, can represent a highly conservative substitution in an appropriate context).

[0210] Conservative substitutions can involve the exchange of a member of one of these classes for another member of the same class. Non-conservative substitutions can involve the exchange of a member of one of these classes for a member from another class.

[0211] Synthetic, rare, or modified amino acid residues having known similar physiochemical properties to those of an above-described grouping can be used as a “conservative” substitute for a particular amino acid residue in a sequence. For example, a D-Arg residue may serve as a substitute for a typical L-Arg residue. It also can be the case that a particular substitution can be described in terms of two or more of the above described classes (e.g., a substitution with a small and hydrophobic residue means substituting one amino acid with a residue(s) that is found in both of the above-described classes or other synthetic, rare, or modified residues that are known in the art to have similar physiochemical properties to such residues meeting both definitions).

[0212] 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.

[0213] 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 vector and after introduction in a suitable host, the sequence can be expressed to produce the encoded polypeptide according to standard cloning and expression techniques, which are known in the art (e.g., as described in Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual* 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989). The invention also relates to such vectors comprising a nucleic acid sequence according to the invention.

[0214] 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.

[0215] 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.

[0216] 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.

[0217] In another aspect of the instant disclosure, host cells comprising the GIPR nucleic acids and vectors disclosed herein are provided. In various embodiments, the vector or nucleic acid is integrated into the host cell genome, which in other embodiments the vector or nucleic acid is extra-chromosomal.

[0218] Recombinant cells, such as yeast, bacterial (e.g., *E. coli*), and mammalian cells (e.g., immortalized mammalian cells) comprising such a nucleic acid, vector, or combinations of either or both thereof are provided. In various embodiments cells comprising a non-integrated nucleic acid, such as a plasmid, cosmid, phagemid, or linear expression element, which comprises a sequence coding for expression of a GIPR polypeptide, are provided.

[0219] 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.

[0220] A GIPR-encoding nucleic acid can be positioned in and/or delivered to a host cell or host animal via a viral vector. Any suitable viral vector can be used in this capacity. A viral vector can comprise any number of viral polynucleotides, alone or in combination with one or more viral proteins, which facilitate delivery, replication, and/or expression of the nucleic acid of the invention in a desired host cell. The viral vector can be a polynucleotide comprising all or part of a viral genome, a viral protein/nucleic acid conjugate, a virus-like particle (VLP), or an intact virus particle comprising viral nucleic acids and a GIPR polypeptide-encoding nucleic acid. A viral particle viral vector can comprise a wild-type viral particle or a modified viral particle. The viral vector can be a vector which requires the presence of another vector or wild-type virus for replication and/or expression (e.g., a viral vector can be a helper-dependent virus), such as an adenoviral vector amplicon. Typically, such viral vectors consist of a wild-type viral particle, or a viral particle modified in its protein and/or nucleic acid content to increase transgene capacity or aid in transfection and/or expression of the nucleic acid (examples of such vectors include the herpes virus/AAV amplicons). Typically, a viral vector is similar to and/or derived from a virus that normally infects humans. Suitable viral vector particles in this respect, include, for example, adenoviral vector particles (including any virus of or derived from a virus of the adenoviridae), adeno-associated viral vector particles (AAV vector particles) or other parvoviruses and parvoviral vector particles, papillomaviral vector particles, flaviviral vectors, alphaviral vectors, herpes viral vectors, pox virus vectors, retroviral vectors, including lentiviral vectors.

[0221] 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.

[0222] 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.

[0223] 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.

[0224] The antigen binding proteins provided are polypeptides into which one or more complementary determining regions (CDRs), as described herein, are embedded and/or joined. In some antigen binding proteins, the CDRs are embedded into a "framework" region, which orients the CDR(s) such that the proper antigen binding properties of the CDR(s) are achieved. Certain antigen binding proteins described herein are antibodies or are derived from antibodies. In other antigen binding proteins, the CDR sequences are embedded in a different type of protein scaffold. The various structures are further described below.

[0225] The antigen binding proteins that are disclosed herein have a variety of utilities. The antigen binding proteins, for instance, are useful in specific binding assays, affinity purification of GIPR, and in screening assays to identify other antagonists of GIPR activity. Other uses for the antigen binding proteins include, for example, diagnosis of GIPR-associated diseases or conditions and screening assays to determine the presence or absence of GIPR. Given that the antigen binding proteins that are provided are antagonists, the GIPR antigen binding proteins have value in therapeutic methods in which it is useful to reduce weight gain, even while maintaining or increasing food intake, increasing % fat mass and increasing % lean mass, improving glucose tolerance, decreasing insulin levels, decreasing cholesterol and triglyceride levels. Accordingly, the antigen binding proteins have utility in the treatment and prevention of diabetes, e.g., type 2 diabetes, obesity, dyslipidemia, elevated glucose levels or elevated insulin levels.

[0226] 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.

[0227] 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.

[0228] 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.

[0229] 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.

[0230] 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:

[0231] (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.

[0232] (b) ability to decrease blood glucose;

[0233] (c) ability to increase glucose tolerance;

[0234] (d) ability to increase insulin sensitivity;

[0235] (e) ability to decrease body weight or reduce body weight gain;

- [0236] (f) ability to decrease fat mass or decrease inflammation in fat tissue;
- [0237] (g) ability to decrease fasting insulin levels;
- [0238] (h) ability to decrease circulating cholesterol levels;
- [0239] (i) ability to decrease circulating triglyceride levels;
- [0240] (j) ability to decrease liver steatosis or reduce triglyceride level in liver;
- [0241] (k) ability to decrease AST, ALT, and/or ALP levels.
- [0242] In one embodiment, a GIPR antigen binding protein has one or more of the following activities:
- [0243] (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.
- [0244] (b) has a half-life in human serum of at least 3 days;
- [0245] Some antigen binding proteins that are provided have an on-rate (k_a) for GIPR of at least 10^4 /M x seconds, at least 10^5 /M x seconds, or at least 10^6 /M x seconds as measured, for instance, as described below. Certain antigen binding proteins that are provided have a slow dissociation rate or off-rate. Some antigen binding proteins, for instance, have a k_d (off-rate) of $1 \times 10^{-2} \text{ s}^{-1}$, or $1 \times 10^{-3} \text{ s}^{-1}$, or $1 \times 10^{-4} \text{ s}^{-1}$, or $1 \times 10^{-5} \text{ s}^{-1}$. In certain embodiments, the antigen binding protein has a 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.
- [0246] 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.
- [0247] Some of the antigen binding proteins that are provided have the structure typically associated with naturally occurring antibodies. The structural units of these antibodies typically comprise one or more tetramers, each composed of two identical couplets of polypeptide chains, though some species of mammals also produce antibodies having only a single heavy chain. In a typical antibody, each pair or couplet includes one full-length "light" chain (in certain embodiments, about 25 kDa) and one full-length "heavy" chain (in certain

embodiments, about 50-70 kDa). Each individual immunoglobulin chain is composed of several "immunoglobulin domains", each consisting of roughly 90 to 110 amino acids and expressing a characteristic folding pattern. These domains are the basic units of which antibody polypeptides are composed. The amino-terminal portion of each chain typically includes a variable domain that is responsible for antigen recognition. The carboxy-terminal portion is more conserved evolutionarily than the other end of the chain and is referred to as the "constant region" or "C region". Human light chains generally are classified as kappa and lambda light chains, and each of these contains one variable domain and one constant domain. Heavy chains are typically classified as mu, delta, gamma, alpha, or epsilon chains, and these define the antibody's isotype as IgM, IgD, IgG, IgA, and IgE, respectively. IgG has several subtypes, including, but not limited to, IgG1, IgG2, IgG3, and IgG4. IgM subtypes include IgM, and IgM2. IgA subtypes include IgA1 and IgA2. In humans, the IgA and IgD isotypes contain four heavy chains and four light chains; the IgG and IgE isotypes contain two heavy chains and two light chains; and the IgM isotype contains five heavy chains and five light chains. The heavy chain C region typically comprises one or more domains that may be responsible for effector function. The number of heavy chain constant region domains will depend on the isotype. IgG heavy chains, for example, each contain three C region domains known as CH1, CH2 and CH3. The antibodies that are provided can have any of these isotypes and subtypes. In certain embodiments, the GIPR antibody is of the IgG1, IgG2, or IgG4 subtype. The terms "GIPR antibody" and "anti-GIPR antibody" are used interchangeably throughout this application and figures. Both terms refer to an antibody that binds to GIPR.

[0248] 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.

[0249] 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.

[0250] 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.

[0251] 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.

[0252] The various light chain and heavy chain variable regions provided herein are depicted in TABLE 3. Each of these variable regions may be attached to a heavy or light chain constant regions to form a complete antibody heavy and light chain, respectively. Furthermore, each of the so generated heavy and light chain sequences may be combined to form a complete antibody structure.

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

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

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

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

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

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

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

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

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

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

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 GGACCCCGGCGAGAGGTCAACCATCTCTTGT CTGGAAGTAGCTCCAACATCGGAAGTAATACTG TAAACTGGTACCAACACCTCCAGGAACGGCCC CCAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCTCCCTGCCATCAGTGGG CTCAGTCTGAGGATGAGGCTGATTATTCTGTG CAACATTCGATGACAGCTGAATGGTCCGGTAT TCGGCGGAGGACCAAGCTGACCGTCTCTAGGT	CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCCGGATACACCTTACCCGGCTACTAT ATGCATTGGGTGCGACAGGCCCTGGACAAGGG CTTGAGTGGATGGATGATCAACCCCTAACAGT GGTGGCACAACTATGCACAGAAGTTTCAGGGC AGGGTCAACCATGACCAAGGACACGTCCATCAGT ACAGCTACATGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGGGATTACGTTTGGGGACTTATCGGCCCTCAC TACTACTACGGTATGACGTCTGGGGCCCAAGGG ACCACGGTCACCGTCTCCTCA
			SEQ ID NO: 1571	SEQ ID NO: 1728
iPS:335914	4B1	NA	QSVLTQPPSASGTPGQRVTISCSGSSNIGSNTVNW YQHLPGTAPKLLIYTNNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDDSLNPGPVFGGGTK LTVLG	QMQVVQSGAEVKKPGASVKVSKASGYTFTGY MHWVRQAPQGQLEWMGWNPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSLRSDDTAVYYCARG GDYVWGTYPHYYYGMDVWVGQGTITVSS
			SEQ ID NO: 1	SEQ ID NO: 158
iPS:335914	4B1	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGATCACCATCATT GCCGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACAGGAAAGCCCCTA AGCGCTGATCTATGGTGCATCCAGTTTGCAA GTGGGTCCCTTCAAGTTACGCGGAGTGGAT CTGGGACAGAAATTCATCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCACTTACTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAGTGGATATCAAAACGA	CAGGTGCAGTGGTGGAGTCTGGGGAGGCGTG GTCCAGCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCACTTTCAGTAACCTTTGGCA TGCATGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGGAA GTAATGAAAACATATGCAGACTCCGTGAAGGGCC GATTACCATCTCCAGAGACAATTCACAAGAATA CGCTGTATCTGCATATGAACAGCTTGAGAGTCG CGGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA
			SEQ ID NO: 1572	SEQ ID NO: 1729

	AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLQSGVPSRFSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVWDGSNENYADSVKG RFTISRDNSKNTLYLHMNSLRVADTAVYYCARDG TIFGVLLGDYWGGQTLVTVSS
!PS:335938	6H1	NA	SEQ ID NO: 2 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACAGGGAAGCCCCCTA AGCCCTGATCTATGTGATCCAGTTTGCAA GTGGGTCCCTTCAAGTTTCAGCGGAGTGGAT CTGGGACAGAAATTCATCTCTCAATCAGCAGCC TGCAGCCTGAAGATTTCGCACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACCTTCGGCCCT GGGACCAAAGTGGATATCAAAACGA
			SEQ ID NO: 1573 DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLQSGVPSRFSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR
!PS:335941	2F11	NA	SEQ ID NO: 3 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTAA ATTGGTATCAGCAGAAACAGGGAAGCCCCCTA AGCTCCTGATCTACGATGCATCCAAATTTGGAA CAGGGGTCCCATCAAGGTTTCAGTGGAAAGTGAT CTGGGACAGATTTAGTTTCACCATCAGCAGCCT GCAGCCTGAAGATATTGCAACATATTACTGTCA ACAGTATGATATTCTCCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGA
			SEQ ID NO: 1574 CAGGTGCAACTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCACTCCCTTCAGTAGCTATGC ATGCACCTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGGA AGTAATAAATACTATGCAGACTCCGTGAAGGGC CGATTCAACCATCTCCAGCGACAATTCGAAGAAC ACGCTGTATCTGCAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGGAGAGAT AGGACGATTTTGGAGTGGTCTTGACTACTGG GGCCAGGGAACCTGGTCAACCGTCTCCTCA
	AA	DIQMTQSPSSLSASIGDRVTITCRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAIVWDGSNKYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGGQTLVTVSS	SEQ ID NO: 1730 QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAIVWDGSNKYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGGQTLVTVSS
	NA	SEQ ID NO: 160 CAGGTGCAACTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCACTCCCTTCAGTAGCTATGC ATGCACCTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGGA AGTAATAAATACTATGCAGACTCCGTGAAGGGC CGATTCAACCATCTCCAGCGACAATTCGAAGAAC ACGCTGTATCTGCAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGGAGAGAT AGGACGATTTTGGAGTGGTCTTGACTACTGG GGCCAGGGAACCTGGTCAACCGTCTCCTCA	SEQ ID NO: 1731

		AA	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGTD FSFTISLQPEDIAITYYCQYDILLTFGGGKVEIKR	SEQ ID NO: 4	QVQLVESGGGVVQGRSLRLSCAASGFTFSYGM HWVRQAPGKGLEWVAIVYDGSNKYYADSVKG RFTISDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLDYWGQGTLVTVSS
		NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTC'TCTGGCGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGT'TTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAAGCAG CAACCAGGACATCTCTTAAGTGTCTCATTTACT GGCATCTACCCGGGAATCCGGGTCCCTGACC GATTCAGTGGCAGCGGTCTGGGACAGATTTC CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTT'TTACTGTCAACAATATTATAGTAC TCCGTGGACGTTTCGGCCAAAGGGACCAAGGTGGA AATCAAAACGA	SEQ ID NO: 161	CAGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCGACAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATCAACCTGACAGT GGTGGCACAGACTATTACAGAGGTTTCAGGGC AGGTTCAACCATGACCAAGGACACGTCCTCAGC ACAGCCTACATGGAAGTGAACAGGCTGAGATCT GACGACACGCGCTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCGTCT CCTCA
	IP:335970	5C2	SEQ ID NO: 1575	SEQ ID NO: 1732	QVPLVQSGAEVKKPGASVKVCKASGYTFTGYI HWVRQAPGQGLEWMGWINPDSSGTDYSQRFQGR FTMRDTSISTAYMELNRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGTLVTVSS
	IP:335978	13H12	SEQ ID NO: 5	SEQ ID NO: 162	CAGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCGACAGGCCCTGGACAAGGA CTTGAGTGGATGGGTGGATCAACCTGACAGT GGTGGCACAGACTATTACAGAGGTTTCAGGGC AGGTTCAACCATGACCAAGGACACGTCCTCAGC ACAGCCTACATGGAAGTGAACAGGCTGAGATCT GACGACACGCGCTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCGTCT CCTCA
		AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQHPKLLIYWASTRESGVPDFRFSGS GSGTDFTLTISSLQAEDVAVFYCQYYSTPWTFGQ GTKVEIKR	SEQ ID NO: 1733	
		NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTC'TCTGGCGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGT'TTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAAGCAG AAACCAAGGACATCTCTTAAGTGTCTCATTTACT GGCATCTACCCGGGAATCCGGGTCCCTGACC GATTCAGTGGCAGCGGTCTGGGACAGATTTC CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTT'TTACTGTCAACAATATTATAGTAC TCCGTGGACGTTTCGGCCAAAGGGACCAAGGTGGA AATCAAAACGA	SEQ ID NO: 1576	

		AA	DIVMTQSPDLSLVSLGERATINCKSSQSVLSSNNK NYIAWYQQKPGHPPKLLIYWASTRESGVPDFSGS GSGTDFLLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR SEQ ID NO: 6	QVPLVQSGAEVKKPGASVKVSKASGYTFTGYYI HWVRQAPGQGLEWMGWINPDSGGTDYSQRFQGR FTMTRDTSISTAYMELSRLSDDTAVYYCAREATI FGMLVFPDYWGQGLVTVSS SEQ ID NO: 163
	IP:335984	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAACAG AACCCAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAGTGGCAGCGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGGACCAAGGTGG AAATCAAAACGA SEQ ID NO: 1577	CAGTGCCGCTGGTACAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATACACTGGGTGCGTCAGGCCCTGGACAAAGG CTTGTTGGATGGGTGGATCAGCCCTAACAGT GGTGACACAAAGCTATGCACAGAAATTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT GACGACACGGCCGTGATTTCTGTACGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCGTCT CCTCA SEQ ID NO: 1734
			DIVMTQSPDLSLVSLGERATINCKSSQSVLSSNNK NYIAWYQQKPGQPPNLLIYWTSRDSGVPDFSG SGSGTDFLLTINSLQAEDVAVYYCQQYYRTPTWTF GQGTKVEIKR SEQ ID NO: 7	QVPLVQSGAEVKKPGASVKVSKASGYTFTGYYI HWVRQAPGQGLVWMGWISPNSGDTSYAQKFQDR VTMTRDTSISTAYMELSRLSDDTAVYYCTREATI FGMLVFPDYWGQGLVTVSS SEQ ID NO: 164
	IP:335994	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAACAG AACCCAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAGTGGCAGCGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGGACCAAGGTGG AAATCAAAACGA SEQ ID NO: 1578	CAGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATACACTGGGTGCGTCAGGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATAAGCCCTAACAAAT GGTGACACAAACTATGCACAGAAATTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT GACGACACGGCCGTGATTTACTGTACGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCGTCT CCTCA SEQ ID NO: 1735

		AA	DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRDGVPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR SEQ ID NO: 8	QVPLVQSGAEVKKPGASVKVSKASGYTFTGYYI HWVRQAPGQGLEWMGWISPNNGDITNYAQKFQD RVTMTDRDTSISTAYMELSRLRSDDTAVYYCTREA TIFGMILVLPEDYWGQGTLLVTVSS SEQ ID NO: 165
IP:336024	18E3	NA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCAGACAGAGTTCAAGTGGCAGTG GGTCTGGACAGACTTCACTCTCACCATCAGCA GACAGGAGCCTGATGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGTTCAACCGCTCACITTCGG CGGAGGGACCAAGGTGGAGATCAAAACGA SEQ ID NO: 1579	CAGGTGCAGTTGCAGGAGTCCGGGCCCAGGACTG GTGAAGCCTTCACAGACCCTGTCCCTCACCTGC ACTGTCTCTGGTGAAGTCCATCAGCAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCAGCCAGGGA AGGGCTGGAGTGGATTGGGTACATCTATTACA GTGGGAGCACCTACTACAACCCGTCCCTCAAGA GTCGAGTTACCATATCATAGTAGACACGTCTAAGA ACCAAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGGACACGGCCGTGTATTACTGTGCGAGAGA TCGTATTACGATTTTGGAGTGGTTATGGGGGGC GGTATGGACGTCTGGGGCCAAAGGGACACCGGTC ACCGTCTCTCTCA SEQ ID NO: 1736
		AA	EIVLTQSPGTLSPGERATLSCRASQISYSYLAW YQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDF TLTISRQEPDDFAVYYCQQYGSPLTFGGGTKEI KR SEQ ID NO: 9	QVQLQESGPGLVKPSQTLSTCTVSGDSISSGGYY WSWIRQHPGKGLEWIGYIYSGSTYYNPISLKSRT ISVDTSKNQFSLKLSSTAAADTAVYYCARDRIITFG VVMGGGMDVWGQGTITVTVSS SEQ ID NO: 166
IP:336041	2G10_1C1	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTG TCTGTGTCTCCAGGGGAAAGAGCCACCCCTCTCC TGCAGGGCCAGTCAGAGTGTAGCAGCAACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACCCAGGGCC ACTGGTATCCAGCCAGGTCAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGCAGTCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTGGCCTCTCACTTTCGGCG GAGGGACCAAGGTGGAGATCAAAACGA SEQ ID NO: 1580	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACTCCATCAGTAAGTATGGC ATGCACCTGGGTCCGCCAGGCTCCAGGCGAGGGG CTGGAGTGGGTGGCAGCTATATGTTTGTATGGA AGTGATAAATACTATGCAGACTCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAACTCCAAAGAAC ACGCTGTATCTGCAAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGCGGATTTTGGAGTGGTCCCGGACTACTGG GGCCAGGGAAACCTGTGTCACCGTCTCCTCTCA SEQ ID NO: 1737

		AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQKPGQAPRLLIYGAAATRAATGIPARVSGSGGTE FTLTISSLQSEDFAVYYCQQYNWPLTFGGGKVE IKR	QVQLVESGGGVVQPRSLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAIWFDGSDKYVADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGLVTVSS
		NA	SEQ ID NO: 10 GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCAACCATCACTT GCCGGCAAGTCAGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACAGGGAAGCCCCCTA AACGCTGATCTATGGTGCATCCAGTTTGCAA GTGGGTCCCATCAAGGTTACGCGGCGAGTGAT CTGGGACAGAGTTCACCTCTCAATCAGCAGCC TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAAATAGTTACCCATTCACTTTCGGCCCT GGGACCAAAGTGGATGTCAAACGA	SEQ ID NO: 167 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTCACTTCACTTGGCA TGCACTGGTCCCGCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGGAA GTAATAAATACTATGCAGACTCCGTGAAGGGCC GCTTCAACCATCTCCAGAGACAATCCAAAGACA CGCTGATCTGCAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTGGAGTGTCTTGGGGGACTACT GGGGCAGGGAACCTGGTCAACCGTCTCCTCA
	4H9.004	AA	SEQ ID NO: 1581 DIQMTQSPSSLSASVGDRTVTITCRASQGIRNELGW YQKPGKAPKRLIYGASLSQSGVPSRFSGSGTE FTLTISSLQPEDFVITYYCLQHNSYPFTFGPGTKVDV KR	SEQ ID NO: 1738 QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIWDGSKNYVADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGLVTVSS
	6A5.004	NA	SEQ ID NO: 11 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGACAGAGTCAACCATCACTT GCCAGCGAGTCAGGACATTACCAACTATTAA ATTGGTATCAGCAGAAACAGGGAAGCCCCCTA AACTCCTGATCTACGATGCTTCCAAATTTGGAGCC AGGGTCCCATCAAGTTTCAGTGAAGTGGATC TGGGACAGATTTTACTTTCACCATCAGCAGCCTG CAGCCTGAAGATAATTGCAACATATTACTGTCAA CAGTATGATGATCTATTCACTTTCGGCCCCTGGGA CCAAAGTGGATATCAAACGA	SEQ ID NO: 168 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCTCCTTCACTAGCTATGGCA TGCACTGGTCCCGCAGCCTCCAGGCAAGGGGC TGGAGTGGTGGCAGCTATATGGTATGATGGAA ATAATAAATACTATGCAGACTCCGTGAAGGGCC GATTCAACCATCTCCAGAGACAGTTCCAAAGACA CGCTGATCTGCAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGGAGAGATC GGACGATTTTGGAGTGTCTTGGTACCTCG GCCAGGGAACCTGGTCAACCGTCTCCTCA
	IPS:336077	AA	SEQ ID NO: 1582 DIQMTQSPSSLSASVGDRTVTITCAASQDITNLYLNW YQKPGKAPKRLIYDASNLEPGVPSRFSGSGGTD	SEQ ID NO: 1739 QVQLVESGGGVVQPRSLRLSCAASGFSFSYGM HWVRQPPGKGLEWVAIWYDGNKNKYVADSVKG
	IPS:336088			

			FTFTISLQPEDIATYYCQYDDLFTFGPGTKVDIK R	SEQ ID NO: 12	SEQ ID NO: 169	RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYLGQGTLVTVSS
		NA	GACATCCAGATGACCCAGTCTCCATCTTCCGTGT CTGCATCTGTAGGAGACAGAGTCAACCATCACTT GTCGGCGAGTCAAGGCTTTATCATCTGGTTAG CCTGGTATCAGCAGAAACCGGGGAAAGCCCCTA AACTCCTGATCTATGCTGCATCCAGTTTGCAAAG TGGGGTCCCATCAAGGTTCAAGCGGCAAGTGGCTC TGGGACAGATTTCACTCTCAACCATCAGCAGCCT ACAGCCTGAAGATTTTGCAACTTACTATTGTCAA CAGACTAACAGTTTCCCTCCGACGTTCCGGCCAA GGGACCAAGGTGGAATCAAAACGA	SEQ ID NO: 1583	SEQ ID NO: 1740	CAGGTGCAGCTGCAGGAGTGGGGCCCAAGGACTG GTGAAGCCTTCGGAGACCCCTGTCCCTCACCTGC ACTGTCTCTCAGGGCTCCATCAGTAGTTACTACT GGAGCTGGATCCGGCAGCCCGCCGGGAAGGGA CTAGAGTGGATTGGCCGTATCTATACCAAGTGGG AGCACC AACTACAACCCCTCCCTCAAGAGTCGA GTCACCATGTCAATAGACACGTCC AAGAACCAG TTCTCCCTGAAACTGAACCTCTGTGACCCGCCGCG GACACGGCCGTGTATTACTGTGCGAGAGATGTA GCAGTGGCTGGCTTTGACTACTGGGGCCAGGGA ACCTGTGCACCGTCTCCTCA
		AA	DIQMTQSPSSVSASVGDRTVTITCRASQGLIWLAW YQQKPGKAPKLLIYAASSLQSGVPSRFSGSGTD FTLTISLQPEDFATYYCQQQTNSFPPTFGQTKVEI KR	SEQ ID NO: 13	SEQ ID NO: 170	QVQLQESGPGLVKPSSETLSLTCTVSQSSISSYYWS WIRQPAKGLEWIGRIYTSGSTNYPNPSLKSRVTMS IDTSKNQFSLKLNSTVAADTAVYYCARDVA VAGF DYWGQGTLVTVSS
		NA	GACATCCAGATGACCCAGTCTCCATCTTCCGTGT CTGCATCTGTAGGAGACAGAGTCAACCATCACTT GTCGGCGAGTCAAGGCTTTATCATCTGGTTAG CCTGGTATCAGCAGAAACCGGGGAAAGCCCCTA AACTCCTGATCTATGCTGCATCCAGTTTGCAAAG TGGGGTCCCATCAAGGTTCAAGCGGCAAGTGGCTC TGGGACAGATTTCACTCTCAACCATCAGCAGCCT ACAGCCTGAAGATTTTGCAACTTACTATTGTCAA CAGACTAACAGTTTCCCTCCGACGTTCCGGCCAA GGGACCAAGGTGGAATCAAAACGA	SEQ ID NO: 1584	SEQ ID NO: 1741	CAGGTGCAGCTGCAGGAGTGGGGCCCAAGGACTG GTGAAGCCTTCGGAGACCCCTGTCCCTCACCTGC ACTGTCTCTGCGGGCTCCATCAGTAGTTACTACT GGAGCTGGATCCGGCAGCCCGCCGGGAAGGGA CTAGAGTGGATTGGCCGTATCTATACCAAGTGGG AGCACC AACTACAACCCCTCCCTCAAGAGTCGA GTCACCATGTCAATAGACACGTCC AAGAACCAG TTCTCCCTGAAACTGAACCTCTGTGACCCGCCGCG GACACGGCCGTGTATTACTGTGCGAGAGATGTA GCAGTGGCTGGCTTTGACTACTGGGGCCAGGGA ACCTGTGCACCGTCTCCTCA
		AA	DIQMTQSPSSVSASVGDRTVTITCRASQGLIWLAW YQQKPGKAPKLLIYAASSLQSGVPSRFSGSGTD	SEQ ID NO: 1584	SEQ ID NO: 1741	QVQLQESGPGLVKPSSETLSLTCTVSQSSISSYYWS WIRQPAKGLEWIGRIYTSGSTNYPNPSLKSRVTMS

		FTLTISSLQPEDFATYYCQQTNSFPPTFGQGTKEI KR	IDTSKNQFSLKLSVTAADTAVYYCARDVA VAGF DYWGQGLVTVSS
		SEQ ID NO: 14	SEQ ID NO: 171
	4H9.004.001	NA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGAATTCACCTTCAGTTACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTC AAGAACA CGCTGTATCTGCA AATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTGGAGTGCTCTTGGGGGACTACT GGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA
		SEQ ID NO: 1585	SEQ ID NO: 1742
		DIQMTQSPSSLSASVGDRTVITCRASQGIRNELGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGTE FTLTISSLQPEDFVITYYCLQHNSYPFTFGQGTKEI VKR	QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIWDASNKYADAVKVG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGLVTVSS
		SEQ ID NO: 15	SEQ ID NO: 172
	4H9.004.002	NA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGAATTCACCTTCAGTTACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACTCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTC AAGAACA CGCTGTATCTGCA AATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTGGAGTGCTCTTGGGGGACTACT GGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA
		SEQ ID NO: 1586	SEQ ID NO: 1743
		DIQMTQSPSSLSASVGDRTVITCRASQGIRNELGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGTE FTLTISSLQPEDFVITYYCLQHNSYPFTFGQGTKEI VKR	QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIWDASNKYADSVKVG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGLVTVSS
		SEQ ID NO: 1586	SEQ ID NO: 1743

		SEQ ID NO: 16	SEQ ID NO: 173
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IP:360936	4H9.004.003	NA	GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCAACCATCACTT GCCGGCAAGTCAGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACAGGGAAGCCCCCTA AACTCCTGATCTATGTTGCATCCAGTTTGCAA GTGGGTCCCATCAAGGTTACGCGCAGTGGAT CTGGGACAGAGTTCATCTCAACAATCAGCAGCC TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAAATAGTTACCCATTCACCTTTCGGCCA AGGACCAAAGTGGATGTCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGTCTGGATTCACTTCACTTCACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGGAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCAACCATCTCCAGAGACAATTCAGAACA CGCTGTATCTGCAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTTACTGTGCGCGAGATG GGACGATTTTGGAGTGCTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
		AA	DIQMTQSPSSLSASVGDRTVTITCRASQGIRNELGW YQKPGKAPKLLIYGASSLQSGVPSRFSGSGSTE FTLTISLQPEDFVTYYCLQHNSYPFTFGQGTKVD VKR	QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAIVYDGSNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGLVTVSS
IP:360943	4H9.004.004	NA	GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCAACCATCACTT GCCGGCAAGTCAGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACAGGGAAGCCCCCTA AACTCCTGATCTATGTTGCATCCAGTTTGCAA GTGGGTCCCATCAAGGTTACGCGCAGTGGAT CTGGGACAGAGTTCATCTCAACAATCAGCAGCC TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAAATAGTTACCCATTCACCTTTCGGCCCT GGGACCAAAGTGGATGTCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGTCTGGATTCACTTCACTTCACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCAACCATCTCCAGAGACAATTCAGAACA CGCTGTATCTGCAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTTACTGTGCGCGAGATG GGACGATTTTGGAGTGCTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
		AA	DIQMTQSPSSLSASVGDRTVTITCRASQGIRNELGW YQKPGKAPKLLIYGASSLQSGVPSRFSGSGSTE FTLTISLQPEDFVTYYCLQHNSYPFTFGPGTKVDV KR	QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAIVYDASNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGLVTVSS

		SEQ ID NO: 18	GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACCAGGGAAGCCCCCTA AACGCTGATCTATGGTGCATCCAGTTTGCAA GTGGGTCCCATCAAGGTTACGCGGCAGTGGAT CTGGACAGAGTTCACTCTCACAATCAGCAGCC TGACGCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAATAGTTACCCATTCACTTTCGGCCA AGGACCAAAGTGGATGTCAAACGA	SEQ ID NO: 1589	SEQ ID NO: 175	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTCACTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATA GGACGATTTTGGAGTGTCTTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
4H9.004.005	!PS:360949	NA			SEQ ID NO: 1746	QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIWYDASNKYADAVKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSS
		SEQ ID NO: 19	GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACCAGGGAAGCCCCCTA AACTCCTGATCTATGGTGCATCCAGTTTGCAA GTGGGTCCCATCAAGGTTACGCGGCAGTGGAT CTGGACAGAGTTCACTCTCACAATCAGCAGCC TGACGCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAATAGTTACCCATTCACTTTCGGCCA AGGACCAAAGTGGATGTCAAACGA	SEQ ID NO: 176	SEQ ID NO: 177	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTCACTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATA GGACGATTTTGGAGTGTCTTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
4H9.004.006	!PS:359761	NA			SEQ ID NO: 1747	QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIWYDASNKYADAVKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLLGDYWGQGTLVTVSS
		SEQ ID NO: 1590	DIQMTQSPSSLSASVGDRTVTITCRASQGIRNELGW YQKPGKAPKLLIYGASSLQSGVPSRFSGSGTE FTLTISLQPEDFVTYYCLQHNSYPFTFGQGTKVD VKR	SEQ ID NO: 1590	SEQ ID NO: 1748	QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIWYDASNKYADAVKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLLGDYWGQGTLVTVSS
		AA				

IP:360955	4B1.010	NA	SEQ ID NO: 20 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTTAG GCTGTATCAGCAGAAACCAAGGAAAGCCCCA AGTCTCTGATCTATGTTGCATCCAGTTTGCAA GTGGGTCCCTTCAAGTTTCAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCACAATCAGCAGCC TGACGCTGAAGATTTGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAAAACGA	SEQ ID NO: 177 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTTCAGTAACCTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAAATTCCAAGAATA CGCTGTATCTGCAAAATGAACAGCCTGAGAGTCG CGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA
		AA	SEQ ID NO: 1591 DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK R	SEQ ID NO: 1748 QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVWYDASNENYADAVKVG RFTISRDN SKNTLYLQMNSLRVADTAVYYCARDG TIFGVVLGDYWGQGGLVTVSS
	4B1.011	NA	SEQ ID NO: 21 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTTAG GCTGTATCAGCAGAAACCAAGGAAAGCCCCA AGCGCTGATCTATGTTGCATCCAGTTTGCAA GTGGGTCCCTTCAAGTTTCAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCACAATCAGCAGCC TGACGCTGAAGATTTGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAAAACGA	SEQ ID NO: 178 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTTCAGTAACCTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAAATTCCAAGAATA CGCTGTATCTGCAAAATGAACAGCCTGAGAGTCG CGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA
		AA	SEQ ID NO: 1592 DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLQSGVPSRFSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK R	SEQ ID NO: 1749 QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVWYDASNENYADAVKVG RFTISRDN SKNTLYLQMNSLRVADTAVYYCARDG TIFGVVLGDYWGQGGLVTVSS
IP:360962	4B1.011			

		SEQ ID NO: 22	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCCTA AGTCCTGATCTATGGTGTCATCCAGTTTGCAAA GTGGGTCCCTTCAAGTTTCAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCTCACAATCAGCAGCC TGACGCCTGAAGATTTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAAACGA	SEQ ID NO: 1593	SEQ ID NO: 179	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTTCAGTAACCTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGCAGACTCCGTGAAGGGCC GATTACCATCTCCAGAGACAATTCACAAGAATA CGCTGTATCTGCACATGAACAGCCTGAGAGTCG CGGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA
IPS:360968	4B1.012	NA			SEQ ID NO: 1750	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVWYDASNENYADAVKGG RFTISRDN SKNTLYLQMNSLRVADTA VYYCARDG TIFGVVLGDYWGQGLVTVSS
		SEQ ID NO: 23	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCCTA AGTCCTGATCTATGGTGTCATCCAGTTTGCAAA GTGGGTCCCTTCAAGTTTCAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCTCACAATCAGCAGCC TGACGCCTGAAGATTTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAAAACGA	SEQ ID NO: 180	SEQ ID NO: 1751	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTTCAGTAACCTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGCAGACTCCGTGAAGGGCC GATTACCATCTCCAGAGACAATTCACAAGAATA CGCTGTATCTGCACATGAACAGCCTGAGAGTCG CGGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA
IPS:360974	4B1.013	NA			SEQ ID NO: 1751	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVWYDASNENYADSVKGG RFTISRDN SKNTLYLHMNSLRVADTA VYYCARDG TIFGVVLGDYWGQGLVTVSS
		SEQ ID NO: 1594	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIK R		SEQ ID NO: 1751	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVWYDASNENYADSVKGG RFTISRDN SKNTLYLHMNSLRVADTA VYYCARDG TIFGVVLGDYWGQGLVTVSS
		AA				

!PS:360978	4B1.014	NA	SEQ ID NO: 24 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACAGGGAAAGCCCCTA AGCTCCTGATCTATGTTGCATCCAGTTTGCAA GTGGGTCCTTCAAGTTTCAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCTCAATCAGCAGCC TGCAGCCTGAAGATTTCGCACTTACTGTCT ACAGCATATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAAAACGA	SEQ ID NO: 181 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCACTTTCAGTAACCTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGGAA GTAATGAAAACATATGCAGACGCCGTGAAGGCC GATTCACCATCTCCAGAGACAATTCACAAGAATA CGCTGTATCTGCACATGAACAGCCTGAGAGTCG CGGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
			SEQ ID NO: 1595 DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK R	SEQ ID NO: 1752 QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVYDGSNENYADAVKG RFTISRDN SKNTLYLHMNSLRVADTAVYYCARDG TIFGVVLGDYWGQGLVTVSS
!PS:359785	4B1.015	NA	SEQ ID NO: 25 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACAGGGAAAGCCCCTA AGCTCCTGATCTATGTTGCATCCAGTTTGCAA GTGGGTCCTTCAAGTTTCAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCTCAATCAGCAGCC TGCAGCCTGAAGATTTCGCACTTACTGTCT ACAGCATATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAAAACGA	SEQ ID NO: 182 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCACTTTCAGTAACCTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGCAGACGCCGTGAAGGCC GATTCACCATCTCCAGAGACAATTCACAAGAATA CGCTGTATCTGCAATGAACAGCCTGAGAGTCG AGGACACGGCTGTGTATTATTGTGCGCGAGATA GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
			SEQ ID NO: 1596 DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK R	SEQ ID NO: 1753 QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVYDGSNENYADAVKG RFTISRDN SKNTLYLQMNSLRVEDTAVYYCARDR TIFGVVLGDYWGQGLVTVSS

		SEQ ID NO: 26	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACCAAGGAAAGCCCCTA AGTCCTGATCTATGGTGATCCAGTTTGCAA GTGGGTCCCTTCAAAGTTTCAGCGGAGTGGAT CTGGGACAGAAATTCATCTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAAAACGA	SEQ ID NO: 1597	SEQ ID NO: 183	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACCTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGCAGACGCCGTGAAGGGCC GATTACCATCTCCAGAGACAATTCACAAGAATA CGCTGTATCTGCAAAATGAACAGCCTGAGAGTCG AGGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
IPs:360982	4B1.016	NA			SEQ ID NO: 1754	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVWYDASNENYADAVKVG RFTISRDN SKNTLYLQMNSLRVEDTAVYYCARDG TIFGVVLGDYWGQGTLVTVSS
		SEQ ID NO: 27	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTAG GCTGGTATCACCAGAAACCAAGGAAAGCCCCTA AGCGCTGATCTATGGTGATCCAGTTTGCAA GTGGGTCCCTTCAAAGTTTCAGCGGAGTGGAT CTGGGACAGAAATTCATCTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAAACGA	SEQ ID NO: 184	SEQ ID NO: 183	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACCTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGCAGACTCCGTGAAGGGCC GATTACCATCTCCAGAGACAATTCACAAGAACA CGCTGTATCTGCACATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
IPs:335922	18F2	NA			SEQ ID NO: 1755	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVWYDGSNENYADSVKVG RFTISRDN SKNTLYLHMNSLRADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSS
		SEQ ID NO: 1598	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YHQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR			
		AA				

		SEQ ID NO: 28	GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTATAGGAGACAGAGTCACCATCACTTGCCGGCAAGTCAGGACCTTAGAAAATTATTTAGGCTGGTATCAACAGAAACCAAGGGAAGCCCCCTAAGTCCTGATCTATGGTGCAATCCAGTTTGCAAA GTGGGTCCCTTCAAGGTTCAAGCGGCAGTGGATCTGGGACAGAAATTCATCTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTGCAACTTATTACTGTCTACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAGTGGATATCAAAACGA	SEQ ID NO: 1599	DIQMTQSPSSLSASIGDRVTITCRASQDLRNLYLGWYQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	AA		18F2.002	NA	SEQ ID NO: 28	GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTATAGGAGACAGAGTCACCATCACTTGCCGGCAAGTCAGGACCTTAGAAAATTATTTAGGCTGGTATCAACAGAAACCAAGGGAAGCCCCCTAAGTCCTGATCTATGGTGCAATCCAGTTTGCAAA GTGGGTCCCTTCAAGGTTCAAGCGGCAGTGGATCTGGGACAGAAATTCATCTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTGCAACTTATTACTGTCTACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAGTGGATATCAAAACGA	SEQ ID NO: 1599	DIQMTQSPSSLSASIGDRVTITCRASQDLRNLYLGWYQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	AA		18F2.002	NA															
	!PS:360986										SEQ ID NO: 185	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGGTGTCCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACTTTCAGTAACCTTTGGCATGCACTGGGTCCGCCAGGCCCAAGCAAGGGGCTGGAGTGGTGGCAGTTATATGGTATGATGCAAGTAATGAAAACATATGCAGACGCCGTGAAGGGCGGATTACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCGCGGACACGGCTGTGTATTACTGTGCGGAGAGATGGACGATCTTTGGAGTGGTCTTGGGGGACTACTGGGCCAGGGAACCTGGTCAACCGTCTCCTCA	SEQ ID NO: 1756	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAIVWYDASNENYADAVKGRFTISRDN SKNTLYLQMNSLR AADTA VYYCARDGTIFGVVLGDYWGQGLVTVSS					SEQ ID NO: 186	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGGTGTCCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACTTTCAGTAACCTTTGGCATGCACTGGGTCCGCCAGGCCCAAGCAAGGGGCTGGAGTGGTGGCAGTTATATGGTATGATGCAAGTAATGAAAACATATGCAGACGCCGTGAAGGGCGGATTACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAATGAACAGCCTGAGAGCCGCGGACACGGCTGTGTATTACTGTGCGGAGAGATGGACGATCTTTGGAGTGGTCTTGGGGGACTACTGGGCCAGGGAACCTGGTCAACCGTCTCCTCA	SEQ ID NO: 1757	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAIVWYDASNENYADAVKGRFTISRDN SKNTLYLHMNSLR AADTA VYYCARDGTIFGVVLGDYWGQGLVTVSS					SEQ ID NO: 1600	DIQMTQSPSSLSASIGDRVTITCRASQDLRNLYLGWYQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	AA		18F2.003	NA
	!PS:360995										SEQ ID NO: 185	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGGTGTCCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACTTTCAGTAACCTTTGGCATGCACTGGGTCCGCCAGGCCCAAGCAAGGGGCTGGAGTGGTGGCAGTTATATGGTATGATGCAAGTAATGAAAACATATGCAGACGCCGTGAAGGGCGGATTACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAATGAACAGCCTGAGAGCCGCGGACACGGCTGTGTATTACTGTGCGGAGAGATGGACGATCTTTGGAGTGGTCTTGGGGGACTACTGGGCCAGGGAACCTGGTCAACCGTCTCCTCA	SEQ ID NO: 1756	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAIVWYDASNENYADAVKGRFTISRDN SKNTLYLQMNSLR AADTA VYYCARDGTIFGVVLGDYWGQGLVTVSS					SEQ ID NO: 186	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGGTGTCCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACTTTCAGTAACCTTTGGCATGCACTGGGTCCGCCAGGCCCAAGCAAGGGGCTGGAGTGGTGGCAGTTATATGGTATGATGCAAGTAATGAAAACATATGCAGACGCCGTGAAGGGCGGATTACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAATGAACAGCCTGAGAGCCGCGGACACGGCTGTGTATTACTGTGCGGAGAGATGGACGATCTTTGGAGTGGTCTTGGGGGACTACTGGGCCAGGGAACCTGGTCAACCGTCTCCTCA	SEQ ID NO: 1757	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAIVWYDASNENYADAVKGRFTISRDN SKNTLYLHMNSLR AADTA VYYCARDGTIFGVVLGDYWGQGLVTVSS					SEQ ID NO: 1600	DIQMTQSPSSLSASIGDRVTITCRASQDLRNLYLGWYQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	AA		18F2.003	NA
											SEQ ID NO: 185	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGGTGTCCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACTTTCAGTAACCTTTGGCATGCACTGGGTCCGCCAGGCCCAAGCAAGGGGCTGGAGTGGTGGCAGTTATATGGTATGATGCAAGTAATGAAAACATATGCAGACGCCGTGAAGGGCGGATTACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAATGAACAGCCTGAGAGCCGCGGACACGGCTGTGTATTACTGTGCGGAGAGATGGACGATCTTTGGAGTGGTCTTGGGGGACTACTGGGCCAGGGAACCTGGTCAACCGTCTCCTCA	SEQ ID NO: 1756	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAIVWYDASNENYADAVKGRFTISRDN SKNTLYLQMNSLR AADTA VYYCARDGTIFGVVLGDYWGQGLVTVSS					SEQ ID NO: 186	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGGTGTCCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACTTTCAGTAACCTTTGGCATGCACTGGGTCCGCCAGGCCCAAGCAAGGGGCTGGAGTGGTGGCAGTTATATGGTATGATGCAAGTAATGAAAACATATGCAGACGCCGTGAAGGGCGGATTACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAATGAACAGCCTGAGAGCCGCGGACACGGCTGTGTATTACTGTGCGGAGAGATGGACGATCTTTGGAGTGGTCTTGGGGGACTACTGGGCCAGGGAACCTGGTCAACCGTCTCCTCA	SEQ ID NO: 1757	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGMHWVRQAPGKGLEWVAIVWYDASNENYADAVKGRFTISRDN SKNTLYLHMNSLR AADTA VYYCARDGTIFGVVLGDYWGQGLVTVSS					SEQ ID NO: 1600	DIQMTQSPSSLSASIGDRVTITCRASQDLRNLYLGWYQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	AA		18F2.003	NA

		SEQ ID NO: 30	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCACACAGAAACCAAGGAAAGCCCTA AGTCCTGATCTATGGTGTCATCCAGTTTGCAA GTGGGTCCCTTCAAGTTTCAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGA	SEQ ID NO: 1601	SEQ ID NO: 1758
!PS:360999	18F2.004	NA		DIQMTQSPSSLSASIGDRVTITCRASQDLRNLYLGW YHQKPGKAPKLLIYGASSLQSGVPSRFSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKVG RFTISRDN SKNTLYLQMNSLRAADTA VYYCARDG TIFGVVLGDYWGQGTLVTVSS
		SEQ ID NO: 31	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCAACAGAAACCAAGGAAAGCCCTA AGCGCTGATCTATGGTGTCATCCAGTTTGCAA GTGGGTCCCTTCAAGTTTCAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGA	SEQ ID NO: 1602	SEQ ID NO: 188
!PS:361005	18F2.005	NA		DIQMTQSPSSLSASIGDRVTITCRASQDLRNLYLGW YQKPGKAPKRLIYGASSLQSGVPSRFSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTTCAGTAACCTTTGGCA TGCACTGGGTCCGCCAGGCCCAAGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGCAGACGCCGTGAAGGGCC GATTACCATCTCCAGAGACAATTCACAAGAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
		SEQ ID NO: 32	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCAACAGAAACCAAGGAAAGCCCTA AGCGCTGATCTATGGTGTCATCCAGTTTGCAA GTGGGTCCCTTCAAGTTTCAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGA	SEQ ID NO: 1603	SEQ ID NO: 1759
!PS:361006	18F2.006	NA		DIQMTQSPSSLSASIGDRVTITCRASQDLRNLYLGW YQKPGKAPKRLIYGASSLQSGVPSRFSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKVG RFTISRDN SKNTLYLQMNSLRAADTA VYYCARDG TIFGVVLGDYWGQGTLVTVSS

!PS:361009	18F2.006	NA	SEQ ID NO: 32 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCAACCATCACTT GCCGGCAAGTCAGGACCTTAGAATATTAG GCTGGTATCAACAGAAACAGGGAAGCCCCCTA AGCCCTGATCTATGGTGCATCCAGTTTGCAA GTGGGTCCTTCAAGGTTACGCGGCAAGTGAT CTGGGACAGAAATTCATCTCTCAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAAACGA	SEQ ID NO: 189 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCACTTTCAGTAACCTTTGGCA TGCACTGGTCCGCCAGGCCCAAGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGCAGACGCCGTGAAGGCC GATTCACCATCTCCAGAGACAATTCACAAGACA CGCTGATCTGCACATGAACAGCCTGAGAGCCG CGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
		AA	SEQ ID NO: 1603 DIQMTQSPSSLSASIGDRVTITCRASQDLRNLYLW YQKPGKAPKRLIYGASSLQSGVPSRFSGSGSTE FTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR	SEQ ID NO: 1760 QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVWYDASNENYADAVKG RFTISRDN SKNTLYLHMNSLRAADTA VYYCARDG TIFGVVLGDYWGQGLVTVSS
!PS:361013	18F2.007	NA	SEQ ID NO: 33 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCAACCATCACTT GCCGGCAAGTCAGGACCTTAGAATATTAG GCTGGTATCAACAGAAACAGGGAAGCCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAA GTGGGTCCTTCAAGGTTCAAGCGGCAAGTGAT CTGGGACAGAAATTCATCTCTCAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAAACGA	SEQ ID NO: 190 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCACTTTCAGTAACCTTTGGCA TGCACTGGTCCGCCAGGCCCAAGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGCAGACGCCGTGAAGGCC GATTCACCATCTCCAGAGACAATTCACAAGACA CGCTGATCTGCACATGAACAGCCTGAGAGCCG CGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
		AA	SEQ ID NO: 1604 DIQMTQSPSSLSASIGDRVTITCRASQDLRNLYLW YHQPGRKAPKLLIYGASSLQSGVPSRFSGSGSTE FTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR	SEQ ID NO: 1761 QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVWYDASNENYADAVKG RFTISRDN SKNTLYLHMNSLRAADTA VYYCARDG TIFGVVLGDYWGQGLVTVSS

[illegible]

		SEQ ID NO: 36	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCAACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAAATTATTTAG GCTGGTATCAACAGAAACCAAGGGAAGCCCCCTA AGTCCTGATCTATGGTGCAATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTCAAGCGGAGTGGAT CTGGGACAGAAATTCATCTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTGCAACTTATTACTGTCT ACAGCATATAAATTACCCCTTCACTTTCGGCCCT GGGACCAAGTGGATATCAAAACGA	SEQ ID NO: 1607	DIQMTQSPSSLSASIGDRVTITCRASQDLRNLYLGW YQKPGKAPKLLIYGASSLQSGVPSRFSGSGGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR	SEQ ID NO: 36	SEQ ID NO: 193	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTTCAGTAACCTTTGGCA TGCACTGGGTCCGCCAGGCCCAAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGCAGACTCCGTGAAGGGCC GATTACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
!PS:361028	18F2.010	NA					SEQ ID NO: 1764	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAWIWYDASNENYADSVKG RFTISRDNKNTLYLQMNSLRAADTA VYYCARDG TIFGVVLGDYWGQGTLVTVSS
		SEQ ID NO: 37	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCAACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAAATTATTTAG GCTGGTATCAACAGAAACCAAGGGAAGCCCCCTA AGTCCTGATCTATGGTGCAATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTCAAGCGGAGTGGAT CTGGGACAGAAATTCATCTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTGCAACTTATTACTGTCT ACAGCATATAAATTACCCCTTCACTTTCGGCCAA GGGACCAAGTGGATATCAAAACGA	SEQ ID NO: 37	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCAACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAAATTATTTAG GCTGGTATCAACAGAAACCAAGGGAAGCCCCCTA AGTCCTGATCTATGGTGCAATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTCAAGCGGAGTGGAT CTGGGACAGAAATTCATCTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTGCAACTTATTACTGTCT ACAGCATATAAATTACCCCTTCACTTTCGGCCAA GGGACCAAGTGGATATCAAAACGA	SEQ ID NO: 194	SEQ ID NO: 194	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTTCAGTAACCTTTGGCA TGCACTGGGTCCGCCAGGCCCAAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGCAGAGCCCTGAAGGGCC GATTACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGGAGAGATA GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
!PS:360535	18F2.011	NA					SEQ ID NO: 1765	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAWIWYDASNENYADAVKG RFTISRDNKNTLYLQMNSLRAEDTA VYYCARDR TIFGVVLGDYWGQGLVTVSS
		SEQ ID NO: 1608	DIQMTQSPSSLSASIGDRVTITCRASQDLRNLYLGW YQKPGKAPKLLIYGASSLQSGVPSRFSGSGGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDI KR	SEQ ID NO: 1608	DIQMTQSPSSLSASIGDRVTITCRASQDLRNLYLGW YQKPGKAPKLLIYGASSLQSGVPSRFSGSGGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDI KR	SEQ ID NO: 194	SEQ ID NO: 194	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTTCAGTAACCTTTGGCA TGCACTGGGTCCGCCAGGCCCAAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGCAGAGCCCTGAAGGGCC GATTACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGGAGAGATA GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
		SEQ ID NO: 1608	DIQMTQSPSSLSASIGDRVTITCRASQDLRNLYLGW YQKPGKAPKLLIYGASSLQSGVPSRFSGSGGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDI KR	SEQ ID NO: 1608	DIQMTQSPSSLSASIGDRVTITCRASQDLRNLYLGW YQKPGKAPKLLIYGASSLQSGVPSRFSGSGGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDI KR	SEQ ID NO: 194	SEQ ID NO: 194	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTTCAGTAACCTTTGGCA TGCACTGGGTCCGCCAGGCCCAAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGCAGAGCCCTGAAGGGCC GATTACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGGAGAGATA GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
		SEQ ID NO: 1608	DIQMTQSPSSLSASIGDRVTITCRASQDLRNLYLGW YQKPGKAPKLLIYGASSLQSGVPSRFSGSGGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDI KR	SEQ ID NO: 1608	DIQMTQSPSSLSASIGDRVTITCRASQDLRNLYLGW YQKPGKAPKLLIYGASSLQSGVPSRFSGSGGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDI KR	SEQ ID NO: 194	SEQ ID NO: 194	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTTCAGTAACCTTTGGCA TGCACTGGGTCCGCCAGGCCCAAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGCAGAGCCCTGAAGGGCC GATTACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGGAGAGATA GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
		SEQ ID NO: 1608	DIQMTQSPSSLSASIGDRVTITCRASQDLRNLYLGW YQKPGKAPKLLIYGASSLQSGVPSRFSGSGGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDI KR	SEQ ID NO: 1608	DIQMTQSPSSLSASIGDRVTITCRASQDLRNLYLGW YQKPGKAPKLLIYGASSLQSGVPSRFSGSGGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDI KR	SEQ ID NO: 194	SEQ ID NO: 194	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTTCAGTAACCTTTGGCA TGCACTGGGTCCGCCAGGCCCAAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGCAGAGCCCTGAAGGGCC GATTACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGGAGAGATA GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA

		SEQ ID NO: 38	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAAATTATTAG GCTGGTATCAACAGAAACCAGGGAAGCCCCTA AGTCCTGATCTATGGTGATCCAGTTTGCAAA GTGGGTCCCTTCAAGTTTCAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCACAATCAGCAGCC TGCAGCCTGAAGATTTGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAAACGA	SEQ ID NO: 1609	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YQKPGKAPKLLIYGASSLQSGVPSRFSGSGTE FTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR	SEQ ID NO: 195	CAGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACCTTTGGCA TGCACTGGGTCCGCCAGGCCAGGCAAGGGGC TGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGCAGACCCGTGAAGGGCC GATTACCATCTCCAGAGACAATTCCAAAGAACA CGCTGTATCTGCAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
IP:361035	18F2.012	NA				SEQ ID NO: 1766	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAIVWYDASNENYADAVKVG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLDYWGQGTLVTVSS
		SEQ ID NO: 39	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTAA ATTGGTATCAGCAGAAACCAGGGAAGCCCCTA AGTCCTGATCTACGATGCATCCCAATTTGAAA CAGGGTCCCATCAAGGTTCAAGTGAAGTGGAT CTGGGACAGATTTTAGTCTCAACCATCAGCAGCC TGCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATATTCTCCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGA	SEQ ID NO: 196	CAGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAGCTATGGC ATGCACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGCAGACGCCGTGAAGGGC CGATTACCATCTCCAGGGACAATTCCAAAGAAC ACGCTGATCTGCAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGGAGAGAT AGGACGATTTTGGAGTGGTCTTGAAGTACTG GGCCAGGGAACCTGGTCAACCGTCTCCTCA		
IP:35940	2F11.002	NA				SEQ ID NO: 1767	QVQLVESGGGVVQPRSLRLSCAASGFTFSYGM HWVRQAPGKGLEWVAIVWYDASNKYADAVKVG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLDYWGQGLVTVSS
		SEQ ID NO: 1610	DIQMTQSPSSLSASVGDRTITCQASQDISNYLNW YQKPGKAPKLLIYDASNLETGVPFSRFSGSGTD FSLTISLQPEDFATYYCQYDILLTTFGGGKVEIK R				
		AA					

IP:361039	2F11.003	SEQ ID NO: 40	<p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCAACCATCACTT GCCAGCGAGTCAGGACATTAGCAACTATTAA ATTGGTATCAGCAGAAACAGGGAAGCCCCCTA AGCTCCTGATCTACGATGCATCCCAATTTGGAA CAGGGTCCCATCAAGGTTCAAGTGGAAAGTGAT CTGGGACAGATTTAGTCTCAACCATCAGCAGCC TGCAGCCTGAAGATTTTGCACATATTACTGTCA ACAGTATGATATTCCTCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGA</p>	SEQ ID NO: 197	<p>CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCACTTCCAGTAGCTATGGC ATGCACCTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGCAGACGCCGTGAAGGC CGATTCAACCATCTCCAGCGACAATTCCAAAGAAC ACGCTGTATCTGCAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTGGAGTGGTTCTTGACTACTGG GGCCAGGGAACCCCTGGTCACCGTCTCCTCA</p>
		SEQ ID NO: 1611	<p>DIQMTQSPSSLSASVGDRTVTITCQASQDISNYLNW YQKPGKAPKLLIYDASNLETGVPSRFSGSGTD FSLTISSLQPEDFATYYCQYDILLTFGGGKVEIK R</p>	SEQ ID NO: 1768	<p>QVQLVESGGGVVQPRSLRLSCAASGFTFSYGM HWVRQAPGKGLEWVAIVWYDASNKYADAVKVG RFTISDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLDYWGQGLVTVSS</p>
IP:361043	2F11.004	SEQ ID NO: 41	<p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCAACCATCACTT GCCAGCGAGTCAGGACATTAGCAACTATTAA ATTGGTATCAGCAGAAACAGGGAAGCCCCCTA AGCTCCTGATCTACGATGCATCCCAATTTGGAA CAGGGTCCCATCAAGGTTCAAGTGGAAAGTGAT CTGGGACAGATTTAGTCTCAACCATCAGCAGCC TGCAGCCTGAAGATATTGCAACATATTACTGTC AACAGTATGATATTCTCCTCACTTTCGGCGGAG GGACCAAGGTGGAGATCAAGCGA</p>	SEQ ID NO: 198	<p>CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCACTTCCAGTAGCTATGGC ATGCACCTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGCAGACGCCGTGAAGGC CGATTCAACCATCTCCAGGACAATTCCAAAGAAC ACGCTGTATCTGCAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTGGAGTGGTTCTTGACTACTGG GGCCAGGGAACCCCTGGTCACCGTCTCCTCA</p>
		SEQ ID NO: 1612	<p>DIQMTQSPSSLSASVGDRTVTITCQASQDISNYLNW YQKPGKAPKLLIYDASNLETGVPSRFSGSGTD FSLTISSLQPEDFATYYCQYDILLTFGGGKVEIKR</p>	SEQ ID NO: 1769	<p>QVQLVESGGGVVQPRSLRLSCAASGFTFSYGM HWVRQAPGKGLEWVAIVWYDASNKYADAVKVG RFTISDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLDYWGQGLVTVSS</p>

IP:361049	2F11.005	NA	<p>SEQ ID NO: 42</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCGAGTCAGGACATTAGCAACTATTTAAATTGGTATCAGCAGAAACCAGGAAAGCCCCTAAGTCTCTGATCTACGATGCATCCAAATTTGAAACAGGGTCCCATCAAGGTTTCAGTGGAAGTGGATCTGGACAGATTTTAGTTTCCACCATCAGCAGCCTGCAGCCTGAAAGATTTTGCAACATATTACTGTCAACAGTATGATAATTCCTCTCACTTTCGGCGGAGGACCAAGGTGGAGATCAAGCGA</p> <p>SEQ ID NO: 1613</p>	<p>SEQ ID NO: 199</p> <p>CAGGTGCAACTGGTGAGTCTGGGGGAGGCGTGTCCAGCCTGGAGGTCCTGAGACTCTCCTGTGCAGGTCCTGGATTACCTTCAGTAGCTATGGCATGCACTGGTCCGCCAGGCTCCAGGCAAGGGCTGGAGTGGTGCGCAGTTATATGTTATGATGCAAGTAATAAATACTATGCAGACGCCGTGAAGGCGGATTCAACCATCTCCAGGGACAAATCCAAAGAACACGCTGTATCTGCAAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGGAGAGATAGGACGATTTTGGAGTGGTTCTTGACTACTGGGCCAGGGAACCCCTGGTCACCGTCTCCTCA</p> <p>SEQ ID NO: 1770</p>
		AA	<p>DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQKPGKAPKLLIYDASNLETGVPSRFSGSGGTD</p> <p>FSFTISLQPEDFATYYCQYDILLTFGGGTKVEIKR</p> <p>SEQ ID NO: 43</p>	<p>QVQLVESGGGVVQPRSLRLSCAASGFTFSYGMHWVRQAPGKGLEWVAWIWYDASNKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVLDYWGQGLVTVSS</p> <p>SEQ ID NO: 200</p>
IP:361055	2F11.006	NA	<p>SEQ ID NO: 42</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCGAGTCAGGACATTAGCAACTATTTAAATTGGTATCAGCAGAAACCAGGAAAGCCCCTAAGTCTCTGATCTACGATGCATCCAAATTTGAAACAGGGTCCCATCAAGGTTTCAGTGGAAGTGGATCTGGACAGATTTTAGTTTCCACCATCAGCAGCCTGCAGCCTGAAAGATTTTGCAACATATTACTGTCAACAGTATGATAATTCCTCTCACTTTCGGCGGAGGACCAAGGTGGAGATCAAGCGA</p> <p>SEQ ID NO: 1614</p>	<p>SEQ ID NO: 1771</p> <p>QVQLVESGGGVVQPRSLRLSCAASGFTFSYGMHWVRQAPGKGLEWVAWIWYDASNKYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVLDYWGQGLVTVSS</p> <p>SEQ ID NO: 200</p>
		AA	<p>DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQKPGKAPKLLIYDASNLETGVPSRFSGSGGTD</p> <p>FSLTISSLQPEDIATYYCQYDILLTFGGGTKVEIKR</p> <p>SEQ ID NO: 43</p>	<p>CAGGTGCAACTGGTGAGTCTGGGGGAGGCGTGTCCAGCCTGGAGGTCCTGAGACTCTCCTGTGCAGGTCCTGGATTACCTTCAGTAGCTATGGCATGCACTGGTCCGCCAGGCTCCAGGCAAGGGCTGGAGTGGTGCGCAGTTATATGTTATGATGCAAGTAATAAATACTATGCAGACGCCGTGAAGGCGGATTCAACCATCTCCAGGACAAATCCAAAGAACACGCTGTATCTGCAAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGGAGAGATAGGACGATTTTGGAGTGGTTCTTGACTACTGGGCCAGGGAACCCCTGGTCACCGTCTCCTCA</p> <p>SEQ ID NO: 1771</p>

		SEQ ID NO: 44	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTAA ATTGGTATCAGCAGAAACCAGGGAAGCCCCTA AGTCCTGATCTACGATGCATCCCAATTTGAAA CAGGGGTCCCATCAAGGTTCAAGTGGAAAGTGAT CTGGGACAGATTTTAGTTTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGC AACATATTACTGTCA ACAGTATGATATTCTCCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGA	SEQ ID NO: 1615	SEQ ID NO: 1772	SEQ ID NO: 201	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTCAGTAGCTATGGC ATGCACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAATACTATGCAGAGCCGTGAAGGGC CGATTACCATCTCCAGGGACAATTCCAAAGAAC ACGCTGTATCTGCAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTGGAGTGGTCTTGACTACTGG GGCCAGGGAACCCCTGGTCACCGTCTCCTCA
IPS:361059	2F11.007	NA					
		SEQ ID NO: 45	DIQMTQSPSSLSASVGDRTVTITCQASQDISNYLNW YQKPGKAPKLLIYDASNLETGVPSRFSGSGGTD FSFTISLQPEDFATYYCQYDILLTFGGGKVEIK R	SEQ ID NO: 1616	SEQ ID NO: 1773	SEQ ID NO: 202	QVQLVESGGGVVQPRSLRLSCAASGFTFSYGM HWVRQAPGKGLEWVAIVWYDASNKYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLDYWGQGTLVTVSS
		SEQ ID NO: 46	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTAA ATTGGTATCAGCAGAAACCAGGGAAGCCCCTA AGTCCTGATCTACGATGCATCCCAATTTGAAA CAGGGGTCCCATCAAGGTTCAAGTGGAAAGTGAT CTGGGACAGATTTTAGTTTCACCATCAGCAGCCT GCAGCCTGAAGATATTGCAACATATTACTGTCA ACAGTATGATATTCTCCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGA	SEQ ID NO: 1617	SEQ ID NO: 1774	SEQ ID NO: 203	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTCAGTAGCTATGGC ATGCACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAATACTATGCAGAGCCGTGAAGGGC CGATTACCATCTCCAGGGACAATTCCAAAGAAC ACGCTGTATCTGCAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTGGAGTGGTCTTGACTACTGG GGCCAGGGAACCCCTGGTCACCGTCTCCTCA
IPS:361063	2F11.008	NA					
		SEQ ID NO: 47	DIQMTQSPSSLSASVGDRTVTITCQASQDISNYLNW YQKPGKAPKLLIYDASNLETGVPSRFSGSGGTD FSFTISLQPEDFATYYCQYDILLTFGGGKVEIKR	SEQ ID NO: 1618	SEQ ID NO: 1775	SEQ ID NO: 204	QVQLVESGGGVVQPRSLRLSCAASGFTFSYGM HWVRQAPGKGLEWVAIVWYDASNKYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLDYWGQGTLVTVSS
		SEQ ID NO: 48	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTAA ATTGGTATCAGCAGAAACCAGGGAAGCCCCTA AGTCCTGATCTACGATGCATCCCAATTTGAAA CAGGGGTCCCATCAAGGTTCAAGTGGAAAGTGAT CTGGGACAGATTTTAGTTTCACCATCAGCAGCCT GCAGCCTGAAGATATTGCAACATATTACTGTCA ACAGTATGATATTCTCCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGA	SEQ ID NO: 1619	SEQ ID NO: 1776	SEQ ID NO: 205	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTCAGTAGCTATGGC ATGCACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAATACTATGCAGAGCCGTGAAGGGC CGATTACCATCTCCAGGGACAATTCCAAAGAAC ACGCTGTATCTGCAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTGGAGTGGTCTTGACTACTGG GGCCAGGGAACCCCTGGTCACCGTCTCCTCA
		SEQ ID NO: 49	DIQMTQSPSSLSASVGDRTVTITCQASQDISNYLNW YQKPGKAPKLLIYDASNLETGVPSRFSGSGGTD FSFTISLQPEDFATYYCQYDILLTFGGGKVEIKR	SEQ ID NO: 1620	SEQ ID NO: 1777	SEQ ID NO: 206	QVQLVESGGGVVQPRSLRLSCAASGFTFSYGM HWVRQAPGKGLEWVAIVWYDASNKYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLDYWGQGTLVTVSS

IP:359949	2F11.009	SEQ ID NO: 46	SEQ ID NO: 1617	SEQ ID NO: 203
		NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGCGAGTCAGGACATTAGCAACTATTAAATTGGTATCAGCAGAAACAGGGAAGCCCCCTAAGCTCTGATCTACGATGCATCCCAATTTGGAAA CAGGGTCCCATCAAGGTTCAAGTGGAAAGTGATCTGGGACAGATTTTAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACATATTACTGTCAACAGTATGATATTCCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGA	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTGTCCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGCTCTGGATTCACTTCCAGTAGCTATGGCATGCACTGGTCCCGCAGGCTCCAGGCAAGGGGCTGGAGTGGTGGCAGTTATATGGTATGATGCAAGTAATAATACTATGCAGACTCCGTGAAGGGCCGATTCAACCATCTCCAGGACAAATCCCAAGAACACGCTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTATTACTGTGCGAGAGATAGGACGATTTTGGAGTGGTTCTTGACTACTGG GGCCAGGGAACCCCTGGTCACCGTCTCCTCA
IP:359956	2F11.010	AA	SEQ ID NO: 1618	SEQ ID NO: 1774
		NA	DIQMTQSPSSLSASVGDRTVTITCQASQDISNYLNWYQKPGKAPKLLIYDASNLETGVPSRFSGSGTD FSLTISSLQPEDFATYYCQYDILLTFGGGKVEIK R	QVQLVESGGGVVQPRSLRLSCAASGFTFSYGMHWVRQAPGKGLEWVAIVWYDASNKYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLDYWGQGLVTVSS
IP:359956	2F11.010	AA	SEQ ID NO: 1618	SEQ ID NO: 1775
		NA	DIQMTQSPSSLSASVGDRTVTITCQASQDISNYLNWYQKPGKAPKLLIYDASNLETGVPSRFSGSGTD FSLTISSLQPEDFATYYCQYDILLTFGGGKVEIK R	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTGTCCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGCTCTGGATTCACTTCCAGTAGCTATGGCATGCACTGGTCCCGCAGGCTCCAGGCAAGGGGCTGGAGTGGTGGCAGTTATATGGTATGATGGAAGTAATAATACTATGCAGACCCGTGAAGGGCCGATTCAACCATCTCCAGGACAAATCCCAAGAACACGCTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTATTACTGTGCGGAGAGATAGGACGATTTTGGAGTGGTTCTTGACTACTGG GGCCAGGGAACCCCTGGTCACCGTCTCCTCA

		SEQ ID NO: 48	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAGCCCCCTA AGCGCTGATCTATGGTGCATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAAATCAGCAGCC TGACGCTGAAGATTTTCGCAACTTATTACTGTCT ACAGCATAAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAAACGA	SEQ ID NO: 1619	SEQ ID NO: 205	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTGGAGTGCTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
IP:359865	6H1.002	NA			SEQ ID NO: 1776	QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAIVWYDASNKYYADAVKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSS
		SEQ ID NO: 49	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAGCCCCCTA AGCGCTGATCTATGGTGCATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAAATCAGCAGCC TGACGCTGAAGATTTTCGCAACTTATTACTGTCT ACAGCATAAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAAACGA	SEQ ID NO: 206	SEQ ID NO: 206	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATA GGACGATTTTGGAGTGCTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
IP:359869	6H1.003	NA			SEQ ID NO: 1777	QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAIVWYDASNKYYADAVKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLLGDYWGQGTLVTVSS
		SEQ ID NO: 1620	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLQSGVPSRFSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	SEQ ID NO: 1620	SEQ ID NO: 1777	QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAIVWYDASNKYYADAVKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLLGDYWGQGTLVTVSS
		AA				

IP:359873	6H1.004	SEQ ID NO: 50	<p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACCAGGAAAGCCCTA AGCTCTGATCTATGTTGATCCAGTTTGCAA GTGGGTCCCTTCAAGTTTACGCGGAGTGGAT CTGGGACAGAAATTCACCTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTCTGTCT ACAGCATATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAAAACGA</p>	SEQ ID NO: 207	<p>CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTCACTTCACTTGGCA TGCACCTGGTCCGCCAGGCTCCAGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCAACCATCTCCAGAGACAATTCAGAACA CGCTGATCTGCAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCTGGTCAACCGTCTCCTCA</p>
		SEQ ID NO: 1621	<p>DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLWY QQKPGKAPKLLIYGASLQSGVPSRFSGSGTEFT LTISLQPEDFATYYCLQHNNYPFTFGQGTKVDIK R</p>	SEQ ID NO: 1778	<p>QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIWYDASNKYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGLVTVSS</p>
IP:359877	6H1.005	SEQ ID NO: 51	<p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACCAGGAAAGCCCTA AGCTCTGATCTATGTTGATCCAGTTTGCAA GTGGGTCCCTTCAAGTTTACGCGGAGTGGAT CTGGGACAGAAATTCACCTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTCTGTCT ACAGCATATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAAAACGA</p>	SEQ ID NO: 208	<p>CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTCACTTCACTTGGCA TGCACCTGGTCCGCCAGGCTCCAGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCAACCATCTCCAGAGACAATTCAGAACA CGCTGATCTGCAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATA GGACGATTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCTGGTCAACCGTCTCCTCA</p>
		SEQ ID NO: 1622	<p>DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLWY QQKPGKAPKLLIYGASLQSGVPSRFSGSGTEFT LTISLQPEDFATYYCLQHNNYPFTFGQGTKVDIK R</p>	SEQ ID NO: 1779	<p>QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIWYDASNKYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLLGDYWGQGLVTVSS</p>

	!PS:361067	6H1.006	NA	SEQ ID NO: 52	SEQ ID NO: 209
				GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTATAGGAGACAGAGTCACCATCACTTGCCGGCAAGTCAGGACATTAGAGATTATTAGGCTGGTATCAGCAGAAACCAGGAAAGCCCCAAGTCTGTATCTATGTTGCATCCAGTTTGCAAAGTGGGTCCCTTCAAGTTTCAGCGGCAAGTGATCTGGGACAGAAATTCATCTCAATCAGCAGCCTGAGCCTGAAGATTTCGCAACTTATTACTGTACAGCATATAATTACCCCTTCACTTTCGGCCCTGGGACCAAGTGGATATCAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCTCTGGATTCACTTCCAGTTACTTTGGCATGCAGTGGTCCGCCAGGTCCAGGCAAGGGGCTGGAGTGGTGGCAGTTATATGTTATGATGGAAGTAATAATACTATGCAGACTCCGTGAAGGGCCGCTTCAACATCTCCAGAGACAATTCAGAACAACGCTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGCGAGATGGACGATTTTGGAGTGTCTTGGGGGACTACTGGGCCAGGGAACCTGGTCAACCGTCTCCTCA
		AA		SEQ ID NO: 1623	SEQ ID NO: 1780
				DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKLLIYGASSLQSGVPSRFSGSGTEFTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	QVQLVESGGGVVQPGRSRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAWIYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGTIFGVLLGDYWGQGLVTVSS
	!PS:361071	6H1.007	NA	SEQ ID NO: 53	SEQ ID NO: 210
				GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTATAGGAGACAGAGTCACCATCACTTGCCGGCAAGTCAGGACATTAGAGATTATTAGGCTGGTATCAGCAGAAACCAGGAAAGCCCCAAGTCTGTATCTATGTTGCATCCAGTTTGCAAAGTGGGTCCCTTCAAGTTTCAGCGGCAAGTGATCTGGGACAGAAATTCATCTCAATCAGCAGCCTGAGCCTGAAGATTTCGCAACTTATTACTGTACAGCATATAATTACCCCTTCACTTTCGGCCCTGGGACCAAGTGGATATCAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCTCTGGATTCACTTCCAGTTACTTTGGCATGCAGTGGTCCGCCAGGTCCAGGCAAGGGCTGGAGTGGTGGCAGTTATATGTTATGATGCAAGTAATAATACTATGCAGACTCCGTGAAGGGCCGCTTCAACATCTCCAGAGACAATTCAGAACAACGCTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGCGAGATGGACGATTTTGGAGTGTCTTGGGGGACTACTGGGCCAGGGAACCTGGTCAACCGTCTCCTCA
		AA		SEQ ID NO: 1624	SEQ ID NO: 1781
				DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWYQQKPGKAPKLLIYGASSLQSGVPSRFSGSGTEFTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	QVQLVESGGGVVQPGRSRLSCAASGFTFSYFGMHWVRQAPGKGLEWVAWIYDASNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGTIFGVLLGDYWGQGLVTVSS
				SEQ ID NO: 54	SEQ ID NO: 211

!PS:361075	6H1.008	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACAGGAAAGCCCCTA AGTCTGTATCTATGTCATCCAGTTTGCAA GTGGGTCCCTTCAAGTTACGCGCAGTGGAT CTGGACAGAAATTCATCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACCTTCGGCCCT GGGACCAAAGTGGATATCAAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCACTTCACTTCACTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGG TGGAGTGGTGGCAGTTATATGGTATGATGGAA GTAATAAATACTATGCAGACGCCGTGAAGGGC GCTTACCATCTCCAGAGACAATTCAGAACA CGCTGATCTGCAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTTACTGTGCGCGAGATG GGACGATTTTGGAGTGCTCTTGGGGGACTACT GGGCCAGGGAACCTGGTCAACCGTCTCCTCA
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAIVWYDGSNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGLVTVSS
!PS:361079	6A5.004.001	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGACAGAGTCAACCATCACTT GCCAGCGAGTCAGGACATTACCAACTATTAA ATTGGTATCAGCAGAAACAGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAAATTTGGAGCC AGGGTCCCATCAAGGTTCAAGTGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAAGTGGATATCAAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCTCTTCACTTCACTTGGCA TGCACTGGTCCGCCAGCCTCCAGGCAAGGGG TGGAGTGGTGGCAGCTATATGGTATGATGCAA ATAATAAATACTATGCAGACGCCGTGAAGGGC GATTCACCATCTCCAGAGACAGTTCCAGAACA CGCTGATCTGCAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTTACTGTGCGGAGAGATC GGACGATTTTGGAGTGCTCTTGGTACTTGGG GCCAGGGAACCTGGTCAACCGTCTCCTCA
		AA	DIQMTQSPSSLSASVGDRTVITCQASQDITNLYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGTD FTLTISSLQPEDFATYYCQYQYDDLFTFGPGTKVDIK R	QVQLVESGGGVVQPRSLRLSCAASGFSYSGM HWVRQPPGKGLEWVAIIWYDANNKYYADAVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGQGLVTVSS

!PS:361085	6A5.004.002	NA	SEQ ID NO: 56	SEQ ID NO: 213
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTGGGGACAGAGTCACCATCACTTGCCAGCGAGTCAGGACATTACCACTATTAAATTGGTATCAGCAGAAACCAGGAAAGCCCCATAACTCCTGATCTACGATGCTTCCAAATTTGAGCCAGGGTCCCATCAAGGTTCAAGTGGAAGTGGATCTGGGACAGATTTTACTCTCACCATCAGCAGCCTGCAGCCTGAAGATATTGCAACATATTACTGTCAACAGTATGATGATCTATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCTCTGGATTCTCCTTCAGTAGCTATGGCATGCACTGGTCCGCCAGCCTCCAGGCAAGGGGCTGGAGTGGTGGCAGCTATATGATGATGCAATAAATAATACTATGCAGACGCCGTGAAGGGCCGATTCAACATCTCCAGAGACAGTTCACAAGAACACGCTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATCGGACGATTTTGGAGTGGTCCCTTGAGTACTGGGGCCAGGGAACCTGGTCAACCGTCTCCTCA
!PS:361091	6A5.004.003	NA	SEQ ID NO: 1627	SEQ ID NO: 1784
			DIQMTQSPSSLSASVGDRTVTITCQASQDITNLYNWYQKPGKAPKLLIYDASNLEPGVPSRFSGSGTDFTLTISSLQPEDIATYYCQYDDLFTFGPGTKVDIKR	QVQLVESGGGVVQPGRSRLSCAASGFSFSSYGMHWVRQPPGKGLEWVAIIWYDANNKYYADAVKGRFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLEYWGQGLVTVSS
!PS:361091	6A5.004.003	NA	SEQ ID NO: 57	SEQ ID NO: 214
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTGGGGACAGAGTCACCATCACTTGCCAGCGAGTCAGGACATTACCACTATTAAATTGGTATCAGCAGAAACCAGGAAAGCCCCATAACTCCTGATCTACGATGCTTCCAAATTTGAGCCAGGGTCCCATCAAGGTTCAAGTGGAAGTGGATCTGGGACAGATTTTACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCACACATATTACTGTCAACAGTATGATGATCTATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCTCTGGATTCTCCTTCAGTAGCTATGGCATGCACTGGTCCGCCAGCCTCCAGGCAAGGGGCTGGAGTGGTGGCAGCTATATGATGATGCAATAAATAATACTATGCAGACGCCGTGAAGGGCCGATTCAACATCTCCAGAGACAGTTCACAAGAACACGCTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATCGGACGATTTTGGAGTGGTCCCTTGAGTACTGGGGCCAGGGAACCTGGTCAACCGTCTCCTCA
!PS:361091	6A5.004.003	AA	SEQ ID NO: 1628	SEQ ID NO: 1785
			DIQMTQSPSSLSASVGDRTVTITCQASQDITNLYNWYQKPGKAPKLLIYDASNLEPGVPSRFSGSGTDFTLTISSLQPEDFATYYCQYDDLFTFGPGTKVDIKR	QVQLVESGGGVVQPGRSRLSCAASGFSFSSYGMHWVRQPPGKGLEWVAIIWYDANNKYYADAVKGRFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLEYLGGQGLVTVSS

IP:361095	6A5.004.004	NA	SEQ ID NO: 58	SEQ ID NO: 215
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTAA ATTGGTATCAGCAGAAACCAGGAAAGCCCCA AACTCCTGATCTACGATGCTTCCAAATTGGAGCC AGGGTCCCCATCAAGGTTCAAGTGAAGTGGATC TGGGACAGATTTTACTTTCCACCATCAGCAGCCTG CAGCCTGAAGATTTTGCACACATATTACTGTCAA CAGTATGATGATCTATTCACTTTCGGCCCTGGGA CCAAAGTGGATATCAAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCTCTTCACTAGTACTATGGCA TGCACTGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGTGGCAGCTATATGATGATGCA ATAATAATACTATGACAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCACAAGAAC CGCTGATCTGCAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTGGAGTGGTCTTGAAGTACTGGG GCCAGGGAACCCCTGGTCACCGTCTCCTCA
IP:361101	6A5.004.005	NA	SEQ ID NO: 59	SEQ ID NO: 216
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTAA ATTGGTATCAGCAGAAACCAGGAAAGCCCCA AACTCCTGATCTACGATGCTTCCAAATTGGAGCC AGGGTCCCCATCAAGGTTCAAGTGAAGTGGATC TGGGACAGATTTTACTTTCCACCATCAGCAGCCT CAGCCTGAAGATTTTGCACACATATTACTGTCAA CAGTATGATGATCTATTCACTTTCGGCCCTGGGA CCAAAGTGGATATCAAAACGA	QVQLVESGGGVVQPRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAIWYDANNKYADAVKVG RFTISRDSKNTLYLQMNSLRAEDTAVYYCARD R TIFGVVLEYWGQGLVTIVSS
IP:361101	6A5.004.005	AA	SEQ ID NO: 1629	SEQ ID NO: 1786
			DIQMTQSPSSLSASVGDRTVTITCQASQDITNLYNW YQKPGKAPKLLIYDASNLEPGVPSRFSGSGTD FTFTISLQPEDFATYYCQYDDLFTFGPGTKVDIK R	QVQLVESGGGVVQPRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAIWYDANNKYADAVKVG RFTISRDSKNTLYLQMNSLRAEDTAVYYCARD R TIFGVVLEYWGQGLVTIVSS
IP:361101	6A5.004.005	AA	SEQ ID NO: 1630	SEQ ID NO: 1787
			DIQMTQSPSSLSASVGDRTVTITCQASQDITNLYNW YQKPGKAPKLLIYDASNLEPGVPSRFSGSGTD FTFTISLQPEDFATYYCQYDDLFTFGPGTKVDIK R	QVQLVESGGGVVQPRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAIWYDANNKYADAVKVG RFTISRDSKNTLYLQMNSLRAEDTAVYYCARD R TIFGVVLEYWGQGLVTIVSS

	IP:361109	6A5.004.007	NA	SEQ ID NO: 60	SEQ ID NO: 217
				GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTGGGGACAGAGTCAACCATCACTTGCCAGCGAGTCAGGACATTACCACTATTAAATTGGTATCAGCAGAAACAGGAAAGCCCCTA AACTCTGATCTACGATGCTTCCAATTGGAGCCAGGGTCCCATCAAGGTTCAAGTGAAGTGATCTGGGACAGATTTACTTTCAACATCAGCAGCTGCAGCCTGAAGATTTGCAACATATTACTGTCAA CAGTATGATGATCTATTCACTTTTCGGCCCTGGGACCAAAGTGGATATCAAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCTCTGGATTCTCTTCAAGTAGCTATGGCATGCAGTGGTCCGCCAGCCTCCAGGCAAGGGGCTGGAGTGGTGGCAGCTATATGATGATGCAATAAATAATACTATGCAGACGCCGTGAAGGGCCGATTACCATCTCCAGAGACAGTTCACAAGAACACGCTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATCGGACGATTTTGGAGTGGTCCCTTGAGTACCTCGGCCAGGGAACCTGGTCAACCGTCTCCTCA
	AA	6A5.004.007	NA	SEQ ID NO: 1631	SEQ ID NO: 1788
				DIQMTQSPSSLSASVGDRVTITCQASQDITNLYNWYQKPGKAPKLLIYDASNLEPGVPSRFSGSGTDFTFTISLQPEDFATYYCQYDDLFTFGPGTKVDIKR	QVQLVESGGGVQPGRSLRLSCAASGFSFSSYGMHWVRQPPGKGLEWVAIWYDANNKYADAVKGRFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLEYLQGQTLVTVSS
	IP:361109	6A5.004.007	NA	SEQ ID NO: 61	SEQ ID NO: 218
				GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTGGGGACAGAGTCAACCATCACTTGCCAGCGAGTCAGGACATTACCACTATTAAATTGGTATCAGCAGAAACAGGAAAGCCCCTA AACTCTGATCTACGATGCTTCCAATTGGAGCCAGGGTCCCATCAAGGTTCAAGTGAAGTGATCTGGGACAGATTTACTTTCAACATCAGCAGCTGCAGCCTGAAGATTTGCAACATATTACTGTCAA CAGTATGATGATCTATTCACTTTTCGGCCCTGGGACCAAAGTGGATATCAAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCTCTGGATTCTCTTCAAGTAGCTATGGCATGCAGTGGTCCGCCAGCCTCCAGGCAAGGGGCTGGAGTGGTGGCAGCTATATGATGATGCAATAAATAATACTATGCAGACGCCGTGAAGGGCCGATTACCATCTCCAGAGACAGTTCACAAGAACACGCTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATCGGACGATTTTGGAGTGGTCCCTTGAGTACTGGGCCAGGGAACCTGGTCAACCGTCTCCTCA
	AA	6A5.004.007	NA	SEQ ID NO: 1632	SEQ ID NO: 1789
				DIQMTQSPSSLSASVGDRVTITCQASQDITNLYNWYQKPGKAPKLLIYDASNLEPGVPSRFSGSGTDFTFTISLQPEDFATYYCQYDDLFTFGPGTKVDIKR	QVQLVESGGGVQPGRSLRLSCAASGFSFSSYGMHWVRQPPGKGLEWVAIWYDANNKYADAVKGRFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLEYWGQGLVTVSS

!PS:36113	6A5.004.008	NA	SEQ ID NO: 62	SEQ ID NO: 219
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTGGGGACAGAGTCACCATCACTTGCCAGCGAGTCAGGACATTACCAACTATTAAATTGGTATCAGCAGAAACAGGGAAGCCCCTA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGGTGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCTCTGGATTCTCTTCACTAGTATGGCA
!PS:361120	6A5.004.009	NA	SEQ ID NO: 63	SEQ ID NO: 220
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTGGGGACAGAGTCACCATCACTTGCCAGCGAGTCAGGACATTACCAACTATTAAATTGGTATCAGCAGAAACAGGGAAGCCCCTA	GCAGCTCTGGATTCTCTTCACTAGTATGGCA
!PS:361120	6A5.004.009	AA	SEQ ID NO: 1633	SEQ ID NO: 1790
			DIQMTQSPSSLSASVGDRTVITCQASQDITNLYNWYQKPGKAPKLLIYDASNLEPGVPSRFSGSGTDFTLTISSLQPEDFATYYCQQYDDLLFTFGPGTKVDIKR	QVQLVESGGGVVQPRSLRLSCAASGFSFSSYGMHWVRQPPGKGLEWVAIWYDGNKYYADAVKGRFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLEYWGQGLVTVSS
!PS:361120	6A5.004.009	AA	SEQ ID NO: 1634	SEQ ID NO: 1791
			DIQMTQSPSSLSASVGDRTVITCQASQDITNLYNWYQKPGKAPKLLIYDASNLEPGVPSRFSGSGTDFTLTISSLQPEDFATYYCQQYDDLLFTFGPGTKVDIKR	QVQLVESGGGVVQPRSLRLSCAASGFSFSSYGMHWVRQPPGKGLEWVAIWYDANNKYYADSVKGRFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLEYWGQGLVTVSS

IP:359890	6A5.004.011	NA	SEQ ID NO: 64	SEQ ID NO: 221	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCTCTCTCAGTAGCTATGGCA TGCACCTGGTCCGCCAGCCTCCAGCAAGGGGC TGGAGTGGTGGCAGCTATATGATGATGCAAA ATAATAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCACAAGACA CGCTGATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTGGAGTGGTCCCTTGAGTACTGGG GCCAGGGAACCTGGTCAACCGTCTCCTCA
		AA	SEQ ID NO: 1635	SEQ ID NO: 1792	QVQLVESGGGVVQGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAIWYDANNKYADAVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGQGLTVTVSS
IP:359890	6A5.004.011	NA	SEQ ID NO: 65	SEQ ID NO: 222	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCTCTCTCAGTAGCTATGGCA TGCACCTGGTCCGCCAGCCTCCAGCAAGGGGC TGGAGTGGTGGCAGCTATATGATGATGCAAA ATAATAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCACAAGACA CGCTGATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTGGAGTGGTCCCTTGAGTACTGGG GCCAGGGAACCTGGTCAACCGTCTCCTCA
		AA	SEQ ID NO: 1636	SEQ ID NO: 1793	QVQLVESGGGVVQGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAIWYDANNKYADAVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGQGLTVTVSS

IP:335965	2A11.003	NA	SEQ ID NO: 66	<p>GAAATTGTGTTGACGCAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCT GCAGGGCCAGTCAGATTTTACCAGCACCTACT TAGCCTGGTACCAAGAGAAACCTGGCCAGGCTC CCAGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCAGACAGGTTCACTGTCAGTGGCAGTG GGTCTGGACAGACTTCACTCTCACCATCAGCA GATTGGAGCCTGAAGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGCTCACCTCGCTTCGGCC AAGGGACACGACTGGAGATTAAACGA</p>	SEQ ID NO: 223	<p>CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTTCAGTAGCTATGGC ATGCACCTGGTCCGCCAGGCTCCAGGCAAGGGA CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAATACTATGAAGACGCCGTGAAGGGC CGATTACCATCTCCAGAGACAAATCCCAAGAAC ACGCTGTTCTGCAAGTGAACAGCCTGAGAGCC GAGGACACGGCTGTATTACTGTGCGAGAGGG ATTACGATTTTGGTCAATGGGTTTGAATATTGGG GCCAGGGAACCCCTGGTCACCGTCTCCTCA</p>
			SEQ ID NO: 1637	<p>EIVLTQSPGTLSPGERATLSCRASQIFSTYLA YQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDF TLTISRLEPEDFAVYYCQQYGSSPRFGQGRLEIKR</p>	SEQ ID NO: 1794	<p>QVQLVESGGGVVQPRSLRLSCAASGFSFSSYGM HWVRQAPGKGLEWVAIVYDASNKYIEDAVKGG RFTISRDNSKNTLFLQVNSLRAEDTAVYYCARGITI FGHGFYWGQGLVTVSS</p>
IP:335965	2A11.003	NA	SEQ ID NO: 67	<p>GAAATTGTGTTGACGCAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCT GCAGGGCCAGTCAGATTTTACCAGCACCTACT TAGCCTGGTACCAAGAGAAACCTGGCCAGGCTC CCAGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCAGACAGGTTCACTGTCAGTGGCAGTG GGTCTGGACAGACTTCACTCTCACCATCAGCA GATTGGAGCCTGAAGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGCTCACCTCGCTTCGGCC AAGGGACACGACTGGAGATTAAACGA</p>	SEQ ID NO: 224	<p>CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTTCAGTAGCTATGGC ATGCACCTGGTCCGCCAGGCTCCAGGCAAGGGA CTGGAGTGGTGGCAGTTATATGGTATGATGGA AGTAATAATACTATGAAGACTCCGTGAAGGGC CGATTACCATCTCCAGAGACAAATCCCAAGAAC ACGCTGTTCTGCAAGTGAACAGCCTGAGAGCC GAGGACACGGCTGTATTACTGTGCGAGAGGG ATTACGATTTTGGTCAATGGGTTTGAATATTGGG GCCAGGGAACCCCTGGTCACCGTCTCCTCA</p>
			SEQ ID NO: 1638	<p>EIVLTQSPGTLSPGERATLSCRASQIFSTYLA YQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDF TLTISRLEPEDFAVYYCQQYGSSPRFGQGRLEIKR</p>	SEQ ID NO: 1795	<p>QVQLVESGGGVVQPRSLRLSCAASGFSFSSYGM HWVRQAPGKGLEWVAIVYDASNKYIEDSVKGG RFTISRDNSKNTLFLQVNSLRAEDTAVYYCARGITI FGHGFYWGQGLVTVSS</p>

!PS:361158	2A11.004	NA	SEQ ID NO: 68	SEQ ID NO: 225
			GAAATTGTTGACGCGAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCT GCAGGCCAGTCAGATTTTACCAGCACCTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCAGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCAGACAGAGTTTCAAGTGGCAGTG GGTCTGGACAGACTTCACTCTCACCATCAGCA GATTGGAGCCTGAAGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGCTCACCTCGCTTCGGCC AAGGGACACGACTGGAGATTAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGAATTCAGTTTCAGTAGCTATGGC ATGCACCTGGTCCGCCAGGCTCCAGGCAAGGGA CTGGAGTGGTGGCAGTTATATGGTATGATGGA AGTAATAAATACTATGAAGACGCCGTGAAGGCG CGATTCAACCATCTCCAGAGACAAATTCCAAGAAC ACGCTGTTTCTGCAAGTGAACAGCCTGAGAGCC GAGGACACGCTGTGTATTACTGTGCGAGAGGG ATTACGATTTTGGTCAATGGGTTTGAATATTGGG GCCAGGGAACCCCTGGTCAACCGTCTCCTCA
!PS:361165	2A11.005	NA	SEQ ID NO: 1639	SEQ ID NO: 1796
			EIVLTQSPGTLSPGERATLSCRASQIFTSYLA YQKPGQAPRLIYGASSRATGIPDRFSGSGTDF TLTISRLEPEDFAVYYCQQYGSSPRFGQGRLEIKR	QVQLVESGGGVVQPRSLRLSCAASGFSFSSYGM HWVRQAPGKGLEWVAWIWDGSKNYIEDAVKG RFTISRDNSKNTLFLQVNSLRAEDTAVYYCARGITI FGHGFYWGQGLVTVSS
!PS:361165	2A11.005	NA	SEQ ID NO: 69	SEQ ID NO: 226
			GAAATTGTTGACGCGAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCT GCAGGCCAGTCAGATTTTACCAGCACCTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCAGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCAGACAGAGTTTCAAGTGGCAGTG GGTCTGGACAGACTTCACTCTCACCATCAGCA GATTGGAGCCTGAAGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGCTCACCTCGCTTCGGCC AAGGGACACGACTGGAGATTAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGAATTCAGTTTCAGTAGCTATGGC ATGCACCTGGTCCGCCAGGCTCCAGGCAAGGGA CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGAAGACTCCGTGAAGGCG CGATTCAACCATCTCCAGAGACAAATTCCAAGAAC ACGCTGTTTCTGCAAGTGAACAGCCTGAGAGCC GAGGACACGCTGTGTATTACTGTGCGAGAGGG ATTACGATTTTGGTCAATGGGTTTGAATATTGGG GCCAGGGAACCCCTGGTCAACCGTCTCCTCA
!PS:361165	2A11.005	AA	SEQ ID NO: 1640	SEQ ID NO: 1797
			EIVLTQSPGTLSPGERATLSCRASQIFTSYLA YQKPGQAPRLIYGASSRATGIPDRFSGSGTDF TLTISRLEPEDFAVYYCQQYGSSPRFGQGRLEIKR	QVQLVESGGGVVQPRSLRLSCAASGFSFSSYGM HWVRQAPGKGLEWVAWIWDGSKNYIEDSVKG RFTISRDNSKNTLFLQVNSLRAEDTAVYYCARGITI FGHGFYWGQGLVTVSS

!PS:361172	2G10_LC1.003	SEQ ID NO: 70	<p>GAAATAGTGATGACGCAGTCTCCAGCCACCCCTG TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTTAGCAGCACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGACGCCACAGGGCC ACTGGTATCCAGCCAGGTTCAGTGGCAGTGGG TCTGGGACAGAGTTCACCTCACCATCAGCAGC CTGCAGTCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTGGCCTCTCACTTTCGGCG GAGGGACCAAGGTGGAGATCAACGA</p>	SEQ ID NO: 227	<p>CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACTTCCAGTA ACTATGGC ATGCACCTGGTCCGCCAGGCTCCAGCGAGGGG CTGGAGTGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGC CGATTCAACCATCTCCAGAGACA ACTCCAAGAAC ACGCTGTATCTGCAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTAATTACTGTGCGAGAGAT CAGCGGATTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCCCTGGTCACCGTCTCCTCA</p>
		SEQ ID NO: 1641	<p>EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQKPGQAPRLLIYGAAATRATGIPARFSGSGSTE FTLTISLQSEDFAVYYCQYNNWPLTFGGGKVE IKR</p>	SEQ ID NO: 1798	<p>QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAIWFDASDKYYADA VKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGLVTVSS</p>
!PS:361178	2G10_LC1.004	SEQ ID NO: 71	<p>GAAATAGTGATGACGCAGTCTCCAGCCACCCCTG TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTTAGCAGCACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGACGCCACAGGGCC ACTGGTATCCAGCCAGGTTCAGTGGCAGTGGG TCTGGGACAGAGTTCACCTCACCATCAGCAGC CTGCAGTCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTGGCCTCTCACTTTCGGCG GAGGGACCAAGGTGGAGATCAACGA</p>	SEQ ID NO: 228	<p>CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACTTCCAGTA ACTATGGC ATGCACCTGGTCCGCCAGGCTCCAGCGAGGGG CTGGAGTGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACTCCGTGAAGGGC CGATTCAACCATCTCCAGAGACA ACTCCAAGAAC ACGCTGTATCTGCAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTAATTACTGTGCGAGAGAT CAGCGGATTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCCCTGGTCACCGTCTCCTCA</p>
		SEQ ID NO: 1642	<p>EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQKPGQAPRLLIYGAAATRATGIPARFSGSGSTE FTLTISLQSEDFAVYYCQYNNWPLTFGGGKVE IKR</p>	SEQ ID NO: 1799	<p>QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAIWFDASDKYYADSVKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGLVTVSS</p>

		SEQ ID NO: 72	SEQ ID NO: 229
!PS:361185	2G10_LC1.005	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGAAAGAGCCACCCTCTCCTG CAGGGCCAGTCAGAGTGTAGCAGCAACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGACGCCACCAGGGCC ACTGGTATCCCAGCCAGGTTCACTGAGGAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGCAGTCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTGGCCTCTCACTTTCGGCG GAGGGACCAAGGTGGAGATCAAAACGA
			SEQ ID NO: 1643
	AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAAATRAATGIPARFSGSGTE FTLTISLSQSEDFAVYYCQQYNWPLTFGGGKVE IKR	QVQLVESGGGVVQPRSLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAIWFDGSDKYYADAVKG RFTISRDNKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGLVTVSS
!PS:361192	2G10_LC1.006	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGAAAGAGCCACCCTCTCC TG CAGGGCCAGTCAGAGTGTAGCAGCAACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGACGCCACCAGGGCC ACTGGTATCCCAGCCAGGTCAGTGGCAGTGGG TCTGGGACAGAGTTCACCTCACCATCAGCAGC CTGCAGTCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTGGCCTCTCACTTTCGGCG GAGGGACCAAGGTGGAGATCAAAACGA
			SEQ ID NO: 1644
	AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAAATRAATGIPARVSGSGTE FTLTISLSQSEDFAVYYCQQYNWPLTFGGGKVE IKR	QVQLVESGGGVVQPRSLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAIWFDASDKYYADAVKG RFTISRDNKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGLVTVSS

!PS:359609	2G10_LC1.007	NA	SEQ ID NO: 74 GAAATAGTGATGACGCAGTCTCCAGCCACCCTG TCTGTCTCCAGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTAGCAGCACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGACGCCACCAGGGCC ACTGGTATCCAGCCAGGTTCACTGAGGAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGGAGCCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTTCCCTCTCACTTTCCGGCGG AGGGACCAAGTGGAGATCAAAACGA	SEQ ID NO: 231 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAACATAGGC ATGCATGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAACTCCAAAGAAC ACGCTGTATCTGCAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGATTACTGTGCGAGAGAT CAGGCGATTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCCCTGTGTACCGTCTCCTCA
		AA	SEQ ID NO: 1645 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAAATRAATGIPARFSGSGTE FTLTISSELPEDFAVYYCQQYNFPLTFGGGKVEI KR	SEQ ID NO: 1802 QVQLVESGGGVVQPRSLRLSCAASGFTFSNYGM HWVRQAPGKGLEWVAIWFDASDKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGLVTVSS
!PS:359615	2G10_LC1.008	NA	SEQ ID NO: 75 GAAATAGTGATGACGCAGTCTCCAGCCACCCTG TCTGTCTCTCCAGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTAGCAGCACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGACGCCACCAGGGCC ACTGGTATCCAGCCAGGTTCACTGAGGAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGGAGCCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTTCCCTCTCACTTTCCGGCGG AGGGACCAAGTGGAGATCAAAACGA	SEQ ID NO: 232 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAACATAGGC ATGCATGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAACTCCAAAGAAC ACGCTGTATCTGCAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGATTACTGTGCGAGAGAT CAGGCGATTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCCCTGTGTACCGTCTCCTCA
		AA	SEQ ID NO: 1646 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAAATRAATGIPARFSGSGTE FTLTISSELPEDFAVYYCQQYNFPLTFGGGKVEI KR	SEQ ID NO: 1803 QVQLVESGGGVVQPRSLRLSCAASGFTFSNYGM HWVRQAPGKGLEWVAIWFDASDKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGLVTVSS

!PS:361196	2G10_LC1.009	NA	SEQ ID NO: 76 GAAATAGTGATGACGCAGTCTCCAGCCACCCTG TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTAGCAGCACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGACGCCACCAGGGCC ACTGGTATCCAGCCAGGTTCACTGAGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGGAGCCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTGGCTCTCACTTTCGGCG GAGGGACCAAGGTGGAGATCAACGA	SEQ ID NO: 233 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAACATGCG ATGCACTGGTCCGCCAGGCTCCAGGCGAGGGG CTGGAGTGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAACTCCAAAGAAC ACGCTGTATCTGCAAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGATTACTGTGCGAGAGAT CAGGCGATTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCCCTGCTCACCGTCTCCTCA
		AA	SEQ ID NO: 1647 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAAATRAATGIPARFSGSGTE FTLTISSELPEDFAVYYCQQYNWPLTFGGGTKVE IKR	SEQ ID NO: 1804 QVQLVESGGGVVQPRSLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAIWFDASDKYYADA VKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGLVTVSS
!PS:361202	2G10_LC1.010	NA	SEQ ID NO: 77 GAAATAGTGATGACGCAGTCTCCAGCCACCCTG TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTAGCAGCACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGACGCCACCAGGGCC ACTGGTATCCAGCCAGGTTCACTGAGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGGAGCCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTGGCTCTCACTTTCGGCG GAGGGACCAAGGTGGAGATCAACGA	SEQ ID NO: 234 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAACATGCG ATGCACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAACTCCAAAGAAC ACGCTGTATCTGCAAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGATTACTGTGCGAGAGAT CAGGCGATTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCCCTGCTCACCGTCTCCTCA
		AA	SEQ ID NO: 1648 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAAATRAATGIPARFSGSGTE FTLTISSELPEDFAVYYCQQYNWPLTFGGGTKVE IKR	SEQ ID NO: 1805 QVQLVESGGGVVQPRSLRLSCAASGFTFSNYGM HWVRQAPGKGLEWVAIWFDASDKYYADA VKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGLVTVSS

IP:359644	18E3.002	SEQ ID NO: 78	<p>GAAATTGTTGACGCAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCT GCAGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCAGACAGGTTCACTGAGGAGTG GGTCTGGACAGACTTCACTCTCACCATCAGCA GACTGGAGCCTGATGATTTGACGTGATTACTG TCAGCAGTATGGTAGTTCAACCGCTCACTTTCGGC GGAGGACCAAGGTGGAGATCAAAACGA</p>	SEQ ID NO: 235	<p>CAGGTGCAGTTGCAGGAGTCGGGCCCCAGGACTG GTGAAGCCTTCAGAGACCCCTGTCCCTCACCTGC ACTGTCTCTGGTGAATCCATCAGCAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCCCCCAGGGA AGGGCTGGAGTGGATTGGGTACATCTATTACA GTGGGAGCACCTACTACAACCCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGCTAAGA ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGGACACGGCCGTGATTACTGTGCGAGAGA TCGTATTACGATTTTGGAGTGGTTATGGGGGGC GGTATGGACGTCTGGGGCCAAAGGGACACCGGTC ACCGTCTCCTCA</p>
		SEQ ID NO: 1649	<p>EIVLTQSPGTLSPGERATLSCRASQISYSYLAW YQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDF TLTISRLEPDDFAVYYCQQYGSSPLTFGGGKVEIK R</p>	SEQ ID NO: 1806	<p>QVQLQESGPGLVKPSSETLSLTCTVSGDSISSGGYY WSWIRQPPGKGLEWIGYIYSGSTYYNPSLKSRT ISVDTSKNQFSLKLSSTVAADTAVYYCARDRTITFG VVMGGMDVWVGQGTITVTVSS</p>
IP:361206	18E3.003	SEQ ID NO: 79	<p>GAAATTGTTGACGCAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCT GCAGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCAGACAGGTTCACTGAGGAGTG GGTCTGGACAGACTTCACTCTCACCATCAGCA GACAGGAGCCTGATGATTTGACGTGATTACT GTCAGCAGTATGGTAGTTCAACCGCTCACTTTCGG CGGAGGACCAAGGTGGAGATCAAAACGA</p>	SEQ ID NO: 236	<p>CAGGTGCAGTTGCAGGAGTCGGGCCCCAGGACTG GTGAAGCCTTCAGAGACCCCTGTCCCTCACCTGC ACTGTCTCTGGTGAATCCATCAGCAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCCCCCAGGGA AGGGCTGGAGTGGATTGGGTACATCTATTACA GTGGGAGCACCTACTACAACCCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGCTAAGA ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGGACACGGCCGTGATTACTGTGCGAGAGA TCGTATTACGATTTTGGAGTGGTTATGGGGGGC GGTATGGACGTCTGGGGCCAAAGGGACACCGGTC ACCGTCTCCTCA</p>
		SEQ ID NO: 1650	<p>EIVLTQSPGTLSPGERATLSCRASQISYSYLAW YQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDF TLTISRQEPDDFAVYYCQQYGSSPLTFGGGKVEI KR</p>	SEQ ID NO: 1807	<p>QVQLQESGPGLVKPSSETLSLTCTVSGDSISSGGYY WSWIRQPPGKGLEWIGYIYSGSTYYNPSLKSRT ISVDTSKNQFSLKLSSTVAADTAVYYCARDRTITFG VVMGGMDVWVGQGTITVTVSS</p>

IP:359628	18E3.004	NA	SEQ ID NO: 80	GAAATTGTGTTGACGCAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCC'TCTCCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCCGCTCCTCATCTATGGTGCAATCCAGCAGGG CCACTGGCATCCAGACAGGTTCAAGTGGCAGTG GGTCTGGGACAGACTTCACTCTCAACCATCAGCA GACTGGAGCCTGATGATTTTGCAGTGATTAATG TCAGCAGTATGGTAGTTCAACCGCTCACTTTTCGGC GGAGGGACC AAGGTGGAGATCAAAACGA	SEQ ID NO: 237	CAGGTGCAGTTGCAGAGTCTGGGCCACGACTG GTGAAGCCTTACAGACCCCTGTCCCTCACCTGC ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCCCCCAGGGA AGGCCCTGGAGTGGAATTGGGTACATCTATTACA GTGGAGCACCTACTACAACCCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGTCTAAGA ACCA GTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGACACGGCCGTGATTACTGTGCGAGAGA TCGTATTACGATTTTGGAGTGTTATGGGGGGC GGTATGGACGTCTGGGGCCAAGGGACACCGGTC ACCGTCTCCTCA
			SEQ ID NO: 1651	EIVLTQSPGTLSPGERATLSCRASQSIYSYLAW YQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDF TLTISRLEPDDFAVYYCQYQGSSPLTFGGGTKVEIK R	SEQ ID NO: 1808	QVQLQESGPGLVKPSQTLSTLCTVSGDSISSGGYY WSWIRQPPGKGLEWIGYIYYSGSTYYPNPSLKS RVT ISVDTSKNQFSLKLSSTVAADTAVYYCARDRIITIFG VVMGGMDVWGQGTITVTVSS
			SEQ ID NO: 81	GAAATTGTGTTGACGCAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCC'TCTCCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCCGCTCCTCATCTATGGTGCAATCCAGCAGGG CCACTGGCATCCAGACAGGTTCAAGTGGCAGTG GGTCTGGGACAGACTTCACTCTCAACCATCAGCA GACTGGAGCCTGATGATTTTGCAGTGATTAATG TCAGCAGTATGGTAGTTCAACCGCTCACTTTTCGGC GGAGGGACC AAGGTGGAGATCAAAACGA	SEQ ID NO: 238	CAGGTGCAGTTGCAGAGTCTGGGCCACGACTG GTGAAGCCTTACAGACCCCTGTCCCTCACCTGC ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCACCCAGGGA AGGCCCTGGAGTGGAATTGGGTACATCTATTACA GTGGAGCACCTACTACAACCCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGTCTAAGA ACCA GTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGACACGGCCGTGATTACTGTGCGAGAGA TCGTATTACGATTTTGGAGTGTTATGGGGGGC GGTATGGACGTCTGGGGCCAAGGGACACCGGTC ACCGTCTCCTCA
			SEQ ID NO: 1652	EIVLTQSPGTLSPGERATLSCRASQSIYSYLAW YQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDF TLTISRLEPDDFAVYYCQYQGSSPLTFGGGTKVEIK R	SEQ ID NO: 1809	QVQLQESGPGLVKPSQTLSTLCTVSGDSISSGGYY WSWIRQHPGKGLEWIGYIYYSGSTYYPNPSLKS RVT ISVDTSKNQFSLKLSSTVAADTAVYYCARDRIITIFG VVMGGMDVWGQGTITVTVSS
IP:359637	18E3.005	NA	SEQ ID NO: 80	GAAATTGTGTTGACGCAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCC'TCTCCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCCGCTCCTCATCTATGGTGCAATCCAGCAGGG CCACTGGCATCCAGACAGGTTCAAGTGGCAGTG GGTCTGGGACAGACTTCACTCTCAACCATCAGCA GACTGGAGCCTGATGATTTTGCAGTGATTAATG TCAGCAGTATGGTAGTTCAACCGCTCACTTTTCGGC GGAGGGACC AAGGTGGAGATCAAAACGA	SEQ ID NO: 237	CAGGTGCAGTTGCAGAGTCTGGGCCACGACTG GTGAAGCCTTACAGACCCCTGTCCCTCACCTGC ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCACCCAGGGA AGGCCCTGGAGTGGAATTGGGTACATCTATTACA GTGGAGCACCTACTACAACCCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGTCTAAGA ACCA GTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGACACGGCCGTGATTACTGTGCGAGAGA TCGTATTACGATTTTGGAGTGTTATGGGGGGC GGTATGGACGTCTGGGGCCAAGGGACACCGGTC ACCGTCTCCTCA
			SEQ ID NO: 1651	EIVLTQSPGTLSPGERATLSCRASQSIYSYLAW YQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDF TLTISRLEPDDFAVYYCQYQGSSPLTFGGGTKVEIK R	SEQ ID NO: 1808	QVQLQESGPGLVKPSQTLSTLCTVSGDSISSGGYY WSWIRQPPGKGLEWIGYIYYSGSTYYPNPSLKS RVT ISVDTSKNQFSLKLSSTVAADTAVYYCARDRIITIFG VVMGGMDVWGQGTITVTVSS
			SEQ ID NO: 81	GAAATTGTGTTGACGCAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCC'TCTCCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCCGCTCCTCATCTATGGTGCAATCCAGCAGGG CCACTGGCATCCAGACAGGTTCAAGTGGCAGTG GGTCTGGGACAGACTTCACTCTCAACCATCAGCA GACTGGAGCCTGATGATTTTGCAGTGATTAATG TCAGCAGTATGGTAGTTCAACCGCTCACTTTTCGGC GGAGGGACC AAGGTGGAGATCAAAACGA	SEQ ID NO: 238	CAGGTGCAGTTGCAGAGTCTGGGCCACGACTG GTGAAGCCTTACAGACCCCTGTCCCTCACCTGC ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCACCCAGGGA AGGCCCTGGAGTGGAATTGGGTACATCTATTACA GTGGAGCACCTACTACAACCCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGTCTAAGA ACCA GTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGACACGGCCGTGATTACTGTGCGAGAGA TCGTATTACGATTTTGGAGTGTTATGGGGGGC GGTATGGACGTCTGGGGCCAAGGGACACCGGTC ACCGTCTCCTCA
			SEQ ID NO: 1652	EIVLTQSPGTLSPGERATLSCRASQSIYSYLAW YQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDF TLTISRLEPDDFAVYYCQYQGSSPLTFGGGTKVEIK R	SEQ ID NO: 1809	QVQLQESGPGLVKPSQTLSTLCTVSGDSISSGGYY WSWIRQHPGKGLEWIGYIYYSGSTYYPNPSLKS RVT ISVDTSKNQFSLKLSSTVAADTAVYYCARDRIITIFG VVMGGMDVWGQGTITVTVSS

	!PS:361210	18E3.006	SEQ ID NO: 82	SEQ ID NO: 239
			<p>NA</p> <p>GAAATTGTTGTTGACGCAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCAGACAGAGTTCAAGTGGCAGTG GGTCTGGACAGACTTCACTCTCACCATCAGCA GACTGGAGCCTGATGATTTTGCAGTGTATTACTG TCAGCAGTATGGTAGTTCAACCGCTCACTTTCGGC GGAGGGACCAAGGTGGAGATCAAAACGA</p>	<p>CAGGTGCAGTTGCAGGAGTCTGGGGCCAGGACTG GTGAAGCCTTACAGACCCTGTCCCTCACCTGC ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCACCAGGGA AGGCCCTGGAGTGGATTGGGTACATCTATTACA GTGGGAGCACCTACTACAACCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGTCTAAGA ACCAAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGGACACGGCCGTGTATTACTGTGCGAGAGA TCGTATTACGATTTTGGAGTGGTTATGGGGGGC GGTATGGACGTCTGGGGCCAAAGGGACCACGGTC ACCGTCTCCTCA</p>
AA			SEQ ID NO: 1653	SEQ ID NO: 1810
			<p>EIVLTQSPGTLSPGERATLSCRASQISYSYLAW YQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDF TLTISRLEPDDFAVYYCQYQYSSPLTFGGGKVEIK R</p>	<p>QVQLQESGPGLVKPSQTLSTCTVSGDSISSGGYY WSWIRQHPGKGLEWIGYIYSGSTYYNPSLKSRT ISVDTSKNQFSLKLSSTVAADTAVYYCARDRTITFG VVMGGMDVWGQGTITVTVSS</p>
	!PS:361214	18E3.007	SEQ ID NO: 83	SEQ ID NO: 240
			<p>NA</p> <p>GAAATTGTTGTTGACGCAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCAGACAGAGTTCAAGTGGCAGTG GGTCTGGACAGACTTCACTCTCACCATCAGCA GACAGGAGCCTGATGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGTTCAACCGCTCACTTTCGG CGGAGGGACCAAGGTGGAGATCAAAACGA</p>	<p>CAGGTGCAGTTGCAGGAGTCTGGGGCCAGGACTG GTGAAGCCTTACAGACCCTGTCCCTCACCTGC ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCACCAGGGA AGGCCCTGGAGTGGATTGGGTACATCTATTACA GTGGGAGCACCTACTACAACCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGTCTAAGA ACCAAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGGACACGGCCGTGTATTACTGTGCGAGAGA TCGTATTACGATTTTGGAGTGGTTATGGGGGGC GGTATGGACGTCTGGGGCCAAAGGGACCACGGTC ACCGTCTCCTCA</p>
AA			SEQ ID NO: 1654	SEQ ID NO: 1811
			<p>EIVLTQSPGTLSPGERATLSCRASQISYSYLAW YQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDF TLTISRQEPDDFAVYYCQYQYSSPLTFGGGKVEI KR</p>	<p>QVQLQESGPGLVKPSQTLSTCTVSGDSISSGGYY WSWIRQHPGKGLEWIGYIYSGSTYYNPSLKSRT ISVDTSKNQFSLKLSSTVAADTAVYYCARDRTITFG VVMGGMDVWGQGTITVTVSS</p>

	!PS:361218	18E3.008	NA	SEQ ID NO: 84	SEQ ID NO: 241
				GAAATTGTGTTGACGCAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCAGACAGAGTTCAAGTGGCAGTG GGTCTGGACAGACTTCACTCTCACCATCAGCA GACAGAGCCTGATGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGTTCACCGCTCCTTTCCGG CGGAGGGACCAAGGTGGAGATCAAAACGA	CAGGTGCAGTTGCAGGAGTCGGGGCCAGGACTG GTGAAGCCTTACAGACCCTGTCCCTCACCTGC ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCCCCAGGGA AGGGCTGGAGTGGATTGGGTACATCTATTACA GTGGGAGCACCTACTACAACCGTCCCTCAAGA GTCGAGTTACCATATCATAGTAGACAGTCTAAGA ACCAAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGGACACGGCCGTGATTACTGTGCGAGAGA TCGTATTACGATTTTGGAGTGGTTATGGGGGGC GGTATGGACGTCTGGGGCCCAAGGGACCACGGTC ACCGTCTCCTCA
		AA	AA	SEQ ID NO: 1655	SEQ ID NO: 1812
				EIVLTQSPGTLSPGERATLSCRASQISYSYLAW YQKPGQAPRLIYGASSRATGIPDRFSGSGGTDF TLTISRQEPDDFAVYYCQQYSSPLTFGGGKVEI KR	QVQLQESGPGLVKPSQTLSTCTVSGDSISSGGYY WSWIRQPPGKGLEWIGYIYSGSTYYNPSLKSRT ISVDTSKNQFSLKLSSTVAADTAVYYCARDRIITFG VVMGGMDVWGQGTITVTVSS
	!PS:361222	5C2.006	NA	SEQ ID NO: 85	SEQ ID NO: 242
				GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG CAACCAGGACATCTCTCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGTCCCTGACC GATTCAGTGGCAGCGGTCTGGGACAGATTICA CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAAATATTATAGTAC TCCGTGGACGTTTCGGCCCAAGGGACCAAGGTGGA AATCAAAACGA	CAGGTGCAGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCGACAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATCAACCTGAAAGT GGTGGCACAGACTATTACAGAGGTTTCAGGGC AGGGTCACCATGACCAAGGACACGTCCATCAGC ACAGCCTACATGGAACCTGAACAGGCTGAGATCT GACGACACGGCCGTGATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCAACCGTCT CCTCA
		AA	AA	SEQ ID NO: 1656	SEQ ID NO: 1813
				DIVMTQSPDSLAVSLGERATINCKSSQVLSNNK NYIAWYQQQHPKLLIYWASTRESGVDPDRFSGS GSGTDFLTIISSLQAEDVAVFYCQQYSTPTWTFGQ GTKVEIKR	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYI HWVRAQPGQGLEWMGWNPESGGTDYSQRFQGR VTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGTITVTVSS

!PS:361229	SC2.007	NA	SEQ ID NO: 86 GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG CAACAGGACATCCTCCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGTCCTGACC GATTCAGTGGCAGCGGCTCTGGACAGATTCA CTCTCACCATCAGCAGCTGCAGGCTGAAGATG TGGCAGTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAAAGGACCAAGGTGGA AATCAAAACGA	SEQ ID NO: 86 CAGTGCCGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGCTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATCAACCTGAAAGT GGTGGCACAGACTATTCACAGAGGTTTCAGGGC AGGTTCAACCATGACCAAGGACACGTCATCAGC ACAGCTACATGGAACCTGAACAGGCTGAGATCT GACGACACGGCCGTGTTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCGTCT CCTCA	SEQ ID NO: 243
		AA	SEQ ID NO: 1657 DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQPGHPPKLLIYWASTRESGVPDFRSGS GSGTDFLTIISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR	SEQ ID NO: 1814 QVPLVQSGAEVKKPGASVKVSKASGYTFTGYYI HWVRAPQGQGLEWMGWINPESGGTDYSQRFQGR FTMTTRDTSISTAYMELNRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGLVTVSS	SEQ ID NO: 244
!PS:361236	SC2.008	NA	SEQ ID NO: 87 GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG CAACAGGACATCCTCCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGTCCTGACC GATTCAGTGGCAGCGGCTCTGGACAGATTCA CTCTCACCATCAGCAGCTGCAGGCTGAAGATG TGGCAGTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAAAGGACCAAGGTGGA AATCAAAACGA	SEQ ID NO: 87 CAGTGCGAGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGCTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATCAACCCCTGACGCT GGTGGCACAGACTATTCACAGAGGTTTCAGGGC AGGGTCACCATGACCAAGGACACGTCATCAGC ACAGCTACATGGAACCTGAACAGGCTGAGATCT GACGACACGGCCGTGTTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCGTCT CCTCA	SEQ ID NO: 1815
		AA	SEQ ID NO: 1658 DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQPGHPPKLLIYWASTRESGVPDFRSGS GSGTDFLTIISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR	SEQ ID NO: 245 QVQLVQSGAEVKKPGASVKVSKASGYTFTGYYI HWVRAPQGQGLEWMGWINPDAGGTDYSQRFQGR RVTMTTRDTSISTAYMELNRLRSDDTAVYYCAREA TIFGMVIVPFDYWGQGLVTVSS	

!PS:359685	SC2.009	NA	SEQ ID NO: 88 GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAAGCAG CAACAGGACATCCTCCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGGTCCCTGACC GATTCAGTGGCAGCGGGTCTGGGACAGATTCA CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAAAGGACCAAGGTGGA AATCAAAACGA	SEQ ID NO: 245 CAGTGCCGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATCAACCTGACGCT GGTGGCACAGACTATTCACAGAGGTTTCAGGGC AGGTTCAACCATGACCAAGGACACGTCATCAGC ACAGCCTACATGGAACCTGAACAGGCTGAGATCT GACGACACGGCCGTGTTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
		AA	SEQ ID NO: 1659 DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQPGHPKLLIYWASTRESGVPDFRFGS GSGTDFLTIISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR	SEQ ID NO: 1816 QVPLVQSGAEVKKPGASVKVCKASGYTFTGYI HWVRAPGQGLEWMGWINPDAGGTDYSQRFQ RFTMTRDTSISTAYMELNRLRSDDTAVYYCAREA TIFGMVIVPFDYWGQGLVTVSS
!PS:361240	SC2.010	NA	SEQ ID NO: 89 GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAAGCAG CAACAGGACATCCTCCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGGTCCCTGACC GATTCAGTGGCAGCGGGTCTGGGACAGATTCA CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAAAGGACCAAGGTGGA AATCAAAACGA	SEQ ID NO: 246 CAGTGCACTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATCAACCTGACAGT GGTGGCACAGACTATTCACAGAGGTTTCAGGGC AGGGTCAACCATGACCAAGGACACGTCATCAGC ACAGCCTACATGGAACCTGAACAGGCTGAGATCT GACGACACGGCCGTGTTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
		AA	SEQ ID NO: 1660 DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQPGHPKLLIYWASTRESGVPDFRFGS GSGTDFLTIISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR	SEQ ID NO: 1817 QVQLVQSGAEVKKPGASVKVCKASGYTFTGYI HWVRAPGQGLEWMGWINPDGSGGTDYSQRFQGR VTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGLVTVSS

!PS:361247	SC2.011	NA	SEQ ID NO: 90 GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAAGCAG CAACAGGACATCCTCCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGGTCCCTGACC GATTCAGTGGCAGCGGGTCTGGGACAGATTCA CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAAAGGACCAAGGTGGA AATCAAAACGA	SEQ ID NO: 247 CAGGTGCAGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATCAACCTTGACAGT GGTGGCACAGACTATTACAGAGGTTTCAGGGC AGGTTCAACCATGACCAAGGACACGTCATCAGC ACAGCCTACATGGAACCTGAACAGGCTGAGATCT GACGACACGGCCGTGTTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
			SEQ ID NO: 1661 DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQPGHPKLLIYWASTRESGVPDFRFGS GSGTDFLTIISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR	SEQ ID NO: 1818 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYI HWVRAPGQGLEWMGWINPDSGGTDYSQRFQGR FTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGLVTVSS
!PS:361254	SC2.012	NA	SEQ ID NO: 91 GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAAGCAG CAACAGGACATCCTCCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGGTCCCTGACC GATTCAGTGGCAGCGGGTCTGGGACAGATTCA CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAAAGGACCAAGGTGGA AATCAAAACGA	SEQ ID NO: 248 CAGGTGCCCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATCAACCTTGACAGT GGTGGCACAGACTATTACAGAGGTTTCAGGGC AGGTCACCATGACCAAGGACACGTCATCAGC ACAGCCTACATGGAACCTGAACAGGCTGAGATCT GACGACACGGCCGTGTTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
			SEQ ID NO: 1662 DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQPGHPKLLIYWASTRESGVPDFRFGS GSGTDFLTIISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR	SEQ ID NO: 1819 QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYI HWVRAPGQGLEWMGWINPDSGGTDYSQRFQGR VTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGLVTVSS

!PS:361261	SC2.013	NA	SEQ ID NO: 92 GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAAGCAG CAACAGGACATCCTCCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGGTCCCTGACC GATTCAGTGGCAGCGGGTCTGGGACAGATTTC CTCTACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAAAGGACCAAGGTGGA AATCAAAACGA	SEQ ID NO: 249 CAGGTGCAGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGCTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCACAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATCAACCTGACGCT GGTGGCACAGACTATTACAGAGGTTTCAGGGC AGGTTCAACCATGACCAAGGACACGTCATCAGC ACAGCTACATGGAACCTGAACAGGCTGAGATCT GACGACACGGCCGTGTTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCGTCT CCTCA
		AA	SEQ ID NO: 1663 DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQPGHPKLLIYWASTRESGVPDFRFGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR	SEQ ID NO: 1820 QVQLVQSGAEVKKPGASVKVSKASGYTFTGYI HWVRAPGQGLEWMGWINPDAGGTDYSQRFQ RFTMTRDTSISTAYMELNRLRSDDTAVYYCAREA TIFGMVIVPFDYWGGQTLVTVSS
!PS:361268	SC2.014	NA	SEQ ID NO: 93 GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAAGCAG CAACAGGACATCCTCCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGGTCCCTGACC GATTCAGTGGCAGCGGGTCTGGGACAGATTTC CTCTACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAAAGGACCAAGGTGGA AATCAAAACGA	SEQ ID NO: 250 CAGGTGCCGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGCTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCACAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATCAACCTGACGCT GGTGGCACAGACTATTACAGAGGTTTCAGGGC AGGGTCACCATGACCAAGGACACGTCATCAGC ACAGCTACATGGAACCTGAACAGGCTGAGATCT GACGACACGGCCGTGTTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCGTCT CCTCA
		AA	SEQ ID NO: 1664 DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQPGHPKLLIYWASTRESGVPDFRFGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR	SEQ ID NO: 1821 QVPLVQSGAEVKKPGASVKVSKASGYTFTGYI HWVRAPGQGLEWMGWINPDAGGTDYSQRFQ RVTMTRDTSISTAYMELNRLRSDDTAVYYCAREA TIFGMVIVPFDYWGGQTLVTVSS

!PS:359678	SC2.015	SEQ ID NO: 94	<p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGCTCTGGGGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAAGCAG AACCAAGGACAACTCTTAAGCTGCTCATTTAC TGGGCATCTACCCGGGAATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAAGCAGCTGCGAGGCTGAAGAT GTGGCAGTTTTTTACTGTCAACAATATTATAGTA CTCCGTGGACGTTGGGCCAAGGGACCAAGGTGG AAATCAAAACGA</p>	SEQ ID NO: 251	<p>CAGGTGCAGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCACAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATCAACCTGACGCT GGTGGCACAGACTATTACAGAGGTTTCAAGGGC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTACATGGAACCTGAACAGCCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA</p>
		SEQ ID NO: 1665	<p>DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQKPGQPPKLLIYWASTRESGVPDFRFGS GSGTDFLTIISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR</p>	SEQ ID NO: 1822	<p>QVQLVQSGAEVKKPGASVKVSKASGYTFTGYYI HWVRAPQGQGLEWMGWINPDAGGTDYSQRFQG RVMTTRDTSISTAYMELNSLRSDDTAVYYCAREA TIFGMVIVPFDYWGQGLVTVSS</p>
!PS:359678	SC2.016	SEQ ID NO: 95	<p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGCTCTGGGGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAAGCAG AACCAAGGACAACTCTTAAGCTGCTCATTTAC TGGGCATCTACCCGGGAATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAAGCAGCTGCGAGGCTGAAGAT GTGGCAGTTTTTTACTGTCAACAATATTATAGTA CTCCGTGGACGTTGGGCCAAGGGACCAAGGTGG AAATCAAAACGA</p>	SEQ ID NO: 252	<p>CAGGTGCAGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCACAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATCAACCTGAAAGT GGTGGCACAGACTATTACAGAGGTTTCAAGGGC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTACATGGAACCTGAACAGCCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA</p>
		SEQ ID NO: 1666	<p>DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQKPGQPPKLLIYWASTRESGVPDFRFGS GSGTDFLTIISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR</p>	SEQ ID NO: 1823	<p>QVQLVQSGAEVKKPGASVKVSKASGYTFTGYYI HWVRAPQGQGLEWMGWINPESGGTDYSQRFQGR VTMTRDTSISTAYMELNSLRSDDTAVYYCAREATI FGMVIVPFDYWGQGLVTVSS</p>

	!PS:361275	11C1.002	SEQ ID NO: 96	SEQ ID NO: 253
			<p>NA</p> <p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGGGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAACAG AACCAAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGAAATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTGGCCAAAGGGACCAAGGTGG AAATCAAAACGA</p>	<p>CAGTGCCCGCTGGTACAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCTCAGGCCCTTGGACAAGGG CTTGTGTGGATGGGTGGATCAGCCCTAACAGT GGTGAACAAAGCTATGCACAGAAGTTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGACTGAGATCT GACGACACGGCCGTGATTTCTGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA</p>
	AA	11C1.003	SEQ ID NO: 1667	SEQ ID NO: 1824
			<p>DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSSTRESGVPDFRSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR</p>	<p>QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLVWMGWISPNSETSYAQKFQDR VTMTRDTSISTAYMELSRLSRDDTAVYFCAREATI FGMLIVPFDYWGQGLVTVSS</p>
	!PS:361282	11C1.003	SEQ ID NO: 97	SEQ ID NO: 254
			<p>NA</p> <p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGGGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAACAG AACCAAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGAAATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTGGCCAAAGGGACCAAGGTGG AAATCAAAACGA</p>	<p>CAGTGCCCGCTGGTACAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCTCAGGCCCTTGGACAAGGG CTTGTGTGGATGGGTGGATCAGCCCTAACAGT GGTGACACAAAGCTATGCACAGAAGTTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGACTGAGATCT GACGACACGGCCGTGATTTCTGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA</p>
	AA	11C1.003	SEQ ID NO: 1668	SEQ ID NO: 1825
			<p>DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSSTRESGVPDFRSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR</p>	<p>QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLVWMGWISPNSETSYAQKFQDR VTMTRDTSISTAYMELSRLSRDDTAVYFCAREATI FGMLIVPFDYWGQGLVTVSS</p>

	IP:361289	11C1.004	SEQ ID NO: 98	SEQ ID NO: 255
			<p>NA</p> <p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGGGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACTTAGCTTGGTACCAACAG AACCAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGTCTGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCAAGGTGG AAATCAAAACGA</p>	<p>CAGTGCCGCTGGTACAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGTGGCTCAGGCCCTTGGACAAGGG CTTGTGTGGATGGGTGGATCAGCCCTAACAGT GGTGAAACAAGCTATGCACAGAAGTTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGACTGAGATCT GACGACACGGCCGTGATTTCTGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA</p>
	IP:359712	11C1.005	SEQ ID NO: 1669	SEQ ID NO: 1826
			<p>AA</p> <p>DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRDSGVPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR</p>	<p>QVPLVQSGAEVKKPGASVKVSKASGYTFTGYYI HWVRQAPGQGLVWMGWISPNSETSYAQKFQDR VTMTRDTSISTAYMELSRLSRDDTAVYFCAREATI FGMLIVPFDYWGQGLVTVSS</p>
	IP:359712	11C1.005	SEQ ID NO: 99	SEQ ID NO: 256
			<p>NA</p> <p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGGGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACTTAGCTTGGTACCAACAG AACCAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGAAATCCGGGTCCCTGAC CGATTCAAGTGGCAGCGGTCTGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCAAGGTGG AAATCAAAACGA</p>	<p>CAGTGCCGCTGGTACAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGTGGCTCAGGCCCTTGGACAAGGG CTTGTGTGGATGGGTGGATCAGCCCTAACAGT GGTGAAACAAGCTATGCACAGAAGTTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGACTGAGATCT GACGACACGGCCGTGATTTCTGTACGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA</p>
	IP:359712	11C1.005	SEQ ID NO: 1670	SEQ ID NO: 1827
			<p>AA</p> <p>DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRDSGVPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR</p>	<p>QVPLVQSGAEVKKPGASVKVSKASGYTFTGYYI HWVRQAPGQGLVWMGWISPNSETSYAQKFQDR VTMTRDTSISTAYMELSRLSRDDTAVYFCAREATI FGMLIVPFDYWGQGLVTVSS</p>

	!PS:361293	11C1.006	SEQ ID NO: 100	SEQ ID NO: 257
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAACAG AACCAAGGACAGCCTCTAACCTGCTCATTTAC TGGACTTCTACCCGAGAAATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGCTCTGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTGGCCAAAGGGACCAAGGTGG AAATCAAAACGA	CAGTGCCGCTGGTACAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGTGGCTCAGGCCCTTGGACAAGGG CTTGTGTGGATGGGTGGATCAGCCCTAACAGT GGTGACACAAGCTATGCACAGAAGTTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGACTGAGATCT GACGACACGGCCGTGATTTCTGTACGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
	AA		SEQ ID NO: 1671	SEQ ID NO: 1828
			DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRESGVPDFRSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	QVPLVQSGAEVKKPGASVKVCKASGYTFTGYYI HWVRQAPGQGLVWMGWISPNSGDTSYAQKFQDR VTMTRDTSISTAYMELSRLSRDDTAVYFCTREATI FGMLIVPFDYWGQGLVTVSS
	!PS:361297	11C1.007	SEQ ID NO: 101	SEQ ID NO: 258
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAACAG AAACCAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGCTCTGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTGGCCAAAGGGACCAAGGTGG AAATCAAAACGA	CAGTGCCGCTGGTACAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGTGGCTCAGGCCCTTGGACAAGGG CTTGTGTGGATGGGTGGATCAGCCCTAACAGT GGTGAAACAAGCTATGCACAGAAGTTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGACTGAGATCT GACGACACGGCCGTGATTTCTGTACGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
		AA	SEQ ID NO: 1672	SEQ ID NO: 1829
			DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRDSGVPDFRSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	QVPLVQSGAEVKKPGASVKVCKASGYTFTGYYI HWVRQAPGQGLVWMGWISPNSETSYAQKFQDR VTMTRDTSISTAYMELSRLSRDDTAVYFCTREATI FGMLIVPFDYWGQGLVTVSS

!PS:361301	11C1.008	SEQ ID NO: 102	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAACAG AACCAAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGCTCTGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 259	CAGTGCCCGCTGGTACAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCTCAGGCCCTTGGACAAGGG CTTGTGTGGATGGGTGGATCAGCCCTAACAGT GGTGACACAAGCTATGCACAGAAGTTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGACTGAGATCT GACGACACGGCCGTGATTTCTGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
		SEQ ID NO: 1673	DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRDSGVPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1830	QVPLVQSGAEVKKPGASVKVCKASGYTFTGYYI HWVRQAPGQGLVWMGWISPNSGDTSYAQKFQDR VTMTRDTSISTAYMELSRLSDDTAVYFCAREATI FGMLIVPFDYWGQGLVTVSS
!PS:359703	11C1.009	SEQ ID NO: 103	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAACAG AAACCAGGACAGCCTCCTAAACTGCTCATTTAC TGGACTTCTACCCGAGAAATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGCTCTGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 260	CAGTGACGCTGGTACAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCTCAGGCCCTTGGACAAGGG CTTGAGTGGATGGGTGGATCAGCCCTAACAGT GGTGAAACAAGCTATGCACAGAAGTTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGCCTGAGATCT GACGACACGGCCGTGATTTCTGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
		SEQ ID NO: 1674	DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRDSGVPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1831	QVQLVQSGAEVKKPGASVKVCKASGYTFTGYYI HWVRQAPGQGLEWMGWISPNSETSYAQKFQDR VTMTRDTSISTAYMELSSLRSDDTAVYFCAREATI FGMLIVPFDYWGQGLVTVSS

		SEQ ID NO: 104	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCCTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACTTAGCTTGGTACCAACAG AAACCAGGACAGCTCCTAACTGCTCATTTAC TGGACTTCTACCCGAGAAATCCGGGTCCCTGAC CGATTCAAGTGCGAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTTCGGCCAAGGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 1675	DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPNNLLIYWTSRESGVDPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1832	QVQLVQSGAEVKKPGASVKVSKASGYTFTGYI HWVRQAPGQGLEWMGWISPNSETSYAQKFQDR VTMTRDTSISTAYMELSRLRSDDTAVYFCAREATI FGMLIVPFDYWGGQGLTVTVSS
!PS:361305	11C1.010	NA			AA		
		SEQ ID NO: 105	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCCTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAAGCAG AAACCAGGACATCCTCCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGTCCCTGACC GATTCAAGTGCGAGCGGGTCTGGGACAGATTTC CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTTCGGCCAAGGGACCAAGGTGGA AATCAAAACGA	SEQ ID NO: 105		SEQ ID NO: 262	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATCCACTGGGTGCGACAGGCCCTGGACAAGGA CTTGAGTGGATGGGTGGATCAACCCCTGAAAGT GGTGGCACAGACTATTACAGAGGTTTCAAGGGC AGGTCACCATGACCAAGGACACGTCCATCAGC ACAGCCTACATGGAACCTGAGCAGGCTGAGATCT GACGACACGGCCGTGATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCAACCGTCT CCTCA
!PS:361312	13H12.002	NA					
		SEQ ID NO: 1676	DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYIAWYQQKPGHPKLLIYWASTRESGVDPDRFSGS GSGTDFLTISLQAEDVAVFYCQQYYSTPWFQ GTKVEIKR	SEQ ID NO: 1676	AA	SEQ ID NO: 1833	QVPLVQSGAEVKKPGASVKVSKASGYTFTGYI HWVRQAPGQGLEWMGWINPESGGTDYSQRFQGR VTMTRDTSISTAYMELSRLRSDDTAVYYCAREATI FGMVIVPFDYWGGQGLTVTVSS

	!PS:359744	13H12.003	SEQ ID NO: 106	SEQ ID NO: 263
			<p>NA</p> <p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGCTCTGGGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG AACCAAGGACATCCTCCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGGTCCCTGACC GATTCAGTGGCAGCGGCTCTGGGACAGATTTC CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAAAGGACCAAGGTGGA AATCAAAACGA</p>	<p>CAGTGCCCGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCACAGGCCCTGGACAAGGA CTTGAGTGGATGGGTGGATCAACCTGAAAGT GGTGGCACAGACTATTCACAGAGTTTACAGGGC AGGTTCAACCATGACCAAGGACACGTCATCAGC ACAGCCTACATGGAACCTGACAGGCTGAGATCT GACGACACGGCCGTGTTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA</p>
AA			SEQ ID NO: 1677	SEQ ID NO: 1834
			<p>DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQKPGHPPKLLIYWASTRESGVPDFRFGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR</p>	<p>QVPLVQSGAEVKKPGASVKVSKASGYTFTGYYI HWVRAPQGQGLEWMGWINPESGGTDYSQRFQGR FTMTRDTSISTAYMELSRLSDDTAVYYCAREATI FGMVVFPFDYWGQGLVTVSS</p>
NA	!PS:361319	13H12.004	SEQ ID NO: 107	SEQ ID NO: 264
			<p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGCTCTGGGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG AAACCAGGACATCCTCCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGGTCCCTGACC GATTCAGTGGCAGCGGCTCTGGGACAGATTTC CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAAAGGACCAAGGTGGA AATCAAAACGA</p>	<p>CAGTGCCCGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCACAGGCCCTGGACAAGGA CTTGAGTGGATGGGTGGATCAACCTGACAGT GGTGGCACAGACTATTCACAGAGTTTACAGGGC AGGTCACCATGACCAAGGACACGTCATCAGC ACAGCCTACATGGAACCTGACAGGCTGAGATCT GACGACACGGCCGTGTTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA</p>
AA			SEQ ID NO: 1678	SEQ ID NO: 1835
			<p>DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQKPGHPPKLLIYWASTRESGVPDFRFGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR</p>	<p>QVPLVQSGAEVKKPGASVKVSKASGYTFTGYYI HWVRAPQGQGLEWMGWINPDSGGTDYSQRFQGR VTMTRDTSISTAYMELSRLSDDTAVYYCAREATI FGMVVFPFDYWGQGLVTVSS</p>

	!PS:359737	13H12.005	SEQ ID NO: 108	SEQ ID NO: 265
			<p>NA</p> <p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAAGCAG AAACGAGGACAACTCTTAAGCTGCTCATTTAC TGGGCATCTACCCGGGAATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAAGCAGCTGCGAGGCTGAAGAT GTGGCAGTTTTTTACTGTCAACAATATTATAGTA CTCCGTGGACGTTGGGCCAAGGGACCAAGGTGG AAATCAAAACGA</p>	<p>CAGGTGCAGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGGTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCACAGGCCCTGGACAAGGA CTTGAGTGGATGGGTGGATCAACCTGAAAGT GGTGGCACAGACTATTACAGAGGTTTCAGGGC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTACATGGAACCTGAGCAGCCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA</p>
AA			SEQ ID NO: 1679	SEQ ID NO: 1836
			<p>DIVMTQSPDLSAVSLGERATINCKSSQSVLSSNNK NYIAWYQQKPGQPPKLLIYWASTRESGVPDFRFGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR</p>	<p>QVQLVQSGAEVKKPGASVKVSKASGYTFTGYYI HWVRAPGQGLEWMGWINPESGGTDYSQRFQGR VTMTRDTSISTAYMELSSLRSDDTAVYYCAREATI FGMVIVPFDYWGQGLVTVSS</p>
NA	!PS:361326	13H12.006	SEQ ID NO: 109	SEQ ID NO: 266
			<p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAAGCAG AAACGAGGACAACTCTTAAGCTGCTCATTTAC TGGGCATCTACCCGGGAATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAAGCAGCTGCGAGGCTGAAGAT GTGGCAGTTTTTTACTGTCAACAATATTATAGTA CTCCGTGGACGTTGGGCCAAGGGACCAAGGTGG AAATCAAAACGA</p>	<p>CAGGTGCCCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGGTTCTGGATACACCTTACCCGGCTACTAT ATCCACTGGGTGCACAGGCCCTGGACAAGGA CTTGAGTGGATGGGTGGATCAACCTGAAAGT GGTGGCACAGACTATTACAGAGGTTTCAGGGC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTACATGGAACCTGAGCAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA</p>
AA			SEQ ID NO: 1680	SEQ ID NO: 1837
			<p>DIVMTQSPDLSAVSLGERATINCKSSQSVLSSNNK NYIAWYQQKPGQPPKLLIYWASTRESGVPDFRFGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR</p>	<p>QVPLVQSGAEVKKPGASVKVSKASGYTFTGYYI HWVRAPGQGLEWMGWINPESGGTDYSQRFQGR VTMTRDTSISTAYMELSSLRSDDTAVYYCAREATI FGMVIVPFDYWGQGLVTVSS</p>

!PS:361330	12H11.002	SEQ ID NO: 110	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCCTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAAGAACTACTTAGCTTGGTACCAGCAG AAACGAGGACAGCCTCCTAACTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAAGTGCGAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTTCGGCCAAGGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 1681	DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPNNLLIYWTSRDSGVPDRFSG SGSGTDFLTINSLQAEDVA VYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1838	QVPLVQSGAEVKPGASVKVSCKASGYTFTGYVI HWVRQAPGQGLEWMGWISPNQGETNYAQKFQD RVMTTRDTSISTAYMELSLRSDDDTAVYYCAREA TIFGMLIVPFDYWGQGLTVTVSS
		NA					
!PS:361337	12H11.003	SEQ ID NO: 111	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCCTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAAGAACTACTTAGCTTGGTACCAGCAG AAACGAGGACAGCCTCCTAACTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAAGTGCGAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTTCGGCCAAGGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 111		SEQ ID NO: 268	CAGTGCCCGCTGGTGCACTCTGGGGCTGAGGTG AAGAAGCCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATACACTGGGTGCGTCAAGGCCCTGGACAAAGG CTTGAGTGGATGGGGTGGATAAGCCCTAACCAA GGTGACACA AACTATGCACAGAAGTTTTCAGGAC AGGTCACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT GACGACACGGCCGTGATTACTGTGCGGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCAACCGTCT CCTCA
		NA					
		SEQ ID NO: 1682	DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPNNLLIYWTSRDSGVPDRFSG SGSGTDFLTINSLQAEDVA VYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1682		SEQ ID NO: 1839	QVPLVQSGAEVKPGASVKVSCKASGYTFTGYVI HWVRQAPGQGLEWMGWISPNQGETNYAQKFQD RVMTTRDTSISTAYMELSLRSDDDTAVYYCAREA TIFGMLIVPFDYWGQGLTVTVSS
		AA					

	!PS:361344	12H11.004	SEQ ID NO: 112	SEQ ID NO: 1122	SEQ ID NO: 269
			NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTGTCTGTGTCTCTGGGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAGCAG AACCAAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGTCTGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCAAGGTGG AAATCAAAACGA	CAGTGCCCGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGCTTCTGGATACACCTTCCACCGGCTACTAT ATACACTGGGTGCTCAGGCCCTTGGACAAAGG CTTGAGTGGATGGGTGGATAAGCCCTAACCAA GGTGAACAAACTATGCACAGAAGTTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGACAGGCTGAGATCT GACGACACGGCCGTGTTACTGTACGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
	!PS:361351	12H11.005	AA	SEQ ID NO: 1683	SEQ ID NO: 1840
			AA	DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRDSGVPDRFSG SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	QVPLVQSGAEVKKPGASVKVCKASGYTFTGYYI HWVRAPQGQLEWMGWISPNQGETNYAQKFQD RVTMTTRDTSISTAYMELSLRSDDTAVYYCTREA TIFGMLIVPFDYWGQGLVTVSS
	!PS:361351	12H11.005	NA	SEQ ID NO: 113	SEQ ID NO: 270
			NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTGT TCTGTGTCTCTGGGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAGCAG AAACCAAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGTCTGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCAAGGTGG AAATCAAAACGA	CAGTGCCCGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGCTTCTGGATACACCTTCCACCGGCTACTAT ATACACTGGGTGCTCAGGCCCTTGGACAAAGG CTTGAGTGGATGGGTGGATAAGCCCTAACCAAT GGTGAACAAACTATGCACAGAAGTTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGACAGGCTGAGATCT GACGACACGGCCGTGTTACTGTGCGGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
			AA	SEQ ID NO: 1684	SEQ ID NO: 1841
			AA	DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRDSGVPDRFSG SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	QVPLVQSGAEVKKPGASVKVCKASGYTFTGYYI HWVRAPQGQLEWMGWISPNQGETNYAQKFQD RVTMTTRDTSISTAYMELSLRSDDTAVYYCAREA TIFGMLIVPFDYWGQGLVTVSS

!PS:361358	12H11.006	SEQ ID NO: 114	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAGCAG AACCAAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGCTCTGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 114	SEQ ID NO: 271	CAGTGCCCGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCTCAGGCCCTTGGACAAAGG CTTGAGTGGATGGGTGGATAAGCCCTAACAAAT GGTGACACAACTATGCACAGAAATTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGACAGGCTGAGATCT GACGACACGGCCGTGATTACTGTGCGGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
		AA	SEQ ID NO: 1685	DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRDSGVPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1842	QVPLVQSGAEVKKPGASVKVSKASGYTFTGYYI HWVRAPQGQLEWMGWISPNNGDTNYAQKFQD RVTMTTRDTSISTAYMELSLRSDDTAVYYCAREA TIFGMLIVPFDYWGQGLTVTVSS
!PS:361365	12H11.007	NA	SEQ ID NO: 115	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAGCAG AAACCAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGCTCTGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 272	CAGTGCCCGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCTCAGGCCCTTGGACAAAGG CTTGAGTGGATGGGTGGATAAGCCCTAACCAA GGTGACACAACTATGCACAGAAATTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGACAGGCTGAGATCT GACGACACGGCCGTGATTACTGTACGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
		AA	SEQ ID NO: 1686	DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRDSGVPDRFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1843	QVPLVQSGAEVKKPGASVKVSKASGYTFTGYYI HWVRAPQGQLEWMGWISPNNGDTNYAQKFQD RVTMTTRDTSISTAYMELSLRSDDTAVYYCTREA TIFGMLIVPFDYWGQGLTVTVSS

	!PS:361372	12H11.008	SEQ ID NO: 116	SEQ ID NO: 117	SEQ ID NO: 118
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAGCAG AACCAAGGACAGCCTCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGCTCTGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCAAGGTGG AAATCAAAACGA	DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRDSGVPDRFSG SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1844 QVPLVQSGAEVKKPGASVKVSKASGYTFTGYI HWVRAPGQGLEWMGWISPNNGETNYAQKFQD RVTMTSDTSISTAYMELSLRSDDTAVYYCTREA TIFGMLIVPFDYWGQGLVTVSS
	!PS:361379	12H11.009	SEQ ID NO: 117	SEQ ID NO: 118	SEQ ID NO: 119
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAGCAG AACCAAGGACAGCCTCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGCTCTGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 1845 QVPLVQSGAEVKKPGASVKVSKASGYTFTGYI HWVRAPGQGLEWMGWISPNNGETNYAQKFQD RVTMTSDTSISTAYMELSLRSDDTAVYYCTREA TIFGMLIVPFDYWGQGLVTVSS	SEQ ID NO: 1846 QVPLVQSGAEVKKPGASVKVSKASGYTFTGYI HWVRAPGQGLEWMGWISPNNGETNYAQKFQD RVTMTSDTSISTAYMELSLRSDDTAVYYCTREA TIFGMLIVPFDYWGQGLVTVSS

!PS:361383	12H11.010	SEQ ID NO: 118	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAAGAACTACTTAGCTTGGTACCAGCAG AAACCAGGACAGCCTCCTAACTGCTCATTTAC TGGACTTCTACCCGAGAAATCCGGGGTCCCTGAC CGATTCAAGTGCGAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTTCGGCCAAGGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 1189	DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPNNLLIYWTSRESGVPDFRSG SGSGTDFLTINSLQAEDVA VYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1689	SEQ ID NO: 1846	QVPLVQSGAEVKPGASVKVSCKASGYTFTGYVI HWVRQAPQGQLEWMGWISPNNGDTNYAQKFQD RVMTTRDTSISTAYMELSLRSDDDTAVYYCAREA TIFGMLIVPFDYWGQGLTVTVSS			
		SEQ ID NO: 119	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAAGAACTACTTAGCTTGGTACCAGCAG AAACCAGGACAGCCTCCTAACTGCTCATTTAC TGGACTTCTACCCGAGAAATCCGGGGTCCCTGAC CGATTCAAGTGCGAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTTCGGCCAAGGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 1690	SEQ ID NO: 1690	SEQ ID NO: 1847	QVPLVQSGAEVKPGASVKVSCKASGYTFTGYVI HWVRQAPQGQLEWMGWISPNQDNTNYAQKFQD RVMTTRDTSISTAYMELSLRSDDDTAVYYCAREA TIFGMLIVPFDYWGQGLTVTVSS				
!PS:361387	12H11.011	SEQ ID NO: 118	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAAGAACTACTTAGCTTGGTACCAGCAG AAACCAGGACAGCCTCCTAACTGCTCATTTAC TGGACTTCTACCCGAGAAATCCGGGGTCCCTGAC CGATTCAAGTGCGAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTTCGGCCAAGGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 119	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAAGAACTACTTAGCTTGGTACCAGCAG AAACCAGGACAGCCTCCTAACTGCTCATTTAC TGGACTTCTACCCGAGAAATCCGGGGTCCCTGAC CGATTCAAGTGCGAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTTCGGCCAAGGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 119	SEQ ID NO: 276	CAGTGCCGCTGGTGCACTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATACACTGGTGCGTCAAGGCCCTGGACAAAGG CTTGAGTGATGGGTGGATAAGCCCTAACCAA GGTGACACA AACTATGCACAGAAGTTTTCAGGAC AGGTCACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT GACGACACGGCCGTGTTATTACTGTGCGGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCGTCT CCTCA	SEQ ID NO: 276	SEQ ID NO: 1847	QVPLVQSGAEVKPGASVKVSCKASGYTFTGYVI HWVRQAPQGQLEWMGWISPNQDNTNYAQKFQD RVMTTRDTSISTAYMELSLRSDDDTAVYYCAREA TIFGMLIVPFDYWGQGLTVTVSS
		SEQ ID NO: 119	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAAGAACTACTTAGCTTGGTACCAGCAG AAACCAGGACAGCCTCCTAACTGCTCATTTAC TGGACTTCTACCCGAGAAATCCGGGGTCCCTGAC CGATTCAAGTGCGAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTTCGGCCAAGGGACCAAGGTGG AAATCAAAACGA	SEQ ID NO: 1690	SEQ ID NO: 1690	SEQ ID NO: 1847	QVPLVQSGAEVKPGASVKVSCKASGYTFTGYVI HWVRQAPQGQLEWMGWISPNQDNTNYAQKFQD RVMTTRDTSISTAYMELSLRSDDDTAVYYCAREA TIFGMLIVPFDYWGQGLTVTVSS				

IPS:361391	12H11.012	NA	SEQ ID NO: 120 GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAAGAAGAACTACTTAGCTTGTAACAGCAG AAACAGGACAGCCTCCTAACCTGCTCATTTAC TGGAATCTACCCGAGAAATCCGGGTCCCTGAC CGATTCAAGTGACGCGGTCTGGGACAGATTTT ACTCTACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTACGAATATTATCGTA CTCCGTGGACGTTTCGGCCAAGGGACCAAGGTGG AAATCAAAACA	SEQ ID NO: 120 GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAAGAAGAACTACTTAGCTTGTAACAGCAG AAACAGGACAGCCTCCTAACCTGCTCATTTAC TGGAATCTACCCGAGAAATCCGGGTCCCTGAC CGATTCAAGTGACGCGGTCTGGGACAGATTTT ACTCTACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTACGAATATTATCGTA CTCCGTGGACGTTTCGGCCAAGGGACCAAGGTGG AAATCAAAACA	SEQ ID NO: 120 GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAAGAAGAACTACTTAGCTTGTAACAGCAG AAACAGGACAGCCTCCTAACCTGCTCATTTAC TGGAATCTACCCGAGAAATCCGGGTCCCTGAC CGATTCAAGTGACGCGGTCTGGGACAGATTTT ACTCTACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTACGAATATTATCGTA CTCCGTGGACGTTTCGGCCAAGGGACCAAGGTGG AAATCAAAACA
		AA	SEQ ID NO: 1691 DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSTRESGVPDFSG SGSGTDFLTINSLQAEDVAVYYCQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1691 DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSTRESGVPDFSG SGSGTDFLTINSLQAEDVAVYYCQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1691 DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSTRESGVPDFSG SGSGTDFLTINSLQAEDVAVYYCQYYRTPWTF GQGTKVEIKR
IPS:361395	12H11.013	NA	SEQ ID NO: 121 GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAAGAAGAACTACTTAGCTTGTAACAGCAG AAACAGGACAGCCTCCTAACCTGCTCATTTAC TGGAATCTACCCGAGAAATCCGGGTCCCTGAC CGATTCAAGTGACGCGGTCTGGGACAGATTTT ACTCTACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTACGAATATTATCGTA CTCCGTGGACGTTTCGGCCAAGGGACCAAGGTGG AAATCAAAACA	SEQ ID NO: 121 GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAAGAAGAACTACTTAGCTTGTAACAGCAG AAACAGGACAGCCTCCTAACCTGCTCATTTAC TGGAATCTACCCGAGAAATCCGGGTCCCTGAC CGATTCAAGTGACGCGGTCTGGGACAGATTTT ACTCTACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTACGAATATTATCGTA CTCCGTGGACGTTTCGGCCAAGGGACCAAGGTGG AAATCAAAACA	SEQ ID NO: 121 GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAAGAAGAACTACTTAGCTTGTAACAGCAG AAACAGGACAGCCTCCTAACCTGCTCATTTAC TGGAATCTACCCGAGAAATCCGGGTCCCTGAC CGATTCAAGTGACGCGGTCTGGGACAGATTTT ACTCTACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTACGAATATTATCGTA CTCCGTGGACGTTTCGGCCAAGGGACCAAGGTGG AAATCAAAACA
		AA	SEQ ID NO: 1692 DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPKLLIYWTSTRDSGVPDFSG SGSGTDFLTINSLQAEDVAVYYCQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1692 DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPKLLIYWTSTRDSGVPDFSG SGSGTDFLTINSLQAEDVAVYYCQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1692 DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPKLLIYWTSTRDSGVPDFSG SGSGTDFLTINSLQAEDVAVYYCQYYRTPWTF GQGTKVEIKR

	!PS:361402	12H11.014	SEQ ID NO: 122	SEQ ID NO: 279
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAGAACTACTTAGCTTGGTACCAGCAG AACCAAGGACAGCTCTTAAACTGCTCATTTAC TGGACTTCTACCCGAGAAATCCGGGTCCTGAC CGATTCAAGTGGCAGCGGCTCTGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTGACGAATATTATCGTA CTCCGTGGACGTTGGCCAAAGGGACCAAGGTGG AAATCAAAACGA	CAGGTGCAGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGCTTCTGGATACACCTTACCCGGCTACTAT ATACACTGGGTGCTCAGGCCCTTGGACAAGGG CTTGAGTGGATGGGTGGATAAGCCCTAACCAA GGTGAACAAACTATGCACAGAAATTTCAGGAC AGGGTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTATATGAGCTGAGCAGCCTGAGATCT GACGACACGGCCGTGATTACTGTGCGGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCCTGGTCACCCGTCT CCTCA
	AA		SEQ ID NO: 1693	SEQ ID NO: 1850
			DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPKLLIYWTSSTRESGVPDFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPTWTF GQGTKVEIKR	QVQLVQSGAEVKKPGASVKVSKASGYTFTGYYI HWVRAPQGQLEWMGWISPNQGETNYAQKFQD RV/TMTRDTSISTAYMELSSLRSDDTAVYYCAREA TIFGMLIVPFDYWGQGLTVTVSS
	!PS:361406	2C2.005.001	SEQ ID NO: 123	SEQ ID NO: 280
			CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGTCACCATCTCTTGT CTGGAAGTAGCTCCAACATCGGAAGTCAAACTG TAAACTGGTACCAGCACCTCCAGGAACGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTCTGTG CAACATTGATGAAGCCTGAGTGTCCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCTCTAGGT	CAGATGCAGGTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGCTTCCGGATACACCTTACCCGGCTACTAT ATGCATTGGGTGCGACAGGCCCTTGGACAAGGG CTTGAGTGGATGGGATGGATCAACCCCTAACAGT GGTGGCACAAACTATGCACAGAAATTTCAGGGC AGGGTCAACCATGACCAAGGACACGTCCATCAGT ACAGCCTACATGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGATTACTGTGCGGAGAGGG GGGGAATTACGTTTGGGGGACTTATCGGCCCTCAC TACTACTACGGTATGGACGCTCTGGGGCCAAAGGG ACCAAGTCAACCGTCTCTCTCA
	AA		SEQ ID NO: 1694	SEQ ID NO: 1851
			QSVLTQPPSASGTPGQRVTISCGSSSNIQSQTWNW YQHLPGTAPKLLIYTNNQRPSPGVPDFSGSKSGTS ASLAISGLQSEDEADYFCATFDESLSGPVFGGK LTVLG	QMQVVQSGAEVKKPGASVKVSKASGYTFTGYY MHWVRQAPQGQLEWMGWISPNQGETNYAQKFQ GRVTMTRDTSISTAYMELSLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWVGQGTTVTVSS

	!PS:361412	2C2.005.002	SEQ ID NO: 124	SEQ ID NO: 281
			CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGGTCACCATCTCTTGT CTGGAAGTAGCTCCAACATCGGAAGTCAAACTG TAAACTGGTACAGCACCTCCAGGAACGGCCC CCAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATGAAGCCTGCAAGGTCGGGTAT TCGGCGGAGGGACCAAGCTGACCGTCTCCTAGGT	CAGATGCAGGTGGTGCACTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGCTTCCGGATACACCTTCACCCGGCTACTAT ATGCATTGGGTGGCAGACGGCCCCCTGGACAAGGG CTTGAGTGGATGGATGGATCAACCCCTAACAGT GGTGGCACAACTATGCACAGAAATTTCAGGGC AGGGTCAACCATGACCAAGGACACGTCCATCAGT ACAGCTACATGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGTAATTACTGTGCGAGAGGG GGGGAATTACGTTTGGGGGACTTATCGGCCCTCAC TACTACTACGGTATGGACGTCTGGGGCCCAAGGG ACCACGGTCACCGTCTCCTCA
AA			SEQ ID NO: 1695	SEQ ID NO: 1852
			QSVLTQPPSASGTPGQRVTISCSGSSNIGSQTVNW YQHLPGTAPKLLIYTNNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDES LQGPVFGGGTK LTVLG	QMQVVQSGAEVKKPGASVKVSKASGYTFTGYY MHWVVRQAPQGQLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSR LRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWVGQGTITVTVSS
NA	!PS:361418	2C2.005.003	SEQ ID NO: 125	SEQ ID NO: 282
			CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGGTCACCATCTCTTGT CTGGAAGTAGCTCCAACATCGGAAGTAAATTATG TAAACTGGTACCAAGCACCTCCAGGAACGGCCC CCAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATGAAGCCTGAGTGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCTCCTAGGT	CAGATGCAGGTGGTGCACTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGCTTCCGGATACACCTTCACCCGGCTACTAT ATGCATTGGGTGGCAGACGGCCCCCTGGACAAGGG CTTGAGTGGATGGATGGATCAACCCCTAACAGT GGTGGCACAACTATGCACAGAAATTTCAGGGC AGGGTCAACCATGACCAAGGACACGTCCATCAGT ACAGCTACATGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGTAATTACTGTGCGAGAGGG GGGGAATTACGTTTGGGGGACTTATCGGCCCTCAC TACTACTACGGTATGGACGTCTGGGGCCCAAGGG ACCACGGTCACCGTCTCCTCA
AA			SEQ ID NO: 1696	SEQ ID NO: 1853
			QSVLTQPPSASGTPGQRVTISCSGSSNIGSNYVNW YQHLPGTAPKLLIYTNNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDES LSGPVFGGGTK LTVLG	QMQVVQSGAEVKKPGASVKVSKASGYTFTGYY MHWVVRQAPQGQLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSR LRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWVGQGTITVTVSS

	!PS:361424	2C2.005.004	SEQ ID NO: 126	SEQ ID NO: 1697	SEQ ID NO: 283
			<p>NA</p> <p>CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGTCACCATCTCTTGTT CTGGAAGTAGCTCCAACATCGGAAGTAATTATG TAAACTGGTACCAGCACCTCCAGGAACGGCCC CCAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATGAAGCCTGCAAGGTCGGGTAT TCGGCGGAGGACCAAGCTGACCGTCTCCTAGGT</p>	<p>SEQ ID NO: 1854</p> <p>QMQVVQSGAEVKKPGASVKVSKASGYTFTGYY MHWVRAQPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWVGQGTITVTVSS</p>	<p>CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCCGGATACACCTTACCCGGCTACTAT ATGCATTGGGTGGCAGAGGCCCTGGACAAGGG CTTGAGTGGATGGGATGGATCAACCCCTAACAGT GGTGGCACAACTATGCACAGAAATTTCAGGGC AGGGTCAACCATGACCAAGGACACGTCCATCAGT ACAGCTACATGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGTAATTACTGTGCGAGAGGG GGGGAATTACGTTTGGGGGACTTATCGGCCCTCAC TACTACTACGGTATGGACGTCTGGGGCCCAAGGG ACCACGGTCACCGTCTCCTCA</p>
	!PS:361430	2C2.005.005	SEQ ID NO: 127	SEQ ID NO: 1698	SEQ ID NO: 284
			<p>NA</p> <p>CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGTCACCATCTCTTGTT CTGGAAGTAGCTCCAACATCGGAAGTCAAACTG TAAACTGGTACCAGCACCTCCAGGAACGGCCC CCAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATGACAGCCTGAATGGTCCGGTAT TCGGCGGAGGACCAAGCTGACCGTCTCCTAGGT</p>	<p>SEQ ID NO: 1855</p> <p>QMQVVQSGAEVKKPGASVKVSKASGYTFTGYY MHWVRAQPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWVGQGTITVTVSS</p>	<p>CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCCGGATACACCTTACCCGGCTACTAT ATGCATTGGGTGGCAGAGGCCCTGGACAAGGG CTTGAGTGGATGGGATGGATCAACCCCTAACAGT GGTGGCACAACTATGCACAGAAATTTCAGGGC AGGGTCAACCATGACCAAGGACACGTCCATCAGT ACAGCTACATGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGTAATTACTGTGCGAGAGGG GGGGAATTACGTTTGGGGGACTTATCGGCCCTCAC TACTACTACGGTATGGACGTCTGGGGCCCAAGGG ACCACGGTCACCGTCTCCTCA</p>

	!PS:361436	2C2.005.006	SEQ ID NO: 128	SEQ ID NO: 185
			CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGTCACCATCTCTTGT CTGGAAGTAGCTCCAACATCGGAAGTAATTATG TAAACTGGTACAGCACCTCCAGGAACGGCCC CCAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATGACAGCCTGAATGGTCCGGTAT TCGGCGGAGGACCAAGCTGACCGTCTCCTAGGT	CAGATGCAGGTGGTGCACTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGCTTCCGGATACACCTTCACCCGGCTACTAT ATGCATGGGTGGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGGCACAACTATGCACAGAAATTTCAGGGC AGGGTCAACCATGACCAAGGACACGTCCATCAGT ACAGCTACATGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGTAATTACTGTGCGAGAGGG GGGGAATTACGTTTGGGGGACTTATCGGCCCTCAC TACTACTACGGTATGGACGTCTGGGGCCCAAGGG ACCACGGTCACCGTCTCCTCA
NA			SEQ ID NO: 1699	SEQ ID NO: 1856
			QSVLTQPPSASGTPGQRVTISCSGSSNIGSNYVNW YQHLPGTAPKLLIYTNNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDDSLNPGPVFGGGTK LTVLG	QMQVVQSGAEVKKPGASVKVSKASGYTFTGY MHWVVRQAPQGQLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWVGQGTITVTVSS
	!PS:361442	2C2.005.007	SEQ ID NO: 129	SEQ ID NO: 286
			CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGTCACCATCTCTTGT CTGGAAGTAGCTCCAACATCGGAAGTAATACTG TAAACTGGTACCAAGCACCTCCAGGAACGGCCC CCAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATGAAGCCTGAATGGTCCGGTAT TCGGCGGAGGACCAAGCTGACCGTCTCCTAGGT	CAGATGCAGGTGGTGCACTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGCTTCCGGATACACCTTCACCCGGCTACTAT ATGCATGGGTGGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGGCACAACTATGCACAGAAATTTCAGGGC AGGGTCAACCATGACCAAGGACACGTCCATCAGT ACAGCTACATGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGTAATTACTGTGCGAGAGGG GGGGAATTACGTTTGGGGGACTTATCGGCCCTCAC TACTACTACGGTATGGACGTCTGGGGCCCAAGGG ACCACGGTCACCGTCTCCTCA
NA			SEQ ID NO: 1700	SEQ ID NO: 1857
			QSVLTQPPSASGTPGQRVTISCSGSSNIGSNYVNW YQHLPGTAPKLLIYTNNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDESINPGPVFGGGTK LTVLG	QMQVVQSGAEVKKPGASVKVSKASGYTFTGY MHWVVRQAPQGQLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWVGQGTITVTVSS
AA				

	!PS:361448	2C2.005.008	SEQ ID NO: 130	SEQ ID NO: 287
			<p>NA</p> <p>CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGTCACCATCTCTTGT CTGGAAGTAGCTCCAACATCGGAAGTAATACTG TAAACTGGTACCAGCACCTCCAGGAACGGCCC CCAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATGACAGCCTGCAAGTCCGGTAT TCGGCGGAGGACCAAGCTGACCGTCTCCTAGGT</p>	<p>CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGTCTCCTGC AAGCTTCCGGATACACCTTCACCCGGCTACTAT ATGCATTGGTGGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGGCACAACTATGCACAGAAATTTCAGGGC AGGGTCAACCATGACCAAGGACACGTCCATCAGT ACAGCTACATGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGTAATTACTGTGCGAGAGGG GGGGAATTACGTTTGGGGGACTTATCGGCCCTCAC TACTACTACGGTATGGACGTCTGGGGCCCAAGGG ACCACGGTCACCGTCTCCTCA</p>
AA			SEQ ID NO: 1701	SEQ ID NO: 1858
			<p>QSVLTQPPSASGTPGQRVTISCSGSSNIGSNTVNW YQHLPGTAPKLLIYTNNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDDSLQGPVFGGGTK LTVLG</p>	<p>QMQVVQSGAEVKKPGASVKVSKASGYTFTGYY MHWVVRQAPQGQLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWVGQGTITVTVSS</p>
	!PS:361454	2C2.005.009	SEQ ID NO: 131	SEQ ID NO: 288
			<p>NA</p> <p>CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGTCACCATCTCTTGT CTGGAAGTAGCTCCAACATCGGAAGTAATACTG TAAACTGGTACCAGCACCTCCAGGAACGGCCC CCAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATGACAGCCTGAGTGGTCCGGTAT TCGGCGGAGGACCAAGCTGACCGTCTCCTAGGT</p>	<p>CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGTCTCCTGC AAGCTTCCGGATACACCTTCACCCGGCTACTAT ATGCATTGGTGGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGGCACAACTATGCACAGAAATTTCAGGGC AGGGTCAACCATGACCAAGGACACGTCCATCAGT ACAGCTACATGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGTAATTACTGTGCGAGAGGG GGGGAATTACGTTTGGGGGACTTATCGGCCCTCAC TACTACTACGGTATGGACGTCTGGGGCCCAAGGG ACCACGGTCACCGTCTCCTCA</p>
AA			SEQ ID NO: 1702	SEQ ID NO: 1859
			<p>QSVLTQPPSASGTPGQRVTISCSGSSNIGSNTVNW YQHLPGTAPKLLIYTNNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDDSLQGPVFGGGTK LTVLG</p>	<p>QMQVVQSGAEVKKPGASVKVSKASGYTFTGYY MHWVVRQAPQGQLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWVGQGTITVTVSS</p>

		SEQ ID NO: 132	CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGTCACCATCTCTTGTT CTGGAAGTAGCTCCAACATCGGAAGTAATACTG TAAACTGGTACAGCACCTCCAGGAACGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTCTGTG CAACATTCGATGACAGCCTGAATGCTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCTCCTAGGT	SEQ ID NO: 1703	QSVLTQPPSASGTPGQRVTISCGSSSNGSNTVNW YQHLPGTAPKLLIYTNNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDDSLNAPVFGGGTK LTVLG	SEQ ID NO: 1860	CAGATGCAGGTGGTGCACTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGCTTCCGGATACACCTTCAACCGGCTACTAT ATGCATTGGGTGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGGCACAACTATGCACAGAAATTTTCAGGGC AGGTCAACCATGACCAAGGACACGTCCATCAGT ACAGCTACATGGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGATTACTGTGCGAGAGGG GGGGATTACGTTTGGGGGACTTATCGGCCCTCAC TACTACTACGGTATGGACGTCTGGGGGCCAAGGG ACCACGGTCACCGTCTCCTCA	SEQ ID NO: 289	CAGATGCAGGTGGTGCACTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGCTTCCGGATACACCTTCAACCGGCTACTAT ATGCATTGGGTGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGGCACAACTATGCACAGAAATTTTCAGGGC AGGTCAACCATGACCAAGGACACGTCCATCAGT ACAGCTACATGGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGATTACTGTGCGAGAGGG GGGGATTACGTTTGGGGGACTTATCGGCCCTCAC TACTACTACGGTATGGACGTCTGGGGGCCAAGGG ACCACGGTCACCGTCTCCTCA
!PS:361460	2C2.005.010	NA			AA				
		SEQ ID NO: 133	CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGTCACCATCTCTTGTT CTGGAAGTAGCTCCAACATCGGAAGTAATACTG TAAACTGGTACCAAGCACCTCCAGGAACGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTCTGTG CAACATTCGATGACAGCCTGAATGCTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCTCCTAGGT	SEQ ID NO: 133	QSVLTQPPSASGTPGQRVTISCGSSSNGSNTVNW YQHLPGTAPKLLIYTNNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDDSLNAPVFGGGTK LTVLG	SEQ ID NO: 1861	CAGATGCAGGTGGTGCACTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGCTTCCGGATACACCTTCAACCGGCTACTAT ATGCATTGGGTGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGGCACAACTATGCACAGAAATTTTCAGGGC AGGTCAACCATGACCAAGGACACGTCCATCAGT ACAGCTACATGGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGATTACTGTGCGAGAGGG GGGGATTACGTTTGGGGGACTTATCGGCCCTCAC TACTACTACGGTATGGACGTCTGGGGGCCAAGGG ACCACGGTCACCGTCTCCTCA	SEQ ID NO: 290	CAGATGCAGGTGGTGCACTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGCTTCCGGATACACCTTCAACCGGCTACTAT ATGCATTGGGTGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGGCACAACTATGCACAGAAATTTTCAGGGC AGGTCAACCATGACCAAGGACACGTCCATCAGT ACAGCTACATGGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGATTACTGTGCGAGAGGG GGGGATTACGTTTGGGGGACTTATCGGCCCTCAC TACTACTACGGTATGGACGTCTGGGGGCCAAGGG ACCACGGTCACCGTCTCCTCA
!PS:361466	2C2.005.011	NA			AA				
		SEQ ID NO: 1704	QSVLTQPPSASGTPGQRVTISCGSSSNGSNTVNW YQHLPGTAPKLLIYTNNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDDSLNAPVFGGGTK LTVLG	SEQ ID NO: 1704	QSVLTQPPSASGTPGQRVTISCGSSSNGSNTVNW YQHLPGTAPKLLIYTNNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDDSLNAPVFGGGTK LTVLG	SEQ ID NO: 1861	QMQVVQSGAEVKKPGASVKVSKASGYTFTGY MHWVRQAPQGQGLEWMGWINPNSGGTNYAQKFK GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG GDYVWGTYPHYYYGMDVWVGQGTTVTVSS	SEQ ID NO: 290	QMQVVQSGAEVKKPGASVKVSKASGYTFTGY MHWVRQAPQGQGLEWMGWINPNSGGTNYAQKFK GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG GDYVWGTYPHYYYGMDVWVGQGTTVTVSS

	!PS:361472	2C2.005.012	SEQ ID NO: 134	SEQ ID NO: 291
			CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGTCACCATCTCTTGTT CTGGAAGTAGCTCCAACATCGGAAGTAATTATG TAAACTGGTACCAGCACCTCCAGGAACGGCCC CCAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATAGCAGCTGAATGCTCCGGTAT TCGGCGGAGGACCAAGCTGACCGTCTCCTAGGT	CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGCTTCCGGATACACCTTCACCCGGCTACTAT ATGCATTGGGTGGCAGACGGCCCCCTGGACAAGGG CTTGAGTGGATGGATGGATCAACCCCTAACAGT GGTGGCACAACTATGCACAGAAATTTCAGGGC AGGGTCAACCATGACCAAGGACACGTCCATCAGT ACAGCTACATGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGTAATTACTGTGCGAGAGGG GGGGAATTACGTTTGGGGGACTTATCGGCCCTCAC TACTACTACGGTATGGACGTCTGGGGCCAAAGGG ACCACGGTCACCGTCTCCTCA
AA			SEQ ID NO: 1705	SEQ ID NO: 1862
			QSVLTQPPSASGTPGQRVTISCSGSSNIGSNYVNW YQHLPGTAPKLLIYTNNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDSSLNAPVFGGGTK LTVLG	QMQVVQSGAEVKKPGASVKVSKASGYTFTGY MHWVVRQAPQGQLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSLRSDDTAVYYCARG GDYVVGTYRPHYYYGMDVWVGQGTIVTVSS
NA	!PS:361478	2C2.005.013	SEQ ID NO: 135	SEQ ID NO: 292
			CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGTCACCATCTCTTGTT CTGGAAGTAGCTCCAACATCGGAAGTAATTATG TAAACTGGTACCAGCACCTCCAGGAACGGCCC CCAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATAGCAGCTGAATGCTCCGGTAT TCGGCGGAGGACCAAGCTGACCGTCTCCTAGGT	CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGCTTCCGGATACACCTTCACCCGGCTACTAT ATGCATTGGGTGGCAGACGGCCCCCTGGACAAGGG CTTGAGTGGATGGATGGATCAACCCCTAACAGT GGTGGCACAACTATGCACAGAAATTTCAGGGC AGGGTCAACCATGACCAAGGACACGTCCATCAGT ACAGCTACATGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGTAATTACTGTGCGAGAGGG GGGGAATTACGTTTCCGGGACTTATCGGCCCTCACT ACTACTACGGTATGGACGTCTGGGGCCAAAGGGA CCACGGTCACCGTCTCCTCA
AA			SEQ ID NO: 1706	SEQ ID NO: 1863
			QSVLTQPPSASGTPGQRVTISCSGSSNIGSNYVNW YQHLPGTAPKLLIYTNNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDSSLNAPVFGGGTK LTVLG	QMQVVQSGAEVKKPGASVKVSKASGYTFTGY MHWVVRQAPQGQLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSLRSDDTAVYYCARG GDYVVGTYRPHYYYGMDVWVGQGTIVTVSS

		SEQ ID NO: 136	CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGTCACCATCTCTTGTT CTGGAAGTAGCTCCAACATCGGAAGTCAAACTG TAAACTGGTACCAGCACCTCCAGGAACGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTCTGTG CAACATTCGATGAAGCCTGAGTGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCTCCTAGGT	SEQ ID NO: 1707	QSVLTQPPSASGTPGQRVTISCSGSSNIGSQTVNW YQHLPGTAPKLLIYTNNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDESLSGPVFGGGTK LTVLG	SEQ ID NO: 1864	QMQVVQSGAEVKKPGASVKVSKASGYTFTGYY MHWVRAQPGQGLEWMGWINPNSGGTNYAQKFPQ GRVTMTRDTSISTAYMELSRLSDDTAVYYCARG GDYVFGTYRPHYYYGMDVWVGQGTITVTVSS
	2C2.005.014	NA					
!PS:361485		AA					
		SEQ ID NO: 137	GACATCCAGATGACCCAGTCTCCATCTCCTCCTGT CTGCATCTATAGGAGACAGAGTCAACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAAATTATTAG GCTGTATCAACAGAAACCAGGGAAGCCCCCTA AGCGCTGATCTATGGTGCATCCAGTTTGCAA GTGGGTCCCCTTCAAGGTTCAAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAGTGGATATCAAAACGA	SEQ ID NO: 137		SEQ ID NO: 294	CAGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCAAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACATATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGGAGAGATA GGACGATCTTTGGAGTGGTCTTTGGGGGACTACT GGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA
!PS:361845	18F2.013	NA					
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YQQKPGKAPKRLIYGASSLQSGVPSRFSGSGSTE FTLTISLQPEDFATYYCLQHNNYPFTFGQGTKVDI KR	SEQ ID NO: 1708		SEQ ID NO: 1865	QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAWIWDASNENYADAVKG RFTISRDNKNTLYLQMNSLRRAEDTAVYYCARDR TIFGVVLGDYWGQGLVTVSS

IP:361851	6H1.009	SEQ ID NO: 138	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCAACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACAGGAAAGCCCTA AGCGCTGATCTATGGTGCATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTACGCGGAGTGGAT CTGGGACAGAAATTCACCTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAAGTGATATCAAAACGA	SEQ ID NO: 295	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTCACTTCACTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATAATACTATGACAGACGCCGTGAAGGGCC GCTTCAACCATCTCCAGAGACAATTCAGAACA CGCTGATCTGCAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTTACTGTGCGCGAGATA GGACGATTTTGGAGTGTCTTGGGGGACTACT GGGGCAGGGAACCTGGTCAACCGTCTCCTCA
		SEQ ID NO: 1709	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLWY QQKPGKAPKRLIYGASSLQSGVPSRFSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK R	SEQ ID NO: 1866	QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAIVWYDASNKYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLLGDYWGQGTLVTVSS
IP:361855	2C2.005.015	SEQ ID NO: 139	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG GGACCCCGGGCAGAGGTCACCATCTCTTGT CTGGAAGTAGCTCCACATCGGAAGTAATACTG TAACTGGTACCAAGCAACTCCCAGGAACGGCCC CCAACTCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATAGCAGCTGAGTGGTCCGGTAT TCGGCGGAGGACCAAGCTGACCGTCTCCTAGGT	SEQ ID NO: 296	CAGATGCAGGTGGTGCAGTCTGGGGGTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGCTTCCGGATACACCTTCAACCGGCTACTAT ATGCATTGGGTGCGACAGCCCCCTGGACAAGGG CTTGAGTGGATGGGATGGATCAACCTTAACAGT GGTGGCAACAACCTATGCACAGAA GTTTCAGGGC AGGGTCAACATGACCAAGGACACGTCCATCAGT ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT GACGACACGCGCGTGTATTACTGTGCGGAGAGGG GGGGAATTACGTTTGGGGGACTTATCGGCCCTCAC TACTACTACGGTATGGACGTCTGGGGCCCAAGGG ACCACGGTCAACCGTCTCCTCA
		SEQ ID NO: 1710	QSVLTQPPSASGTPGQRVTISCSGSSNIGSNTVNW YQQLPGTAPKLLIYTNNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDSSLSGPVFGGGTK LTVLG	SEQ ID NO: 1867	QMQVVQSGAEVKKPGASVKVSKASGYTFTGYY MHWVRQAPQGQGLEWMGWINPNSGNTNYAQKFQ GRVTMTRDTSISTAYMELSLRSDDDTAVYYCARG GDYVWGTYRPHYYYGMDVWVGQGTTVTVSS

IP:336067	SG12.006	SEQ ID NO: 140	SEQ ID NO: 297
		NA	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT ACAGGCTCTGGATTCACTTCACTAGCTATGGC ATACACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGGA AGTAATAAGTTCCATGCAGACTCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAATCCCAAGAAC ACGCTGTATCTGCAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCCTGAAGCTTTTGAATC TGGGGCCAAAGGGACAAGGTCAACCGTCTCTTCA
IP:336169	17B11.002	SEQ ID NO: 1711	SEQ ID NO: 1868
		AA	QVQLVESGGGVVQPRSLRLSCTASGFTFSSYGIH WVRQAPGKGLEWVAIVWYDGSNKFHADSVKGRF TISRDNKNTLYLQMNSLRAEDSAMFYFCARGKVA GMPEAFEIWGQGTKVTVSS
IP:336169	17B11.002	SEQ ID NO: 141	SEQ ID NO: 298
		NA	CAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCCACCAGTTATGAT ATCAACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGATGGATGAACCCCTAACAGT GGTAACACAGGCTATGCACAGAAATTCCAGGGC AGAGTCAACATGACAGGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGTTACTGTGCGAGAGGG GGTGATTACGTTTGGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCAAAG GGACCACGGTCAACCGTCTCCTCA
IP:336169	17B11.002	SEQ ID NO: 1712	SEQ ID NO: 1869
		AA	QMLVQSGAEVKKPGASVKVSKKASGYTFTSYDI NWVRQATGQGLEWMGMWNPNSGNTGYAQKFQ GRVTMTRDTSISTAYMELSSLSRSDTA VYYCARG GDYVWGSYRPYYYYGYGMDVWVGQGTITVTVSS

	IP:361127	5G12.006.001	NA	SEQ ID NO: 142	SEQ ID NO: 299
				GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGCAAGTCAGACCAATTAGCAGGTTTAA ATTGGTATCAGCAGAAACCTGGAAAGCCCTG AGTCTGTATCTATGTTGCATCCAGTTTGCAAAG TGGGTCCCATCAAGATTCACTGCGCAGTGGTTC TGGGACAGATTTCACTCTCAACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCTGATCAGTTTGGCCA GGGACCAAGCTGGAGATCAAAACGA	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACCTTCAGTAGCTATGGC ATACACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAATTCCAAAGAAC ACGCTGTATCTGCAAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCGTGAAGCTTTTGAATC TGGGGCCAAAGGGACAAAGGTCACCGTCTCTTCA
	IP:361136	5G12.006.002	NA	SEQ ID NO: 143	SEQ ID NO: 300
				GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGCAAGTCAGACCAATTAGCAGGTTTAA ATTGGTATCAGCAGAAACCTGGAAAGCCCTG AGTCTGTATCTATGTTGCATCCAGTTTGCAAAG TGGGTCCCATCAAGATTCACTGCGCAGTGGTTC TGGGACAGATTTCACTCTCAACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCTGATCAGTTTGGCCA GGGACCAAGCTGGAGATCAAAACGA	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT ACAGGCTCTGGATTCACCTTCAGTAGCTATGGC ATACACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAATTCCAAAGAAC ACGCTGTATCTGCAAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCGTGAAGCTTTTGAATC TGGGGCCAAAGGGACAAAGGTCACCGTCTCTTCA
			AA	SEQ ID NO: 1713	SEQ ID NO: 1870
				DIQLTQSPSSLASVGDRTTITCRASQTISRFLNWX QQKPGKAPELLIYVASSLQSGVPSRFSGSGTDFT LTISSLQPEDFATYYCQQSYSTLISFGGQGTKLEIKR	QVQLVESGGGVVQPRSLRLSCAASGFTFSYGIH WVRQAPGKGLEWVAIVWYDASNKFHADA VKGR FTISRDNSKNTLYLQMNSLRAEDSAM YFCARGKV AGMPEAFEIWGQGTKVTVSS
			AA	SEQ ID NO: 1714	SEQ ID NO: 1871
				DIQLTQSPSSLASVGDRTTITCRASQTISRFLNWX QQKPGKAPELLIYVASSLQSGVPSRFSGSGTDFT LTISSLQPEDFATYYCQQSYSTLISFGGQGTKLEIKR	QVQLVESGGGVVQPRSLRLSCTASGFTFSYGIH WVRQAPGKGLEWVAIVWYDASNKFHADA VKGR FTISRDNSKNTLYLQMNSLRAEDSAM YFCARGKV AGMPEAFEIWGQGTKVTVSS

!PS:361140	5G12.006.003	NA	SEQ ID NO: 144	SEQ ID NO: 301
			GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGCAAGTCAGACCAATTAGCAGGTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCTG AGTCTGTATCTATGTTGCATCCAGTTTGCAAAG TGGGTCCCATCAAGATTCACTGCGCAGTGGTTC TGGGACAGATTTCACTCTCAACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCTGATCAGTTTGGCCA GGGACCAAGCTGGAGATCACACGA	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACCTTCAGTAGCTATGGC ATACACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAAATCCCAAGAAC ACGCTGTATCTGCAAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCGTGAAGCTTTTGAAATC TGGGGCCAAAGGACAAAGGTCACCGTCTCTTCA
!PS:359919	5G12.006.004	NA	SEQ ID NO: 145	SEQ ID NO: 302
			GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGCAAGTCAGACCAATTAGCAGGTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCTA AGTCTGTATCTATGTTGCATCCAGTTTGCAAAG TGGGTCCCATCAAGATTCACTGCGCAGTGGTTC TGGGACAGATTTCACTCTCAACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCTGATCAGTTTGGCCA GGGACCAAGCTGGAGATCAACGA	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACCTTCAGTAGCTATGGC ATACACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAAATCCCAAGAAC ACGCTGTATCTGCAAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCGTGAAGCTTTTGAAATC TGGGGCCAAAGGACAAAGGTCACCGTCTCTTCA
AA		AA	SEQ ID NO: 1715	SEQ ID NO: 1872
			DIQLTQSPSSLASVGDRTVTITCRASQTISRFLNWX QQKPGKAPELLIYVASSLQSGVPSRFSGSGTDFT LTISSLQPEDFATYYCQQSYSTLISFGGQTKLEIR	QVQLVESGGGVVQPRSLRLSCAASGFTFSYGIH WVRQAPGKGLEWVAIVYDASNKFHADA VKGR FTISRDNSKNTLYLQMNSLRAEDSAMFYFCARGKV AGMPEAFEIWGQGTKVTVSS
AA		AA	SEQ ID NO: 1716	SEQ ID NO: 1873
			DIQLTQSPSSLASVGDRTVTITCRASQTISRFLNWX QQKPGKAPKLLIYVASSLQSGVPSRFSGSGTDF LTISSLQPEDFATYYCQQSYSTLISFGGQTKLEIKR	QVQLVESGGGVVQPRSLRLSCAASGFTFSYGIH WVRQAPGKGLEWVAIVYDASNKFHADA VKGR FTISRDNSKNTLYLQMNSLRAEDSAMFYFCARGKV AGMPEAFEIWGQGTKVTVSS

	IP:361144	5G12.006.005	NA	SEQ ID NO: 146	SEQ ID NO: 303
				GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGCAAGTCAGACCATTAGCAGGTTTAA ATTGGTATCAGCAGAAACCTGGAAAGCCCTG AGTCTGTATCTATGTTGCATCCAGTTTGAAG TGGGTCCCATCAAGATTCACTGCGAGTGGTTC TGGGACAGATTTCACTCTCAACATCAGCAGTCT GCAACCTGAAGATTTTGAACCTTACTACTGTCA ACAGAGTTACAGTACCTGATCAGTTTGGCCA GGGACCAAGCTGGAGATCAAAACGA	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACCTTCAGTAGCTATGGC ATACACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAGTTCCATGCAGACTCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAAATCCAAAGAAC ACGCTGTATCTGCAAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCGTAAGCTTTTGAATC TGGGGCCAAAGGACAAAGGTCACCGTCTCTTCA
	AA			SEQ ID NO: 1717	SEQ ID NO: 1874
				DIQLTQSPSSLASVGDRTVTITCRASQTISRFLNWX QQKPGKAPELLIYVASSLQSGVPSRFSGSGTDFT LTISSLQPEDFATYYCQQSYSTLISFGGQGTKLEIKR	QVQLVESGGGVVQPRSLRLSCAASGFTFSYGIH WVRQAPGKGLEWVAIVWYDASNKFHADS VKGRF TISRDN SKNTLYLQMNSLRAEDSAM YFCARGKVA GMPEAF EIWGGQTKVT VSS
	IP:361151	5G12.006.006	NA	SEQ ID NO: 147	SEQ ID NO: 304
				GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGCAAGTCAGACCATTAGCAGGTTTAA ATTGGTATCAGCAGAAACCTGGAAAGCCCTG AGTCTGTATCTATGTTGCATCCAGTTTGAAG TGGGTCCCATCAAGATTCACTGCGAGTGGTTC TGGGACAGATTTCACTCTCAACATCAGCAGTCT GCAACCTGAAGATTTTGAACCTTACTACTGTCA ACAGAGTTACAGTACCTGATCAGTTTGGCCA GGGACCAAGCTGGAGATCAAAACGA	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACCTTCAGTAGCTATGGC ATACACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGGA AGTAATAAGTTCCATGCAGACGCGCTGAAGGGC CGATTCAACCATCTCCAGAGACAAATCCAAAGAAC ACGCTGTATCTGCAAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCGTAAGCTTTTGAATC TGGGGCCAAAGGACAAAGGTCACCGTCTCTTCA
	AA			SEQ ID NO: 1718	SEQ ID NO: 1875
				DIQLTQSPSSLASVGDRTVTITCRASQTISRFLNWX QQKPGKAPELLIYVASSLQSGVPSRFSGSGTDFT LTISSLQPEDFATYYCQQSYSTLISFGGQGTKLEIKR	QVQLVESGGGVVQPRSLRLSCAASGFTFSYGIH WVRQAPGKGLEWVAIVWYDGSNKFHADAVKGR FTISRDN SKNTLYLQMNSLRAEDSAM YFCARGKV AGMPEAF EIWGGQTKVT VSS

!PS:361491	17B11.002.001	NA	SEQ ID NO: 148 CAGTCTGTGTGACGCGAGCCGCCCTCAGTGTCTG CGCCCCAGGACAGAAGGTCAACATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAATAATTATG TATCCTGGTATCAGCAGCTCCAGGAACAGCCC CCAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTCAGCCACCCCTGGGCATCACCG ACTCCAGACTGGGACGAGGCCGATTATTACTG CGGAACATGGATAGCAGCCTGAGTGTGTGGT ATTCGGCGGAGGACCAAACTGACCGTCTCTAGG T	SEQ ID NO: 305 CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCCACCAAGTTATGAT ATCAACTGGTGCAGACAGGCCACTGGACAAGGG CTTGAGTGGATGGATGGATGAACCCCTAACAGT GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCAACCATGACCAAGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGTTACTGTGCGAGAGGG GGTGATTACGTTTGGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCCAAG GGACCACGGTCAACCGTCTCCTCA
			SEQ ID NO: 1719 QSVLTQPPSVSAAPGQKVTISCSGSSNIGNNNYVS WYQQLPGTAPKLLIYDNNKRPSPGIPDRFSGSKSGT SATLGITGLQTGDEADYYCGTWDSSLSAVVFGGG TKLTVLG	SEQ ID NO: 1876 QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQATGQGLEWMGMWNPNSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDTA VYYCARG GDYVWGSYRPPY YYYGMDVWVGQTTVTVSS
!PS:361499	17B11.002.002	NA	SEQ ID NO: 149 CAGTCTGTGTGACGCGAGCCGCCCTCAGTGTCTG CGCCCCAGGACAGAAGGTCAACATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAATAATTATG TATCCTGGTATCAGCAGCTCCAGGAACAGCCC CCAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTCAGCCACCCCTGGGCATCACCG ACTCCAGACTGGGACGAGGCCGATTATTACTG CGGAACATGGATAGCAGCCTGAGTGTGTGGT ATTCGGCGGAGGACCAAACTGACCGTCTCTAGG T	SEQ ID NO: 306 CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCCACCAAGTTATGAT ATCAACTGGTGCAGACAGGCCACTGGACAAGGG CTTGAGTGGATGGATGGATGAACCCCTAACAGT GGTAACACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCAACCATGACCAAGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGTTACTGTGCGAGAGGG GGTGATTACGTTTGGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCCAAG GGACCACGGTCAACCGTCTCCTCA
			SEQ ID NO: 1720 QSVLTQPPSVSAAPGQKVTISCSGSSNIGNNNYVS WYQQLPGTAPKLLIYDNNKRPSPGIPDRFSGSKSGT SATLGITGLQTGDEADYYCGTWDSSLSAVVFGGG TKLTVLG	SEQ ID NO: 1877 QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQATGQGLEWMGMWNPNSGNTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDTA VYYCARG GDYVWGSYRPPY YYYGMDVWVGQTTVTVSS

	!PS:361503	17B11.002.003	NA	SEQ ID NO: 150 CAGTCTGTGTTGACGCGAGCGGCCCTCAGTGTCTG CGCCCCAGGACAGAAAGGTCAACATCTCCTGCT CTGGAAGCAGCTCCAAACATTGGAAATAATTATG TATCCTGGTATGAGCAGTTCCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCAGTCAGCCACCCCTGGCATCACCGG ACTCCAGACTGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGTGTGGT ATTCGGCGGAGGACCAAACTGACCGTCTCTAGG T	SEQ ID NO: 307 CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGCTTCTGGATACACCTTACCAAGTTATGAT ATCAACTGGTGCAGACAGGCCACTGGACAAGGG CTTGAGTGGATGGATGGATGAACCCCTAACAGT GGTGGCACAGGCTATGCACAGAAAGTTCCAGGGC AGAGTCAACATGACCAAGGACACCTCCATAAGC ACAGCTACATGAGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGTTACTGTGCGAGAGGG GGTGATTACGTTTGGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGGCCAAG GGACCACGGTCAACCGTCTCCTCA
				SEQ ID NO: 1721 QSVLTQPPSVSAAPGQKVTISCSGSSNIGNNYVS WYEQPFGTAPKLLIYDNNKRPSGIPDRFSGSKSGTS ATLGTGLQTGDEADYYCGTWDSSL SAVVFGGGT KLTVLG	SEQ ID NO: 1878 QMQLVQSGAEVKKPGASVKVSKKASGYTFTSYDI NWVRQATGQGLEWMGMNPNSSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDTAVYYCARG GDYVWGSYRPPYYYGYGMDVWVGQGTITVTVSS
	!PS:361507	17B11.002.004	NA	SEQ ID NO: 151 CAGTCTGTGTTGACGCGAGCGGCCCTCAGTGTCTG CGCCCCAGGACAGAAAGGTCAACATCTCCTGCT CTGGAAGCAGCTCCAAACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCAGTCAGCCACCCCTGGCATCACCGG ACTCCAGACTGGGACGAGGCCGATTATTACTG CGGAACATTCGAAAGCAGCCTGAGTGTGTGGT ATTCGGCGGAGGACCAAACTGACCGTCTCTAGG T	SEQ ID NO: 308 CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGCTTCTGGATACACCTTACCAAGTTATGAT ATCAACTGGTGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGATGGATGAACCCCTAACAGT GGTGGCACAGGCTATGCACAGAAAGTTCCAGGGC AGAGTCAACATGACCAAGGACACCTCCATAAGC ACAGCTACATGAGAGCTGAGCAGCCTGAGATCT GACGACACGGCCGTGTTACTGTGCGGAGAGGG GGTGATTACGTTTGGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGGCCAAG GGACCACGGTCAACCGTCTCCTCA
				SEQ ID NO: 1722 QSVLTQPPSVSAAPGQKVTISCSGSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLAITGLQTGDEADYYCGTFESSLSAVVFGGGT KLTVLG	SEQ ID NO: 1879 QMQLVQSGAEVKKPGASVKVSKKASGYTFTSYDI NWVRQAPGQGLEWMGMNPNSSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDDTAVYYCARG GDYVWGSYRPPYYYGYGMDVWVGQGTITVTVSS

	!PS:361514	17B11.002.005	NA	SEQ ID NO: 152	SEQ ID NO: 309
				CAGTCTGTGTTGACGCAGCGCCCTCAGTGTCTG CGCCCCAGGACAGAAAGGTCAACATCTCCTGCT CTGGAAGCAGCTCCAAACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCAGTCAGCCACCTGGCCATCACCGG ACTCCAGACTGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGTGTGGT ATTCCGGCGGAGGACCAAACTGACCGTCTTAGG T	CAAATGCAGCTGGTGCACTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGCTTCTGGATACACCTTCCACCAAGTTATGAT ATCAACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGATGGATGAACCCCTAACAGT GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCACCATGACCAAGGACACCTCCATAAGC ACAGCTACATGAGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGTTACTGTGCGGAGAGGG GGTGATTACGTTTGGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGGCCAAG GGACCACGGTCAACCGTCTCCTCA
AA				SEQ ID NO: 1723	SEQ ID NO: 1880
				QSVLTQPPSVSAAPGQKVTISCSGSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLAITGLQTGDEADYYCGTWDSSLSAVVFGGG TKLTVLG	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQATGQGLEWMGMNPNSSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDTAVYYCARG GDYVWGSYRPPYYYGYGMDVWVGQGTITVTVSS
NA	!PS:360582	17B11.002.006		SEQ ID NO: 153	SEQ ID NO: 310
				CAGTCTGTGTTGACGCAGCGCCCTCAGTGTCTG CGCCCCAGGACAGAAAGGTCAACATCTCCTGCT CTGGAAGCAGCTCCAAACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCAGTCAGCCACCTGGCCATCACCGG ACTCCAGACTGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGTGTGGT ATTCCGGCGGAGGACCAAACTGACCGTCTTAGG T	CAAATGCAGCTGGTGCACTCTGGGGCTGAGGTG AAGAACCTGGGGCTCAGTGAAGGTCTCCTGC AAGCTTCTGGATACACCTTCCACCAAGTTATGAT ATCAACTGGGTGCGACAGGCCCTGGACAAGGG CTTGAGTGGATGGATGGATGAACCCCTAACAGT GGTAACACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCACCATGACCAAGGACACCTCCATAAGC ACAGCTACATGAGAGCTGAGCAGCCTGAGATCT GACGACACGGCCGTGTTACTGTGCGGAGAGGG GGTGATTACGTTTGGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGGCCAAG GGACCACGGTCAACCGTCTCCTCA
AA				SEQ ID NO: 1724	SEQ ID NO: 1881
				QSVLTQPPSVSAAPGQKVTISCSGSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLAITGLQTGDEADYYCGTWDSSLSAVVFGGG TKLTVLG	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQAPGQGLEWMGMNPNSSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDTAVYYCARG GDYVWGSYRPPYYYGYGMDVWVGQGTITVTVSS

	!PS:361518	17B11.002.007	NA	SEQ ID NO: 154 CAGTCTGTGTTGACGCGAGCGGCCCTCAGTGTCTG CGCCCCAGGACAGAAAGGTCAACATCTCCTGCT CTGGAAGCAGCTCCAAACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCAGTCAGCCACCCCTGGCATCACCGG ACTCCAGACTGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGTGTGGT ATTCCGGCGGAGGACCAAACTGACCGTCTTAGG T	SEQ ID NO: 311 CAAATGCAGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACACAGTTATGAT ATCAACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGATGGATGAACCCATAACAGT GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCAACATGACCAAGGACACCTCCATAAGC ACAGCCTACATGAGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGTAATTACTGTGCGAGAGGG GGTGATTACGTTTTCGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGGCCAAG GGACCACGGTCAACCGTCTCCTCA
			AA	SEQ ID NO: 1725 QSVLTQPPSVSAAPGQKVTISCSGSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLGITGLQTGDEADYYCGTWDSSL SAVVFGGG TKLTVLG	SEQ ID NO: 1882 QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQATGQGLEWMGMWNPNSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDTA VYYCARG GDYVFGSYRPPYYYYGMDVWGQGTITVTVSS
	!PS:360570	17B11.002.008	NA	SEQ ID NO: 155 CAGTCTGTGTTGACGCGAGCGGCCCTCAGTGTCTG CGCCCCAGGACAGAAAGGTCAACATCTCCTGCT CTGGAAGCAGCTCCAAACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCAGTCAGCCACCCCTGGCATCACCGG ACTCCAGACTGGGACGAGGCCGATTATTACTG CGGAACATTCGAAAGCAGCCTGAGTGTGTGGT ATTCCGGCGGAGGACCAAACTGACCGTCTTAGG T	SEQ ID NO: 312 CAAATGCAGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTACACAGTTATGAT ATCAACTGGGTGCGACAGGCCCTGGACAAGGG CTTGAGTGGATGGATGGATGAACCCATAACAGT GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCAACATGACCAAGGACACCTCCATAAGC ACAGCCTACATGAGAGCTGAGCAGCCTGAGATCT GACGACACGGCCGTGTAATTACTGTGCGAGAGGG GGTGATTACGTTTTCGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGGCCAAG GGACCACGGTCAACCGTCTCCTCA
			AA	SEQ ID NO: 1726 QSVLTQPPSVSAAPGQKVTISCSGSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLAITGLQTGDEADYYCGTFESSLSAVVFGGGT KLTVLG	SEQ ID NO: 1883 QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQAPGQGLEWMGMWNPNSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDDTAVYYCARG GDYVFGSYRPPYYYYGMDVWGQGTITVTVSS

!PS:362051	5G12.005.001	NA	SEQ ID NO: 156 GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGCAAGTCAGACCATTAGCAGGTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCTA AGTCTGTATCTATGTTGCATCCAGTTGCAAAAG TGGGTCCCATCAAGATTCACTGAGTGGAGTGTTC TGGGACAGATTTCACCTCAACCATCAGCAGTCT GCAACCTGAAGATTTTGAACCTTACTACTGTCA ACAGAGTTACAGTACCTGCTCAGTTTGGCCA GGGACCAAGCTGGAGATCAACGA	SEQ ID NO: 313 CAGGTGCAGTTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCACTTCCAGTAGCTATGGC ATACACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAGTTCATGCAGACGCCGTGAAGGC CGATTCAACCATCTCCAGAGACAATTCCAAAGAAC ACGCTGTATCTGCAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCTGAAAGCTTTTGAATC TGGGCCAAGGGACATTGGTCAACCGTCTCTTCA
			SEQ ID NO: 1727 DIQLTQSPSSLASVGDRTVTITCRASQTISRFLNRY QQKPGKAPKLLIYVASSLQSGVPSRFSGSGTDF TLTISSLQPEDFATYYCQQSYSTLLSFGGQGTKLEIK R	SEQ ID NO: 1884 QQVLVESGGGVVQPRSLRLSCAASGFTFSSYGIH WVRQAPGKGLEWVAWIYDASNKPHADAVKGR FTISRDNSKNTLYLQMNSLRAEDSAMYPFCARGKV AGMPEAFEIWGQGTLVTVSS
			SEQ ID NO: 157	SEQ ID NO: 314

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

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

IPS#	Ab	Type	CDRL1	CDRL2	CDRL3
!PS:336175	2C2.005	NA	TCTGGAAGTAGCTCCAAACATCG GAAAGTAATACTGTAAAC	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	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2200	SEQ ID NO: 2357	SEQ ID NO: 2514
			RASQDIRDYL	GASSLQS	LQHNNYPFT
			SEQ ID NO: 630	SEQ ID NO: 787	SEQ ID NO: 944

!PS:335938	6H1	NA	CGGGCAAGTCAGGACATTAGAG ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2201	SEQ ID NO: 2358	SEQ ID NO: 2515
		AA	RASQDIRDYL	GASSLOS	LQHNNYPFT
!PS:335941	2F11	NA	SEQ ID NO: 631	SEQ ID NO: 788	SEQ ID NO: 945
		AA	CAGCGAGTCAGGACATTAGCA ACTATTTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCCTCA CT
		AA	SEQ ID NO: 2202	SEQ ID NO: 2359	SEQ ID NO: 2516
!PS:335970	5C2	NA	QASQDISNYLN	DASNLET	QQYDILLT
		AA	SEQ ID NO: 632	SEQ ID NO: 789	SEQ ID NO: 946
		AA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
!PS:335978	13H12	NA	SEQ ID NO: 2203	SEQ ID NO: 2360	SEQ ID NO: 2517
		AA	KSSQSVLSSNNKNYIA	WASTRES	QQYYSTPWT
		AA	SEQ ID NO: 633	SEQ ID NO: 790	SEQ ID NO: 947
!PS:335986	11C1	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
		AA	SEQ ID NO: 2204	SEQ ID NO: 2361	SEQ ID NO: 2518
		AA	KSSQSVLSSNNKNYIA	WASTRES	QQYYSTPWT
!PS:335994	12H11	NA	SEQ ID NO: 634	SEQ ID NO: 791	SEQ ID NO: 948
		AA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC	CAGCAATATTATCGTACTCCGT GGACG
		AA	SEQ ID NO: 2205	SEQ ID NO: 2362	SEQ ID NO: 2519
!PS:335999	12H11	NA	KSSQSVLSSNNKNYLA	WTSTRDS	QQYYRTPWT
		AA	SEQ ID NO: 635	SEQ ID NO: 792	SEQ ID NO: 949
		AA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC	CAGCAATATTATCGTACTCCGT GGACG
!PS:335999	12H11	NA	SEQ ID NO: 2206	SEQ ID NO: 2363	SEQ ID NO: 2520
		AA	SEQ ID NO: 636	SEQ ID NO: 793	SEQ ID NO: 950
		AA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC	CAGCAATATTATCGTACTCCGT GGACG

		AA	KSSQSVLSSNNKNLYLA SEQ ID NO: 636	WTSTRDS SEQ ID NO: 793	QYYRTPWT SEQ ID NO: 950
!PS:336024	18E3	NA	AGGCCAGTCAGAGTATTAGTT ACAGTTACTTAGCC	GGTGCATCCAGCAGGGGCCACT	CAGCAGTATGGTAGTTCACCGC TCACT
		AA	SEQ ID NO: 2207 RASQISYSYLA	SEQ ID NO: 2364 GASSRAT	SEQ ID NO: 2521 QQYGSSPLT
!PS:336041	2G10_LC1	NA	SEQ ID NO: 637 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

!PS:359621	17H11.004.00	NA	CGGGCAGTCAGGGTCTTATCA TCTGGTTAGCC	GCTGCATCCAGTTTGCAAAAGT	CAACAGACTAACAGTTTCCCTC CGACG
			SEQ ID NO: 2212	SEQ ID NO: 2369	SEQ ID NO: 2526
		AA	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
		AA	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
		NA	CGGGCAAGTCAGGGCATTAGAA ATGAGTTAGGC	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATAATAGTTACCCAT TCACT
!PS:360936	4H9.004.003	AA	SEQ ID NO: 2214	SEQ ID NO: 2371	SEQ ID NO: 2528
			RASQGIRNELG	GASSLQS	LQHNSYPFT
		NA	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
		NA	RASQGIRNELG	GASSLQS	LQHNSYPFT
!PS:360949	4H9.004.005	AA	SEQ ID NO: 645	SEQ ID NO: 802	SEQ ID NO: 959
			CGGGCAAGTCAGGGCATTAGAA ATGAGTTAGGC	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATAATAGTTACCCAT TCACT
		NA	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
		NA	CGGGCAAGTCAGGGCATTAGAA ATGAGTTAGGC	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATAATAGTTACCCAT TCACT
!PS:360949	4H9.004.005	AA	SEQ ID NO: 2217	SEQ ID NO: 2374	SEQ ID NO: 2531
			RASQGIRNELG	GASSLQS	LQHNSYPFT
		NA	SEQ ID NO: 647	SEQ ID NO: 804	SEQ ID NO: 961

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

!PS:359785	4B1.015	NA	CGGGCAAGTCAGGACATTAGAG ATTATTAGGC	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2224	SEQ ID NO: 2381	SEQ ID NO: 2538
			RASQDLRDYLG	GASSLQS	LQHNNYPFT
!PS:360982	4B1.016	NA	CGGGCAAGTCAGGACATTAGAG ATTATTAGGC	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2225	SEQ ID NO: 2382	SEQ ID NO: 2539
			RASQDLRDYLG	GASSLQS	LQHNNYPFT
!PS:335922	18F2	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTAGGC	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2226	SEQ ID NO: 2383	SEQ ID NO: 2540
			RASQDLRNYLG	GASSLQS	LQHNNYPFT
!PS:360986	18F2.002	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTAGGC	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2227	SEQ ID NO: 2384	SEQ ID NO: 2541
			RASQDLRNYLG	GASSLQS	LQHNNYPFT
!PS:360995	18F2.003	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTAGGC	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2228	SEQ ID NO: 2385	SEQ ID NO: 2542
			RASQDLRNYLG	GASSLQS	LQHNNYPFT
!PS:360999	18F2.004	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTAGGC	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2229	SEQ ID NO: 2386	SEQ ID NO: 2543
			RASQDLRNYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 659	SEQ ID NO: 816	SEQ ID NO: 973

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

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

!PS:361055	2F11.006	NA	CAGCGAGTCAGGACATTAGCA ACTATTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCTCA CT
		AA	SEQ ID NO: 2242	SEQ ID NO: 2399	SEQ ID NO: 2556
			QASQDISNYLN	DASNLET	QQYDILLT
!PS:361059	2F11.007	NA	CAGCGAGTCAGGACATTAGCA ACTATTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCTCA CT
		AA	SEQ ID NO: 2243	SEQ ID NO: 2400	SEQ ID NO: 2557
			QASQDISNYLN	DASNLET	QQYDILLT
!PS:361063	2F11.008	NA	CAGCGAGTCAGGACATTAGCA ACTATTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCTCA CT
		AA	SEQ ID NO: 2244	SEQ ID NO: 2401	SEQ ID NO: 2558
			QASQDISNYLN	DASNLET	QQYDILLT
!PS:359949	2F11.009	NA	CAGCGAGTCAGGACATTAGCA ACTATTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCTCA CT
		AA	SEQ ID NO: 2245	SEQ ID NO: 2402	SEQ ID NO: 2559
			QASQDISNYLN	DASNLET	QQYDILLT
!PS:359956	2F11.010	NA	CAGCGAGTCAGGACATTAGCA ACTATTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCTCA CT
		AA	SEQ ID NO: 2246	SEQ ID NO: 2403	SEQ ID NO: 2560
			QASQDISNYLN	DASNLET	QQYDILLT
!PS:359865	6H1.002	NA	CGGCAAGTCAGGACATTAGAG ATTATTAGGC	GGTGCATCCAGTTTGCAAAAGT	CTACAGCATAATAATTACCCCT TCACT
		AA	SEQ ID NO: 2247	SEQ ID NO: 2404	SEQ ID NO: 2561
			RASQDIRDYL	GASSLQS	LQHNNYPFT
			SEQ ID NO: 677	SEQ ID NO: 834	SEQ ID NO: 991

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

!PS:361079	6A5.004.001	NA	CAGCGAGTCAGGACATTACCA ACTATTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
		AA	SEQ ID NO: 2254 QASQDITNYLN SEQ ID NO: 684	SEQ ID NO: 2411 DASNLEP SEQ ID NO: 841	SEQ ID NO: 2568 QQYDDLFT SEQ ID NO: 998
		NA	CAGCGAGTCAGGACATTACCA ACTATTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
!PS:361085	6A5.004.002	AA	SEQ ID NO: 2255 QASQDITNYLN SEQ ID NO: 685	SEQ ID NO: 2412 DASNLEP SEQ ID NO: 842	SEQ ID NO: 2569 QQYDDLFT SEQ ID NO: 999
		NA	CAGCGAGTCAGGACATTACCA ACTATTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
		AA	SEQ ID NO: 2256 QASQDITNYLN SEQ ID NO: 686	SEQ ID NO: 2413 DASNLEP SEQ ID NO: 843	SEQ ID NO: 2570 QQYDDLFT SEQ ID NO: 1000
!PS:361095	6A5.004.004	NA	CAGCGAGTCAGGACATTACCA ACTATTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
		AA	SEQ ID NO: 2257 QASQDITNYLN SEQ ID NO: 687	SEQ ID NO: 2414 DASNLEP SEQ ID NO: 844	SEQ ID NO: 2571 QQYDDLFT SEQ ID NO: 1001
		NA	CAGCGAGTCAGGACATTACCA ACTATTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
!PS:361101	6A5.004.005	AA	SEQ ID NO: 2258 QASQDITNYLN SEQ ID NO: 688	SEQ ID NO: 2415 DASNLEP SEQ ID NO: 845	SEQ ID NO: 2572 QQYDDLFT SEQ ID NO: 1002
		NA	CAGCGAGTCAGGACATTACCA ACTATTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
		AA	SEQ ID NO: 2259 QASQDITNYLN SEQ ID NO: 689	SEQ ID NO: 2416 DASNLEP SEQ ID NO: 846	SEQ ID NO: 2573 QQYDDLFT SEQ ID NO: 1003

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

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

!PS:361192	2G10_LC1.00 6	NA	AGGGCCAGTCAGAGTGTTAGCA GCAACTTAGCC	GGTGCAGCCACCAGGGCCACT	CAGCAGTATAATAACTGGCCTC TCACT
		AA	SEQ ID NO: 2272 RASQSVSSNLA SEQ ID NO: 702	SEQ ID NO: 2429 GAATRAT SEQ ID NO: 859	SEQ ID NO: 2586 QQYNNWPLT SEQ ID NO: 1016
		NA	AGGGCCAGTCAGAGTGTTAGCA GCAACTTAGCC	GGTGCAGCCACCAGGGCCACT	CAGCAGTATAATAACTTCCCTC TCACT
!PS:359609	2G10_LC1.00 7	AA	SEQ ID NO: 2273 RASQSVSSNLA SEQ ID NO: 703	SEQ ID NO: 2430 GAATRAT SEQ ID NO: 860	SEQ ID NO: 2587 QQYNNFPLT SEQ ID NO: 1017
		NA	AGGGCCAGTCAGAGTGTTAGCA GCAACTTAGCC	GGTGCAGCCACCAGGGCCACT	CAGCAGTATAATAACTATCCTC TCACT
		AA	SEQ ID NO: 2274 RASQSVSSNLA SEQ ID NO: 704	SEQ ID NO: 2431 GAATRAT SEQ ID NO: 861	SEQ ID NO: 2588 QQYNNYPLT SEQ ID NO: 1018
!PS:361196	2G10_LC1.00 9	NA	AGGGCCAGTCAGAGTGTTAGCA GCAACTTAGCC	GGTGCAGCCACCAGGGCCACT	CAGCAGTATAATAACTGGCCTC TCACT
		AA	SEQ ID NO: 2275 RASQSVSSNLA SEQ ID NO: 705	SEQ ID NO: 2432 GAATRAT SEQ ID NO: 862	SEQ ID NO: 2589 QQYNNWPLT SEQ ID NO: 1019
		NA	AGGGCCAGTCAGAGTGTTAGCA GCAACTTAGCC	GGTGCAGCCACCAGGGCCACT	CAGCAGTATAATAACTGGCCTC TCACT
!PS:361202	2G10_LC1.01 0	AA	SEQ ID NO: 2276 RASQSVSSNLA SEQ ID NO: 706	SEQ ID NO: 2433 GAATRAT SEQ ID NO: 863	SEQ ID NO: 2590 QQYNNWPLT SEQ ID NO: 1020
		NA	AGGGCCAGTCAGAGTATTAGTT ACAGTACTTAGCC	GGTGCATCCAGCAGGGCCACT	CAGCAGTATGGTAGTTCACCGC TCACT
		AA	SEQ ID NO: 2277 RASQSVSSNLA SEQ ID NO: 707	SEQ ID NO: 2434 GASSRAT SEQ ID NO: 864	SEQ ID NO: 2591 QQYSSPLT SEQ ID NO: 1021

!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

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

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

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

!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	TGGACTTCTACCCGAGATTCC	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	TGGACTTCTACCCGAGATTCC	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

!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

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

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

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

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

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

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

!PS:361136	5G12.006.002	NA	CGGGCAAGTCAGACCATTAGCA GGTTTTTAAAT	GTTGCATCCAGTTTGC AAAAGT	CAACAGAGTTACAGTACCCCTG 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	CAACAGAGTTACAGTACCCCTG 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	CAACAGAGTTACAGTACCCCTG 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	CAACAGAGTTACAGTACCCCTG 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	CAACAGAGTTACAGTACCCCTG ATCAGT
		AA	SEQ ID NO: 2346	SEQ ID NO: 2503	SEQ ID NO: 2660
			RASQTISRFLN	VASSLQS	QQSYSTLIS
!PS:361491	17B11.002.001	NA	TCTGGAAAGCAGCTCCAACATTG GAAATAATTATGTATCC	GACAATAATAAGCGACCCCTCA	GGAACATGGGATAGCAGCCCTG AGTGCTGTGGTA
		AA	SEQ ID NO: 2347	SEQ ID NO: 2504	SEQ ID NO: 2661
			SGSSSNIGNNYVS	DNNKRPS	GTWDSSL SAVV
			SEQ ID NO: 777	SEQ ID NO: 934	SEQ ID NO: 1091

!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
!PS:361518	17B11.002.00 7	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
		NA	TCTGGAAGCAGCTCCAACATTG GAAATAATTATGTATCC	GACAATAAAGCGACCCCTCA	GGAACATGGGATAGCAGCCTG AGTGCTGTGGTA

IPS:360570	17B11.002.008	NA	TCTGGAAGCAGCTCCAACATTG GAAATAATTATGTATCC	GACAATAATAAGCGACCCCTCA	GGAACATTGAAAGCAGCCTG AGTGCTGTGGTA
		AA	SEQ ID NO: 2354 SGSSSNIGNNYVS SEQ ID NO: 784	SEQ ID NO: 2511 DNNKRPS SEQ ID NO: 941	SEQ ID NO: 2668 GTFESSLSAVV SEQ ID NO: 1098
IPS:362051	5G12.005.001	NA	CGGCAAGTCAGACCATTAGCA GGTTTTTAAT	GTTGCATCCAGTTTGCAAGT	CAACAGAGTTACAGTACCCCTGC TCAGT
		AA	SEQ ID NO: 2355 RASQTISRFLN SEQ ID NO: 785	SEQ ID NO: 2512 VASSLQS SEQ ID NO: 942	SEQ ID NO: 2669 QQSYSTLLS 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 GYVMH	SEQ ID NO: 2827 WINPNSGGTNYAQKFQG	SEQ ID NO: 2984 GGDYVWGTYPHYYYGMDV
		AA	SEQ ID NO: 1100	SEQ ID NO: 1257	SEQ ID NO: 1414
IPS:335914	4B1	NA	AAC TTGGCATGCAC	GTTATATGGTATGATGGAAGTA ATGAAAACTATGCAGACTCCGT GAAGGC	GATGGACGATCTTTGGAGTGG TC TTGGGGGACTAC
			SEQ ID NO: 2671 NFGMH	SEQ ID NO: 2828 VIWYDGSNIENYADSVKG	SEQ ID NO: 2985 DGTIFGVVLGDY
		AA	SEQ ID NO: 1101	SEQ ID NO: 1258	SEQ ID NO: 1415

!PS:335938	6H1	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGGAAGTA ATAAATACTATGCAGACTCCGT GAAGGC	GATGGGACGATTTTGGAGTGC TC TTGGGGGACTAC
			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	WINPDSGGTDYSQRFGQ	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	WINPDSGGTDYSQRFGQ	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

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

!PS:336099	17H11.004	NA	AGTTACTACTGGAGC	CGTATCTATACCAGTGGGAGCA CCAACACTACAACCCCTCCCTCAA GAGT	GATGTAGCAGTGGCTGGCTTTG ACTAC
			SEQ ID NO: 2682	SEQ ID NO: 2839	SEQ ID NO: 2996
			SYWWS	RIYTSGSTNYPNPSLKS	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	RIYTSGSTNYPNPSLKS	DVAVAGFDY
			SEQ ID NO: 1113	SEQ ID NO: 1270	SEQ ID NO: 1427
			TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC	GATGGGACGATTTTGGAGTGC TCCTGGGGGACTAC
!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 GAAGGGC	GATGGGACGATTTTGGAGTGC TCCTGGGGGACTAC
			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 GAAGGGC	GATGGGACGATTTTGGAGTGC TCCTGGGGGACTAC
			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

!PS:360943	4H9.004.004	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC	GATGGGACGATTTTGGAGTGC TCCTGGGGGACTAC
			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 TCCTGGGGGACTAC
			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	GATAGGACGATTTTGGAGTGC TCCTGGGGGACTAC
!PS:360955	4B1.010	NA	SEQ ID NO: 2689	SEQ ID NO: 2846	SEQ ID NO: 3003
			YFGMH	VIWYDASNKYYADAVKG	DRTIFGVLLGDY
			SEQ ID NO: 1119	SEQ ID NO: 1276	SEQ ID NO: 1433
!PS:360962	4B1.011	AA	AACCTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACCTATGCAGACGCCG TGAAGGGC	GATGGGACGATCTTTGGAGTGG TCCTGGGGGACTAC
			SEQ ID NO: 2690	SEQ ID NO: 2847	SEQ ID NO: 3004
			NFGMH	VIWYDASNENYADAVKG	DGTIFGVVLLGDY
!PS:360962	4B1.011	NA	SEQ ID NO: 1120	SEQ ID NO: 1277	SEQ ID NO: 1434
			AACCTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACCTATGCAGACGCCG TGAAGGGC	GATGGGACGATCTTTGGAGTGG TCCTGGGGGACTAC
			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

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

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

!PS:361009	18F2.006	NA	AACCTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGC	GATGGACGATCTTTGGAGTGG TCCTGGGGGACTAC
			SEQ ID NO: 2702	SEQ ID NO: 2859	SEQ ID NO: 3016
			NFGMH	VIWYDASNENYADAVKG	DGTIFGVVLGDY
!PS:361013	18F2.007	AA	SEQ ID NO: 1132	SEQ ID NO: 1289	SEQ ID NO: 1446
			AACCTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGC	GATGGACGATCTTTGGAGTGG TCCTGGGGGACTAC
			SEQ ID NO: 2703	SEQ ID NO: 2860	SEQ ID NO: 3017
!PS:361017	18F2.008	AA	NFGMH	VIWYDASNENYADAVKG	DGTIFGVVLGDY
			SEQ ID NO: 1133	SEQ ID NO: 1290	SEQ ID NO: 1447
			AACCTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGC	GATGGACGATCTTTGGAGTGG TCCTGGGGGACTAC
!PS:361021	18F2.009	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
!PS:361028	18F2.010	AA	AACCTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGC	GATGGACGATCTTTGGAGTGG TCCTGGGGGACTAC
			SEQ ID NO: 2705	SEQ ID NO: 2862	SEQ ID NO: 3019
			NFGMH	VIWYDASNENYADAVKG	DGTIFGVVLGDY
!PS:361028	18F2.010	AA	SEQ ID NO: 1135	SEQ ID NO: 1292	SEQ ID NO: 1449
			AACCTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACTCCGT GAAGGC	GATGGACGATCTTTGGAGTGG TCCTGGGGGACTAC
			SEQ ID NO: 2706	SEQ ID NO: 2863	SEQ ID NO: 3020
!PS:361028	18F2.010	AA	NFGMH	VIWYDASNENYADSVKG	DGTIFGVVLGDY
			SEQ ID NO: 1136	SEQ ID NO: 1293	SEQ ID NO: 1450

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

!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:359949	2F11.009	AA	AGCTATGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC	GATAGGACGATTTTGGAGTGG TTCTTGACTAC
			SEQ ID NO: 2715	SEQ ID NO: 2872	SEQ ID NO: 3029
			SYGMH	VIWYDASNKYYADAVKG	DRTIFGVVLDY
!PS:361063	2F11.008	NA	SEQ ID NO: 1145	SEQ ID NO: 1302	SEQ ID NO: 1459
			AGCTATGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC	GATAGGACGATTTTGGAGTGG TTCTTGACTAC
			SEQ ID NO: 2716	SEQ ID NO: 2873	SEQ ID NO: 3030
!PS:361063	2F11.009	AA	SYGMH	VIWYDASNKYYADSVKG	DRTIFGVVLDY
			SEQ ID NO: 1146	SEQ ID NO: 1303	SEQ ID NO: 1460

!PS:359865	2F11.010	NA	AGCTATGGCATGCAC	GTTATATGGTATGATGGAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC	GATAGGACGATTTTGGAGTGG TTCTTGACTAC
			SEQ ID NO: 2717	SEQ ID NO: 2874	SEQ ID NO: 3031
			SYGMH	VIWYDASNKYYADAVKG	DRTIFGVLLDY
!PS:359865	6H1.002	AA	SEQ ID NO: 1147	SEQ ID NO: 1304	SEQ ID NO: 1461
			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	DGTIFGVLLGDY
			SEQ ID NO: 1148	SEQ ID NO: 1305	SEQ ID NO: 1462
			TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC	GATAGGACGATTTTGGAGTGC TCCTGGGGGACTAC
!PS:359873	6H1.004	NA	SEQ ID NO: 2719	SEQ ID NO: 2876	SEQ ID NO: 3033
			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
			YFGMH	VIWYDASNKYYADAVKG	DGTIFGVLLGDY
!PS:359877	6H1.005	AA	SEQ ID NO: 1150	SEQ ID NO: 1307	SEQ ID NO: 1464
			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

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

!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

!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: 2734	SEQ ID NO: 2891	SEQ ID NO: 3048
			SYGMH	AIWYDANNKYYADAVKG	DRTIFGVVLEY
!PS:359890	6A5.004.011	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	NA	AGCTATGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGAAGACGCCGT GAAGGC	GGGATTACGATTTTGGTCATG GGTTTGAATAT
			SEQ ID NO: 2736	SEQ ID NO: 2893	SEQ ID NO: 3050
			SYGMH	VIWYDASNKYYEDAVKG	GITIFGHGFEY
		AA	SEQ ID NO: 1166	SEQ ID NO: 1323	SEQ ID NO: 1480

!PS:335965	2A11.003	NA	AGCTATGGCATGCAC		GTTATATGGTATGATGGAAGTA ATAAATACTATGAAGACTCCGT GAAGGC	GGGATTACGATTTTTTGGTCATG GGTTTGAATAT
		AA	SEQ ID NO: 2737	SEQ ID NO: 2894	SEQ ID NO: 3051	
			SYGMH	VIWYDGSNKYYEDSVKG	GITIFGHGEY	
!PS:361158	2A11.004	NA	AGCTATGGCATGCAC		GTTATATGGTATGATGGAAGTA ATAAATACTATGAAGACGCCGT GAAGGC	GGGATTACGATTTTTTGGTCATG GGTTTGAATAT
		AA	SEQ ID NO: 2738	SEQ ID NO: 2895	SEQ ID NO: 3052	
			SYGMH	VIWYDGSNKYYEDAVKG	GITIFGHGEY	
!PS:361165	2A11.005	NA	AGCTATGGCATGCAC		GTTATATGGTATGATGCAAGTA ATAAATACTATGAAGACTCCGT GAAGGC	GGGATTACGATTTTTTGGTCATG GGTTTGAATAT
		AA	SEQ ID NO: 2739	SEQ ID NO: 2896	SEQ ID NO: 3053	
			SYGMH	VIWYDASNKYYEDSVKG	GITIFGHGEY	
!PS:361172	2G10_LC1.003	NA	AACTATGGCATGCAC		GCTATATGGTTTGATGCAAGTG ATAAATACTATGCAGACGCCGT GAAGGC	GATCAGGCGATTTTTTGGAGTGG TCCCCGACTAC
		AA	SEQ ID NO: 2740	SEQ ID NO: 2897	SEQ ID NO: 3054	
			NYGMH	AIWFDASDKYYADAVKG	DQAIFGVVPDY	
!PS:361178	2G10_LC1.004	NA	AACTATGGCATGCAC		GCTATATGGTTTGATGCAAGTG ATAAATACTATGCAGACTCCGT GAAGGC	GATCAGGCGATTTTTTGGAGTGG TCCCCGACTAC
		AA	SEQ ID NO: 2741	SEQ ID NO: 2898	SEQ ID NO: 3055	
			NYGMH	AIWFDASDKYYADSVKG	DQAIFGVVPDY	
		AA	SEQ ID NO: 1171	SEQ ID NO: 1328	SEQ ID NO: 1485	

!PS:361185	2G10_LC1.005	NA	AACTATGGCATGCAC	GCTATATGTTTGATGGAAGTG ATAAATACTATGCAGACGCCGT GAAGGGC	GATCAGCGATTTTTGGAGTGG TCCCCGACTAC
		AA	SEQ ID NO: 2742	SEQ ID NO: 2899	SEQ ID NO: 3056
			NYGMH	AIWFDGSDKYYADAVKG	DQAIFGVVPDY
!PS:361192	2G10_LC1.006	NA	AACTATGGCATGCAC	GCTATATGTTTGATGCAAGTG ATAAATACTATGCAGACGCCGT GAAGGGC	SEQ ID NO: 1486
		AA	SEQ ID NO: 1172	SEQ ID NO: 1329	SEQ ID NO: 1486
			SEQ ID NO: 2743	SEQ ID NO: 2900	SEQ ID NO: 3057
!PS:359609	2G10_LC1.007	NA	AACTATGGCATGCAC	GCTATATGTTTGATGCAAGTG ATAAATACTATGCAGACGCCGT GAAGGGC	GATCAGCGATTTTTGGAGTGG TCCCCGACTAC
		AA	SEQ ID NO: 1173	SEQ ID NO: 1330	SEQ ID NO: 1487
			SEQ ID NO: 2744	SEQ ID NO: 2901	SEQ ID NO: 3058
!PS:359615	2G10_LC1.008	NA	AACTATGGCATGCAC	GCTATATGTTTGATGCAAGTG ATAAATACTATGCAGACGCCGT GAAGGGC	GATCAGCGATTTTTGGAGTGG TCCCCGACTAC
		AA	SEQ ID NO: 1174	SEQ ID NO: 1331	SEQ ID NO: 1488
			SEQ ID NO: 2745	SEQ ID NO: 2902	SEQ ID NO: 3059
!PS:361196	2G10_LC1.009	NA	AACTATGGCATGCAC	GCTATATGTTTGATGCAAGTG ATAAATACTATGCAGACGCCGT GAAGGGC	GATCAGCGATTTTTGGAGTGG TCCCCGACTAC
		AA	SEQ ID NO: 1175	SEQ ID NO: 1332	SEQ ID NO: 1489
			SEQ ID NO: 2746	SEQ ID NO: 2903	SEQ ID NO: 3060
!PS:361196	2G10_LC1.009	AA	AACTATGGCATGCAC	GCTATATGTTTGATGCAAGTG ATAAATACTATGCAGACGCCGT GAAGGGC	GATCAGCGATTTTTGGAGTGG TCCCCGACTAC
		AA	SEQ ID NO: 1176	SEQ ID NO: 1333	SEQ ID NO: 1490

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

!PS:361210	18E3.006	NA	AGTGGTGGTTACTACTGGAGC	TACATCTATTACAGTGGGAGCA CCTACTACAACCCGTCCCTCAA GAGT	GATCGTATTACGATTTTGGAG TGGTTATGGGGGCGGTATGG ACGTC
			SEQ ID NO: 2752	SEQ ID NO: 2909	SEQ ID NO: 3066
			SGGYYS	YIYSGSTYYNPSLKS	DRITFGVVMGGGMDV
!PS:361214	18E3.007	AA	SEQ ID NO: 1182	SEQ ID NO: 1339	SEQ ID NO: 1496
			AGTGGTGGTTACTACTGGAGC	TACATCTATTACAGTGGGAGCA CCTACTACAACCCGTCCCTCAA GAGT	GATCGTATTACGATTTTGGAG TGGTTATGGGGGCGGTATGG ACGTC
			SEQ ID NO: 2753	SEQ ID NO: 2910	SEQ ID NO: 3067
!PS:361218	18E3.008	AA	SGGYYS	YIYSGSTYYNPSLKS	DRITFGVVMGGGMDV
			SEQ ID NO: 1183	SEQ ID NO: 1340	SEQ ID NO: 1497
			AGTGGTGGTTACTACTGGAGC	TACATCTATTACAGTGGGAGCA CCTACTACAACCCGTCCCTCAA GAGT	GATCGTATTACGATTTTGGAG TGGTTATGGGGGCGGTATGG ACGTC
!PS:361222	5C2.006	NA	SEQ ID NO: 2754	SEQ ID NO: 2911	SEQ ID NO: 3068
			SGGYYS	YIYSGSTYYNPSLKS	DRITFGVVMGGGMDV
			SEQ ID NO: 1184	SEQ ID NO: 1341	SEQ ID NO: 1498
!PS:361229	5C2.007	NA	GGCTACTATATCCAC	TGGATCAACCCCTGAAAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGGCCACGATTTTGGAAATGG TTATTGTACCGTTTGACTAC
			SEQ ID NO: 2755	SEQ ID NO: 2912	SEQ ID NO: 3069
			GYIYH	WINPESGGTDYSQRFQG	EATIFGMVIVPFDY
!PS:361229	5C2.007	AA	SEQ ID NO: 1185	SEQ ID NO: 1342	SEQ ID NO: 1499
			GGCTACTATATCCAC	TGGATCAACCCCTGAAAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGGCCACGATTTTGGAAATGG TTATTGTACCGTTTGACTAC
			SEQ ID NO: 2756	SEQ ID NO: 2913	SEQ ID NO: 3070
!PS:361229	5C2.007	AA	GYIYH	WINPESGGTDYSQRFQG	EATIFGMVIVPFDY
			SEQ ID NO: 1186	SEQ ID NO: 1343	SEQ ID NO: 1500

!PS:361236	5C2.008	NA	GGCTACTATATCCAC	TGGATCAACCCCTGACGCTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGCCACGATTTTGGAAATGG TTATTGTACCGTTTGACTAC
			SEQ ID NO: 2757	SEQ ID NO: 2914	SEQ ID NO: 3071
			GYIYH	WINPDAGGTDYSQRFQG	EATIFGMVIVPFDY
!PS:359685	5C2.009	NA	SEQ ID NO: 1187	SEQ ID NO: 1344	SEQ ID NO: 1501
			GGCTACTATATCCAC	TGGATCAACCCCTGACGCTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGCCACGATTTTGGAAATGG TTATTGTACCGTTTGACTAC
			SEQ ID NO: 2758	SEQ ID NO: 2915	SEQ ID NO: 3072
!PS:361240	5C2.010	AA	GYIYH	WINPDAGGTDYSQRFQG	EATIFGMVIVPFDY
			SEQ ID NO: 1188	SEQ ID NO: 1345	SEQ ID NO: 1502
			GGCTACTATATCCAC	TGGATCAACCCCTGACGCTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGCCACGATTTTGGAAATGG TTATTGTACCGTTTGACTAC
!PS:361247	5C2.011	NA	SEQ ID NO: 2759	SEQ ID NO: 2916	SEQ ID NO: 3073
			GYIYH	WINPDSGGTDYSQRFQG	EATIFGMVIVPFDY
			SEQ ID NO: 1189	SEQ ID NO: 1346	SEQ ID NO: 1503
!PS:361254	5C2.012	NA	GGCTACTATATCCAC	TGGATCAACCCCTGACGCTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGCCACGATTTTGGAAATGG TTATTGTACCGTTTGACTAC
			SEQ ID NO: 2760	SEQ ID NO: 2917	SEQ ID NO: 3074
			GYIYH	WINPDSGGTDYSQRFQG	EATIFGMVIVPFDY
!PS:361254	5C2.012	AA	SEQ ID NO: 1190	SEQ ID NO: 1347	SEQ ID NO: 1504
			GGCTACTATATCCAC	TGGATCAACCCCTGACGCTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGCCACGATTTTGGAAATGG TTATTGTACCGTTTGACTAC
			SEQ ID NO: 2761	SEQ ID NO: 2918	SEQ ID NO: 3075
!PS:361254	5C2.012	AA	GYIYH	WINPDSGGTDYSQRFQG	EATIFGMVIVPFDY
			SEQ ID NO: 1191	SEQ ID NO: 1348	SEQ ID NO: 1505

!PS:361261	5C2.013	NA	GGCTACTATATCCAC	TGGATCAACCCCTGACGCTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGCCACGATTTTGGAAATGG TTATTGTACCGTTTGACTAC
			SEQ ID NO: 2762	SEQ ID NO: 2919	SEQ ID NO: 3076
			GYIYH	WINPDAGGTDYSQRFG	EATIFGMVIVPFDY
!PS:361268	5C2.014	AA	SEQ ID NO: 1192	SEQ ID NO: 1349	SEQ ID NO: 1506
			GGCTACTATATCCAC	TGGATCAACCCCTGACGCTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGCCACGATTTTGGAAATGG TTATTGTACCGTTTGACTAC
			SEQ ID NO: 2763	SEQ ID NO: 2920	SEQ ID NO: 3077
!PS:359669	5C2.015	AA	GYIYH	WINPDAGGTDYSQRFG	EATIFGMVIVPFDY
			SEQ ID NO: 1193	SEQ ID NO: 1350	SEQ ID NO: 1507
			GGCTACTATATCCAC	TGGATCAACCCCTGACGCTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGCCACGATTTTGGAAATGG TTATTGTACCGTTTGACTAC
!PS:359678	5C2.016	NA	SEQ ID NO: 2764	SEQ ID NO: 2921	SEQ ID NO: 3078
			GYIYH	WINPDAGGTDYSQRFG	EATIFGMVIVPFDY
			SEQ ID NO: 1194	SEQ ID NO: 1351	SEQ ID NO: 1508
!PS:359678	5C2.016	NA	GGCTACTATATCCAC	TGGATCAACCCCTGAAAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGCCACGATTTTGGAAATGG TTATTGTACCGTTTGACTAC
			SEQ ID NO: 2765	SEQ ID NO: 2922	SEQ ID NO: 3079
			GYIYH	WINPESGGTDYSQRFG	EATIFGMVIVPFDY
!PS:361275	11C1.002	AA	SEQ ID NO: 1195	SEQ ID NO: 1352	SEQ ID NO: 1509
			GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG AAACAAGCTATGCACAGAAAGT TTCAGGAC	GAGCCACGATTTTGGAAATGG TTATTGTACCATTTTGACTAC
			SEQ ID NO: 2766	SEQ ID NO: 2923	SEQ ID NO: 3080
!PS:361275	11C1.002	AA	GYIYH	WISPNSGETSYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1196	SEQ ID NO: 1353	SEQ ID NO: 1510

!PS:361282	11C1.003	NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG ACACAAGCTATGCACAGAAAGT TTCAGGAC	GAGGCCACGATTTTGGAAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2767	SEQ ID NO: 2924	SEQ ID NO: 3081
			GYIYH	WISPSGDTSYAQKFQD	EATIFGMLIVPFDY
!PS:361289	11C1.004	AA	SEQ ID NO: 1197	SEQ ID NO: 1354	SEQ ID NO: 1511
			GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG AAACAAGCTATGCACAGAAAGT TTCAGGAC	GAGGCCACGATTTTGGAAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2768	SEQ ID NO: 2925	SEQ ID NO: 3082
!PS:359712	11C1.005	AA	GYIYH	WISPSGDTSYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1198	SEQ ID NO: 1355	SEQ ID NO: 1512
			GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG AAACAAGCTATGCACAGAAAGT TTCAGGAC	GAGGCCACGATTTTGGAAATGC TTATTGTACCATTTGACTAC
!PS:359712	11C1.005	NA	SEQ ID NO: 2769	SEQ ID NO: 2926	SEQ ID NO: 3083
			GYIYH	WISPSGDTSYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1199	SEQ ID NO: 1356	SEQ ID NO: 1513
!PS:361293	11C1.006	NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG ACACAAGCTATGCACAGAAAGT TTCAGGAC	GAGGCCACGATTTTGGAAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2770	SEQ ID NO: 2927	SEQ ID NO: 3084
			GYIYH	WISPSGDTSYAQKFQD	EATIFGMLIVPFDY
!PS:361297	11C1.007	AA	SEQ ID NO: 1200	SEQ ID NO: 1357	SEQ ID NO: 1514
			GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG AAACAAGCTATGCACAGAAAGT TTCAGGAC	GAGGCCACGATTTTGGAAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2771	SEQ ID NO: 2928	SEQ ID NO: 3085
!PS:361297	11C1.007	NA	GYIYH	WISPSGDTSYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1201	SEQ ID NO: 1358	SEQ ID NO: 1515

!PS:361301	11C1.008	NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG ACACAAGCTATGCACAGAAAGT 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 AAACAAGCTATGCACAGAAAGT 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 AAACAAGCTATGCACAGAAAGT 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

!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 GAAACAAACTATGCACAGAAG TTTCAGGAC	GAGGCCACGATTTTGGAAATGC TTATTGTACCATTTGACTAC
			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 GACACAAACTATGCACAGAAG TTTCAGGAC	GAGGCCACGATTTTGGAAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2781	SEQ ID NO: 2938	SEQ ID NO: 3095
!PS:361337	12H11.003	AA	GYIYH	WISPNQGDNTY AQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1211	SEQ ID NO: 1368	SEQ ID NO: 1525

!PS:361344	12H11.004	NA	GGCTACTATATACAC	TGGATAAGCCCTAACCAAGGT GAAACAAACTATGCACAGAAG TTCAGGAC	GAGCCACGATTTTGGAAATGC 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 AAACAAACTATGCACAGAAAGT TTCAGGAC	GAGCCACGATTTTGGAAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2783	SEQ ID NO: 2940	SEQ ID NO: 3097
!PS:361358	12H11.006	AA	GYIYH	WISPNNGETNYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1213	SEQ ID NO: 1370	SEQ ID NO: 1527
			GGCTACTATATACAC	TGGATAAGCCCTAACCAATGGTG ACACAAACTATGCACAGAAAGT TTCAGGAC	GAGCCACGATTTTGGAAATGC 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 GACACAAACTATGCACAGAAG TTCAGGAC	GAGCCACGATTTTGGAAATGC 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 AAACAAACTATGCACAGAAAGT TTCAGGAC	GAGCCACGATTTTGGAAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2786	SEQ ID NO: 2943	SEQ ID NO: 3100
!PS:361372	12H11.008	AA	GYIYH	WISPNNGETNYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1216	SEQ ID NO: 1373	SEQ ID NO: 1530

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

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

!PS:361430	2C2.005.005	NA	GGCTACTATATGCAT	TGGATCAACCCCTAACAGTGGTG GCACAAACTATGCACAGAAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACTACT ACGGTATGGACGTC
			SEQ ID NO: 2797	SEQ ID NO: 2954	SEQ ID NO: 3111
			GYMH	WINPNSGGTNYAQKFQG	GGDYVWGTYPHYYYGMDV
!PS:361436	2C2.005.006	NA	GGCTACTATATGCAT	TGGATCAACCCCTAACAGTGGTG GCACAAACTATGCACAGAAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACTACT ACGGTATGGACGTC
			SEQ ID NO: 2798	SEQ ID NO: 2955	SEQ ID NO: 3112
			GYMH	WINPNSGGTNYAQKFQG	GGDYVWGTYPHYYYGMDV
!PS:361442	2C2.005.007	NA	GGCTACTATATGCAT	TGGATCAACCCCTAACAGTGGTG GCACAAACTATGCACAGAAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACTACT ACGGTATGGACGTC
			SEQ ID NO: 1228	SEQ ID NO: 1385	SEQ ID NO: 1542
			GYMH	WINPNSGGTNYAQKFQG	GGDYVWGTYPHYYYGMDV
!PS:361448	2C2.005.008	NA	GGCTACTATATGCAT	TGGATCAACCCCTAACAGTGGTG GCACAAACTATGCACAGAAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACTACT ACGGTATGGACGTC
			SEQ ID NO: 1229	SEQ ID NO: 1386	SEQ ID NO: 1543
			GYMH	WINPNSGGTNYAQKFQG	GGDYVWGTYPHYYYGMDV
!PS:361454	2C2.005.009	NA	GGCTACTATATGCAT	TGGATCAACCCCTAACAGTGGTG GCACAAACTATGCACAGAAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACTACT ACGGTATGGACGTC
			SEQ ID NO: 1230	SEQ ID NO: 1387	SEQ ID NO: 1544
			GYMH	WINPNSGGTNYAQKFQG	GGDYVWGTYPHYYYGMDV
!PS:361454	2C2.005.009	AA	GGCTACTATATGCAT	TGGATCAACCCCTAACAGTGGTG GCACAAACTATGCACAGAAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACTACT ACGGTATGGACGTC
			SEQ ID NO: 2800	SEQ ID NO: 2957	SEQ ID NO: 3114
			GYMH	WINPNSGGTNYAQKFQG	GGDYVWGTYPHYYYGMDV
!PS:361454	2C2.005.009	NA	GGCTACTATATGCAT	TGGATCAACCCCTAACAGTGGTG GCACAAACTATGCACAGAAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACTACT ACGGTATGGACGTC
			SEQ ID NO: 1231	SEQ ID NO: 1388	SEQ ID NO: 1545
			GYMH	WINPNSGGTNYAQKFQG	GGDYVWGTYPHYYYGMDV

IPS:361460	2C2.005.010	NA	GGCTACTATATGCAT	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACAGAAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACTACT ACGGTATGGACGTC
			SEQ ID NO: 2802	SEQ ID NO: 2959	SEQ ID NO: 3116
			GYVMH	WINPNSGGTNYAQKFQG	GGDYVWGTYPHYYYGMDV
IPS:361466	2C2.005.011	NA	GGCTACTATATGCAT	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACAGAAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACTACT ACGGTATGGACGTC
			SEQ ID NO: 2803	SEQ ID NO: 1389	SEQ ID NO: 1546
			GYVMH	WINPNSGGTNYAQKFQG	GGDYVWGTYPHYYYGMDV
IPS:361472	2C2.005.012	NA	GGCTACTATATGCAT	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACAGAAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACTACT ACGGTATGGACGTC
			SEQ ID NO: 2804	SEQ ID NO: 1390	SEQ ID NO: 1547
			GYVMH	WINPNSGGTNYAQKFQG	GGDYVWGTYPHYYYGMDV
IPS:361478	2C2.005.013	NA	GGCTACTATATGCAT	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACAGAAAGT TTCAGGGC	GGGGGGGATTACGTTTTCGGGA CTTATCGGCCTCACTACTACTA CGGTATGGACGTC
			SEQ ID NO: 2805	SEQ ID NO: 1391	SEQ ID NO: 1548
			GYVMH	WINPNSGGTNYAQKFQG	GGDYVWGTYPHYYYGMDV
IPS:361485	2C2.005.014	NA	GGCTACTATATGCAT	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACAGAAAGT TTCAGGGC	GGGGGGGATTACGTTTTCGGGA CTTATCGGCCTCACTACTACTA CGGTATGGACGTC
			SEQ ID NO: 2806	SEQ ID NO: 1392	SEQ ID NO: 1549
			GYVMH	WINPNSGGTNYAQKFQG	GGDYVWGTYPHYYYGMDV
IPS:361485	2C2.005.014	AA	GGCTACTATATGCAT	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACAGAAAGT TTCAGGGC	GGGGGGGATTACGTTTTCGGGA CTTATCGGCCTCACTACTACTA CGGTATGGACGTC
			SEQ ID NO: 2806	SEQ ID NO: 2963	SEQ ID NO: 3120
			GYVMH	WINPNSGGTNYAQKFQG	GGDYVWGTYPHYYYGMDV
IPS:361485	2C2.005.014	AA	GGCTACTATATGCAT	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACAGAAAGT TTCAGGGC	GGGGGGGATTACGTTTTCGGGA CTTATCGGCCTCACTACTACTA CGGTATGGACGTC
			SEQ ID NO: 2806	SEQ ID NO: 1393	SEQ ID NO: 1550
			GYVMH	WINPNSGGTNYAQKFQG	GGDYVWGTYPHYYYGMDV

!PS:361845	18F2.013	NA	AAC	TTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGC	GATAGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
		AA	SEQ ID NO: 2807	SEQ ID NO: 2964	SEQ ID NO: 3121	
			NFGMH	VIWYDASNENYADAVKG	DRTIFGVVLGDY	
!PS:361851	6H1.009	NA	TAC	TTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGC	GATAGGACGATTTTGGAGTGC TCTTGGGGGACTAC
		AA	SEQ ID NO: 2808	SEQ ID NO: 2965	SEQ ID NO: 3122	
			YFGMH	VIWYDASNKYYADAVKG	DRTIFGVLLGDY	
!PS:361855	2C2.005.015	NA	GGC	TACTATATGCAT	TGGATCAACCCCTAACAGTGGTG GCACAACTATGCACAGAAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACT ACGGTATGGACGTC
		AA	SEQ ID NO: 2809	SEQ ID NO: 2966	SEQ ID NO: 3123	
			GYYMH	WINPNSGGTNYAQKFQG	GGDYVWGTYPHYYYGMDV	
!PS:336067	5G12.006	NA	AGC	TATGGCATAAC	GTTATATGGTATGATGGAAGTA ATAAGTTCCATGCAGACTCCGT GAAGGC	GGAAAAGTGGCTGGTATGCCT GAAAGCTTTTGAATC
		AA	SEQ ID NO: 2810	SEQ ID NO: 2967	SEQ ID NO: 3124	
			SYGIH	VIWYDGSNKFHADSVKG	GKVAGMPEAFEI	
!PS:336169	17B11.002	NA	AGT	TATGATATCAAC	TGGATGAACCCCTAACAGTGGTA ACACAGGCTATGCACAGAAAGT TCCAGGGC	GGGGGTGATTACGTTTGGGGG AGTTATCGTCCCTACTACT ACTACGGTATGGACGTC
		AA	SEQ ID NO: 2811	SEQ ID NO: 2968	SEQ ID NO: 3125	
			SYDIN	WMNPNSGNTGYAQKFQG	GGDYVWGSYRPPYYYGMDV	
			SEQ ID NO: 1241	SEQ ID NO: 1398	SEQ ID NO: 1555	

!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	VIWYDASNKFHADA VKG	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	VIWYDASNKFHADA VKG	GKVAGMPEAFEI
			SEQ ID NO: 1243	SEQ ID NO: 1400	SEQ ID NO: 1557
			AGCTATGGCATAAC	GTTATATGGTATGATGCAAGTA ATAAGTTCCATGCAGACGCCGT GAAGGGC	GGAAAAAGTGGTGGTATGCCT GAAAGCTTTTGAAATC
!PS:361144	5G12.006.004	NA	SEQ ID NO: 2814	SEQ ID NO: 2971	SEQ ID NO: 3128
			SYGIH	VIWYDASNKFHADA VKG	GKVAGMPEAFEI
			SEQ ID NO: 1244	SEQ ID NO: 1401	SEQ ID NO: 1558
!PS:359919	5G12.006.004	AA	AGCTATGGCATAAC	GTTATATGGTATGATGCAAGTA ATAAGTTCCATGCAGACGCCGT GAAGGGC	GGAAAAAGTGGTGGTATGCCT GAAAGCTTTTGAAATC
			SEQ ID NO: 2815	SEQ ID NO: 2972	SEQ ID NO: 3129
			SYGIH	VIWYDASNKFHADA VKG	GKVAGMPEAFEI
!PS:361144	5G12.006.005	NA	SEQ ID NO: 1245	SEQ ID NO: 1402	SEQ ID NO: 1559
			AGCTATGGCATAAC	GTTATATGGTATGATGCAAGTA ATAAGTTCCATGCAGACTCCGT GAAGGGC	GGAAAAAGTGGTGGTATGCCT GAAAGCTTTTGAAATC
			SEQ ID NO: 2816	SEQ ID NO: 2973	SEQ ID NO: 3130
!PS:361144	5G12.006.005	AA	SYGIH	VIWYDASNKFHADS VKG	GKVAGMPEAFEI
			SEQ ID NO: 1246	SEQ ID NO: 1403	SEQ ID NO: 1560

!PS:361151	5G12.006.006	NA	AGCTATGGCATAAC	GTTATATGGTATGATGGAAGTA ATAAGTTCCATGCAGACGCCGT GAAGGGC	GGAAAAAGTGGCTGGTATGCCT 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

!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
		AA	SYDIN	WMNPNSGGTGYAQKFQG	GGDYVWGSYRPPYYYYYGM DV
!PS:360582	17B11.002.006	NA	SEQ ID NO: 1252	SEQ ID NO: 1409	SEQ ID NO: 1566
			AGTTATGATATCAAC	TGGATGAACCCCTAACAGTGGTA ACACAGGCTATGCACAGAAAGT TCCAGGGC	GGGGGTGATTACGTTTGGGGG AGTTATCGTCCCTACTACT ACTACGGTATGGACGTC
		AA	SYDIN	WMNPNSGNTGYAQKFQG	GGDYVWGSYRPPYYYYYGM DV
!PS:361518	17B11.002.007	NA	SEQ ID NO: 1253	SEQ ID NO: 1410	SEQ ID NO: 1567
			AGTTATGATATCAAC	TGGATGAACCCCTAACAGTGGTG GCACAGGCTATGCACAGAAAGT TCCAGGGC	GGGGGTGATTACGTTTTCGGGA GTTATCGTCCCTACTACTA CTACGGTATGGACGTC
		AA	SYDIN	WMNPNSGGTGYAQKFQG	GGDYVFGSYRPPYYYYYGM DV
!PS:360570	17B11.002.008	NA	SEQ ID NO: 1254	SEQ ID NO: 1411	SEQ ID NO: 1568
			AGTTATGATATCAAC	TGGATGAACCCCTAACAGTGGTG GCACAGGCTATGCACAGAAAGT TCCAGGGC	GGGGGTGATTACGTTTTCGGGA GTTATCGTCCCTACTACTA CTACGGTATGGACGTC
		AA	SYDIN	WMNPNSGGTGYAQKFQG	GGDYVFGSYRPPYYYYYGM DV
!PS:362051	5G12.005.001	NA	SEQ ID NO: 2825	SEQ ID NO: 2982	SEQ ID NO: 3139
			AGCTATGGCATAAC	TGGATGAACCCCTAACAGTGGTG GCACAGGCTATGCACAGAAAGT TCCAGGGC	GGGGGTGATTACGTTTTCGGGA GTTATCGTCCCTACTACTA CTACGGTATGGACGTC
		AA	SYDIN	WMNPNSGGTGYAQKFQG	GGDYVFGSYRPPYYYYYGM DV
!PS:362051	5G12.005.001	NA	SEQ ID NO: 1255	SEQ ID NO: 1412	SEQ ID NO: 1569
			AGCTATGGCATAAC	GTTATATGGTATGATGCAAGTA ATAAGTTCCATGCACAGCGCGT GAAGGGC	GGAAAAGTGGCTGGTATGCCT GAAAGCTTTTGAATC
		AA	SYGIH	VIWYDASNKFHADAVKG	GKVAGMPEAFEI
!PS:362051	5G12.005.001	NA	SEQ ID NO: 2826	SEQ ID NO: 2983	SEQ ID NO: 3140
			AGCTATGGCATAAC	GTTATATGGTATGATGCAAGTA ATAAGTTCCATGCACAGCGCGT GAAGGGC	GGAAAAGTGGCTGGTATGCCT GAAAGCTTTTGAATC
		AA	SYGIH	VIWYDASNKFHADAVKG	GKVAGMPEAFEI
!PS:362051	5G12.005.001	NA	SEQ ID NO: 1256	SEQ ID NO: 1413	SEQ ID NO: 1570
			AGCTATGGCATAAC	GTTATATGGTATGATGCAAGTA ATAAGTTCCATGCACAGCGCGT GAAGGGC	GGAAAAGTGGCTGGTATGCCT GAAAGCTTTTGAATC
		AA	SYGIH	VIWYDASNKFHADAVKG	GKVAGMPEAFEI

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	<p>CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGGTCACCATCTCTGT CTGGAAGTAGCTCCAAACATCGGAAGTAATACTG TAAACTGGTACCAGCACCTCCAGGAACGGCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTCTGTG CAACATTCGATGACAGCCTGAATGCTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCCTAGGTC AGCCCAAGGTGCCCCCTCGGTCACTCTGTTCCT GCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGC CACACTGGTGTGCTCATAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCTGGAAGGCAGATAG CAGCCCCGTCAAGCGGGAGTGGAACCAACCAC ACCCCTCCAAACAAGCAACAACAAGTACGCGGC CAGCAGCTATCTGAGCCTGACGCTGAGCAGTG GAAGTCCACAGAAAGCTACAGCTGCCAGGTCAC GCATGAAGGGAGCACCGTGGAGAAAGACAGTGG CCCCACAGAAATGTTCA</p>	<p>CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCCGGATACACCTTACCCGGCTACTAT ATGCATTGGGTGCACAGGCCCCTGGACAAGGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGGCACAACTATGCACAGAAATTTTCAGGGC AGGTCACCATGACAGGACACGTCCATCAGT ACAGCCTACATGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGGGATTACGTTTGGGGGACTTATCGGCCCTCAC TACTACTACGGTATGGACGTCTGGGGCCAAAGG ACCACGGTCACCGTCTCCCTCAGCCTCCACCAAG GGCCCATCGGTCTTCCCCCTGGCACCTCCTCCA AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA CGGTGTCTGTGAACCTCAGGCGCCCTGACCAGCG GCGTGCACACCTTCCCCGGCTGTCTACAGTCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT CTGCAACGTGAATCAACAAGCCAGCAACACCAA GGTGACACAAGAAAGTTGAGCCCCAATCTTGTGA CAAACTCACACATGCCACCCGTGCCAGCACCC TGAACTCCTGGGGGACCGTCAGTCTTCTCTTC CCCCAAAACCCAAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTACATGCGTGGTGGTGGAC GTGAGCCACGAAGACCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCC AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG CACGTACCGTTGTGTACGCGTCCACCGTCTCTG CACCAGGACTGGCTGAATGGCAAGGAGTACAA GTGCAAGGTCTCCAAACAAGCCCTCCAGCCCC CATCGAGAAACCATCTCCAAGCCAAAGGGCA</p>

			<p> GCGCCGAGAACACAGGTGTACACCTGCCCCC ATCCGGGAGGAGATGACCAAGAACACAGGTCA GCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA GCGACATCGCCGTGGAGTGGGAGAGCAATGGG CAGCCGAGAACAACTACAGACACGCTCCCTCC GTGCTGGACTCCGACGGCTCCTTCTCCTCTATA GCAAGCTCACCGTGGACAAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAAACCACTACACGCAAGAGAGC CTCTCCCTGTCTCCGGGTAA </p>
			<p> SEQ ID NO: 1885 QSVLTQPPSASGTPGQQRVTISCSGSSNIGSNTVNW YQHLPGTAPKLLIYTNNQRPSPGVDRFSGSKSGTS ASLAISGLOSEDEADYFCATFDDSLNGPVFGGGTK LTVLGGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTTPSKQSNKKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS </p>
	AA		<p> SEQ ID NO: 2042 QMQVVQSGAEVKKPGASVKVCKASGYTFTGYY MHWVRQAPGQGLEWMGWINPNNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLSDDTAVYYCARG GDYVWGTYPHYYYGMDVWVGQGTITVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPPELLGGPSVFLFPPKPKDITLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LDDSGSFELYSKLTVDKSRWQQGNVFSQSVMHFA LHNHYTQKLSLSLSPGK </p>
			<p> SEQ ID NO: 315 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCATT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGTATCAGCAGAAACCAAGGAAAGCCCTA AGCGCTGATCTATGGTGATCCAGTTTGCAAA GTGGGTCCCTTCAAGGTTTCAGCGGCAGTGGAT CTGGACAGAAATTCATCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAAGTGGATATCAACGAACGGTGGCT </p>
IPS:335914	4B1	NA	<p> SEQ ID NO: 472 CAGGTGCAGCTGGTGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACCTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGCAAGGGGC TGGAGTGGTGCGCAGTTATATGGTATGATGGAA GTAATGAAAACTATGCAGACTCCGTGAAGGGCC GATTACCATCTCCAGAGACAAATCCAAAGAATA CGCTGTATCTGCACATGAACAGCCTGAGAGTCG CGGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTTGGGGGACTACT </p>

		<p>GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAATCTGGAACCTGCCTCTGTTGTGT GCCTGCTGAATACTTCTATCCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAAT CGGGTAAC'TCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCCCTGCCGAAGTCACCCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT</p>	<p>GGGGCAGGGAACCCCTGGTCACCGTCTCCTCAG CTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGCTGCTGCTGCTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGTGGAATCAGGCGC CTGACCAAGCGGCGTGACACACCTTCCCGGCTGT CTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAAACCCAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCAATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCCTGTGTGTCAGCGT CCTCACCGTCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAAACAAGC CTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCATCCCGGAGGAGATGACCA AGAACCAAGTCAAGCTGACCTGCCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGAGAACAACTACAAG ACACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
	AA	<p>DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLSQGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA</p>	<p>SEQ ID NO: 1886</p> <p>SEQ ID NO: 2043</p> <p>QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAWIYDGSNENYADSVKIG RFTISRDNSKNTLYLHMNSLRVADTA VYYCARDG TIFGVVLGDYWGQGTLTITVSSASTKGPSVFPLAPS</p>

			<p>KVQWKVDNALQSGNSQESVTEQDSKDSYSTYLSST LTLKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC</p>		<p>SKSTSGGT AALGCLVKDYFPEPVT VSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPETVTVVDVSHED PEVKFNWYVDGVEVHNATKPKCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK</p>	
			<p>SEQ ID NO: 316</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAGCCCCTA AGCGCTGATCTATGGTGCAATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTCAAGCGGCAGTGGAT CTGGGACAGAAATTCACCTCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAGTGGATATCAAAACGAAACGGTGGCT GCACCATCTGTCTTCAATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACCTGCCCTCTGTTGTGT GCCTGCTGAATAACTTCTATATCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCCTGCGAAGTCAACCATCAGG GCCTGAGCTCGCCCGTCAAAAGAGCTTCAACA GGGGAGAGTGT</p>	6H1	NA	<p>SEQ ID NO: 473</p> <p>CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGATTCACTTCACTTCACTTTGGCA TGCAC TGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGGA GTAATAAATACTATGACAGACTCCGTGAAGGGCC GCTTCAACCATCTCCAGAGACAATTCCAAGAACA CGCTGATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGAACCTGGTCAACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCTCTCCAAAGACACCTCTGGGGGCACAGC GGCCTGGGCTGCCTGGTCAAGGACTACTTCCC CGAAACGGTGACGGTGTCTGTGGAACCTCAGGCG CCTGACAGCGGCTGCACACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAACTTTGTGACAAAACTCACACATGCCACC GTGCCAGCACCTGAAC TCTCTGGGGGACCCTC AGTCTTCTCTTCCCCCAAAACCCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCCTGA</p>

			GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTCAAGCGT CCTACCGTCTCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGC AAGGTCTCCAACAAGC CTCCCAAGCCCCATCGAGAAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACAGGTACGCTGACCTGCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGAGTGGG AGAGCAATGGCAGCCGGAACAACATACAAG ACCACGCTCCCGTCTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAAGAAGAGCCTCTCCCTGTCTCCGGGTAAA SEQ ID NO: 1887					
	AA		DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLSQGVPSRFSGSGSGTEFT LTISLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR TVAAPSVFIPTPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSITYSLST LTLKADYEEKHKVYACEVTHQGLSSPVTKSFNRG EC	SEQ ID NO: 2044	QVQLVESGGGVVQGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIYDGSNKYYADSVKQ RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGLTVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNATKPCPEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK	SEQ ID NO: 474		
	NA	2F11	IP5:335 941			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTAA ATTGGTATCAGCAGAAACCAAGGGAAGCCCCCTA	SEQ ID NO: 317	CAGGTGCAACTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCAACCTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG

AGCTCTGATCTACGATGCATCCAAATTTGAAA CAGGGTCCCATCAAGGTTCAAGTGGAGTGGAT CTGGGACAGATTTTAGTTTCACCATCAGCAGCCT GCAGCCTGAAGATATTGCAACATATTACTGTCA ACAGTATGATATTCTCCTCACITTCGGCGGAGG GACC AAGTGGAGATCAAGCGAACGGTGGCTG CACCATCTGCTTCATCTTCCCGCCATCTGATGA GCAGTTGAAATCTGGAACCTGCCCTCTGTTGTGTC CTGCTGAATAACTTCTATCCAGAGAGGCCAAA GTACAGTGG AAGTGGATAACGCCCTCCCAATCG GGTA ACTCCCAGGAGAGTGTCAAGAGCAGGAC AGCAAGGACAGCACCTACAGCCTCAGCAGCAC CTGACGCTGAGCAAAAGCAGACTACGAGAAACA CAAAGTCTACGCCTGCGAAGTCAACCCATCAGGG CCTGAGCTCGCCCGTCACAAAGAGCTTCAACAG GGGAGAGTGT	CTGAGTGGTGGCAGTTATATGGTATGATGGA AGTAATAAATACTATGCAGACTCCGTGAAGGC CGATTCACCATCTCCAGCGACAATTCCAAGAAC ACGCTGATCTGCAAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTGGAGTGGTCTTGACTACTGG GGCCAGGGAACCTGGTCAACCGTCTCCTCAGCC TCCACCAAGGCCCATCGGTCTTCCCCCTGGCA CCCTCTCCAAAGAGCACCTCTGGGGGCACAGCG GCCCCGGCTGCCCTGGTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCTGTGGAACCTCAGGGGCC CTGACCAGCGCGTGCACACCTTCCCCGGCTGTC CTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGGCTTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACCTCACACATGCCACCC GTGCCAGCACCTGAACCTCTGGGGGACCGTCT AGTCTTCTCTTCCCCCAAAACCC AAGGACAC CCTCATGATCTCCCGACCCCTGAGGTACATG CGTGTGGTGGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTACGCGT CCTCACCGTCTTGCAACAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACCAGGTGAGCCTGACCTGCCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
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			SEQ ID NO: 1888	TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAAA
			SEQ ID NO: 2045	QVQLVESGGGVVQGRSLRLSCAASGFTSSYGM HWVRQAPGKGLEWVAWIYDGSNKYYADSVKG RFTISDNTSKNTLYLQMNLSRAEDTAVYYCARDR TIFGVLDYWQGQGLVTVSSASTKGPSVFLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGQTYYICNV NHKPSNTKVDKKEPKSCDKTHITCPPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDSDGSEFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
	AA		SEQ ID NO: 318	SEQ ID NO: 475
			DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSTRFSGSGGTD FSFTISLSLPEDIAYYCQQYDILLTFGGGKVEIKR TVAAPSVFIIPPSDEQLKSGTASVCLLNFPYREA KVQWKVDNALQSGNSQESVTEQDSKDSYLSST LTLISKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC	CAGTGCCGCTGGTGAGTCTGGGGCTGAGGTG AAGAAGCCTGGGCTCAGTGAAGTCTCCTGC AAGCTTCTGGATACACCTTCAACCGGCTACTAT ATCCACTGGTGCGACAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATCAACCTGACAGT GGTGACACAGACTATTACAGAGGTTTCAGGGC AGGTTACCATGACCAAGGACACGTCATCAGC ACAGCCTACATGGAACCTGAACAGGCTGAGATCT GACGACACGGCGTGATTAATGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGAAACCTGGTACCGTCT CCTCAGCCTCCACCAAGGGCCATCGGTCTTCCC CCTGGACCCCTCCTCCAAGAGCACCTCTGGGGG CACAGCGCCCTGGGTGCTGGTCAAGGACTA CTTCCCAGAACCGGTGACGGTGTGCGGAACCTC AGCGCCCTGACCAAGCGGTGACACACCTTCCC GGCTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG
	5C2	IPS:335970	NA	GACATCGTATGACCCAGTCTCCAGACTCCCTG GCTGTGCTCTGGCGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAGAACTACATAGCTTGGTACCAGCAG CAACAGGACATCTCTCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGTCCCTGACC GATTCAAGTGGCAGCGGTCTGGGACAGATTTC CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGCCAAGGGACCAAGGTGGA AATCAACGAACGGTGGCTGCACCATCTGTCTT CATCTTCCCGCCATCTGATGAGCAGTTGAAATCT GGAACCTGCTCTGTGTGTGCTGCTGAATAACT TCTATCCAGAGAGGCCAAAGTACAGTGGAAAG TGGATAACGCCCTCCAATCGGGTAACCTCCAGG AGAGTGTACAGAGCAGGACAGCAAGGACAGC ACCTACAGCCTCAGCAGCACCCCTGACGCTGAGC AAAGCAGACTACGAGAAACACAAAGTCTACGC

		<p>CTGCGAAGTCACCCATCAGGGCCTGAGCTCGCC CGTCACAAAGAGCTTCAACAGGGGAGAGTGT</p>	<p>GGACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGTGGACAAAGAAAGT TGAGCCCAAATCTTGTGACAAACTCACACATG CCCACCGTGCCAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGGACGTGAGCCACGAAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTG AGCTCTCACCGTCTTGCACCAAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGCAGCCCCGAGAAACCACA GGGTACACCTGCCCTCCCATCCCGGAGGAGAT GACCAAGAACAGGTACGCTGACCTGCCTGGT CAAAGGCTTCTATCCAGCGACATCGCCGTGGA GTGGAGAGCAATGGCAGCCGAGAGAACAACT ACAAGACCAGCTTCCCGTGTGGACTCCGACG GCTCTTCTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAAGAGCCTCTCCCTGTCTCCGGG TAAA</p>
	AA	<p>SEQ ID NO: 1889</p> <p>DIVMTQSPDSLAVSLGERATINCKSSQSVLSNNK NYIAWYQQQPGHPPKLLIYWASTRESGVPDFSGS GSGTDFTLTISSLAEDVAVFYCCQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC</p>	<p>SEQ ID NO: 2046</p> <p>QVPLVQSGAEVKKPGASVKVSKASGYTFTGYI HWVIRQAPQGQLEWMGWINPDSGTDYSQRFQGR FTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLMISRTPETVTVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF</p>

				YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
				SEQ ID NO: 476
				CAGTGCCGCTGGTGCGAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGTACTAT ATCCACTGGTGCGACAGGCCCTGGACAAGGA CTTGAGTGGATGGGTGGATCAACCTTGACAGT GGTGGCACAGACTATTACAGAGGTTTCAGGGC AGGTTACCATGACCAAGGACACGTCCATCAGC ACAGCCTACATGGAACCTGAGCAGGCTGAGATCT GACGACACGGCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGAAACCTGGTCAACCGTCT CCTCAGCCTCCACCAAGGGCCATCGGTCTTCCC CCTGGACCCCTCCTCCAAGAGCACCTCTGGGGG CACAGGGCCCTGGCTGCCCTGGTCAAGGACTA CTTCCCGCAACCGGTGACGGTGTCTGGAACCTC AGCGCCCTGACCAAGCGGTGACACACCTTCCC GGTGTCTCAGTCTCAGGACTCTACTCCCTC AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACCAAGGTGGACAAGAAAGT TGAGCCCAATCTTGTGACAAACTCACACATG CCCACCGTGCCAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGACGTGAGCCACGAAGAC CCTGAGGTCAAGTTCACCTGGTACGTGGACGGC GTGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCAGTACCGTTGTGTC AGCTCTCACCGTCTGACCCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGGCAGCCCCCGAGAACACACA
				SEQ ID NO: 319
				GACATCGTATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAAGAACTACATAGCTTGGTACCAGCAG AAACAGGACATCCTCCTAAGCTGCTCATTTACT GGGCATCTACCCGGGAATCCGGGTCCCTGACC GATTCAAGTGGACGGGTCTGGGACAGATTTCAC CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAGGGACCAAGGTGGA AATCAACGAACGGTGGCTGCACCATCTGTCTT CATCTTCCCGCCATCTGATGAGCAGTTGAAATCT GGAACCTGCCCTGTGTGTGCTGCTGAATAACT TCTATCCAGAGAGGCCAAAGTACAGTGGAAAG TGGATAACGCCCTCCAATCGGGTAACCTCCAGG AGAGTGTACAGAGCAGGACAGCAAGGACAGC ACCTACAGCCTCAGCAGCACCCCTGACGCTGAGC AAAGCAGACTACGAGAAACACAAAGTCTACGC CTGCGAAGTCAACCATCAGGGCCTGAGCTCGCC CGTCACAAAGAGCTTCAACAGGGGAGAGTGT
				NA
				13H12
				IPS:335978

			GGGTACACCCCTGCCCATCCCGGAGGAGAT GACCAAGAACAGGTGAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCAGCAGCATCGCCGTGGA GTGGGAGAGCAATGGCAGCCGGAGAACAACT ACAAAGACCAGCCTCCCGTGTGGACTCCGACG GCTCCTTCTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGAGAAAGCCCTCTCCCTGTCTCCCGG TAAA
		SEQ ID NO: 1890	SEQ ID NO: 2047
	AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQKPGHPPKLLIYWASTRESGVPDFRSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYI HWVRAQAPQGQLEWMGWINPDSGTDYSQRFQGR FTMTRDTSISTAYMELSLRLRDDTA VYYCAREATI FGMVIVPFDYWGQGLVTVSSASTKGPSVFPLAPS SKSTSGGT AALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTKISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
		SEQ ID NO: 320	SEQ ID NO: 477
IPS:335986	11C1	NA	CAGGTCCCGCTGGTACAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATACACTGGTGCCTCAGGCCCTGGACAAGGG CTTGTGTGGATGGGTGGATCAGCCCTAACAGT GGTGACACAAAGCTATGCACAGAAAGTTTCAGGAC AGGTCACCATGACCAGGGACACGTCCATCAGC ACAGCCTATATGAGCTGAGCAGACTGAGATCT GACGACACGGCGTGTATTTCTGTACGAGAGAG

		<p>CTCCGTGGACGTTCCGGCCAAAGGACCACCAAGGTGG AAATCAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACCTGCC'TCTGTTGTGTGCCTGCTGAATAAC TTCTATCCACAGAGAGGCCAAAGTACAGTGGAAG GTGGATAACGCCCTCCAAATCGGGTAACTCCACG GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCAACCATCAGGGCCTGAGCTCGC CCGTCAACAAGAGCTTCAACAGGGGAGAGTGT</p>	<p>GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGAAACCCCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCTTCTCTCAAGAGCACCTCTTGGGG CACAGGGCCCTGGGTGCTTGGTCAAGGACTA CTTCCCAGAACCGGTGACGGTGTCTGTGGAATC AGGCGCCTTGACAGCGGGCTGCACACCTTCCC GGTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCAATCTTGTGACAAACTCACACATG CCCACCGTGCCAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGACGTGAGCCACGAAAGAC CCTGAGGTCAAGTTCACTGGTACGTGGACGGC GTGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCAGTACCGTTGTGTC AGCTCTCACCGTCTTGCAACAGGACTGGCTG AATGGCAAGGAGTCAAGTGCAGGCTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACACACA GGTGTACACCTGCCCTCCATCCCGGAGGAGAT GACCAAGAACAGGTGACGCTGACCTGCCCTGGT CAAAGGCTTCTATCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGAGCCGAGCGGAGAACACT ACAAAGCCACGCTTCCCGTGTGGACTCCGACG GCTCTTCTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGAGAAAGAGCCTCTCCCTGTCTCCGGG TAAA</p>
	AA	<p>SEQ ID NO: 1891</p> <p>DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSRDSGVPDFSG</p>	<p>SEQ ID NO: 2048</p> <p>QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYI HWVRRQAPGGQLVWMGWISPNSGDTSYAQKFQDR</p>

			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSYLSSTLTLSKADYEEKHKVYACEVTHQGLSS PVTKSFNRGEC	VTMRDTSISTAYMELSRRLRSDDTAVYFCTREATI FGMLIVPFDYWGGQTLVTVSSASTKGPSVFPLAPS SKSTSGGTAAAGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLISRTPETVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFFSCSVMHEALHNHYTQKS LSLSPGK
			SEQ ID NO: 321	SEQ ID NO: 478
IPS:335994	12H11	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAGAACTACTTAGCTTGGTACCAGCAG AAACGAGCAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTACCATCAACAGCCTGCAAGGCTGAAGAT GTGGTGTTTATTACTGTACGCAATATTATCGTA CTCCGTGGACGTTCCGGCCAGGGACCAAGGTGG AAATCAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACCTGCCCTCTGTGTGTGCTGCTGAATAAC TTCTATCCAGAGAGGCCAAAGTACAGTGGAG GTGGATAACGCCCTCCAAATCGGGTAACTCCAG GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCCTGACGCTGAG CAAAAGCAGACTACGAGAAACACAAGTCTACG CCTGCGAAGTCAACCATCAGGGCCTGAGCTCGC CCGTACAAAGAGCTTCAACAGGGGAGAGTGT	CAGTGCCGCTGGTGCAAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAGTCTCCTGC AAGCTTCTGGATACACCTTCAACGGCTACTAT ATACACTGGTGCGTCAAGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATAAGCCCTAACAT GGTGACACAACTATGCACAGAAAGTTTCAGGAC AGGTCAACATGACAGGACACGTCATCAGC ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT GACGACACGGCGTGTATTACTGTACGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCAATTG ACTACTGGGCCAGGGAACCCCTGGTCAACGCTCT CCTCAGCCTCCACCAAGGGCCATCGGTCTTCCC CCTGGCACCTCTCTCCAAGAGCACCTCTGGGGG CACAGCGCCCTGGGTGCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCTGGAACTC AGCGCCCTGACACAGCGGTGACACACCTTCCC GGTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCCCAACAACCAAGGTGGACAAGAAAGT TGAGCCCCAATCTTGTGACAAACTCACACATG CCCACCGTGCCAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCCCCAAACCCAAAG

			<p>GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGACGTGAGCCACGAAGAC CCTGAGGTCAGTTCACTGGTACGTGACGGC GTGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCTCCTCACCGTCTGCACCAAGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGCAGCCCCGAGAACACACA GGGTACACCTGCCCTCCCATCCCGGAGGAGAT GACCAAGAACAGGTACGCTGACCTGCCTGGT CAAGGCTTCTATCCAGCGACATCGCCGTGGA GTGGAGAGCAATGGCAGCCGAGACAACACT ACAAGACCAGCTCCCGTGTGGACTCCGACG GCTCTTCTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGAACGTCTTCTC ATGCTCCGTGATGATGAGGCTCTGCACAACCA CTACACGAGAAAGGCTCTCCCTGTCTCCGGG TAAA</p>
	SEQ ID NO: 1892	SEQ ID NO: 2049	
	<p>DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLA WYQQKPGQPPNLLIYWTSRDSGVPDFSG SGSGTDFTLTINSLQAEDVA VYQCQQY YRTPWTF GQGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVC LLNFIYPREA KVQWKVDNALQSGNSQESVTEQDS KDSTYLSSTLTLSKADYEKHKVYACEVTHQQLSS PVTKSFNRGEC</p>	<p>QVPLVQSGAEVKKPGASVKVSKASGYTFTGYYI HWVRQAPGQGLEWMGWISPNNGDTNYAQKFQD RVMTTRDTSISTAYMELSRLRSDDTAVYCTREA TIFGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYIC NVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLEPPKPKDITLMISRTPETVTVVDVSHE DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVVFSCSVMEALHNHYTQK SLSLSPGK</p>	AA

			SEQ ID NO: 322	SEQ ID NO: 479
IPS:336024	18E3	NA	<p>GAAATTGTGTGACGCGAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCCGCTCCTCATCTATGGTGCATCCAGCAGGG CCTAGGATCCAGACAGGTTCACTGAGGAGTG GGTCTGGGACAGACTTCACTCTCACCATCAGCA GACAGGAGCCTGATGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGTTTCAACCGCTCACTTTCGG CGAGGGACCAAGGTGGAGATCAACGAAACGG TGGCTGCACCATCTGTCTTCACTCTCCCGCCATC TGATGAGCAGTTGAAATCTGGAACCTGCCTCTGT TGTGTGCTGCTGAATAACTTCTATCCAGAGA GGCCAAAGTACAGTGGAGGTGGATAACGCCCT CCAATCGGGTAACTCCAGGAGAGTGTACACAGA GCAGGACAGCAAGGACAGCACCTACAGCCTCA GCAGCACCCCTGACGCTGAGCAAAAGCAGACTACG AGAAACACAAAGTCTACGCTGCGAAAGTACCC ATCAGGGCCTGAGCTCGCCCGTCCACAAAGAGCT TCAACAGGGGAGAGTGT</p>	<p>CAGTGCAGTTGCAGGAGTCTGGGCCCCAGGACTG GTGAAGCCTTTCACAGACCCCTGTCCCTCACCTGC ACTGTCTCTGGTGAATCCATCAGCAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCACCCAGGGA AGGGCCTGGAGTGGATTGGGTACATCTATTACA GTGGGAGCACCTACTACAACCCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGCTCTAAGA ACCAAGTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGGACACGGCCGTGTATTACTGTGCGAGAGA TCGTATTACGATTTTGGAGTGGTTATGGGGGGC GGTATGGAGCTGTGGGGCCAAAGGACCAACGGTC ACCGTCTCTCAGCCTCCACCAAGGGGCCCATCG GTCCTCCCTGGCACCCCTCCCTCCAAGAGCACCT CTGGGGGCACAGCGGCCCTGGGCTGCCCTGGTCA AGGACTACTTCCCCGAAACCGGTGACGGTGTCTGT GGAAGTACAGGGCCCTGACCAAGCGGCGTGCACA CCTTCCCGGTGTCTCAGTCTCAGTCTCAGGACTCTA CTCCCTCAGCAGCGTGTGACCGTCCCTCCAG CAGCTTGGGACCCAGACCTACATCTGCAACGT GAATCACAAGCCAGCAACCAAGGTGGACA AGAAAGTTGAGCCCAATCTTGTGACAAACTC ACACATGCCACCCGTGCCAGCACCTGAACCTC TGGGGGACCGTCACTCTCTTCCCCCCTCAA ACCAAGGACACCCCTCATGATCTCCCGGACCC TGAGGTACATGCGTGGTGGTGGACGTGAGCCA CGAAGACCCCTGAGTCAAGTTCAACTGGTACGT GGACGGCTGGAGGTGCATAATGCCAAGACAA AGCCGTGTGAGGAGCAGTACGGCAGCACGTACC GTTGTGTACGCTCTCAGGCTCTGACCCAGG ACTGGCTGAATGGCAAGGAGTACAAGTGCAAG GTCTCCAACAAGCCCTCCAGCCCCCATCGAG AAAACCATCTCCAAGCCAAAGGGCAGCCCCGA GAACACAGGTGTACACCTGCCCCCATCCCGG GAGGAGATGACCAAGAACCCAGGTGACGCTGAC CTGCCTGGTCAAGGCTTCTATCCAGCGGACAT</p>

			CGCCGTGGAGTGGGAGAGCAATGGGCAGCCGG AGAACAATAACAAGACACGCCTCCCGTGTGG ACTCCGACGGCTCTTCTTCCCTCTATAGCAAGCT CACCGTGGACAAGACAGGTGGCAGCAGGGGA ACGTCTTCTCATGCTCCGTGATGCATGAGGCTCT GCACAACCACTACACGCAGAGAAGGCCTCTCCCT GTCTCCGGGTAAA
		SEQ ID NO: 1893	SEQ ID NO: 2050
	AA	EIVLTQSPGTLSPGERATLSCRASQISYSYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGTDF TLTIHQEPDDFAVYYCQQYGSSPLTFGGGTKEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLS STLTLSKADYEKHKVYACEVTHQGLSPVTKSFN RGEC	QVQLQESGPGLVKPSQTLSTCTVSGDSISSGGYY WSWIRHPGKGLEWIGYIYSGSTYYNPSLKSRTV ISVDTSKNQFSLKLSVTAADTA VYYCARDRITIFG VVMGGMDVWVGQGTTVTVSSASTKGPSVPFLAP SSKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLMISRTEPVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
		SEQ ID NO: 323	SEQ ID NO: 480
IPS:336041	2G10 LCI	NA	CAGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACTTCACTAAGTATGGC ATGCACTGGTCCGCGAGGTCCAGGCGAGGGG CTGGAGTGGTGGCAGCTATATGGTTTGTGGA AGTGATAAATACTATGCAGACTCCGTGAAGGC CGATTCACTATCTCCAGAGACAACCTCCAGAAC ACGTGTATCTGCAATGAACAGCTGAGAGCC GAGGACACGGCTGTGTATTAAGTGTGAGAGAT CAGGCGATTTTGGAGTGTGTCCTCCGACTACTGG GGCCAGGGAACCTGGTCACTCCCTCTCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA CCCTCTCCAGAGCACTCTGGGGGACAGCG

		<p>CCAAAGTACAGTGGAAGGTGGATAACGCCCTCC AATCGGGTAACCTCCAGGAGAGTGTCACAGAGC AGGACAGCAAGGACAGCACCTACAGCCTCAGC AGCACCTGACGCTGAGCAAAAGCAGACTACGAG AAACACAAAGTCTACGCCTGCGAAGTCACCCAT CAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTC AACAGGGGAGAGTGT</p>	<p>GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC GAACCGGTACGGTGTCTGTGGAACCTCAGGGGCC CTGACCAGCGGCTGCACACCTTCCCGGCTGTC CTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAAACCAAGGACAC CCTCATGATCTCCCGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCAATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCCTGTGTGTCAGCGT CCTCACCGTCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAAACAAGC CCTCCAGCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCATCCCGGAGGAGATGACCA AGAACAGGTGAGCCTGACCTGCCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAAGCCGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAAG</p>
AA	RGE	<p>EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLIYGAAATRAATGIPARVSGSGSGTE FTLTISLSQSEDFAVYQCQYNNWPLTFGGGTKVE IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN</p>	<p>SEQ ID NO: 1894</p> <p>SEQ ID NO: 2051</p> <p>QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAIWFDSGDKYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVDPDYWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNV NHPKSTNTKVDKKEPKSCDKTHHTCPCPAPELLG</p>

				GPSVFLPFPKPKDTLMISRTPVTCVVVVDVSHEDPE VKFNWYVVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDJAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQOQGNVFSCSVMHEALHNHYTQKSLS LSPGK
				SEQ ID NO: 324 GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACCAAGGGAAGCCCCTA AACGCCGTGATCTATGGTGCATCCAGTTTGCAAA GTGGGTCCCATCAAGGTTCAAGCGGCAGTGGAT CTGGGACAGAGTTCACTCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTTGTAACTTAATTACTGTCT ACAGCATAATAGTTACCCATTCACTTTCGGCCCT GGGACCAAGTGGATGTCAAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACCTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAGTCTACGCCTGCGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT
			4H9.004	NA
			IPS:336077	SEQ ID NO: 481 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAAGCTCTGGATTCAACCTTCAGTTACTTTGGCA TGCACCTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGGAA GTAATAAATACTATGCAGACTCCGTGAAGGGCC GCTTCAACCATCTCCAGAGACAATTCCAAAGAACA CGCTGATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTGGAGTGTCTTGGGGGACTACT GGGCCAGGGAACCCCTGGTCAACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGTGCTGCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTGCGTGAACTCAGGCGC CCTGACCAAGCGCGTGCACACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACCTCACACATGCCACC GTGCCAGCACCTGAACCTCTGGGGGACCGTCT AGTCTTCTCTTCCCCCAAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAGTTCAACTGGTACGTGGACGCGGTGGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTACGCGT

				<p>SEQ ID NO: 1895</p> <p>DIQMTQSPSSLSASVGDRVTITCRASQGIKELGW YQQKPGKAPKRLIYGASSLSQSGVPSRFSGSGTE FTLTISLQPEDFVITYCLQHNSYPFTFGPGTKVDV KRTVAAPSVFIFPPSDEQLKSGTASVVCCLLNNFYPR EAKVQWIKVDNALQSGNSQESVTEQDSKDSYSL STLTLSKADYEKHKVYACEVTHQGLSPVTKSFN RGEK</p>	<p>SEQ ID NO: 1895</p> <p>CCTACCGTCTGCACCAAGGACTGGCTGAATGG CAAGGAGTACAAAGTGCAAGGTCTCCAAACAAGC CTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCAACAGGTGT ACACCTGCCCATCCCGGAGGAGATGACCA AGAACAGGTCAAGCTGACCTGCCTGGTCAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGAGAACCAACTACAAG ACCAGCCTCCCGTCTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCCTGGACAAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCTCTCCCTGTCTCCGGGTAAA</p>
	AA			<p>SEQ ID NO: 2052</p> <p>QVQLVESGGGVVQPGRLSLRSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIYDGSNKYYADSVKG RFTISRDNSKNTLYQMNSLR AEDTAVYYCARDG TIFGVLGDYWGQGTLLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLMISRTPETCVVDVSHED PEVKFNWYVDGVEVHNATKPKCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFELY SKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPGK</p>	<p>SEQ ID NO: 2052</p> <p>QVQLVESGGGVVQPGRLSLRSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIYDGSNKYYADSVKG RFTISRDNSKNTLYQMNSLR AEDTAVYYCARDG TIFGVLGDYWGQGTLLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLMISRTPETCVVDVSHED PEVKFNWYVDGVEVHNATKPKCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFELY SKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPGK</p>
IPS:336088	6A5.004	NA		<p>SEQ ID NO: 325</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTAA ATTGGTATCAGCAGAAACCAAGGAAAGCCCTA AACTCCTGATCTACGATGCTTCCAAATTTGGAGCC AGGGTCCCATCAAGGTTTCAGTGGAAAGTGGATC TGGGACAGATTTTACTTTTACCATCATCAGCAGCCTG</p>	<p>SEQ ID NO: 482</p> <p>CAGTGCAGCTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCTTCAGTAGCTATGGCA TGCACTGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGTGGCAGCTATATGGTATGATGGAA ATAATAAATACTATGCAGACTCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTTCCAAAGACA</p>

CAGCCTGAAGATATTGCAACATATTACTGTCAA CAGTATGATGATCTATTCACTTTCGGCCCTGGGA CCAAAGTGGATATCAACGAACGGTGGCTGCAC CATCTGCTTTCATCTTCCCGCCATCTGATGAGCA GTTGAATCTGGAACCTGCTCTGTTGTGCTG CTGAATAACTTCTATCCCAGAGAGGCCAAAGTA CAGTGGAAAGTGGATAACGCCCTCCAATCGGGT AACTCCAGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGCAGCACCTT GACGCTGAGCAAGCAGACTACGAGAAACACA AAGTCTACGCCCTGCGAAGTCAACCCATCAGGGCC TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGG GAGAGTGT	CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGGTGTATTACTGTGCGAGAGATC GGACGATTTTGGAGTGGTCTTGAGTACCTCG GCCAGGAACCTGGTCAACCGTCTCCTCAGCCT CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC CCTCTCCAAGAGCACCTCTGCGGGCACAGCGG CCCTGGGTGCCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCTGGAACCTCAGGCGCCC TGACCAGCGGTGCACACCTTCCCCGGCTGTCC TACAGTCTCAGGACTCTACTCTCCCTCAGCAGCGT GGTGACCGTGGCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAGCCAG CAACACCAAGGTGGACAAAGAAATTGAGCCCCA AATCTGTGACAAAACTCACACATGCCACCCGT GCCCAGCACTGAATCTCTGGGGGACCGTCAG TCTTCTCTTCCCCCCAAACCCAAAGGACACCT CATGATCTCCCGGACCCCTGAGGTACATGCGT GGTGTGACGTGAGCCACGAAGACCTGAGGT CAAGTTCAACTGGTACGTGGACGGCTGGAGGT GCATAATGCCAAGACAAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTACGCGTCC TCACCGTCTGCACCCAGGACTGGCTGAATGGCA AGGAGTACAAGTGCAAGGTCTCCAAACAAAGCCC TCCCAGCCCCCATCGAGAAACCATCTCCAAAG CCAAAGGCGAGCCCCCGAGAACCCACAGGTGTAC ACCTGCCCCCATCCC'GGGAGGAGATGACCAAG AACAGGTACGCTGACCTGCCCTGGTCAAAGGC TTCTATCCCAGCAGATCGCCGTGGAGTGGGAG AGCAATGGGCGAGCCGGAACAACACACAGAC CACGCTCCCGTGTCTGGACTCCGACGGCTCCTC TTCTCTATAGCAAGTCAACCGTGGACAAAGC AGGTGGCAGCAGGGGAACGTCTTCTCATGTCTC GTGATGCATGAGGCTCTGCACAACCACTACAG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
SEQ ID NO: 1896	SEQ ID NO: 2053

		AA	<p>DIQMTQSPSSLSASVGDRVTITCQASQDITNLYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGGTD FTFTISLQPEDIATYYCQQYDDLFTFGPGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSLSS TLTLKADYEEKHKVYACEVTHQGLSSPVTKSFNR GEC</p>	<p>QVQLVESGGGVVQGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLVWAIAIWDGNNKYYADSVKG RFTISRDSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYLGQGTLVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCDKTHTCPCPAPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVFSQSVMHREALHNHYTQKLSL SPGK</p>
IPS:336099	17H11.004	NA	<p>GACATCCAGATGACCCAGTCTCCATCTTCCGTGT CTGCATCTGTAGGAGACAGAGTACCATCACTT GTCGGCGAGTCAGGTCTTATCATCTGGTTAG CCTGGTATCAGCAGAAACGGGGAAGCCCCCTA AACTCTGATCTATGCTGCATCCAGTTTGCAAAG TGGGTCCCATCAAGGTTCAAGCGGCAGTGGCTC TGGGACAGATTTCACTCTCACCATCAGCAGCCT ACAGCCTGAAGATTTTGCAACTTACTATTGTCAA CAGACTAACAGTTTCCCTCCGACGTTCCGGCCAA GGGACCAAGGTGGAATCAACGAAACGGTGGC TGCACCATCTGTCTTCACTCTTCCCGCCATCTGAT GAGCAGTTGAATCTGGAACTGCCTCTGTTGTG TGCCTGCTGAATAACTTCTATCCAGAGAGGCC AAAGTACAGTGAAGGTGGATAACGCCCTCCAA TCGGGTAACTCCAGGAGAGTGTACAGAGCAG GACAGCAAGGACAGCACCTACAGCCTCAGCAGC ACCCGTGACGCTGAGCAAGCAGACTACGAGAA ACACAAAGTCTACGCTGCGAAGTCAACCCATCA GGGCTGAGCTCGCCGTCACAAAGAGCTTCAA CAGGGGAGAGTGT</p>	<p>SEQ ID NO: 483</p> <p>CAGGTGAGCTGCAGGAGTCGGGCCAGGACTG GTGAAGCCTTCGGAGACCTGTCCCTCACCTGC ACTGTCTCTAGGGTCCATCAGTAGTTACTACT GGAGCTGGATCCGCGACGCCCGGGAAGGGA CTAGAGTGGATTGGCGTATCTATACAGTGGG AGCACCAACTCAACCCCTCCCTCAAGAGTCGA GTCACCATGTCAATAGACACGTCCAAAGAACCAG TTCTCCCTGAACACTGAACCTGTGACCCGCCGCG GACACGGCCGTGATTAATGTGCGAGAGATGTA GCAGTGGCTGGCTTTGACTACTGGGGCCAGGGA ACCTGGTCAACCGTCTCCTCAGCTCCACCCAAAG GGCCATCGGTCTTCCCTCCCTGGCACCCCTCCCA AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT GCCGTGGTCAAGGACTACTTCCCCGAACCGGTGA CGGTGTCTGGAACTCAGGCGCCCTGACCAAGC GCGTGACACCTTCCCGGCTGTCTACAGTCCCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT GCCCTCCAGCAGCTTGGGCAACCCAGACCTACAT CTGCAACGTGAATCAAGGCCAGCAACACCAA GGTGGACAAGAAAGTTGAGCCCAATCTTGTGA CAAACCTCACACATGCCCCACCGTGCCCCAGCAC</p>

		TGAACTCCTGGGGGACCGTCAGTCTTCTCTTC CCCCAAAACCCAAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTCACATGCGTGGTGGTGAC GTGAGCCACGAAGACCCTGAGGTCAAGTTC AAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCC AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG CACGTACCGTTGTGTACGCGTCTCACCGTCTCTG CACCAGGACTGGCTGAATGGCAAGGAGTACAA GTGCAAGGTCTCCAAACAAAGCCCTCCCAGCCCC CATCGAGAAACCATCTCCAAGCCAAAGGCA GCCCCGAGAACACAGGTGTACACCTGCCCCC ATCCCGGAGGAGATGACCAAGACACAGGTCA GCCTGACCTGCCCTGGTCAAGGCTTCTATCCCCA GCGACATCGCCGTGGAGTGGGAGAGCAATGGG CAGCCGAGAACAACTACAGACCACGCTCCC GTGCTGGACTCCGACGGCTCTTCTTCTCTATA GCAAGCTCACCGTGGACAAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAAACCACTACACGCAAGAGAGC CTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1897	SEQ ID NO: 2054
	DIQMTQSPSSVSASVGDRVTITCRASQGLIWLAW YQQKPGKAPKLLIYAASLQSGVPSRFSGSGGTD FTLTISLQPEDFATYYCQQTNFPPTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWVKVDNALQSGNSQESVTEQDSKDSYSTLS STLTLSKADYEKHKVYACEVTHQGLSPVTKSFN RGEK	QVQLQESGPGLVKPSETLSLTCTVSQGSISYYWS WIRQPAAGKGLEWIGRIYTSGSTNYPNPSLKSRVTMS IDTSKNQFSLKLSNVTAAADTA VYFCARDVAVAGF DYWGQGTLLVTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNT KVDKKVEPKSCDKTHTCPPCPAPELGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGSYRCVSVLTVLHQ DWLNGKEYKCKVSNKALPAPIEK TISKAKGQPREP QVYVTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS RWQQGNVVFSCSVMEALHNHYTQKLSLSLSPGK
AA		

SEQ ID NO: 327	SEQ ID NO: 484
<p>GACATCCAGATGACCCAGTCTCCATCTTCCGTGT CTGCATCTGTAGGAGACAGAGTCAACCATCACTT GTCGGCGAGTCAGGGTCTTATCATCTGGTTAG CCTGGTATCAGCAGAAACCGGGAAAGCCCCTA AACTCTGATCTATGCTGCATCCAGTTTGCAAAG TGGGTCCCATCAAGGTTCAAGCGGCAAGTGGCTC TGGGACAGATTTCACTCTCAACCATCAGCAGCCT ACAGCCTGAAGATTTTGCAACTTACTATTGTCAA CAGACTAACAGTTTCCCTCCGACGTTTCGGCCAA GGGACCAAGGTGGAATCAACGAACGGTGGC TGCACCATCTGTCTTCATCTTCCCGCCATCTGAT GAGCAGTTGAAATCTGGAACTGCTCTGTGTG TGCCTGCTGAATAACTTCTATCCAGAGAGGCC AAAGTACAGTGAAGGTGGATAACGCCCTCCAA TCGGGTAACTCCAGGAGAGTGTACAGAGCAG GACAGCAAGGACAGCACCTACAGCCTCAGCAGC ACCCTGACGCTGAGCAAGCAGACTACGAGAA ACACAAAGTCTACGCTGCGAAGTCAACCCATCA GGGCTGAGCTCGCCCGTCCACAAAGAGCTTCAA CAGGGGAGAGTGT</p>	<p>CAGGTGCAGCTGCAGGAGTCCGGCCAGGACTG GTGAAGCCTTCGGAGACCTGTCCCTCACCTGC ACTGTCTCTGGGGCTCCATCAGTAGTACTACT GGAGCTGGATCCGGCAGCCCGCCGGGAAGGGA CTAGAGTGGATTGGCCGTATCTATACAGTGGG AGCACCAACTACAACCCCTCCCTCAAGAGTCA GTCACCATGTCAATAGACACGTCCCAAGAACCA TTCTCCCTGAAACTGAACCTCTGTGACCCGCCG GACACGGCCTGTATTACTGTGCGAGAGATGTA GCAGTGGCTGGCTTTGACTACTGGGGCCAGGGA ACCTGGTCAACCGTCTCCCTCAGCCTCCACCAAG GGCCCATCGTCTTCCCTGGCACCTCTCTCCA AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA CGGTGTCTGGAACTCAGGGCCCTGACCAAGCG GCGTGACACCTTCCCGGCTGTCTACAGTCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT CTGCAACGTGAATCAAGCCCAAGCAACACCAA GGTGACAAAGAAAGTTGAGCCCAATCTTGTGA CAAACCTCACACATGCCCAACCGTGGCCAGCAC TGAACTCTGGGGGACCGTCACTTCTCTCTTC CCCCAAACCAAGGACACCTCATGATCTCC CGGACCCCTGAGGTACATGCGTGGTGGTGAC GTGAGCCACGAAGACCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCC AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG CACGTACCGTTGTGTCAGCGTCTCACCGTCTG CACCAGGACTGGTGAATGGCAAGGAGTACAA GTGCAAGGTCTCCAAACAAAGCCCTCCAGCCCC CATCGAGAAACCATCTCTCCAAGCCAAAGGGA GCCCCGAGAACCAAGGTGTACACCTGCCCTCC ATCCCGGGAGGAGATGACCAAGAACCAAGTCA GCCTGACCTGCCTGGTCAAGAGGCTTCTATCCCA GCGACATCGCCGTGGAGTGGGAGAGCAATGGG</p>
IP:359621	17H11.004.001
NA	

				<p>CAGCCGAGAACAACTACAAGACCACGCCTCCC GTGCTGACTCCGACGGCTCTTCTTCTCTATA GCAAGCTCACCGTGGACAAAGAGCAGGTGGCAG CAGGGAAACGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACCACTACACGCAAGAGAGC CTCTCCCTGTCTCCGGTAAA</p> <p>SEQ ID NO: 2055</p> <p>QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWS WIRQPAKGLEWIGRIYTSGSTNYPNPSLKSRVTMS IDTSKNQFSKLNSTAAADTA VYCARDVA VAGF DYWGQGTLLVTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVTVPSSSLGTQTYICNVNHNKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQ DWLNGKEYKCKVSNKALPAPIEK TISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHEALHNHYTQKLSLSPGK</p> <p>SEQ ID NO: 485</p> <p>CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCA GCGTCTGGATTCACTTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCAACCATCTCCAGAGACAATTCCAAAGAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTGGAGTGTCTTTGGGGGACTACT GGGGCCAGGGAACCTGGTCAACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCTCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCGTGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGTGGAACACTCAGGCGC</p>
				<p>SEQ ID NO: 1898</p> <p>DIQMTQSPSSVSASVGDRVTITCRASQGLIWLAW YQQKPGKAPKLLIYAASLQSGVPSRFSGSGGTD FTLTISLQPEDFATYYCQQTNFPPTFGQGTKVEI KRTVAAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSITYSL STLTLSKADYEKHKVYACEVTHQGLSPVTKSFN RGEK</p> <p>AA</p> <p>SEQ ID NO: 328</p> <p>GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCATT GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACCAAGGGAAGCCCCCTA AACTCCTGATCTATGGTGATCCAGTTTGCAA GTGGGTCCCATCAAGGTTTCAGCGGCAGTGGAT CTGGGACAGAGTTCACTCTCACAAATCAGCAGCC TGACGCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAAATAGTTACCCATTCACTTTCGGCCA AGGACCAAAAGTGATGTCAAAACGAACGGTGG CTGCACCATCTGTCTTCACTTCCCGCCATCTGA TGAGCAGTTGAAAATCTGGAACCTGCCTCTGTTGT GTGCTGTGCTGAATAACTTCTATCCAGAGAGGC CAAAAGTACAGTGGAAGGTGGATAACGCCCTCCA ATCGGGTAACCTCCAGGAGAGTGTACAGAGCA</p> <p>NA</p>
		4H9.004.001	IPS:359781	

		<p>GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCTGACGCTGAGCAAGCAGACTACGAGA AACACAAAGTCTACGCCCTGCGAAGTCACCCATC AGGCCCTGAGCTCGCCCCGTCACAAAGAGCTTCA ACAGGGGAGAGTGT</p>	<p>CCTGACCAGCGGCGTGACACACCTTCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACAC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAAACCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCAATATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCCTGTGTGTCAGCGT CCTACCGTCTTGACCAAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCATCCCGGAGGAGATGACCA AGAACAGGTGACCTGACCTGCCTGTGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
	AA	<p>DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISLQPEDFVITYCLQHNSYPFTFGQGTKVD VKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWVKVDNALQSGNSQESVTEQDSKDSSTYS LSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSF NRGEC</p>	<p>SEQ ID NO: 1899</p> <p>SEQ ID NO: 2056</p> <p>QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIWYDASNKYADAVKYG RFTISRDNSKNTLYQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLMISRTPETVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV</p>

				SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVVFSCSVMHEALHNHYTQKS LSLSPGK
				SEQ ID NO: 486
				CAGGTGAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAAGCTCTGGATTCAACCTTCAGTTACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACTCCGTGAAGGGCC GCTTCAACCATCTCCAGAGACAATTCCAAAGAACA CGTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTATTACTGTGCGCGAGATG GGACGATTTTGGAGTGTCTTGGGGGACTACT GGGGCAGGGAACCCCTGGTCAACCTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCTCTCAAAGAGCACCTCTGGGGGCACAGC GGCCCTGGCTGCTGTGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGTGGAATCAGGCGC CCTGACCAAGCGGTGTGCACACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGCGGTGGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCTCCACAAGC
				SEQ ID NO: 329
				GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG GCTGTTATCAGCAGAACCAAGGGAAGCCCCCTA AACTCTGATCTATGGTGCAATCCAGTTTGCAA GTGGGTCCCATCAAGGTTCAAGCGGCAGTGGAT CTGGGACAGAGTTCACTCTCACAAATCAGCAGCC TGCAAGCCTGAAGATTTTGTAACTTAATTAATGCT ACAGCATAAATAGTTACCCATTCACTTTCGGCCA AGGACCAAAAGTGGATGTCAAACGAACGGTGG CTGCACCATCTGTCTTCACTTCCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGT GTGCTGTCTGAATACTTCTATCCCAGAGAGGC CAAAAGTACAGTGAAGGTGGATAACGCCCTCCA ATCGGGTAATCCCCAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACTACAGCCCTCAGCA GCACCTGACGCTGAGCAAAAGCAGACTACGAGA AACACAAAGTCTACGCCCTGCGAAGTCAACCATC AGGGCCTGAGCTCGCCCGTCAACAAAGAGCTTCA ACAGGGGAGAGTGT
				NA
				4H9.004.002
				IPS:360929

			<p>CTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACACACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACAGGTGAGCCTGACCTGCCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGAGAACAACTACAAG ACCACGCTCCCGTCTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
			<p>SEQ ID NO: 1900</p> <p>DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSTE FTLTISLQPEDFVITYCLQHNSYPFTFGQGTKVD VKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYS LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF NRGEC</p>
	AA		<p>SEQ ID NO: 2057</p> <p>QVQLVESGGGVVQPGRLSLRSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIWYDASNKYIYADSVKVG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLISRTEPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFELY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK</p>
IPS:360936	4H9.004.003	NA	<p>SEQ ID NO: 330</p> <p>GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGAGAGACAGATCACCATCACTT GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACCAAGGAAAGCCCCCTA AACTCTGATCTATGGTGATCCAGTTTGCAA GTGGGTCCCATCAAGTTTCAGCGGCAGTGGAT CTGGGACAGAGTTCACTCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAAATAGTTACCCATTCACTTTCGGCCA</p>
			<p>SEQ ID NO: 487</p> <p>CAGTGCAGCTGGTGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAAGCTCTGGATTCACTTCAAGTTACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGCGCAGTTATATGGTATGATGAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCAACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG</p>

		<p>AGGACCACAAAGTGGATGTCAACGAACGGTGG CTGCACCATCTGTCTTCACTTCCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCCTCTGTTGT GTGCTGTCTGAATAACTTCTATCCACAGAGGC CAAAGTACAGTGAAGGTGGATAACGCCCTCCA ATCGGTAACCTCCAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCTGACGCTGAGCAAGCAGACTACGAGA AACACAAAGTCTACGCCTGCGAAGTCAACCCATC AGGCCTGAGCTCGCCCGTCAACAAAGAGCTTCA ACAGGGGAGAGTGT</p>	<p>GGACGATTTTGGAGTGCTCTTGGGGGACTACT GGGGCAGGGAACCCGTGTCACCGTCTCCTCAG CTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGCTGCCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGC CCTGACCAGCGCGTGCACACCTTCCC GGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACCC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCAATATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAAGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCGAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACCAAGTCAAGCTGACCTGCCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCGAGCCGGAGACAACATACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
	AA	<p>DIQMTQSPSSLSASVGDRTVTITCRASQGIRNELGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFVITYYCLQHNSYPFTFGQGTKVD</p>	<p>SEQ ID NO: 1901</p> <p>SEQ ID NO: 2058</p> <p>QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIYDGSNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG</p>

			VKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTS LSSLTLTKADYEEKHKVYACEVTHQGLSSPVTKSF NRGEC			TIFGVLLGDYWGQGTLLVTVSSASTKGPSVFPLAPS SKSTSGGT AALGCLVKDYFPEPVT VSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVVFSCVMHEALHNHYTQKS LSLSPGK
			SEQ ID NO: 331 GACATTCAGATGACCCAGTCTCCATCCTCCTCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACCAAGGAAAGCCCCTA AACTCCTGATCTATGGTGCAATCCAGTTTGCAA GTGGGTCCCATCAAGGTTCAAGCGGCAGTGGAT CTGGGACAGAGTTCACTCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAATAGTTACCCATTCACTTTCGGCCCT GGGACCAAAGTGGATGTCAAACGAACGGTGGCT GCACCATCTGTCTTCAATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACCTGCCCTCTGTTGTGT GCCTGCTGAATAACTTCTATATCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCCTGCGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCAAAAGAGCTTCAACA GGGGAGAGTGT	NA	4H9.004.004	IPS:360943
			SEQ ID NO: 488 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGAATCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAAGAACA CGCTGATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTGGAGTGTCTTTGGGGGACTACT GGGGCCAGGAACCTGGTCAACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCTCTCCAAAGACACCTCTGGGGGCACAGC GGCCCTGGGCTGCCGTGGTCAAGGACTACTTCCC CGAAACCGGTGACGGTGTCTGTGGAACCTCAGGCG CCTGACAGCGGCGTGCAACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGGCC CAAACTTTGTGACAAAACTCACACATGCCACC GTGCCAGCACCTGAACCTCTGGGGGACCGTCT AGTCTTCTCTTCCCCCAAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACTG			

		CGTGTGGTGACGTGAGCCACGAAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCAATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTGACGCGT CCTCACCGTCTTGACCAAGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCATCGAGAAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACACAGGTGT ACACCTGCCCCATCCGGGAGGAGATGACCA AGAACCAAGTCAAGCTGACCTGCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGGAAGAACAACTACAAG ACCACGCCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1902	SEQ ID NO: 2059
	DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSTE FTLTISLQPEDFVITYYCLQHNSYPFTFGPGTKVDV KRTVAAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSITYSL STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEK	QVQLVESGGGVVQPGRLSLRSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIWYDASNKYADAVKVG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGLTVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNATKPCPEEQYGYSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVVFSCVMHEALHNHYTQKS LSLSPGK
		AA

		SEQ ID NO: 332	SEQ ID NO: 489
	IP:360949	4H9.004.005	NA
		GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACCAAGGGAAGCCCCTA AACGCCCTGATCTATGGTGCATCCAGTTTGCAA GTGGGGTCCCATCAAGGTTCAAGCGGCAGTGGAT CTGGGACAGAGTTCACTCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTTGTAACTTAATTACTGTCT ACAGCATAAATAGTTACCCATTCACTTTTCGGCCA AGGGACCAAAAGTGGATGTCAAACGAACGGTGG CTGCACCATCTGTCTTCATCTTCCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACCTGCCCTCTGTTGT GTGCCTGCTGAATAACTTCTATCCCAGAGAGGC CAAAGTACAGTGGAAAGGTGGATAACGCCCTCCA ATCGGGTAACCTCCCAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCC'TGACGCTGAGCAAAAGCAGACTACGAGA AACACAAAGTCTACGCCCTGCGAAAGTCACCCATC AGGGCCTGAGCTCGCCCCGTCAACAAGAGCTTCA ACAGGGGAGAGTGT	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTCACTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCAACCATCTCCAAGAGACAATTCACAAGACA CGCTGATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTAATTACTGTGCGCGAGATG GGACGATTTTGGAGTGTCTTGGGGGACTACT GGGGCCAGGAACCCCTGGTCAACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCGTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGC CCTGACCAAGCGGTGTGCAACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGGCTTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACCTCACACATGCCACC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAAACCCAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTCAAGCGT CCTCACCGTCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGAAGGTCTCCACAAGCAAGC CCTCCAGCCCCCATCGAGAAAACCATCTCCAA AGCCAAGGGCAGCCCCGAGAACCCAGGTGT ACACCTTGCCCCCATCCCCGGGAGGAGATGACCA AGAACAGGTCAAGCTGACCTGCCTGTGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG

			<p>AGAGCAATGGCAGCCGGAGAACAACTACAAG ACCACGCTCCCGTCTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTAAA</p> <p>SEQ ID NO: 2060</p>	<p>AGAGCAATGGCAGCCGGAGAACAACTACAAG ACCACGCTCCCGTCTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTAAA</p> <p>SEQ ID NO: 2060</p>
			<p>DIQMTQSPSSLSASVGDRVTITCRASQGINELGW YQQKPGKAPKRLIYGASSLQSGVPSRFSGSGTE FTLTISLQPEDFVITYCLQHNYPFTFGQGTKVD VKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYS LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF NRGEC</p> <p>AA</p>	<p>QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIWYDASNKYADAVKVG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLISRTPETVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVVFSCVMHEALHNHYTQKS LSLSPGK</p> <p>SEQ ID NO: 490</p>
IPS:359761	4H9.004.006	NA	<p>GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACCAAGGAAAGCCCCCTA AACTCCTGATCTATGGTGATCCAGTTTGCAA GTGGGTCCCATCAAGGTTTCAGCGGCAGTGGAT CTGGGACAGAGTTCACTCTCACAAATCAGCAGCC TGACGCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAATAGTTACCCATTCACTTTCGGCCA AGGACCAAAAGTGATGTCAAAACGAACGGTGG CTGCACCATCTGTCTTCTATCTTCCCGCCATCTGA TGAGCAGTTGAAAATCTGGAACCTGCCTCTGTTGT GTGCTGTGTAATAACTTCTATCCACAGAGAGGC CAAAAGTACAGTGGAAGGTGGATAACGCCCTCCA</p> <p>SEQ ID NO: 333</p>	<p>CAGGTGCACTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTCACTTACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCAACCATCTCCAGAGACAATTCCAAAGAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGCTGTGTATTACTGTGCGCGAGATA GGACGATTTTGGAGTGTCTTGGGGGACTACT GGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCAG CCTCCACCAAGGGGCCATCGGTCTTCCCCCTGGC ACCTCTCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCC</p> <p>SEQ ID NO: 490</p>

		<p>ATCGGGTAACCTCCAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCCTGACGCTGAGCAAGCAGACTACGAGA AACACAAAGTCTACGCCCTGCGAAGTCACCCATC AGGCCCTGAGCTCGCCCGTCAACAAAGAGCTTCA ACAGGGGAGAGTGT</p>	<p>CGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGC CCTGACCAAGCGCGTGCACACCTTCCCGGTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACAC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAAACCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCAATATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCCTGTGTGTCAGCGT CCTCACCGTCTGCACCAAGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACAGGTGAGCCTGACCTGCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAA</p>
	AA	<p>DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISLQPEDFVITYCLQHNSYPFTFGQGTKVD VKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWVKVDNALQSGNSQESVTEQDSKDSSTYS LSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSF NRGEC</p>	<p>SEQ ID NO: 1904</p> <p>SEQ ID NO: 2061</p> <p>QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIYDASNKYADAVKYG RFTISRDNSKNTLYQMNSLRAEDTAVYYCARDR TIFGVLLGDYWGQGTSLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLMISRTPETVTCVVVDVSHED</p>

				<p>PEVKFNWYVVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVVFSCVMHEALHNHYTQKS LSLSPGK</p>
				<p>SEQ ID NO: 334</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACCAAGGAAAGCCCCA AGCTCTGATCTATGGTGCAATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTCAAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAGTGGATATCAACGAACGGTGGCT GCACCATCTGTCTTCACTTCCCGCCATCTGATG AGCAGTTGAATCTGGAACCTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAGTGGATAACGCCCTCCAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT</p>
				<p>SEQ ID NO: 491</p> <p>CAGGTGAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTTTCACTAACCTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAATA CGTGTATCTGCAAAATGAACAGCCTGAGAGTCG CGGACACGGCTGTATTATTGTGCGCGAGATG GGACGATCTTGGAGTGGTCTTGGGGGACTACT GGGGCAGGAAACCTGGTCAACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCTGGCTGCTGTCAGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGC CCTGACCAAGGGCGTGCAACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACCTACACATGCCACC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGCGGTGGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAAGGACTGGCTGAATGG</p>

			<p>CAAGGAGTACAAAGTGCAAGGTCTCCAAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACAGGTGAGCCTGACCTGCCGTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGAGAACAACTACAAG ACCAGCCTCCCGTCTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAAA</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 RFTISRDNSKNTLYQMNSLRVADTA VYCARDG TIFGVLDGYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLMISRTPETCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFELY SKLTVDKSRWQQGNVVFSCSVMEALHNHYTQKS LSLSPGK</p>
IPS:360962	4B1.011	NA	<p>SEQ ID NO: 335</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGAGACAGAGTCACCATCATT GCCGGGCAAGTCAGGACATTAGAGATTATTAG GCTGTATCAGCAGAAACCAAGGAAAGCCCTA AGCGCTGATCTATGGTGATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT</p>

		<p>ACAGCATAAATAATTACCCCTTCACTTTTCGGCCAA GGGACCAAAGTGGATATCAACGAACGGTGGCT GCACCATCTGTCTTTCATCTTCCCGCCATCTGATG AGCAGTTGAATCTGGAACCTGCCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAAGAGAGGCCA AAGTACAGTGGAAAGGTGGATAACGCCCTCCAAAT CGGGTAAC'TCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCCGAAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT</p>	<p>CGGACACGGCTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTTGGGGGACTACT GGGGCCAGGGAACCCCTGGTCACCGTCTCCTCAG CTCCACCAAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCTCTCAAAGAGCACCTCTGGGGGACACAGC GGCCCTGGCTGCTTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGTGGAATCAGGCGC CCTGACCAAGCGGCGTGACACACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCACC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCAATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCACAAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACCAAGGTACGCTGACCTGCCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGAGCGGAGACAACATAACAAG ACCAAGCCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
	AA	<p>DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QOKPGKAPKRLIYGASSLSQSGVPSRFSGSGSGTEFT</p>	<p>SEQ ID NO: 1906</p> <p>SEQ ID NO: 2063</p> <p>QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG</p>

			<p>LTISLQPEDFATYYCLQHNPNYPFTFGQGTKVDIK RTVAAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSLSS TLTLKADYKHKVYACEVTHQGLSSPVTKSFNR GEC</p>	<p>RFTISRDN SKNTLYLQMNSLRVADTA VYVCARDG TIFGVVLGDYWGQGT LVTVSSASTKGPSVFFLAPS SKSTSGGT AALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQSSGL YSLSSVTVVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPKPKD TLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHN AAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKS LSLSPGK</p>
			<p>SEQ ID NO: 336</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACCAAGGGAAGCCCCCTA AGCTCTGATCTATGGTGCAATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTCAAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAACGAACGGTGGCT GCACCATCTGCTTTCATCTTCCCGCCATCTGATG AGCAGTTGAATCTGGAACCTGCCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAGTGGATACGCCCTCCCAAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCGGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCAAAAGAGCTTCAACA GGGAGAGTGT</p>	<p>SEQ ID NO: 493</p> <p>CAGGTGCAGTGGTGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAACATATGCAGACGCCGTGAAGGGCC GATTACCATCTCCAGAGACAATTCCAAGAATA CGCTGATCTGCAAAATGAACAGCCTGAGAGTCG CGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCCTGGTCAACCTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCTGGCTGCCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGGAACCTCAGGCGC CCTGACCAAGCGGTGTGCAACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTTGACCGTGGCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCCCCAAACCCCAAGGACAC</p>
IPS:360968	4B1.012	NA	<p>SEQ ID NO: 336</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACCAAGGGAAGCCCCCTA AGCTCTGATCTATGGTGCAATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTCAAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAACGAACGGTGGCT GCACCATCTGCTTTCATCTTCCCGCCATCTGATG AGCAGTTGAATCTGGAACCTGCCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAGTGGATACGCCCTCCCAAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCGGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCAAAAGAGCTTCAACA GGGAGAGTGT</p>	<p>SEQ ID NO: 493</p> <p>CAGGTGCAGTGGTGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAACATATGCAGACGCCGTGAAGGGCC GATTACCATCTCCAGAGACAATTCCAAGAATA CGCTGATCTGCAAAATGAACAGCCTGAGAGTCG CGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCCTGGTCAACCTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCTGGCTGCCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGGAACCTCAGGCGC CCTGACCAAGCGGTGTGCAACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTTGACCGTGGCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCCCCAAACCCCAAGGACAC</p>

	<div>SEQ ID NO: 1907</div> <div>DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QOKPGKAPKLLIYGASSLQSGVPSRFSGSGSTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR TVAAPSVFIIPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSITYLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC</div>	<div>SEQ ID NO: 2064</div> <div>QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKGG RFTISRDNSKNTLYLQMNSLRVADTA VYYCARDG TIFGVVLGDYWGQGTLLTVVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNATKPCPEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGGSFFLY SKLTVDKSRWQQGNVVFSCSVMHAEALHNHYTQKS LSLSPGK</div>
AA		

				SEQ ID NO: 337	SEQ ID NO: 494
				<p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAAGGAAAGCCCTA AGCTCTGATCTATGGTGCATCCAGTTTGCAA GTGGGTCCCCTTCAAGGTTCAAGGCGAGTGGAT CTGGGACAGAAATTCATCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAGTGGATATCAACGAACGGTGGCT GCACCATCTGCTTTCATCTTCCCGCCATCTGATG AGCAGTTGAATCTGGAACTGCCTCTGTTGTGT GCCTGCTGAATACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAA CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCCGAAATCAGCCATCAGG GCCTGAGCTCGCCCGTCAAAAGAGCTTCAACA GGGGAGAGTGT</p>	<p>CAGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCACTAATTTGGCA TGCACTGGTCCGCCAGGCTCCAGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACTCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAATA CGCTGATCTGCACATGAACAGCCTGAGAGTCG CGACACGGCTGTATTATTGTGCGCGAGATG GGACGATCTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGAACCCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGCTGCCGTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGC CCTGACCAAGCGGTGCACACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAAGCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAAACCCAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGGTGGGACGTGAGCCACGAAGACCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTGAGCGT CCTCACCGTCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCACAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCGAGCCCCGAGAACCCAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACCAAGTCAAGCTGACCTGCCTGCTGTCAAAG GCTTCTATCCAGCGGACATCGCCGTGGAGTGGG</p>
			4B1.013	NA	
			IPS:360974		

			<p>AGAGCAATGGCAGCCGGAGAACAACTACAAG ACCACGCTCCCGTCTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTAAA</p> <p>SEQ ID NO: 2065</p>	
			<p>QVQLVESGGGVVQGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAWIWYDASNENYADSVKVG RFTISRDNSKNTLYLHMNSLRVADTA VYCARDG TIFGVVLGDYWGQGTLLVTVSSASTKGPSVFPLAPS SKSTSGGT AALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK</p> <p>SEQ ID NO: 495</p>	
			<p>DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSTEFT LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLS TLTLTKADYEKHKVYACEVTHQGLSSLSPVTKSFNR GEC</p> <p>AA</p> <p>SEQ ID NO: 1908</p>	
			<p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACCAAGGAAAGCCCTA AGCTCTGATCTATGGTGATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTCAAGGCGCAGTGGAT CTGGGACAGAAATTCATCTCACAATCAGCAGCC TGACGCTGAAGATTTCGCAACTTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATAACAACGAACGGTGGCT GCACCATCTGTCTTCACTTCCCGCCATCTGATG AGCAGTTGAATCTGGAACCTGCCTCTGTGTGT GCCTGCTGAATAACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT</p> <p>NA</p> <p>SEQ ID NO: 338</p>	
IPS:360978	4B1.014		<p>CAGGTGCAGCTGGTGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGCGCAGTTATATGGTATGATGGA GTAATGAAAACTATGCAGAGCCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCACAAGAATA CGCTGATCTGCACATGAACAGCCTGAGAGTCG CGGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCAG CCTCCACCAAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCTCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCC</p>	

		<p>CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT</p>	<p>CGAACCGGTGACGGTGTCTGTGGAACCTCAGGCG CCTGACCAGCGGCGTGACACACCTTCCCGGCTGT CCTACAGTCTTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCCCACC GTGCCAGCACCTGAACCTCTGGGGGACCCGTC AGTCTTCTCTTCCCCCAAAACCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCAATATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAAGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACAGGTGACCTGACCTGCTGCTGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAA</p>
	AA	<p>DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT LTISLQPEDFATYYCLQHNNYPFTFGQGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLS TLTLTKADYEEKHKVYACEVTHQGLSPVTKSFNR GEC</p>	<p>SEQ ID NO: 2066</p> <p>QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAWIYDGSNENYADAVKG RFTISRDNSKNTLYLHMNSLRVADTA VYCARDG TIFGVVLGDYWGQGTLT VTVSSASTKGPSVFPLAPS SKSTSGGT AALGLCLVKDYFPEPVT VSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLMISRTPETVTCVVDVSHED</p>

				PEVKFNWYVVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVVFSCVMHEALHNHYTQKS LSLSPGK
				SEQ ID NO: 496 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTTCAGTAACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAACATATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAATA CGCTGATCTGCAAAATGAACAGCCTGAGAGTCG AGGACACGGCTGTGTAATTATTGTGCGCGAGATA GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGAAACCCGTGTCACCGTCTCCTCAG CCTCCACCAAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGCTGCCGTGTGTCAGGACTACTTCCC CGAACCGGTGACGGTGTGTCGTCAGGAACTCAGGCGC CCTGACCAAGCGGTGTCACACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACCTACACATGCCACC GTGCCAGCACCTGAACTCTGGGGGACCGTCT AGTCTTCCTCTTCCCCCAAACCCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGCGGTGGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAAGGACTGGCTGAATGG
				SEQ ID NO: 339 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACCAAGGAAAGCCCCA AGCTCTGATCTATGGTGCAATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTCAAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAGTGGATATCAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAATCTGGAACCTGCCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAAGAGAGGCCA AAGTACAGTGGAAGTGGATAACGCCCTCCAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT
				NA
		4B1.015		
		IPS:359785		

			<p>CAAGGAGTACAAAGTGCAAGGTCTCCAAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACAGGTGAGCCTGACCTGCCGTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGAGAACAACTACAAG ACCAGCCTCCCGTCTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
			<p>SEQ ID NO: 1910</p> <p>DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSITYSLSS TLTLTKADYEEKHKVYACEVTHQGLSSPVTKSFNR GEC</p>
		AA	<p>SEQ ID NO: 2067</p> <p>QVQLVESGGGVVQPGRLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDNSKNTLYQMNSLRVEDTAVYYCARDR TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAAAGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK</p>
IPS:360982	4B1.016	NA	<p>SEQ ID NO: 340</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGAGACAGAGTCACCATCATT GCCGGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACCAAGGAAAGCCCTA AGCTCTGATCTATGGTGATCCAGTTTGCAA GTGGGGTCCCTTCAAAGTTTCAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT</p>
			<p>SEQ ID NO: 497</p> <p>CAGTGCAGCTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTTCAGTAACTTTGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTACCATCTCCAGAGACAATTCCAAGAATA CGCTGTATCTGCAAAATGAACAGCCTGAGAGTCG</p>

	ACAGCATAAATAATTACCCCTTCACTTTTCGGCCAA GGGACCAAAGTGGATATCAACGAACGGTGGCT GCACCATCTGTCTTCACTTTCCCGCCATCTGATG AGCAGTTGAATCTGGAACCTGCCCTCTGTTGT GCCTGCTGAATAACTTCTATCCCAAGAGAGGCCA AAGTACAGTGGAAAGGTGGATAACGCCCTCCAAT CGGGTAAC'TCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCCGAAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	AGGACACGGCTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTTGGGGGACTACT GGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCAG CTCCACCAAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCTCTCAAAGAGCACCTCTGGGGGCACAGC GGCCCTGGCTGCTTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGTGGAATCAGGCGC CCTGACCAAGCGGCTGCACACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAAGCCC AGCAACACCAAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCACC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCAATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACCAAGGTGACCTGACCTGCCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGAGCGGAGACAACACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1911	SEQ ID NO: 2068
AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT	QVQLVESGGGVVQPGRSRLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVA VIWYDASNENYADAVKG

			<p>LTISLQPEDFATYYCLQHNPNYPFTFGQGTKVDIK RTVAAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSLSS TLTLKADYKHKVYACEVTHQGLSSPVTKSFNR GEC</p>	<p>RFTISRDN SKNTLYLQMNSLRVEDTAVYYCARDG TIFGVVLGDYWGQGTTLVTSSASTKGPSVFFLAPS SKSTSGGT AALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKD TLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNV FSCSV MHEALHNHYTQKS LSLSPGK</p>
			<p>SEQ ID NO: 341</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCACAGAAACCAAGGAAAGCCCCA AGGCCGTGATCTATGGTGATCCAGTTTGC AAA GTGGGTCCCTTCAAGGTTCAAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCTCACAAATCAGCAGCC TGACGCCGTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAACGAAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAATCTGGAACTGCCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAGTGGATACGCCCTCCCAAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCGGAAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCAAAAGAGCTTCAACA GGGAGAGTGT</p>	<p>SEQ ID NO: 498</p> <p>CAGGTGCAGTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTTCAGTAACTTTGGCA TGCACTGGTCCGCCAGGCCCAAGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGGA GTAATGAA AACTATGCAGACTCCGTGAAGGGCC GATTCAACCATCTCCAGAGACAATTCCAAGAAC CGCTGATCTGCACATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGTGCCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGGAACCTCAGGCGC CCTGACCAAGCGGTGTGCAACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTTGACCGTGGCTTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCACC GTGCCAGCACCTGAACTCTGGGGGACCGTCT AGTCTTCTCTTCCCCCCCCAAACCCCAAGGACAC</p>
IPS:335922	18F2	NA	<p>SEQ ID NO: 341</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCACAGAAACCAAGGAAAGCCCCA AGGCCGTGATCTATGGTGATCCAGTTTGC AAA GTGGGTCCCTTCAAGGTTCAAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCTCACAAATCAGCAGCC TGACGCCGTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAACGAAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAATCTGGAACTGCCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAGTGGATACGCCCTCCCAAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCGGAAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCAAAAGAGCTTCAACA GGGAGAGTGT</p>	<p>SEQ ID NO: 498</p> <p>CAGGTGCAGTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTTCAGTAACTTTGGCA TGCACTGGTCCGCCAGGCCCAAGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGGA GTAATGAA AACTATGCAGACTCCGTGAAGGGCC GATTCAACCATCTCCAGAGACAATTCCAAGAAC CGCTGATCTGCACATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGTGCCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGGAACCTCAGGCGC CCTGACCAAGCGGTGTGCAACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTTGACCGTGGCTTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCACC GTGCCAGCACCTGAACTCTGGGGGACCGTCT AGTCTTCTCTTCCCCCCCCAAACCCCAAGGACAC</p>

		<div>SEQ ID NO: 1912</div> <div>DIQMTQSPSSLSASIGDRVTITCRASQDLRNLYLGW YHQPGRKAPKRLIYGASSLQSGVPSRFSGSGSGTE FTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDI KRTVAAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSITYSL STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEN</div>	<div>SEQ ID NO: 2069</div> <div>QVQLVESGGGVVQPGRLSLRSCAASGFTFSNFGM HWVRQAPGKGLEWVAWIWYDGSNENYADSVKIG RFTISRDNSKNTLYLHMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLLTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNATKTPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVVFSCSVMEALHNHYTQKS LSLSPGK</div>
	AA		

				SEQ ID NO: 342	SEQ ID NO: 499
IP:360986	18F2.002	NA		<p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCAACAGAAACCAAGGAAAGCCCCTA AGCTCTGATCTATGGTGCATCCAGTTTGCAA GTGGGTCCCCTTCAAGGTTCAAGGCGAGTGGAT CTGGGACAGAATTCACTCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTGCAACTTATTACTGTCT ACAGCATAAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAGTGGATATCAACGAACGGTGGCT GCACCATCTGCTTTCATCTTCCCGCCATCTGATG AGCAGTTGAATCTGGAACCTGCCTCTGTTGTGT GCCTGCTGAATACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCCGAAATCACCCATCAGG GCCTGAGCTCGCCCGTCAAAAGAGCTTCAACA GGGGAGAGTGT</p>	<p>CAGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCACTAATTTGGCA TGCACTGGTCCGCCAGGCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCAGAAACA CGCTGATCTGCAAAATGAACAGCCTGAGAGCCG CGACACGGCTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGAACCCCTGGTCAACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGCTGCCGTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGC CCTGACCAAGCGGTGTCACACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGGCTTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAAGCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAAACCCAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGGTGGGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTGAGCGT CCTCACCGTCTGCACCAGGACTGGTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCGAGCCCCGAGAACCCAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACCAAGTCAAGCTGACCTGCCTGCTGTCAAAG GCTTCTATCCAGCGGACATCGCCGTGGAGTGGG</p>

			<p>AGAGCAATGGCAGCCGGAGAACAACTACAAG ACCACGCTCCCGTCTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCCTGGACAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTAAA</p> <p>SEQ ID NO: 1913</p> <p>DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSTE FTLTISLQPEDFATYYCLQHNYPFTFGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSITYSL STLTLSKADYEKHKVYACEVTHQGLSPVTKSFN RGEK</p>	<p>QVQLVESGGGVVQPGSRSLRSLSCAASGFTFSNFGM HWVRQAPGKGLEWVAWIWYDASNENYADAVKG RFTISRDNSKNTLYLQMNSLRAADTA VYCARDG TIFGVVLGDYWGQGTLLVTVSSASTKGPSVFPLAPS SKSTSGGT AALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLMISRTPETVTVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK</p> <p>SEQ ID NO: 2070</p>
		AA	<p>SEQ ID NO: 343</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCAATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTAG GCTGGTATCAACAGAAACCAAGGAAAGCCCTA AGCTCTGATCTATGGTGATCCAGTTTGCAAA GTGGGTCCCTTCAAGGTTCAAGGGCAGTGGAT CTGGGACAGAAATTCATCTCACAATCAGCAGCC TGACGCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAACGAAACGGTGGCT GCACCATCTGTCTTCACTTCCCGCCATCTGATG AGCAGTTGAATCTGGAACCTGCCTCTGTGTGT GCCTGCTGAATAACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT</p>	<p>CAGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTTCAGTAACCTTTGGCA TGCACTGGTCCGCCAGGCCCAAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGAGCCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAAACA CGCTGATCTGCACATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCAG CCTCCACCAAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCTCTCCAAGAGCACCTCTTGGGGGACAGC GGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCC</p> <p>SEQ ID NO: 500</p>
IPS:360995	18F2.003	NA	<p>SEQ ID NO: 343</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCAATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTAG GCTGGTATCAACAGAAACCAAGGAAAGCCCTA AGCTCTGATCTATGGTGATCCAGTTTGCAAA GTGGGTCCCTTCAAGGTTCAAGGGCAGTGGAT CTGGGACAGAAATTCATCTCACAATCAGCAGCC TGACGCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAACGAAACGGTGGCT GCACCATCTGTCTTCACTTCCCGCCATCTGATG AGCAGTTGAATCTGGAACCTGCCTCTGTGTGT GCCTGCTGAATAACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT</p>	<p>CAGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTTCAGTAACCTTTGGCA TGCACTGGTCCGCCAGGCCCAAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGAGCCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAAACA CGCTGATCTGCACATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCAG CCTCCACCAAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCTCTCCAAGAGCACCTCTTGGGGGACAGC GGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCC</p> <p>SEQ ID NO: 500</p>

		<p>CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGAGAGTGT</p>	<p>CGAACCGGTGACGGTGTCTGTGGAACCTCAGGCG CCTGACCAGCGGCGTGACACACCTTCCCGGTGT CCTACAGTCTTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCCCACC GTGCCAGCACCTGAACCTCTGGGGGACCCGTC AGTCTTCTCTTCCCCCAAAACCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCAATATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAAGACTGGCTGAATGG CAAGGAGTACAAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCATCCCGGAGGAGATGACCA AGAACAGGTGACCTGACCTGCTGCTGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAA</p>
	AA	<p>DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSTE FTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP EAKVQWVKVDNALQSGNSQESVTEQDSKDSYSTLS STLTLSKADYEKHKVYACEVTHQGLSPVTKSFN RGEC</p>	<p>SEQ ID NO: 1914</p> <p>SEQ ID NO: 2071</p> <p>QVQLVESGGGVVQGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAWIYDASNENYADAVKG RFTISRDNSKNTLYLHMNSLRAADTA VYCARDG TIFGVLDGYWGGQTLTVTSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLMISRTPETVTCVVDVSHED</p>

				PEVKFNWYVVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVVFSCVMHEALHNHYTQKS LSLSPGK
			SEQ ID NO: 344	SEQ ID NO: 501
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCACACAGAAACCAAGGAAAGCCCCA AGCTCTGATCTATGGTGCAATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTCAAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTGCAACTTATTACTGTCT ACAGCATAAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAGTGGATATCAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAATCTGGAACCTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCACAGAGAGGCCA AAGTACAGTGGAAGTGGATAACGCCCTCCAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	CAAGTGCAGCTGGTGGAGTCTGGGGGAGGCGGTG GTCCAGCCTGGGAGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTTCACTAACCTTTGGCA TGCACTGGTCCGCCAGGCCCAAGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAACATATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCACAGAACAA CGCTGATCTGCAATGAACAGCCTGAGAGCCG CGGACACGGCTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCAGGGAACCTGTGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCTGGCTGCCGTGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGC CCTGACCAAGGGCGTGCACACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAGCCC AGCAACACCAAGGTGGACAAAGAAAGTTGAGCC CAAATCTTGTGACAAACCTACACATGCCACC GTGCCACGACCTGAACCTCTGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGCGGTGGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAAGGACTGGCTGAATGG
			18F2.004	
			IPS:360999	

			<p>CAAGGAGTACAAAGTCAAGGTCTCCACAAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACAGGTCAAGCTGACCTGCCGTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGAGAACAACTACAAG ACCAGCCTCCCGTCTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAAA</p> <p>SEQ ID NO: 1915</p>	<p>QVQLVESGGGVVQPGRLSLRSCAASGFTFSFGM HWVRQAPGKGLEWVAWIWYDASNENYADAVKG RFTISRDNSKNTLYQMNSLRAADTA VYCARDG TIFGVLDGYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGT AALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFELY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK</p> <p>SEQ ID NO: 2072</p>
	AA		<p>DIQMTQSPSSLSASIGDRVTITCRASQDLRNLYLGW YHQPGRKAPKLLIYGASSLQSGVPSRFSGSGGTE FTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDI KRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSITYSL STLTLSKADYEKHKVYACEVTHQGLSPVTKSFN RGEK</p> <p>SEQ ID NO: 345</p>	<p>QVQLVESGGGVVQPGRLSLRSCAASGFTFSFGM HWVRQAPGKGLEWVAWIWYDASNENYADAVKG RFTISRDNSKNTLYQMNSLRAADTA VYCARDG TIFGVLDGYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGT AALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFELY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK</p> <p>SEQ ID NO: 502</p>
IPS:361005	18F2.005	NA	<p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGAGACAGAGTCACCATCATT GCCGGGCAAGTCAGGACCTTAGAAATTATTAG GCTGGTATCAACAGAAACCAAGGAAAGCCCTA AGCGCTGTATCTATGGTGATCCAGTTTGCAA GTGGGGTCCCTTCAAGGTTCAAGGCGCAGTGGAT CTGGGACAGAAATTCATCTCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT</p> <p>SEQ ID NO: 345</p>	<p>CAGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTTCAGTAACTTTGCA TGCACTGGTCCGCCAGGCCCAAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAACATATGCAGACGCCGTGAAGGGCC GATTACCATCTCCAGAGACAATTCCAAAGAAC CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG</p> <p>SEQ ID NO: 502</p>

	ACAGCATAAATAATTACCCCTTCACTTTTCGGCCCT GGGACCAAAGTGGATATCAACGAACGGTGGCT GCACCATCTGTCTTTCATCTTCCCGCCATCTGATG AGCAGTTGAATCTGGAACCTGCCCTCTGTTGT GCCTGCTGAATAACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAAGGTGGATAACGCCCTCCAT CGGGTAAC'TCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCCGAAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	CGGACACGGCTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTTGGGGGACTACT GGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCAG CTCCACCAAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGACACAGC GGCCCTGGCTGCTTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGTGGAATCAGGCGC CCTGACCAAGCGGCTGCACACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACC GTGCCAGCACCTGAATCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCAATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACCAAGTCAAGCTGACCTGCCCTGGTCAAAG GCTTCTATCCAGCGCATCGCCGTGGAGTGGG AGAGCAATGGGAGCCGGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1916	SEQ ID NO: 2073
AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRLNYLGW YQQKPGKAPKRLIYGASSLSQGVPSRFSGSGSGTE	QVQLVESGGGVVQPGSRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVA VIWYDASNENYADAVKG

			FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNFFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSITYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEK	RFTISRDN SKNTLYLQMNSLRAADTA VYYCARDG TIFGVVLGDYWGQGT LVTVSSASTKGPSVFPLAPS SKSTS SGT AALGCL VKDYPPEPVT VSWNSGALTS GVHTFPAVLQSSGL YSLSSVTVVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHN AKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKS LSLSPGK
			SEQ ID NO: 346	SEQ ID NO: 503
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCAACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCAACAGAAACCAAGGAAAGCCCCTA AGCGCTGATCTATGGTGCAATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTTCAGCGGCAGTGGAT CTGGGACAGAAATTCACCTCTCACAAATCAGCAGCC TGACGCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAGTGGATATCAAAACGAAACGGTGGCT GCACCATCTGTCTTCACTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACCTGCCCTCTGTTGTGT GCCTGCTGAATAACTTCTATATCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT CGGGTAAC TCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCAACCATCAGG GCCTGAGCTCGCCCGTCAAAAGAGCTTCAACA GGGGAGAGTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCAAGCAAGGGGC TGGAGTGGTGGCAGTTATATGTTGATGATGCAA GTAATGAAAAC TATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACAA CGCTGTATCTGCACATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGAACCTGGTCAACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCTCTCAAAGAGCACCTCTGGGGGCAACAGC GGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCC CGAAACGGTGACGGTGTCTGTGGAAC TCAAGGCG CCTGACCAAGCGGTGCACACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAA TCTTGTGACAA AACTCACACATGCCACC GTGCCACGACCTGA ACTCTGGGGGACCGTCT AGTCTTCTCTTCCCCCCCCAAACCCCAAGGACAC
IPS:361009	18F2.006	NA		

		<div>SEQ ID NO: 1917</div> <div>DIQMTQSPSSLSASIGDRVTITCRASQDLRNLYLGW YQQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTE FTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSYSTYSL STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEN</div>	<div>SEQ ID NO: 2074</div> <div>QVQLVESGGGVVQPGRLSLRSCAASGFTFSNFGM HWVRQAPGKGLEWVAWIWYDASNENYADAVKVG RFTISRDNSKNTLYLHMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLLTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNATKPCPEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVVFSCSVMHAEALHNHYTQKS LSLSPGK</div>
	AA		

				SEQ ID NO: 347	SEQ ID NO: 504			
				GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCACAGAAACCAAGGAAAAGCCCCTA AGCTCCTGATCTATGGTGCAATCCAGTTTGCAA GTGGGGTCCCCTTCAAGGTTCAAGCGGCAGTGGAT CTGGGACAGAAATTCAC'TCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATATAATTACCCCTTCACTTTTCGGCCCT GGGACCAAAGTGGATATCAAAAGAACGGTGGCT GCACCATCTGTCTTCAATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAAC'TGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT CGGGTAACTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCCTGCGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCAACAAGAGCTTCAACA GGGGAGAGTGT				CAGGTGCAGCTGGTGAGTCTGGGGGAGGCGTGT GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAAC'TTGGCA TGCACTGGGTCCGCCAGGCCCAAGCAAGGGGC TGGAGTGGGTGGCAGTTATATGATGATGCAAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCAACCATCTCCAGAGACAATTCAGAAACA CGCTGATCTGCACATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGAACCCCTGGTCAACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGTGCCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGTGGAAC'TCAGGCGC CCTGACCAGCGCGTGCACACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCTC'TCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCACC GTGCCAGCACCTGAAC'TCCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGACGTGAGCCACGAAGACCC'TGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTCAAGCT CCTCACCGTCTGCACCAAGACTGGCTGAATGG CAAGGAGTACAAGTGC'AAGGTCTCCAAACAAGC CCTCCAGCCCCCATCGAGAAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCCAGGTGT ACACCC'TGCCCTCATCCCGGGAGGAGATGACCA AGAACAGGTCAAGCTGACCTGACCTGCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG
				NA				
			18F2.007					
			IPS:361013					

			<div>SEQ ID NO: 1918</div> <div>DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YHQKPGKAPKLLIYGASSLQSGVPSRFSGSGGTE FTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNFFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSITYSLS STLTLSKADYEKHKVYACEVTHQGLSPVTKSFN RGEK</div>	<div>SEQ ID NO: 2075</div> <div>QVQLVESGGGVVQPGRLSLRSLSCAASGFTFSNFGM HWVRQAPGKGLEWVAWIWYDASNENYADAVKGG RFTISRDNSKNTLYLHMNSLRAADTA VYYCARDG TIFGVVLGDYWGQGTLLTVVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPTVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK</div>
	AA		<div>SEQ ID NO: 348</div> <div>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTAATTAG GCTGGTATCACACAGAAACCAGGGAAGCCCCCTA AGCGCTGATCTATGGTGCAATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTCAAGCGGCAGTGGAT CTGGGACAGAAATTCATCTTCACAAATCAGCAGCC TGCAAGCTGAAGATTTCGCAACTTAATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCCGGCCCT GGGACCAAAAGTGGATATCAAACGAACGGTGGCT GCACCATCTGTCTTCACTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACTGCCCTCTGTTGTGT GCCTGCTGAATAACTTCTATATCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT</div>	<div>SEQ ID NO: 505</div> <div>CAGGTGCAAGCTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGAGGTCCTCTGAGACTCTCCTGT GCAGGCTCTGGATTCACTTTCAGTAACCTTTGGCA TGCACTGGGTCCGCCAGGCCCAAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGTTATGATGCAA GTAATGAAAACATATGACAGACCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAAACA CGCTGATCTGCAATATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTAATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGAACCCCTGGTCAACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCTCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCC</div>
IPS:361017	18F2.008	NA		

		<p>CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT</p>	<p>CGAACCGGTGACGGTGTCTGTGGAACCTCAGGCG CCTGACCAGCGGCGTGACACACCTTCCCGGCTGT CCTACAGTCTTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCCCACC GTGCCAGCACCTGAACCTCTGGGGGACCCGTC AGTCTTCTCTTCCCCCACAACCCAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCAATATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAAGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACAGGTGACCTGACCTGCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
	AA	<p>DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YHQPGRKAPKRLIYGASSLQSGVPSRFSGSGGTE FTLTISLQPEDFATYYCLQHNHYPTFGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWVKVDNALQSGNSQESVTEQDSKDSSTYSLS STLTLSKADYEKHKVYACEVTHQGLSPVTKSFN RGEC</p>	<p>SEQ ID NO: 1919</p> <p>SEQ ID NO: 2076</p> <p>QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAWIYDASNENYADAVKG RFTISRDNSKNTLYQMNSLRAADTAVYCARDG TIFGVLDGYWGQGTLTIVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLMISRTPETVTCVVDVSHED</p>

			PEVKFNWYVVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVVFSCVMHEALHNHYTQKS LSLSPGK
			SEQ ID NO: 506 CAGGTGACGTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTTCAGTAACTTTGGCA TGCACTGGTCCGCCAGGCCCAAGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGGAA GTAATGAAACATATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAAC CGTGTATCTGCAATGAACAGCCTGAGAGCCG CGGACACGGCTGTATTACTGTGCGGAGAGATG GGACGATCTTGGAGTGGTCTTGGGGGACTACT GGGGCAGGGAACCTGGTCAACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCTGGCTGCTGTCAGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTGTCGTCGAACTCAGGCGC CCTGACCAAGGGCGTGCAACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACCTACACATGCCACC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGCGGTGGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAAGGACTGGCTGAATGG
			SEQ ID NO: 349 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTTATTAG GCTGGTATCAACAGAAACCAAGGAAAGCCCCA AGCTCTGATCTATGGTGCAATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTCAAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTGCAACTTATTACTGTCT ACAGCATAAATTAATACCCCTTCACTTTCGGCCCT GGGACCAAGTGGATATCAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAATCTGGAACCTGCCTCTGTTGTGT GCCTGCTGAATACTTCTATCCCAAGAGAGGCCA AAGTACAGTGGAAGTGGATACGCCCTCCCAAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT
			NA
		18F2.009	
		IPS:361021	

			<p>CAAGGAGTACAAAGTGCAAGGTCTCCAAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACAGGTGAGCCTGACCTGCCGTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGAGAACAACTACAAG ACCAGCCTCCCGTCTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAAA</p> <p>SEQ ID NO: 1920</p>	<p>QVQLVESGGGVVQPGRLSLRSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDGSNENYADAVKG RFTISRDNSKNTLYQMNSLRRAADTA VYCARDG TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGT AALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLISRTPETVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK</p> <p>SEQ ID NO: 2077</p>
	AA		<p>DIQMTQSPSSLSASIGDRVTITCRASQDLRNLYLGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSTE FTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQW/KVDNALQSGNSQESVTEQDSKDSITYSL STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEK</p> <p>SEQ ID NO: 350</p>	<p>CAGTGCAGCTGGTGGAGTCTGGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTTCAGTAACTTTGGCA TGCACTGGTCCGCCAGGCCCAAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAA AACTATGCAGACTCCCGTGAAGGGCC GATTCAACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG</p> <p>SEQ ID NO: 507</p>
IPS:361028	18F2.010	NA	<p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGAGACAGAGTCACCATCATT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCAACAGAAACCAAGGAAAGCCCTA AGCTCTGATCTATGGTGATCCAGTTTGC AAA GTGGGGTCCCTTCAAGGTTCAAGGGCAGTGGAT CTGGGACAGAAATTCATCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT</p> <p>SEQ ID NO: 350</p>	

	ACAGCATAAATAATTACCCCTTCACTTTCCGGCCCT GGGACCAAAGTGGATATCAACGAACGGTGGCT GCACCATCTGTCTTTCATCTTCCCGCCATCTGATG AGCAGTTGAATCTGGAACCTGCCCTCTGTTGT GCCTGCTGAATAACTTCTATCCCAAGAGAGGCCA AAGTACAGTGGAAAGGTGGATAACGCCCTCCAT CGGGTAAC'TCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCCGAAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGAGAGTGT	CGGACACGGCTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTTGGGGACTACT GGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCAG CTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCTCTCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGCTGCTTGGTCAAGGACTACTTCCC CGAACGGTGACGGTGTCTGTGGAATCAGGCGC CTGACCAAGCGGCTGCACACCTTCCCCGGCTGT CTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAAGCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCAATATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACCAAGTCAAGCTGACCTGCCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGAGCCGGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGAGAAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1921	SEQ ID NO: 2078
AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE	QVQLVESGGGVVQPGSRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVA VIWYDASNENYADSVKKG

			FTLTISSLQPEDFATYYCLQHNNYPFTGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNFFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSYLSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEK	RFTISRDN SKNTLYLQMNSLRAADTA VYYCARDG TIFGVVLGDYWGQGT LVTVSSASTKGPSVFLAPS SKSTSGGT AALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQSSGL YLSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKD TLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHN A KTKPCEEQYGYSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFELY SKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKS LSLSPGK
			SEQ ID NO: 351	SEQ ID NO: 508
IP:360535	18F2.011	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGAGACAGAGTCACCATCATT GCCGGCAAGTCAGGACCTTAGAAAATTATTAG GCTGATATCAACAGAAACCAAGGAAAGCCCTA AGCTCCTGATCTATGTCATCCAGTTTGCAA GTGGGTCCCTTCAAGGTT CAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCACAAATCAGCAGCC TGACGCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAAACGAACGGTGGCT GCACCATCTGTCTTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAAC TGCCTCTGTGTGT GCCTGCTGAATAACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAAGTGGATAACGCCCTCCAAT CGGGTAAC TCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCGAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCA CAAAGAGCTTCAACA GGGGAGAGTGT	CAGGTG CAGCTGGTGAGTCTGGGGAGGCGTG GTCCAGCCTGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAAC TTTGGCA TGCACTGGGTCCGCCAGGCC CAGCAAGGGC TGGAGTGGTGCGAGTTATATGTTATGATGCAA GTAATGAA AACTATG CAGACGCCGTGAAGGCC GATTCACCATCTCCAGAGACAATTCAGAAACA CGCTGATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTAATTACTGTGCGAGAGATA GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGAAACCTGGTCACCGTCTCCTCAG CCTCCACCAAAGGCCCATCGGTCTTCCCTGGC ACCTCCTCCAAGAGCACCTCTGGCAAGGACTACTCCC GGCCTGGGTGCTGGTGTCTGCAACCTCAGGCGC CGAACCGGTGACGGTGTGTCACCTTCCCGGTGT CCTGAC CAGCGGTGCACACTCTCCTCAGCAGC CCTACAGTCTCAGGACTCTACTCCTCAGCAGC GTGTGACCGTGCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAA AACTCACACATGCCACC GTGCCAGCACCTGAACTCTTGGGGGACCGTC AGTCTCCTCTTCCCCC CAAACCCCAAGGACAC

		<div>SEQ ID NO: 1922</div> <div>DIQMTQSPSSLSASIGDRVTITCRASQDLRNLYLGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSTE FTLTISLQPEDFATYYCLQHNNYPFTFGQGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSITYSL STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEN</div>
	AA	<div>SEQ ID NO: 2079</div> <div>QVQLVESGGGVVQPGRLSLRSCAASGFTFSNFGM HWVRQAPGKGLEWVAWIYDASNENYADAVKGV RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLGDYWGQGTLLTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNATKTPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVVFSCSVMHEALHNHYTQKS LSLSPGK</div>

IP:361035	18F2.012	NA	SEQ ID NO: 352	SEQ ID NO: 509
			<p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCAACAGAAACCAAGGAAAGCCCTA AGCTCTGATCTATGGTGCATCCAGTTTGCAA GTGGGTCCCCTTCAAGGTTCAAGGCGAGTGGAT CTGGGACAGAATTCACTCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTGCAACTTATTACTGTCT ACAGCATAAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAGTGGATATCAACGAACGGTGGCT GCACCATCTGCTTTCATCTTCCCGCCATCTGATG AGCAGTTGAATCTGGAACCTGCCTCTGTTGTGT GCCTGCTGAATACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCCGAAATCAGCCATCAGG GCCTGAGCTGCCCCGTACAAAGAGCTTCAACA GGGGAGAGTGT</p>	<p>CAGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCACTAATTTGGCA TGCACTGGTCCGCCAGGCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAAACA CGCTGATCTGCAAAATGAACAGCCTGAGAGCCG AGGACAGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGAACCCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGCTGCCGTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGC CCTGACCAAGCGGTGTCACACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACC GTGCCAGCACCTGAACCTCTGGGGGACCGTCT AGTCTTCTCTTCCCCCAAACCCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAAGACCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTGAGCGT CCTCACCGTCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCACAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCGAGCCCCGAGAACCCAGGTGT ACACCTGCCCTCCATCCCGGAGGAGATGACCA AGAACCAGGTCAAGCTGACCTGCCTGCTCAAG GCTTCTATCCAGCGGACATCGCCGTGGAGTGGG</p>

			<div>AGAGCAATGGCAGCCGGAGAACAACTACAAG ACCACGCTCCCGTCTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAAA</div> <div>SEQ ID NO: 1923</div> <div>DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSTE FTLTISLQPEDFATYYCLQHNNYPFTFGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLS STLTLSKADYEKHKVYACEVTHQGLSPVTKSFN RGEK</div>
	AA		<div>QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAWIWYDASNENYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR DGTIFGVVLGDYWGQGTLLTVVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPETVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVVFSCSVMHEALHNHYTQKS LSLSPGK</div> <div>SEQ ID NO: 2080</div>
IPS:359940	2F11.002	NA	<div>GACATCCAGATGACCCAGTCTCCATCCTCCTCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTAA ATTGGTATCAGCAGAAACCAAGGAAAGCCCTA AGCTCCTGATCTACGATGCATCCAATTTGGAAA CAGGGTCCCATCAAGGTTCAAGTGGAAAGTGGAT CTGGGACAGATTTTAGTCTCACCATCAGCAGCC TGCAGCCTGAAGATTTTGCAACATAATTACTGTCA ACAGTATGATATTCTCCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGAACGGTGGCTG CACCATCTGTCTTCACTTCTCCCGCCATCTGATGA GCAGTTGAAAATCTGGAACTGCCTCTGTTGTGTGC CTGCTGAATAACTTCTATCCCAAGAGAGGCCAAA GTACAGTGGAAAGGTGGATAACGCCCTCCCAATCG</div> <div>SEQ ID NO: 353</div>
			<div>CAGGTGCAACTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTCACTAGCTATGGC ATGCACCTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAATACTATGCAGACGCCGTGAAGGGC CGATTCAACCATCTCCAGGGACAAATCCAAAGAAC ACGCTGTATCTGCAAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTGGAGTGGTCTTACTACTGTG GGCCAGGGAACCTGGTCAACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA CCCTCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC</div> <div>SEQ ID NO: 510</div>

		<p>GGTAACTCCCAGGAGAGTGTCACAGAGCAGGAC AGCAAGGACAGCACCTACAGCCTCAGCAGCACC CTGACGCTGAGCAAGCAGACTACGAGAAACA CAAAGTCTACGCCTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCACAAAGAGCTTCAACAG GGGAGAGTGT</p>	<p>GAACCGGTGACGGTGTCTGTGGAACCTCAGGGGCC CTGACCAGCGGCGTGACACACCTTCCCGGCTGTC CTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCCCACC GTGCCAGCACCTGAACCTCTGGGGGACCCGTC AGTCTTCTCTTCCCCCAAAACCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCAATATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAAGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACAGGTGACCTGACCTGCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGAGAACAACTACAAG ACACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAA</p>
	AA	<p>DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGGTD FSLTISLQPEDFATYYCQQYDILLTFGGGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLS TLTLTKADYEEKHKVYACEVTHQGLSSPVTKSFNR GEC</p>	<p>SEQ ID NO: 2081</p> <p>QVQLVESGGGVVQPRSLRLSCAASGFTFSYGM HWVRQAPGKGLEWVAWIYDASNKYADAVKVG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLDYWQGQTLVTVSSASTKGPSVFPLAPSS KSTSGGTAAALGCLVKDYFPEPTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKEPKSCDKTHHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE</p>

				<p>VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK</p>
				<p>SEQ ID NO: 354</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTTAA ATTGGTATCAGCAGAAACCAAGGGAAGCCCCTA AGCTCTGATCTACGATGCATCCAAATTTGGAAA CAGGGTCCCATCAAGGTTCAAGTGGAAAGTGGAT CTGGGACAGATTTTAGTCTCACCATCAGCAGCC TGCAGCCTGAAGATTTTGGCAACATATTACTGTCA ACAGTATGATATTCTCCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGAACGGTGGCTG CACCATCTGTCTTCACTTCCCGCCCATCTGATGA GCAGTTGAAATCTGGAACCTGCTCTGTTGTGTGC CTGCTGAATAACTTCTATCCAGAGAGGCCAAA GTACAGTGGAGGTGGATAACGCCCTCCCAATCG GGTAACCTCCAGGAGAGTGTACAGAGCAGGAC AGCAAGGACAGCACCTACAGCCTCAGCAGCACCC CTGACGCTGAGCAAGCAGACTACGAGAAACA CAAAAGTCTACGCTGCGAAGTCAACCATCAGGG CCTGAGCTCGCCCGTCAAAAGAGCTTCAACAG GGGAGAGTGT</p>
				<p>SEQ ID NO: 511</p> <p>CAGTGCAACTGGTGGAGTCTGGGGGAGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCAACCTTCAGTAGCTATGGC ATGCACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAATACTATGCAGACGCCGTGAAGGGC CGATTCAACATCTCCAGCGACAATTCCAAGAAC ACGCTGATCTGCAAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTGGAGTGGTCTTGACTACTGG GGCCAGGGAACCTGGTCAACCGTCTCCTCAGCC TCCACAAAGGCCCATCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCAACCTCTGGGGGCACAGCG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCC CTGACCAAGCGGTGCACACCTTCCCCGGCTGTC CTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACC GTGCCAGCACCTGAACCTCTGGGGGACCGTCTC AGTCTTCTCTTCCCCCAAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGCGGTGGA GGTGCAATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTACGCGT CCTCACCGTCTTGCAACCAAGGACTGGCTGAATGG</p>

			<p>CAAGGAGTACAAAGTGCAAGGTCTCCAAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACAGGTGAGCCTGACCTGCCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGAGAACAACTACAAG ACCAGCCTCCCGTCTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAAA</p> <p>SEQ ID NO: 1925</p>	
			<p>QVQLVESGGGVVQGRSLRLSCAASGFTSSYGM HWVRQAPGKGLEWVAVIWYDASNKYAYADA VKG RFTISSDNSKNTLYLQMNLSRAEDTAVYYCARDR TIFGVLDYWGQGTLVTVSSASTKGPSVPFLAPSS KSTSGGTAAALGCLVKDYFPEPTVSWNSGALTSG VHTFPAVLQSSGLYSLSVTVTPSSSLGTQTYICNV NHKPSNTKVDKKEPKSCDKTHTCTPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFNCSVMHEALHNHYTQKSLS LSPGK</p> <p>SEQ ID NO: 2082</p>	
	AA		<p>DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGGTD FSLTISLQPEDFATYYCQQYDILLTFGGGKVEIK RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSITYSLSS TLTLTKADYEKHKVYACEVTHQGLSPVTKSFNR GEC</p> <p>SEQ ID NO: 355</p>	
IPS:361043	2F11.004	NA	<p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCACTCTGTAGGAGACAGAGTCACCATCATT GCCAGGCGAGTCAGGACATTAGCAACTATTAA ATTGGTATCAGCAGAAACCAAGGAAAGCCCCCTA AGCTCTGATCTACGATGCATCCCAATTTGGAAA CAGGGTCCCATCAAGGTTTCAGTGGAAGTGGAT CTGGGACAGATTTTAGTCTCACCATCAGCAGCC TGCAGCCTGAAGATATTGCAACATATTACTGTC</p> <p>SEQ ID NO: 512</p>	

		AACAGTATGATATTCTCCTCACTTTTCGGCGGAG GGACCAAGGTGGAGATCAAGCGAACGGTGGCT GCACCATCTGTCTTTCATCTTCCCGCCATCTGATG AGCAGTTGAATCTGGAACCTGCCCTCTGTTGT GCCTGCTGAATACTTCTATCCAGAGAGGCCA AAGTACAGTGAAGGTGGATAACGCCCTCCAAT CGGGTAAC'TCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGACGATTTTGGAGTGGTCTTGACTACTGG GGCCAGGGAACCTGGTCAACCGTCTCCTCAGCC TCCACCAAGGCCCATCGGTCTTCCCCCTGGCA CCCTCTCCAAGAGCACCTCTGGGGGCACAGG GCCC'TGGCTGCCTGGTCAAGGACTACTTCCCC GAACCGGTACGGTGTCTGTGGAAC'TCAGGGGCC CTGACCAAGCGGTGCACACCTTCCCGGCTGTC CTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCTTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACC GTGCCAGCACCTGAAC'TCCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACCAAGGTACGCTGACCTGCCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGACAACATACAAG ACCAAGCCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAAA
	AA	SEQ ID NO: 1926 DIQMTQSPSSLSASVGDRTVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD	SEQ ID NO: 2083 QVQLVESGGGVVQPRSLRLSCAASGFTFSYGM HWVRQAPGKGLEWVA VIWYDASNKY YADAVKG

			<p>FSLTISSLQPEDIATYYCQYDILLTFGGGKVEIKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNFFYPREA KVQWKVDNALQSGNSQESVTEQDSKSDSTYLSST LTLKADYEEKHKVYACEVTHQGLSSPVTKSFNRG EC</p>	
IPS:361049	2F11.005	NA	<p>SEQ ID NO: 356</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTAA ATTGGTATCAGCAGAAACCAAGGAAAGCCCCTA AGCTCCTGATCTACGATGCATCCAAATTTGGAAA CAGGGTCCCATCAAGGTTCAAGTGGAAAGTGGAT CTGGGACAGATTTTAGTTTCAACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATATTCTCCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGAACGGTGGCTG CACCATCTGTCTTCACTCTCCCGCCATCTGATGA GCAGTTGAAAATCTGGAACCTGCCCTCTGTTGTGCG CTGCTGAATAAAGTCTATATCCAGAGAGGCCAAA GTACAGTGGAAAGGTGGATAACGCCCTCCAAATCG GGTAACTCCAGAGAGAGTGTCACAGAGCAGGAC AGCAAGGACAGCACCTACAGCCTCAGCAGCACCC CTGACGCTGAGCAAGCAGAGACTACGAGAAACA CAAAAGTCTACGCTGCGAAGTCAACCCATCAGGG CCTGAGCTCGCCCGTCACAAAGAGCTTCAACAG GGGAGAGTGT</p>	
			<p>SEQ ID NO: 513</p> <p>CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTCAGTAGCTATGGC ATGCACTGGTCCCGCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAATACTATGCAGAGCGCGTGAAGGGC CGATTACCATCTCCAGGGACAATTCCAAGAAC ACGCTGATCTGCAAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTGGAGTGGTCTTGACTACTGG GGCCAGGGAACCTGGTCAACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCTCTGGGGGCAACAGCG GCCCTGGGCTGCCGTGGTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCTGTGGAAC TCAAGGCGC CTGACCAAGCGGTGCACACCTTCCCCGGCTGTC CTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAAATCTTGTGACAAAAC TCAACATGCCACC GTGCCAGCACCTGAAC TCTGGGGGACCGTCTC AGTCTTCTCTTCCCCCCTCAACCC AAGGACAC</p>	

		<p>CCTCATGATCTCCGGACCCCTGAGGTACATG CGTGGTGGTGACGTGAGCCACGAAGACCC'TGA GGTCAAGT'TCAACTGGTACGTGGACGGCGTGGA GGTGCAATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTCAAGCGT CCTCACCGTCTCGACCAAGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCCATCGAGAAAACCATCTCCAA AGCCAAGGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCGGGAGGAGATGACCA AGAACAGGTACGCTGACCTGACCTGGTCAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGGAACAACACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
	SEQ ID NO: 1927	SEQ ID NO: 2084
	<p>DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGGTD FSFTISSLPQEDFATYYCQQYDILLTFGGGKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSYSTYSLSS TLTSLKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC</p>	<p>QVQLVESGGGVVQPGRLRLSCAASGFTFSYGM HWVRQAPGKGLEWVAWIWDASNKYADAVKVG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLDYWGQGTLYTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCTPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKSA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK LTVDKSRWQQGNVVFSCSVMHEALHNHYTQKSLS LSPGK</p>
	AA	

IP:361055	2F11.006	NA	SEQ ID NO: 357	SEQ ID NO: 514
			<p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTTAA ATTGGTATCAGCAGAAACCAAGGAAAGCCCCTA AGCTCTGATCTACGATGCATCCAATTTGGAAA CAGGGTCCCATCAAGGTTCAAGTGGAGTGGAT CTGGGACAGATTTTAGTCTCACCATCAGCAGCC TGCAGCCTGAAGATATTGCAACATATTACTGTC AACAGTATGATATTCTCTCACTTTCGGCGGAG GGACCAAGGTGGAGATCAAGCGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACCTGCCTCTGTTGT GCCTGCTGAATACTTCTATCCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCCGAAATCACCCTCAGG GCCTGAGCTCGCCCGTCAAAAGAGCTTCAACA GGGGAGAGTGT</p>	<p>CAGTGCAACTGGTGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCTCTGGATTCACTTTCAGTAGCTATGGC ATGCACTGGTCCCGCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAATACTATGCAGACGCCGTGAAGGGC CGATTCAACATCTCCAGCGACAATTCCAAGAAC ACGCTGATCTGCAAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTGGAGTGGTCTTGACTACTGG GGCCAGGGAACCTGGTCAACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA CCCTCTCCAAGAGCACCTCTGGGGGCACAGG GCCCTGGCTGCCTGGTCAAGGACTACTTCCCC GAACCGGTACGGTGTCTGTGGAACCTCAGGGCC CTGACCAAGCGGTGCACACCTTCCCGGCTGTC CTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAGCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGGTGGTGACGTGAGCCACGAAGACCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCCTTGTGTGACCGT CCTCACCGTCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAAGTGAAGGTCTCCAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCGAGCCCCGAGAACCCAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACCAAGTCAAGCTGACCTGCCTGCTCAAG GCTTCTATCCAGCGGACATCGCCGTGGAGTGGG</p>

			<p>AGAGCAATGGGAGCCGGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCCTGGACAAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAAA</p> <p>SEQ ID NO: 1928</p> <p>DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGGTD FSLTISLQPEDATYYCQQYDILLTFGGGKVEIKR TVAAPSVFIIPPSDEQLKSGTASVCLLNFFPREA KVQWKVDNALQSGNSQESVTEQDSKDSYSTLSST LTLKADYEEKHKVYACEVTHQGLSSPVTKSFNRG EC</p>	<p>AGAGCAATGGGAGCCGGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCCTGGACAAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAAA</p> <p>SEQ ID NO: 2085</p> <p>QVQLVESGGGVVQPGSRSLRSLSCAASGFTFSYGM HWVRQAPGKGLEWVAWIWYDASNKYADAVKVG RFTISSDNKNTLYLQMNLSRAEDTAVYYCARDR TIFGVLDYWGQGTLVTVSSASTKGPSVFPPLAPSS KSTSGGTAAALGCLVKDYFPEPTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHITCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK</p>
	AA		<p>SEQ ID NO: 358</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCACTCTGTAGGAGACAGAGTCACCAATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTAA ATTGGTATCAGCAGAAACCAAGGAAAGCCCCCTA AGCTCTGATCTACGATGCATCCCAATTTGGAAA CAGGGTCCCATCAAGGTTCAAGTGGAAAGTGGAT CTGGGACAGATTTTAGTTTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATATTCTCTCACTTTCCGGCGGAGG GACCAAAGTGGAGATCAAGCGAAACGGTGGCTG CACCATCTGTCTTCATCTTCCCGCCATCTGATGA GCAGTTGAAATCTGGAACCTGCTCTGTTGTGTGC CTGCTGAATAACTTCTATCCAGAGAGGCCAAA GTACAGTGAAGGTGGATAACGCCCTCCCAATCG</p>	<p>SEQ ID NO: 515</p> <p>CAGGTGCAACTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCAACCTTCAGTAGCTATGGC ATGC ACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAATACTATGACAGACGCCGTGAAGGGC CGATTACCATCTCCAGCGACAAATTCAGAAAGAAC ACGCTGATCTGCAAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTGGAGTGGTCTTGACTACTGG GGCCAGGGAACCCCTGGTCAACCGTCTCCTCAGCC TCCACCAAGGGCCCAATCGGTCTTCCCCCTGGCA CCCTCTCCAAAGAGCACCTCTGGGGGCAACAGCG GCCCCGGGCTGCCTGGTCAAGGACTACTTCCCC</p>

		<p>GGTAACCTCCAGGAGAGTGTCACAGAGCAGGAC AGCAAGGACAGCACCTACAGCCTCAGCAGCACC CTGACGCTGAGCAAGCAGACTACGAGAAACA CAAAGTCTACGCCTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCACAAAGAGCTTCAACAG GGGAGAGTGT</p>	<p>GAACCGGTGACGGTGTCTGTGGAACCTCAGGGGCC CTGACCAGCGGCGTGACACACCTTCCCGGCTGTC CTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCACC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAAACCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACAGGTGACCTGACCTGCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAA</p>
		<p>SEQ ID NO: 1929</p>	<p>SEQ ID NO: 2086</p>
	AA	<p>DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGGTD FSFTISLQPEDFATYYCQQYDILLTFGGGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLS TLTLTKADYEEKHKVYACEVTHQGLSSPVTKSFNR GEC</p>	<p>QVQLVESGGGVVQPRSLRLSCAASGFTFSYGM HWVRQAPGKGLEWVAWIYDASNKYADAVKVG RFTISSDNKNTLYLQMNLSRAEDTAVYYCARDR TIFGVLDYWQGQTLVTVSSASTKGPSVFPLAPSS KSTSGGTAAALGCLVKDYFPEPTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKEPKSCDKTHHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE</p>

				<p>VKFNWYVVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK</p>
				<p>SEQ ID NO: 359</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCACTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTAA ATTGGTATCAGCAGAAACCAAGGAAAGCCCCA AGCTCTGATCTACGATGCATCCCAATTTGAAA CAGGGTCCCATCAAGGTTCAAGTGAAGTGGAT CTGGGACAGATTTTAGTTTCACCATCAGCAGCCT GCAGCCTGAAGATATTGCAACATATTACTGTCA ACAGTATGATATTCTCTCCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGAAACGGTGGCTG CACCATCTGTCTTCATCTTCCCGCCCATCTGATGA GCAGTTGAAATCTGGAACCTGCTCTGTTGTGTGC CTGCTGAATAACTTCTATCCAGAGAGGCCAAA GTACAGTGAAGGTGGATAACGCCCTCCCAATCG GGTAACTCCAGGAGAGTGTACAGAGCAGGAC AGCAAGGACAGCACCTACAGCCTCAGCAGCACCC CTGACGCTGAGCAAAAGCAGACTACGAGAAACA CAAAAGTCTACGCTGCGAAGTCAACCCATCAGGG CCTGAGCTCGCCCGTCAAAAGAGCTTCAACAG GGGAGAGTGT</p>
				<p>SEQ ID NO: 516</p> <p>CAGTGCAACTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCAACCTTCAGTAGCTATGGC ATGCACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGACAGACGCCGTGAAGGGC CGATTACCAATCTCCAGGGACAATTCCAAGAAC ACGCTGATCTGCAAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTGGAGTGGTCAACGCTCTCCTCAGCC GGCCAGGGAACCTGGTCAACGCTCTCCTCAGCC TCCACAAAGGGCCCACTCGGTCTTCCCCCTGGCA CCCTCTCCAAAGAGCACCTCTGGGGGCAACAGG GCCCTGGCTGCTGGTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCTGTGGAACCTCAGGGGCC CTGACCAAGCGGTGCAACACTTCCCCGGCTGTC CTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACCTCACACATGCCACCC GTGCCAGCACCTGAACCTCTGGGGGACCCGTC AGTCTTCTCTTCCCCCAAAACCCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGGTGGGACGTGAGCCACGAAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCAATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTGACGCT CCTCACCGTCTCGCACCAAGGACTGGCTGAATGG</p>

			<p>CAAGGAGTACAAAGTCAAGGTCTCCAAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACAGGTCAAGCTGACCTGCCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGAGAACAACTACAAG ACCAGCCTCCCGTCTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCCTGGACAAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
			<p>SEQ ID NO: 1930</p> <p>DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGGTD FSFTISLQPEDIATYYCQQYDILLTFGGGKVEIKR TVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSITYLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC</p>
	AA		<p>SEQ ID NO: 2087</p> <p>QVQLVESGGGVVQPGRLSLRSCAASGFTFSYGM HWVRQAPGKGLEWVAWIWYDASNKYADAVKGG RFTISRDNSKNTLYQMNSLRRAEDTAVYYCARDR TIFGVLDYWGQGLTVTVSSASTKGPSVFPLAPSS KSTSGGTAAALGCLVKDYFPEPTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKEPKSCDKTHTCTCPPEPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSQSVMHREALHNHYTQKSLS LSPGK</p>
			<p>SEQ ID NO: 360</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCACTCTGTAGGAGACAGAGTCACCATCATT GCCAGGCGAGTCAGGACATTAGCAACTATTAA ATTGGTATCAGCAGAAACCAAGGAAAGCCCCCTA AGCTCTGATCTACGATGCATCCCAATTTGGAAA CAGGGTCCCATCAAGGTTTCAGTGGAAGTGGAT CTGGGACAGATTTTAGTCTCACCATCAGCAGCC TGCAGCCTGAAGATTTTGCAACATATTACTGTCA</p>
IPS:359949	2F11.009	NA	<p>SEQ ID NO: 517</p> <p>CAGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCAACCTTCAGTAGCTATGGC ATGCACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGACAGACTCCGTGAAGGC CGATTACCATCTCCAGGGGACAAATCCAAAGAAC ACGCTGTATCTGCAAAATGAACAGCCTGAGAGCC</p>

		<p>ACAGTATGATATTCTCCTCACCTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGAACGGTGGCTG CACCATCTGTCTTCATCTTCCCGCCATCTGATGA GCAGTTGAAATCTGGAACCTGCTCTGTGTGTGC CTGCTGAATAACTTCTATCCAGAGAGGCCAAA GTACAGTGAAGGTGGATAACGCCCTCCCAATCG GGTAACCTCCAGGAGAGTGTACAGAGCAGGAC AGCAAGGACAGCACCTACAGCCTCAGCAGCAC CTGACGCTGAGCAAAAGCAGACTACGAGAAACA CAAAGTCTACGCTGCGAAGTCAACCCATCAGGG CCTGAGCTCGCCCGTCACAAAGAGCTTCAACAG GGGAGAGTGT</p>	<p>GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTGGAGTGGTCTTGACTACTGG GGCCAGGGAACCTGGTCAACCGTCTCCTCAGCC TCCACCAAGGCCCATCGGTCTTCCCCCTGGCA CCCTCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCCTGGCTGCCTGGTCAAGGACTACTTCCCC GAACCGGTACGGTGTCTGCGGAACCTCAGGGGCC CTGACCAGCGGCTGCACACCTTCCCGGCTGTC CTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGCTTCTCTTCCCCCAAAACCAAGGACAC CCTCATGATCTCCCGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCGAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACCAAGGTACGCTGACCTGCCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCGAGCCGGAGAACAACTACAAG ACCAAGCTTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
	AA	<p>SEQ ID NO: 1931</p> <p>DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGGTD</p>	<p>SEQ ID NO: 2088</p> <p>QVQLVESGGGVVQPRSLRLSCAASGFTFSYGM HWVRQAPGKGLEWVAVIWYDASNKYADSVKYG</p>

			<p>FSLTISSLQPEDFATYYCQYDILLTFGGGKVEIK RTVAAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLS TLTLKADYKHKVYACEVTHQGLSSPVTKSFNR GEC</p>
			<p>RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLDYWGQGLTVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHSTCPPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDSDGSEFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK</p>
			<p>SEQ ID NO: 361</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTAA ATTGGTATCAGCAGAAACCAAGGAAAGCCCCA AGCTCTGATCTACGATGCATCCAAATTTGGAAA CAGGGTCCCATCAAGGTTCAAGTGAAGTGGAT CTGGGACAGATTTTAGTCTCACCATCAGCAGCC TGACGCTGAAGATTTTGCAACATAATTACTGTCA ACAGTATGATATTCTCCTCACITTCGGCGGAGG GACCAAGGTGGAGATCAAGCGAACGGTGGCTG CACCATCTGTCTTCATCTTCCCGCCATCTGATGA GCAGTTGAAATCTGGAACCTGCCCTCTGTTGTGTC CTGCTGAATAACTTCTATCCAGAGAGGCCAAA GTACAGTGGAGGTGGATAACGCCCTCCCAATCG GGTAACCTCCAGGAGAGTGTCACAGAGCAGGAC AGCAAGGACAGCACCTACAGCCTCAGCAGCACCC CTGACGCTGAGCAAAAGCAGACTACGAGAAACA CAAAAGTCTACGCTGCGAAGTCAACCCATCAGGG CCTGAGCTCGCCCGTCACAAAGAGCTTCAACAG GGGAGAGTGT</p>
		NA	
IPS:359956	2F11.010		<p>SEQ ID NO: 518</p> <p>CAGGTGCAACTGGTGGAGTCTGGGGGAGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCAACCTTCAGTAGCTATGGC ATGCACTGGTCCCGAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGGA AGTAATAATACTATGCAGACGCCGTGAAGGGC CGATTACCATCTCCAGGGACAATTCCAGAAC ACGCTGATCTGCAAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTGGAGTGGTCTTGACTACTGG GGCCAGGGAACCTGGTCAACCTCTCCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA CCCTCTCCAAAGAGCACCTCTGGGGGCAACAGG GCCCTGGGCTGCCGTGGTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCC CTGACCAAGCGGTGCACACCTTCCCCGGCTGTC CTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTTGACCGTGGCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACCTCACACATGCCACC GTGCCAGCACCTGAACCTCTGGGGGACCGTCT AGTCTTCTCTTCCCCCCCCAAACCCCAAGGACAC</p>

		<p>CCTCATGATCTCCGGACCCCTGAGGTACATG CGTGGTGGTGACGTGAGCCACGAAGACCC'TGA GGTCAAGT'TCAACTGGTACGTGGACGGCGTGGA GGTGCAATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTCAAGCGT CCTCACCGTCTCGACCAAGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCCATCGAGAAAACCATCTCCAA AGCCAAGGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGGAGGAGATGACCA AGAACAGGTACGCTGACCTGCCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCCTGGACAAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
	SEQ ID NO: 1932	SEQ ID NO: 2089
	<p>DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGGTD FSLTISLQPEDFATYYCQQYDILLTFGGGKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSLS TLTLTKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC</p>	<p>QVQLVESGGGVVQGRSLRLSCAASGFTFSYGM HWVRQAPGKGLEWVAWIYDGSNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLDYWGGQGLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK</p>
AA		

				SEQ ID NO: 362	SEQ ID NO: 519
IPS:359865	6H1.002	NA		<p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACCAAGGAAAGCCCTA AGCCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGTCCCTTCAAGGTTCAAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAGTGGATATCAACGAACGGTGGCT GCACCATCTGTCTTCACTTCCCGCCATCTGATG AGCAGTTGAATCTGGAACTGCCCTCTGTTGTGT GCCTGCTGAATACTTCTATCCCAAGAGAGGCCA AAGTACAGTGGAAGTGGATAACGCCCTCCAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCGGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCAACAAGAGCTTCAACA GGGGAGAGTGT</p>	<p>CAGTGCAGCTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAAGCTCTGGATTCAACCTTCAAGTTACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCAACCATCTCCAGAGACAATTCCAAGAACAA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACAGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTGGAGTGTCTTTGGGGGACTACT GGGGCCAGGAAACCCCTGGTCAACGCTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGCTGCCGTGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGTTGAACTCAGGCGC CCTGACCAAGCGGCTGCACACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAAGCC AGCAACACCAAGGTGGACAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACC GTGCCAGCACCTGAACCTCTGGGGGACCGTCTC AGTCTTCTCTTCCCCCAAAACCCAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTGAGCGT CCTCACCGTCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGAAGGTCTCCAAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAAGCCCCGAGAACCCAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACCAGGTCAACCTGACCTGCCTGGTCAAG GCTTCTATCCAGCGGACATCGCCGTGGAGTGGG</p>

			<p>AGAGCAATGGCAGCCGGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTAAA</p> <p>SEQ ID NO: 1933</p>	
			<p>DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLQSGVPSRFSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSYSTLSST LTLTKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC</p> <p>AA</p> <p>SEQ ID NO: 2090</p> <p>QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIWYDASNKYADAVKVG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTSIK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK</p>	
IPS:359869	6H1.003	NA	<p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTAG GCTGTATCAGCAGAAACCAAGGAAAGCCCTA AGCCCTGATCTATGGTGCAATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTCAAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCACAATCAGCAGCC TGACGCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTCGGCCCT GGGACCAAAGTGGATATCAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACCTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT</p> <p>SEQ ID NO: 363</p> <p>CAGTGCAGCTGGTGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTCAGTTACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCAACCATCTCCAGAGACAATCCAAAGAACA CGCTGATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATA GGACGATTTTGGAGTGTCTTTGGGGGACTACT GGGGCCAGGGAACCTGGTCAACCTCTCCTCAG CCTCCACCAAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCTCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGTGTCAAGGACTACTTCCC</p>	

		<p>CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCCAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGAGAGTGT</p>	<p>CGAACCGGTGACGGTGTCTGTGGAACCTCAGGCG CCTGACCAGCGGCGTGACACACCTTCCCGGCTGT CCTACAGTCTTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCCCACC GTGCCAGCACCTGAACCTCTGGGGGACCCGTC AGTCTTCTCTTCCCCCACAACCCAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCAATATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCCTGTGTGTCAGCGT CCTCACCGTCTGCACCAAGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCATCCCGGAGGAGATGACCA AGAACAGGTGACCTGACCTGCCTGTCACAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAA</p>
	AA	<p>DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTEFT LTISLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR TVAAPSVFIPTPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSYSTYLSST LTLKADYEEKHKVYACEVTHQGLSSPVTKSFNRG EC</p>	<p>SEQ ID NO: 1934</p> <p>SEQ ID NO: 2091</p> <p>QVQLVESGGGVVQGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIYDASNKYADAVKVG RFTISRDNSKNTLYQMNSLRAEDTAVYYCARDR TIFGVLLGDYWGQGTLLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLMISRTPETVTCVVDVSHED</p>

			<p>PEVKFNWYVVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVVFSCSVMHEALHNHYTQKS LSLSPGK</p>
			<p>SEQ ID NO: 364</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACCAAGGAAAGCCCCA AGCTCTGATCTATGGTGCAATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTCAAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAGTGGATATCAACGAACGGTGGCT GCACCATCTGTCTTCACTTCCCGCCATCTGATG AGCAGTTGAATCTGGAACCTGCCTCTGTTGTGT GCCTGCTGAATACTTCTATCCCAAGAGAGGCCA AAGTACAGTGGAAGTGGATAACGCCCTCCAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT</p>
			<p>SEQ ID NO: 521</p> <p>CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAAGCTCTGGATTCAACCTTCAAGTTACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCAACCATCTCCAGAGACAATTCCAAAGAACA CGCTGATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTATTACTGTGCGCGAGATG GGACGATTTTGGAGTGTCTTGGGGGACTACT GGGGCAGGAAACCCCTGGTCAACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGCTGCTGTGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTGTGGAACCTCAGGCGC CCTGACCAAGCGGTGTGCACACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGTGGACAAAGAAAGTTGAGCC CAAATCTTGTGACAAACCTACACATGCCACCC GTGCCAGCACCTGAACCTCTGGGGGAGCCGTC AGTCTTCTCTTCCCCCAAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGCGGTGGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAAGGACTGGCTGAATGG</p>

			<p>CAAGGAGTACAAAGTCAAGGTCTCCAAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACAGGTGAGCCTGACCTGCCGTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGAGAACAACTACAAG ACCAGCCTCCCGTCTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
			<p>SEQ ID NO: 1935</p> <p>DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSTEFT LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSITYSLSS TLTLTKADYEKHKVYACEVTHQGLSPVTKSFNR GEC</p>
		AA	<p>SEQ ID NO: 2092</p> <p>QVQLVESGGGVVQPGRLSLRSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDASNKYADAVKGG RFTISRDNSKNTLYQMNSLR AEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGT AALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLMISRTPETCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK</p>
IPS:359877	6H1.005	NA	<p>SEQ ID NO: 365</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGAGACAGAGTCACCATCCTT GCCGGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACCAAGGAAAGCCCTA AGCTCCTGATCTATGGTGATCCAGTTTGCAA GTGGGGTCCCTTCAAAGTTTCAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT</p>
			<p>SEQ ID NO: 522</p> <p>CAGTGCAGCTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCA GCGTCTGGATTCAACCTTCAGTTACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG</p>

	AA	ACAGCATAAATAATTACCCCTTCACTTTTCGGCCAA GGGACCAAAGTGGATATCAACGAACGGTGGCT GCACCATCTGTCTTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACCTGCCCTCTGTTGT GCCTGCTGAATAACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAAGGTGGATAACGCCCTCCAT CGGGTAAC'TCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCCGAAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	AGGACACGGCTGTGTATTACTGTGCGGAGATA GGACGATTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCAG CTCCACCAAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCTCTCAAAGAGCACCTCTGGGGGCACAGC GGCCCTGGCTGCTTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGTGGAATCAGGCGC CCTGACCAAGCGGCTGCACACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAAGCCC AGCAACACCAAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCACC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCAATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACCAAGGTGACCTGACCTGCCCTGGTCAAAG GCTTCTATCCAGCGCATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGACAACATACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAAA
		SEQ ID NO: 1936	SEQ ID NO: 2093
	AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT	QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDASNKYADAVKYG

			<p>LTISLQPEDFATYYCLQHNPNYPFTFGQGTKVDIK RTVAAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKSDSTYSLSS TLTLKADYKHKVYACEVTHQGLSSPVTKSFNR GEC</p>	<p>RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLLGDYWGQGLTVTVSSASTKGPSVFPLAPS SKSTSGGT AALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKD TLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKS LSLSPGK</p>
			<p>SEQ ID NO: 366</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGATCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACCAAGGGAAGCCCCCTA AGCTCTGATCTATGGTGCATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTCAAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCTCACAAATCAGCAGCC TGACGCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAACGAACGGTGGCT GCACCATCTGCTTTCATCTTCCCGCCATCTGATG AGCAGTTGAATCTGGAACCTGCCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAGTGGATACGCCCTCCCAAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCGGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCAAAAGAGCTTCAACA GGGGAGAGTGT</p>	<p>SEQ ID NO: 523</p> <p>CAGGTGCAGTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAAGCTCTGGATTCAACCTTCAGTTACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGGAA GTAATAATACTATGCAGACTCCGTGAAGGCC GCTTCAACCATCTCCAGAGACAATTCCAAAGAACA CGTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTGGAGTGTCTTGGGGGACTACT GGGGCCAGGGAACCCCTGGTCAACCTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGCTGCCGTGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGGAACCTCAGGCGC CCTGACCAAGCGGTGTGCAACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTTGACCGTGGCTTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACC GTGCCAGCACCTGAACCTCTGGGGGACCGTCT AGTCTTCTCTTCCCCCCCCAAACCCAAAGGACAC</p>
IPS:361067	6H1.006	NA	<p>SEQ ID NO: 366</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGATCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACCAAGGGAAGCCCCCTA AGCTCTGATCTATGGTGCATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTCAAGCGGCAGTGGAT CTGGGACAGAAATTCATCTCTCACAAATCAGCAGCC TGACGCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAACGAACGGTGGCT GCACCATCTGCTTTCATCTTCCCGCCATCTGATG AGCAGTTGAATCTGGAACCTGCCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAGTGGATACGCCCTCCCAAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCTGCGGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCAAAAGAGCTTCAACA GGGGAGAGTGT</p>	<p>SEQ ID NO: 523</p> <p>CAGGTGCAGTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAAGCTCTGGATTCAACCTTCAGTTACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGGAA GTAATAATACTATGCAGACTCCGTGAAGGCC GCTTCAACCATCTCCAGAGACAATTCCAAAGAACA CGTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTGGAGTGTCTTGGGGGACTACT GGGGCCAGGGAACCCCTGGTCAACCTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGCTGCCGTGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGGAACCTCAGGCGC CCTGACCAAGCGGTGTGCAACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTTGACCGTGGCTTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACC GTGCCAGCACCTGAACCTCTGGGGGACCGTCT AGTCTTCTCTTCCCCCCCCAAACCCAAAGGACAC</p>

		<div>SEQ ID NO: 1937</div> <div>DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR TVAAPSVFIIPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSITYSLST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC</div>	<div>SEQ ID NO: 2094</div> <div>QVQLVESGGGVVQPGRLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIWYDGSNKYYADSVKVG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLGDIYWGGQGTLLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNATKPCPEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGGSFFLY SKLTVDKSRWQQGNVVFSCSVMHAEALHNHYTQKS LSLSPGK</div>
	AA		

				SEQ ID NO: 367	SEQ ID NO: 524	
				GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGAAAGCCCCTA AGCTCCTGATCTATGGTGCAATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTCAAGCGCAGTGGAT CTGGGACAGAAATTCAC'TCTCACAAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCAC'TTTCGGCCCT GGGACCAAAAGTGGATATCAAAACGAAACGGTGGCT GCACCATCTGTCTTCAATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACCTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCAGAGAGGCCA AAGTACAGTGAAGGTGGATAACGCCCTCCAAAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCAAAAGAGCTTCAACA GGGGAGAGTGT		CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGTTATGATGCAA GTAATAAATACTATGCAGACTCCGTGAAGGGCC GCTTCAACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTGGAGTGTCTTTGGGGGACTACT GGGGCCAGGAACCCCTGGTCAACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGTGGAACCTCAGGCG CCTGACACGCGGTGCAACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAAC'TCACACATGCCACC GTGCCAGCACCTGAAC'TCCTGGGGGACCGTGC AGTCTTCTCTTCCCCCAAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAAGTTCAA'CTGGTACGTGGACGGCGTGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTCAAGCT CCTCACCGTCTGCACCGAGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAAACAAGC CCTCCAGCCCCATCGAGAAAACCATCTCCAA AGCCAAGGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCCGGGAGGAGATGACCA AGAACAGGTACGCTGACCTGCCTGCTCAAAAG GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
			NA			
		6H1.007				
		IPS:361071				

			<p>AGAGCAATGGCAGCCGGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTAAA</p> <p>SEQ ID NO: 1938</p>	
			<p>DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT LTISLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR TVAAPSVFIIPPSDEQLKSGTASVVCLLNFPREA KVQWKVDNALQSGNSQESVTEQDSKDSYSTLSST LTLISKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC</p> <p>AA</p>	
			<p>QVQLVESGGGVVQPGRLSLRSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDASNKYIYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVVFSCVMHEALHNHYTQKS LSLSPGK</p> <p>SEQ ID NO: 2095</p>	
IPS:361075	6H1.008	NA	<p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTAG GCTGGTATCAGCAGAAACCAAGGAAAGCCCTA AGCTCTGATCTATGGTGATCCAGTTTGCAA GTGGGTCCCTTCAAAGTTTCAGGGCAGTGGAT CTGGGACAGAAATTCATCTCACAATCAGCAGCC TGACGCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAAATAATTACCCCTTCACTTCGGCCCT GGGACCAAAGTGGATATCAACGAAACGGTGGCT GCACCATCTGTCTTCACTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACCTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT</p> <p>SEQ ID NO: 368</p>	
			<p>CAGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTCACTTACTTTGGCA TGCACTGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGGAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCAACCATCTCCAGAGACAATCCAAAGAACA CGCTGATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTTACTGTGCGCGAGATG GGACGATTTTGGAGTGTCTTGGGGGACTACT GGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCAG CCTCCACCAAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCTCTCCAAGAGCACCTCTTGGGGGCACAGC GGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCC</p> <p>SEQ ID NO: 525</p>	

		<p>CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCCGAAATCAGCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT</p>	<p>CGAACCGGTGACGGTGTCTGTGGAACCTCAGGCG CCTGACCAGCGGCGTGACACACCTTCCCGGCTGT CCTACAGTCTTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCCCACC GTGCCAGCACCTGAACCTCTGGGGGACCCGTC AGTCTTCTCTTCCCCCACAACCCAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCAATATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAAGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACAGGTGACCTGACCTGCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAA</p>
	AA	<p>DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT LTISLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR TVAAPSVFIPTPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSYSTYLSST LTLKADYEEKHKVYACEVTHQGLSSPVTKSFNRG EC</p>	<p>SEQ ID NO: 1939</p> <p>SEQ ID NO: 2096</p> <p>QVQLVESGGGVVQPRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAWIYDGSNKYYADAVKG RFTISRDNSKNTLYQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLMISRTPETVTCVVDVSHED</p>

			<p>PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVVFSCVMHEALHNHYTQKS LSLSPGK</p>
			<p>SEQ ID NO: 369</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAGCCCCTA AACTCTGATCTACGATGCTTCCAAATTTGGAGCC AGGGTCCCATCAAGGTTCAAGTGGAAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAGTGGATATCAACGAACGGTGGCTGCA CCATCTGTCTTCACTTCCCGCCATCTGATGAGC AGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCT GCTGAATAACTTCTATCCAGAGAGGCCAAAGT ACAGTGGAAAGGTGGATAACGCCCTCCAAATCGGG TAAC'TCCAGGAGAGTGTACAGCCTCAGCAGCACCT CAAGGACAGCACCTACAGCCTCAGCAGCACCT GACGCTGAGCAAGCAGACTACGAGAAACACA AAGTCTACGCTGCGAAGTCAACCCATCAGGGCC TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGG GAGAGTGT</p>
		6A5.004.001	NA
		IPS:361079	<p>SEQ ID NO: 526</p> <p>CAGGTGCAGCTGGTGGAGTCTGGGGGAGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGTGGCAGCTATATGGTATGATGCAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAAGAAC CGTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTATTACTGTGCGAGAGATC GGACGATTTTGGAGTGGTCTTGGAGTACTGGG GCCAGGGAACCTGTGTACCGTCTCCTCAGCCT CCACCAAGGCCCATCGGTCTTCCCCCTGGCAC CCTCCTCCAAGACACCTCTGGGGGACACAGCG CCCTGGGTGCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCTGTGGAACTCAGGCGCCC TGACCAGCGCGTGCACACCTTCCCCGGCTGTCC TACAGTCTCAGGACTCTACTCCTCAGCAGCGT GGTGACCGTGCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAGCCCCAG CAACCAAGGTGGACAAAGAAAGTTGAGCCCCA AATCTTGTGACAAAACTCACACATGCCACCGT GCCCCAGCACTGAATCCTGGGGGACCGTCAG TCTTCTCTTCCCCCAAAACCCAAAGGACACCT CATGATCTCCCGGACCCCTGAGGTACATGCGT GGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGT GCATAATGCCAAGACAAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTACGCGTCC TCACCGTCTTGCAACCAAGGACTGGCTGAATGGCA</p>

			<p>AGGAGTAC AAGTGCAAGGTCTCCAAACAAAGCCC TCCAGCCCCCATCGAGAAACCATCTCCAAAG CCAAAGGCAGCCCCGAGAACACACAGGTGTAC ACCTGCCCCCATCCCGGAGGAGATGACCAAG AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC TTCTATCCAGCGACATCGCCGTGGAGTGGGAG AGCAATGGCAGCGGAGAACAACTACAAGAC CACGCCTCCGTGCTGGAATCCGACGGCTCCTTC TTCCTATAGCAAGCTACCGTGGACAAAGAGC AGTGGCAGCAGGGGAACGTCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACAG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
			<p>SEQ ID NO: 1940</p> <p>DIQMTQSPSSLSASVGDRVTITCQASQDITNLYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGGTD FTLTISLQPEDFATYYCQQYDDLFTFGPGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLS TLTLKADYEKHKVYACEVTHQGLSPVTKSFNR GEC</p>
	AA		<p>SEQ ID NO: 2097</p> <p>QVQLVESGGGVVQPGRSRLRSCAASGFSFSSYGM HWVRQPPGKGLWVAAIWYDANNKYADAVKGG RFTISRDSSKNTLYLQMNSLR AEDTAVYYCARDR TIFGVLEYWGQGLTVTVSSASTKGPSVFPLAPSS KSTSGGT AALGCLVKDYFPEPTVSWNSGALTSG VHTFPAVLQSSGLYSLSVTVVPSSSLGTQTYICNV NHKPSNTKVDKKEPKSCDKTHTCTPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSQSVMH EALHNHYTQKSLS LSPGK</p>
IPS:361085	6A5.004.002	NA	<p>SEQ ID NO: 370</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGACAGAGTCACCAATCATT GCCAGGCGAGTCAGGACATTACCAACTATTAA ATTGGTATCAGCAGAAACCAAGGAAAGCCCCA AACTCTGATCTACGATGCTTCCAAATTGGAGCC AGGGTCCCATCAAGGTTTCAGTGGAAAGTGGATC TGGGACACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATATTGCAACATATTACTGTCA</p>
			<p>SEQ ID NO: 527</p> <p>CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCTTCAGTAGCTATGGCA TGCACTGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGTGGCAGCTATATGGTATGATGCAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCAACCATCTCCAGAGACAGTTTCCAAAGACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG</p>

		<p>ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAGTGGATATCAACGAACGGTGGCTGCA CCATCTGTCTTCATCTTCCCGCCATCTGATGAGC AGTTGAAATCTGGAACTGCCTCTGTGTGTGCCT GCTGAATAACTTCTATCCAGAGAGGCCAAAGT ACAGTGGAAGGTGGATAACGCCCTCCAAATCGGG TAAC'TCCAGGAGAGGTGTCACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGCAGCACCT GACGCTGAGCAAAGCAGACTACGAGAAACACA AAGTCTACGCCCTGCGAAGTCAACCCATCAGGGCC TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGG GAGAGTGT</p>	<p>AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTGGAGTGGTCTTGAGTACTGGG GCCAGGAACCTGGTCAACCGTCTCCTCAGCCT CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC CCTCTCCAAGAGCACCTCTGGGGGACACAGCG CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCTGGAAC'TCAGGCGCCC TGACCAGCGGCTGCACACCTTCCCCGGCTGTCC TACAGTCTCAGGACTCTACTCTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAGCCAG CAACACCAAGGTGGACAAAGAAATTGAGCCCCA AATCTTGTGACAAAACTCACACATGCCACCCGT GCCCAGCACTGAATCTCTGGGGGACCGTCAG TCTTCTCTTCCCCCACAACCCAAAGGACACCCCT CATGATCTCCCGGACCCCTGAGGTACATGCGT GGTGGTGGACGTGAGCCACGAAGACCC'TGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGT GCATAATGCCAAGACAAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTACGCGTCC TCACCGTCTGCCACAGGACTGGCTGAATGGCA AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC TCCCAGCCCCCATCGAGAAACCATCTCCAAG CCAAAGGCGAGCCCCGAGAACCCACAGGTGTAC ACCTGCCCCCATCCC'GGGAGGAGATGACCAAG AACAGGTACGCTGACCTGCCCTGGTCAAAGGC TTCTATCCCAGCGACATCGCCGTGGAGTGGGAG AGCAATGGGCAGCCGGAGAACACTACAGAC CACGCCCTCCGTGTGTGGACTCCGACGGCTCCTC TTCTCTATAGCAAGCTCACCGTGGACAAAGC AGGTGGCAGCAGGGGAACGTCTTCTCATGTCTC GTGATGCATGAGGCTCTGCACAACCACTACAG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
	AA	<p>SEQ ID NO: 1941</p> <p>DIQMTQSPSSLSASVGDRTVITTCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD</p>	<p>SEQ ID NO: 2098</p> <p>QVQLVESGGGVQPGRSRLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAIIWYDANNKYYADAVKG</p>

			FTLTISSLQPEDIATYYCQQYDDLFTFGPGTKVDIK RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSLSS TLTLISKADYEHKHYVACEVTHQGLSSPVTKSFN GEC	SEQ ID NO: 371	RFTISRDSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGQGLTVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVVDGVEVHNAAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
IPS:361091	6A5.004.003	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTAA ATTGGTATCAGCAGAAACCAAGGAAAGCCCCA AACTCTGATCTACGATGCTTCCAAATTGGAGCC AGGGTCCCATCAAGGTTCAAGTGGAAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCACACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAGTGGATATCAACGAACGGTGGCTGCA CCATCTGTCTTCACTTCCCGCCATCTGATGAGC AGTTGAAATCTGGAACTGCCTCTGTTGTGTCCT GCTGAATAACTTCTATCCAGAGAGGCCAAAGT ACAGTGGAAAGTGGATAACGCCCTCCAAATCGGG TAAC'TCCAGGAGAGTGTACAGCAGAGCAGACAG CAAGGACAGACCTACAGCCTCAGCAGCACCTT GACGCTGAGCAAGCAGACTACGAGAAACACA AAGTCTACGCTGCGAAGTCAACCCATCAGGGCC TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGG GAGAGTGT	SEQ ID NO: 528	CAGGTGAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCTCTTCAGTAGCTATGGCA TGCACTGGTCCGCCAGCCTCCAGGCAAGGGC TGGAGTGGTGGCAGCTATATGGTATGATGCAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTACCATCTCCAGAGACAGTTCCAAAGAAC CGCTGATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTGGAGTGGTCTTGGAGTACCTCG GCCAGGGAACCTGGTCACTCTGCGGCGACAGCG CCACCAAGGGCCATCGGTCTTCCCCCTGGCAC CCTCTCCAAAGACACCTCTGGGGGACAGCGG CCCTGGGCTGCCGTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCTGTTGGAACCTCAGGCGCC TGACCAAGCGGTGCAACACTTCCCCGGCTGTCC TACAGTCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGGCTCCAGCAGCTTGGGCAACCA GACCTACATCTGCAACGTGAATCACAAGCCCA CAACCAAGGTGGACAAAGAAAGTTGAGCCCA AATCTGTGACAAACTCACACATGCCACCGT GCCCAGCACCTGAATCTCTGGGGGACCGTCAG TCTTCTCTTCCCCCAAAACCAAGGACACCT

			<p>CATGATCTCCCGGACCCCTGAGGTACATGCGT GGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGAGGT GCATAATGCCAAGACAAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTACGCGTCC TCACCGTCTGCACCAAGGACTGGCTGAATGGCA AGGAGTACAAGTGCAAGGTCTCCAAACAAAGCCC TCCCAGCCCCCATCGAGAAACCATCTCCAAAG CCAAAGGCAGCCCCGAGAACACACAGGTGTAC ACCTGCCCCCATCCCGGAGGAGATGACCAAG AACCAGGTACGCTGACCTGCCTGGTCAAAGGC TTCTATCCAGCGACATCGCCGTGGAGTGGGAG AGCAATGGCAGCCGAGAACAACTACAAGAC CACGCTCCCGTGTGACTCCGACGGCTCCTTC TTCCTCTATAGCAAGCTACCGTGGACAAAGC AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACAG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
	SEQ ID NO: 1942	SEQ ID NO: 2099	<p>QVQLVESGGGVVQPGRLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAIIWYDANNKYYADAVKG RFTISRDSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYLGQGTLVTVSSASTKGPSVFPLAPSSK STSGGTAAALGCLVKDYFPEPTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCDKTHTCPPCPAPPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVFCSSVMHEALHNHYTQKLSL SPGK</p>
	<p>DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGGTD FTLTISLQPEDFATYYCQQYDDLFTFGPGTKVDIK RTVAAPSVFIPPSDEQLKSGTASVCLLNFPYRE AKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSLSS TLTLISKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC</p>	AA	

				SEQ ID NO: 372	SEQ ID NO: 529
				<p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTAA ATTGGTATCAGCAGAACCCAGGGAAGCCCCA AACTCTGATCTACGATGCTTCCAAATTGGAGCC AGGGTCCCATCAAGGTTCAAGTGGAAGTGGATC TGGGACAGATTTTACTTTCAACCATCAGCAGCCTG CAGCCTGAAGATTTTGCAACATATTACTGTCAA CAGTATGATGATCTATTCACTTTCGGCCCTGGGA CCAAAGTGGATATCAACGAACGGTGGCTGCAC CATCTGCTTCATCTTCCCGCCATCTGATGAGCA GTTGAAATCTGGAACCTGCCCTCTGTTGTGCTG CTGAATAACTTCTATCCCAGAGAGGCCAAAGTA CAGTGGAAAGTGGATAACGCCCTCCAATCGGGT AACTCCAGGAGAGTGTACAGCCTCAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGCAGCACCTT GACGCTGAGCAAGCAGACTACGAGAAACACA AAGTCTACGCTGCGAAGTCAACCCATCAGGGCC TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGG GAGAGTGT</p>	<p>CAGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCTTTCAGTAGCTATGGCA TGCACTGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGTGGCAGCTATATGGTATGATGCAA ATAATAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAAGAAC CGTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACAGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTGGAGTGGTCTTGGAGTACTGGG GCCAGGGAACCTGGTCAACGCTCTCCTCAGCCT CCACCAAGGGCCATCGGTCTTCCCCCTGGCAC CCTCCTCCAAGAGACCTCTGGGGGACAGCGG CCCTGGGCTGCCGTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCTGGAACCTCAGCGGCC TGACCAGCGGCTGCACACCTTCCCCGGCTGTCC TACAGTCTCAGGACTCTACTCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAGCCCCAG CAACCAAGGTGGACAAAGAAAGTTGAGCCCCA AATCTTGTGACAAAACTCACACATGCCACCGT GCCCAGCACCTGAACCTCCTGGGGGACCGTCAG TCTTCTCTTCCCCCACAACCCAAAGGACACCT CATGATCTCCCGGACCCCTGAGGTACATGCGT GGTGGTGGACGTGAGCCACGAAGACCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGT GCATAATGCCAAGACAAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTACGCGTCC TCACCGTCTGCACCAAGGACTGGGTGAATGGCA AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC TCCCAGCCCCCATCGAGAAACCATCTCCAAAG CCAAAGGCGACCCCGAGAACCAAGGTGTAC ACCTGCCCCCATCCCCGGGAGGAGATGACCAAG AACCAGGTACGCTGACCTGCCTGGTCAAGGCG TTCTATCCCAAGCAGACATCGCCGTGGAGTGGGAG</p>
				NA	
			6A5.004.004		
			IPS:361095		

				AGCAATGGGCAGCCGAGACAACACTACAAGAC CACGCTCCCCTGCTGGACTCCGACGGCTCCTTC TTCCTCTATAGCAAGCTCACCGTGACAAGAGC AGGTGCAGCAGGGGAACGTCTTCTCATGCTCC GTGATGCATGAGGCTCTTGACAACCACTACACG CAGAAAGAGCCTCTCCCTGTCTCCGGGTAAA SEQ ID NO: 2100 QVQLVESGGGVVQPGRLRLSCAASGFSFSYGM HWVRQPPGKGLEWVAIIWYDANNKYYADAVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLEYWGQGTLLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSEFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK SEQ ID NO: 530
				CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCTCTGAGACTCTCCTGT GCAGGCTCTGATTCTCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGCAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAAGAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGGAGAGATC GGACGATTTTGGAGTGGTCTTGTGAGTACCTCG GCCAGGGAACCTGGTCAACCTCCTCCTCAGCCT
				DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGGTD FTFTISLQPEDFATYYCQQYDDLFTFGPGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS TLTLKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC SEQ ID NO: 1943
		AA		
		NA	6A5.004.005	IPS:361101
				GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTAA ATTGGTATCAGCAGAAACCAGGGAAGCCCCTA AACTCCTGATCTACGATGCTTCCAAATTTGGAGCC AGGGTCCCATCAAGGTTCAAGTGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATATTGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAAGTGGATATCAACGAACGGTGGCTGCA CCATCTGTCTCATCTTCCCGCCATCTGATGAGC

		<p>AGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCT GCTGAATAACTTCTATCCCAGAGAGGCCAAAGT ACAGTGGAAGGTGGATAACGCCCTCCAATCGGG TAAC'TCCAGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGCAGCACCT GACGCTGAGCAAAGCAGACTACGAGAAACACA AAGTCTACGCCCTGCGAAGTCAACCCATCAGGGCC TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGG GAGAGTGT</p>	<p>CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC CCTCTCCAAGAGCACCTCTGGGGCACAGCGG CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG AACCGTACGGTGTCTGTGGAACCTCAGGCGCCC TGACCAGCGGCTGCACACCTTCCCCGGCTGTCC TACAGTCTCAGGACTCTACTCTCCCTCAGCAGCGT GGTGACCGTGGCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAGCCACG CAACACCAAGGTGGACAAAGAAAGTTGAGCCCCA AATCTGTGACAAAACTCACACATGCCACCCGT GCCCAGCACCTGAATCTCTGGGGGACCGTCAAG TCTTCTCTTCCCCCACAACCCAAAGGACACCCCT CATGATCTCCCGGACCCCTGAGGTACATGCGT GGTGTGACGTGAGCCACGAAGACCCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGT GCATAATGCCAAGACAAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTACGCGTCC TCACCGTCTGCACCAAGGACTGGCTGAATGGCA AGGAGTACAAGTGCAAGGTCTCCAAACAAAGCCC TCCCAGCCCCCATCGAGAAACCATCTCCCAAAG CCAAAGGCAGCCCCCGAGAACCAAGGTGTAC ACCTGCCCCCATCCCGGGAGGAGATGACCAAG AACAGGTACGCTGACCTGCCTGGTCAAGGC TTCTATCCAGCGACATCGCCGTGGAGTGGGAG AGCAATGGGCAGCCGAGAACACTACAGAC CACGCTCCCTGTCTGGACTCCGACGGCTCCTTC TTCCTCTATAGCAAGCTCACCGTGGACAAAGC AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACAG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
	AA	<p>DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGGTD FTLTISLQPEDIAITYCQQYDDLFTFGPGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSL</p>	<p>SEQ ID NO: 1944</p> <p>SEQ ID NO: 2101</p> <p>QVQLVESGGGVVQPGSRSLRSLSCAASGFSFSSYGM HWVRQPPGKGLEWVAIIWYDANNKYYADAVKGG RFTISRDSKNTLYLQMNSLRRAEDTAVYYCARDR TIFGVVLEYLGQGTLVTVSSASTKGPSVFPLAPSSK STSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGV</p>

			TLTLKADYKHKVYACEVTHQGLSSPVTKSFNR GEC		HTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVN HKPSNTKVDKKEPKSCDKTHTCPAPPELLGGP SVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNKATKPCEEQYGSTYRCVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVFSQSVMHREALHNHYTQKSLSL SPGK
					SEQ ID NO: 531
					SEQ ID NO: 374
					SEQ ID NO: 361105
					6A5.004.006
					NA

				GCATAATGCCAAGACAAAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTACGCGTCC TCACCGTCTGCACACGAGACTGGCTGAATGGCA AGGAGTACAAGTGCAAGGTCTCCAAACAAAGCCC TCCCAGCCCCCATCGAGAAACCATCTCCAAAG CCAAAGGCAGCCCCCGAGAACACACAGGTGTAC ACCTGCCCCCATCCCGGAGGAGATGACCAAG AACAGGTCAGCCTGACCTGCCTGGTCAAAGGC TTCTATCCAGCGACATCGCCGTGGAGTGGGAG AGCAATGGCAGCGCGAGAACAACTACAAGAC CACGCTCCCGTGTGACTCCGACGGCTCCTTC TTCCTATAGCAAGCTCACCGTGGACAAGAGC AGTGGCAGCAGGGGAACGTCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACAG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
				SEQ ID NO: 2102
				QVQLVESGGGVVQGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLWVAAIWYDANNKYYADAVKG RFTISRDSSKNTLYIQMNSLRAREDYAVYYCARDR TIFGVVLEYLGQGTLVTVSSASTKGPSVFPLAPSSK STSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVN HKPSN'TKVDKKVEPKSCDKTHTCPCPAPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYITLPPSRREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVVFSCSVMHEALHNHYTQKSLSL SPGK
				SEQ ID NO: 532
				CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGCAA
				SEQ ID NO: 1945
				DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGTGD FTFTISLQPEDFATYYCQQYDDLFTFGPGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSLSS TLTLISKADYEKHKVYACEVTHQGLSSLSPVTKSFNR GEC
			AA	
				SEQ ID NO: 375
				GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGACAGAGTCACCATCATT GCCAGGCGAGTCAGGACATTACCAACTATTAA ATTGGTATCAGCAGAAACCAAGGGAAGCCCCCTA AACTCCTGATCTACGATGCTTCCAAATTGGAGCC
			NA	
		6A5,004.00	7	
		IPS:36110	9	

AGGGTCCCATCAAGGTTCAAGTGGAGTGGATC TGGGACAGATTTTACTTTCAACATCAGCAGCCTG CAGCTGAAGATATTGCAACATATTACTGTCAA CAGTATGATGATCTATTCACTTTGGCCCTGGGA CCAAAGTGGATATCAACGAACGGTGGCTGCAC CATCTGCTTTCATCTTCCCGCCATCTGATGAGCA GTTGAAATCTGGAACTGCCCTCTGTTGTGCTG CTGAATAACTTCTATCCCAGAGAGGCCAAAGTA CAGTGGAAAGTGGATAACGCCCTCCAATCGGGT AACTCCCAGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGCAGCACCTT GACGCTGAGCAAGCAGACTACGAGAAACACA AAGTCTACGCCCTGCGAAGTCAACCCATCAGGGC TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGG GAGAGTGT	ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAAGAACA CGCTGATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTGGAGTGGTCTTGGAGTACTGGG GCCAGGAACCTGGTCAACCTCTCCTCAGCCT CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC CCTCTCCAAGAGCACCTCTGGGGGACACAGCG CCCTGGGCTGCCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCC TGACCAGCGGCTGCACACCTTCCCCGGCTGTCC TACAGTCTCAGGACTCTACTCTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAGCCACG CAACACCAAGGTGGACAAAGAAATTGAGCCCCA AATCTGTGACAAAACTCACACATGCCACCCGT GCCCAGCACCTGAACCTCCTGGGGGACCGTCAG TCTTCTCTTCCCCCCTCAACCCAAAGGACACCT CATGATCTCCCGGACCCCTGAGGTACATGCGT GGTGGTGGACGTGAGCCACGAAGACCTGAGGT CAAGTTCAACTGGTACGTGGACGGCTGGAGGT GCATAATGCCAAGACAAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTACGCGTCC TCACCGTCTGCACCAAGGACTGGCTGAATGGCA AGGAGTACAAGTGCAAGGTCTCCAAACAAAGCCC TCCCAGCCCCCATCGAGAAACCATCTCCAAAG CCAAAGGCGAGCCCCGAGAACCCACAGGTGTAC ACCTGCCCCCATCCCGGGAGGAGATGACCAAG AACCAGGTACGCTGACCTGCCCTGGTCAAAGGC TTCTATCCCAGCAGATCGCCGTGGAGTGGGAG AGCAATGGGCGAGCCGGAACAACACTACAAGAC CACGCCCTCCGTGTGTGACTCCGACGGCTCCTTC TTCCTCTATAGCAAGCTCACCCTGGACAAAGC AGGTGGCAGCAGGGGAACGTCTTCTCATGTCTC GTGATGCATGAGGCTCTGCACAACCACTACAG CAGAAGAGCCTCTCCCTGTCTCCGGGTAA
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		SEQ ID NO: 1946	SEQ ID NO: 2103
	AA	DIQMTQSPSSLSASVGDRAVITITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGGTD FTFTISLQPEDATYYCQQYDDLFTFGPGTKVDIK RTVAAPSVEFPPSDEQLKSGTASVCLLNFFPRE AKVQW'KVDNALQSGNSQESVTEQDSKDSYSLSS TLTLKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC	QVQLVESGGGVVQPGSRSLRLSCAASGFSFSSYGM HWVRQPPGKGLVVAIWDANNKYADA VKG RFTISRDSSKNTLYIQMNSLR AEDTAVYYCARDR TIFGVVLEYWGQGLVTVSSASTKGPSVFP LAPSS KSTSGGT AALGCLVKDYFPEPTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCTPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYITLPPSRREMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
		SEQ ID NO: 376	SEQ ID NO: 533
	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTAA ATTGGTATCAGCAGAAACCAGGGAAGCCCCA AACTCTGATCTACGATGCTTCCAAATTTGGAGCC AGGGTCCCATCAAGGTTTCAGTGGAAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAGTGGATATCAACGAAACGGTGGCTGCA CCATCTGTCTTCATCTTCCCGCCATCTGATGAGC AGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCT GCTGAATAACTTCTATCCAGAGAGGCCAAAAGT ACAGTGGAAAGGTGGATAACGCCCTCCAAATCGGG TAACCTCCAGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGCAGCACCT GACGCTGAGCAAAAGCAGACTACGAGAAACACA AAGTCTACGCTGCGAAGTCAACCCATCAGGGCC TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGG GAGAGTGT	CAGTGCAGCTGGTGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCTTCAGTAGCTATGGCA TGCACTGGTCCGCCAGCCTCCAGGCAAGGGC TGGAGTGGTGGCAGCTATATGGTATGATGGAA ATAATAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAAGAAC CGCTGATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTGGAGTGGTCTTGAAGTACTGGG GCCAGGGAACCTGGTCAACCTCTCCTCAGCCT CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC CCTCCTCCAAAGACACCTCTGGGGGCAACAGCG CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCTGTGGAACCTCAGCGGCC TGACACGCGGTGCACACCTTCCCCGGCTGTCC TACAGTCTCAGGACTCTACTCCTCAGCAGCGT GGTGACCGTGCCTCCAGCAGCTTGGGCAACCA GACCTACATCTGCAACGTGAATCACAAGCCCA CAACACCAAGGTGGACAAAGAAAGTTGAGCCCA

		<p>AATCTTGTGACAAAACCTCACACATGCCCACCGT GCCCAGCACTGAACCTCCTGGGGGACCGTCAG TCTTCTCTTCCCCCAAACCCAAAGGACACCCCT CATGATCTCCCGGACCCCTGAGGTACATGCGT GGTGTGACGTGAGCCACGAAGACCCGTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGAGGT GCATAATGCCAAGACAAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTACGCGTCC TCACCGTCTGCACCAAGGACTGGCTGAATGGCA AGGAGTACAAGTGCAAGGTCTCCAAACAAAGCCC TCCCAGCCCCATCGAGAAACCATCTCCAAAG CCAAAGGCAGCCCCGAGAACACACAGGTGTAC ACCTGCCCCCATCCCGGAGGAGATGACCAAG AACCAGGTACGCTGACCTGCCTGGTCAAAGGC TTCTATCCAGCGACATCGCCGTGGAGTGGGAG AGCAATGGCAGCCGAGAACAACTACAAGAC CACGCTCCCGTGTGACTCCGACGGCTCCTTC TTCCTATAGCAAGCTCACCGTGGACAAGAGC AGTGGCAGCAGGGGAACGTCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACAG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
	SEQ ID NO: 1947	SEQ ID NO: 2104
	<p>DIQMTQSPSSLSASVGDRVTITCQASQDITNLYNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGGTD FTLTISLQPEDFATYYCQQYDDLFTFGPGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLS TLTLTKADYEKHKVYACEVTHQGLSPVTKSFNR GEC</p>	<p>QVQLVESGGGVVQPGRLRLSCAASGFSFSSYGM HWVRQPPGKGLVVAAIWYDGNKKYYADAVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWQQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAAALGCLVKDYFPEPTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKEPKSCDKTHCTCPPELPG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK LTVDKSRWQQGNVFSQSVMHENHNTQKSL LSPGK</p>
	AA	

			SEQ ID NO: 377	SEQ ID NO: 534		
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTAA ATTGGTATCAGCAGAAACCAGGGAAGCCCCTA AACTCCTGATCTACGATGCTTCCAAATTTGGAGCC AGGGTCCCATCAAGGTTCAAGTGGAAAGTGGATC TGGGACAGATTTTACTCTCAACCATCAGCAGCCT GCAGCCTGAAGATTTTGC AACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAGTGGATATCA AACGAACGGTGGCTGCA CCATCTGCTTCATCTTCCCGCCATCTGATGAGC AGTTGAAATCTGGAAC'TGCCTCTGTTGTGTGCT GCTGAATAACTTCTATCCCAAGAGAGGCCAAAGT ACAGTGGAAAGTGGATAACGCCCTCCAATCGGG TAACTCCCAGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGCAGCACCCCT GACGCTGAGCA AAGCAGACTACGAGAAACACA AAGTCTACGCC'TGCGAAGTCACCCCATCAGGGCC TGAGCTCGCCCCGTCAAAAGAGCTTCAACAGGG GAGAGTGT			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGGTC'TGGATTCTCCTTCAAGTAGCTATGGCA TGCACTGGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATG'TATGATGCAA ATAATAAATACTATGCAGACTCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAAGAACA CGCTGATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTG'TATTACTGTGCGGAGAGATC GGACGATTTTGGAGTGGTCTT'GAGTACTTGGG GCCAGGAAACCTGGTCAACC'GTCTCCTCAGCCT CCACCAAGGGCCCATCGGTCTT'CCCCCTGGCAC CCTCTCC AAGAGCACCTCTGGGGGCACAGCGG CCCTGGGTGCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTG'TG'TGGAAC'TCAGGCGCC TGACCAGCGGCTGCACACCTT'CCCGGCTGTCC TACAGTCTCAGGACTCTACTCCTCAGCAGCGCT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCAACAAGCCACG CAACACCAAGGTGGACAAGAAAGTTGAGCCCA AATCTTGTGACA AAAC'TCACACATGCCCAACCGT GCCAGCACCTGAAC'TCCTGGGGGACCGTCAG TCTTCTCTTCCCCCACA AAACCAAGGACACCCCT CATGATCTCCGGACCCCTGAGGTACATGCGT GGTGTGGACGTGAGCCACGAAGACCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGT GCATAATGCCAAGACA AAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTCAAGCTCC TCACCGTCTGCACCAAGGACTGGCTGAATGGCA AGGAGTACAAGTGCAAGGTCTCCAAACAAGCCC TCCCAGCCCCCATCGAGAAACCATCTCCAAAG CCAAAGGCGAGCCCCGAGAACCAACAGGTGTAC ACCTGCCCCCATCCCGGGAGGAGATGACCAAG AACCAGGTACGCTGACCTGCCTGGTCAAGGC TTCTATCCCAGCGACATCGCCGTGGAGTGGGAG
		6A5.004.009	NA			
		IPS:361120				

			<p>AGCAATGGGAGCCGGAGAACAACTACAAGAC CACGCCTCCCTGCTGGACTCCGACGGCTCCTTC TTCCTCTATAGCAAGCTCACCCTGGACAAGAGC AGTGGCAGCAGGGGAACGTCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACAG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA</p> <p>SEQ ID NO: 2105</p> <p>QVQLVESGGGVVQGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLWVAAIWYDANNKYVADSVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWQQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAAALGCLVKDYFPEPTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHITCPPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPVLDSDGSEFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK</p>
			<p>DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGGTD FTLTISLQPEDFATYYCQQYDDLFTFGPGTKVDIK RTVAAPSVFIPPPSDEQLKSGTASVCLLNFFPRE AKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLS TLTLKADYEEKHKVYACEVTHQGLSSPVTKSFNR GEC</p> <p>SEQ ID NO: 1948</p>
		AA	
IPS:359896	6A5.004.010	NA	<p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCACTCTGTGGGGACAGAGTCACCAATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTAA ATTGGTATCAGCAGAAACCAAGGAAAGCCCTA AACTCTGATCTACGATGCTTCCAAATTTGGAGCC AGGGTCCCATCAAGGTTTCAGTGGAAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATGATCTATTACCTTTCGGCCAAGG GACCAAAGTGGATATCAAAACGAACGGTGGCTGC ACCATCTGTCTTCACTTCCCGCCATCTGATGAG CAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCC TGCTGAATAACTTCTATCCACAGAGAGGCCAAAG TACAGTGGAAAGGTGGATAACGCCCTCCAAATCGG</p> <p>SEQ ID NO: 378</p> <p>CAGGTGCAGCTGGTGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGTGCGCAGCTATATGGTATGATGCAAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCCAAGAACAA CGCTGATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTGGAGTGGTCTTGTAGTACTGGG GCCAGGGAACCTGTGTACCGCTCTCCTCAGCCT CCACCAAGGGCCCAATCGGTCTTCCCCCTGGCAC CCTCCTCCAAGAGCACCTCTGGGGGCAACAGCGG CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG</p> <p>SEQ ID NO: 535</p>

		<p>GTAAGGACAGCACTACAGCCTCAGCAGCACCC TGACGCTGAGCAAGCAGACTACGAGAAACAC AAAGTCTACGCTGCGAAGTCACCCATCAGGCG CTGAGCTCGCCCGTCACAAAGAGCTTCAACAGG GGAGAGTGT</p>	<p>AACCGGTGACGGTGTCTGGAACCTCAGCGCCC TGACCAGCGGCTGCACACCTTCCCAGCTGTCC TACAGTCTCAGGACTCTACTCCCTCAGCAGCGT GGTACCGTGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAGCCAG CAACACCAAGTGGACAAAGAAATTGAGCCCA AATCTGTGACAAAACTCACACATGCCACCGT GCCCAGCACTGAATCTCTGGGGGACCGTCAG TCTTCTCTTCCCCCAAACCCAAAGGACACCCCT CATGATCTCCCGGACCCCTGAGGTACATGCGT GGTGTGACGTGAGCCACGAAGACCTGAGGT CAAGTTCAACTGGTACGTGGACGGCTGGAGGT GCATAATGCCAAGACAAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTACGCGTCC TCACCGTCTGCCACGAGGACTGGCTGAATGGCA AGGAGTACAAGTGCAAGGTCTCCAAACAAAGCCC TCCCAGCCCCATCGAGAAACCATCTCCAAAG CCAAAGGCAGCCCCGAGAACCAACAGGTGTAC ACCTGCCCCATCCCGGAGGAGATGACCAAG AACAGGTACGCTGACCTGCCTGGTCAAAGGC TTCTATCCAGCGACATCGCCGTGGAGTGGGAG AGCAATGGCAGCCGAGAACAACTACAAGAC CACGCTCCCGTGTGACTCCGACGGCTCCTTC TTCCTCTATAGCAAGCTCACCGTGGACAAGAGC AGTGGCAGCAGGGGAACGTCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACAG CAGAAGAGCCTCTCCCTGTCTCCGGGTAA</p>
	AA	<p>DIQMTQSPSSLSASVGDRVTITCQASQDITNLYNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGGTD FTLTISLQPEDFATYYCQQYDDLFTFGQGTQKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLS STLTLSKADYEKHKVYACEVTHQGLSPVTKSFN RGEC</p>	<p>SEQ ID NO: 1949</p> <p>SEQ ID NO: 2106</p> <p>QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAIIWYDANNKYVADAVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGQGTLLVTVSSASTKGPSVFPAPSS KSTSGGTAAALGCLVKDYFPEPTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCTPCPAPELLG GPSVFLFPPKPKDITLMISRTPETVTVVVDVSHEDPE</p>

				<p>VKFNWYVVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDSGSEFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK</p>
				<p>SEQ ID NO: 379</p> <p>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAAGGAAAGCCCCTA AACTCTGATCTACGATGCTTCCAAATTTGGAGCC AGGGTCCCATCAAGGTTCAAGTGGAAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCAAAG GACCAAAGTGGATATCAAAACGAACGGTGGCTGC ACCATCTGTCTTCACTTCCCGCCATCTGATGAG CAGTTGAAATCTGGAACCTGCCCTCTGTTGTGGCC TGCTGAATAACTTCTATCCACAGAGAGGCCAAAG TACAGTGGAAAGGTGGATAACGCCCTCCAAATCGG GTAACTCCAGGAGAGTGTACAGAGCAGGACA GCAAGGACAGCACTACAGCCTCAGCAGCACCCC TGACGCTGAGCAAAAGCAGACTACGAGAAACAC AAAGTCTACGCCCTGCGAAGTCACCCATCAGGGC CTGAGCTCGCCCGTCAACAAAGAGCTTCAACAGG GGAGAGTGT</p>
			6A5.004.011	NA
		IPS:359890		<p>SEQ ID NO: 536</p> <p>CAGGTGCAGCTGGTGGAGTCTGGGGGAGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAAGCTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGTGGCAGCTATATGGTATGATGCAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAAGAAC CGCTGATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTATTACTGTGCGAGAGATC GGACGATTTTGGAGTGGTCTTGAGTAGCTCG GCCAGGAAACCTGTGTACCGCTCCTCCTCAGCCT CCACCAAGGCCCAATCGGTCTTCCCCCTGGCAC CCTCCTCCAAGACACCTCTGGGGGCAACAGCGG CCCTGGGTGCCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCTGTGGAACTCAGGCGCCC TGACCAGCGCGTGCACACCTTCCCCGGCTGTCC TACAGTCTCAGGACTCTACTCCTCAGCAGCGT GGTGACCGTGGCCTCCAGCAGCTTGGGCAACCA GACCTACATCTGCAACGTGAATCACAAGCCCCAG CAACCAAGGTGGACAAAGAAAGTTGAGCCCCA AATCTTGTGACAAAACTCACACATGCCACCGT GCCCCAGCACTGAATCCTGGGGGACCGTCAG TCTTCTCTTCCCCCAAAACCCAAAGGACACCCCT CATGATCTCCGGACCCCTGAGGTACATGCGT GGTGGTGGACGTGAGCCACGAAGACCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGT GCATAATGCCAAGACAAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTACGCGTCC TCACCGTCTTGCAACCAAGGACTGGCTGAATGGCA</p>

			<p>AGGAGTAC AAGTGCAAGGTCTCCAAACAAAGCCC TCCAGCCCCCATCGAGAAACCATCTCCAAAG CCAAAGGCAGCCCCGAGAACACACAGGTGTAC ACCTGCCCCCATCCCGGAGGAGATGACCAAG AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC TTCTATCCAGCGACATCGCCGTGGAGTGGGAG AGCAATGGCAGCGGAGAACAACTACAAGAC CACGCCTCCGTGCTGGACTCCGACGGCTCCTTC TTCCTATAGCAAGCTACCGTGGACAAAGAC AGGTGCAGCAGGGGAACGTCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACAG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
			<p>SEQ ID NO: 1950</p> <p>DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGGTD FTLTISLQPEDFATYYCQQYDDLFTFGQGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS STLTLSKADYEKHKVYACEVTHQGLSPVTKSFN RGEK</p>
		AA	<p>SEQ ID NO: 2107</p> <p>QVQLVESGGGVVQPGRLSLRSCAASGFSFSSYGM HWVRQPPGKGLWVAAIWYDANNKYYADAVKG RFTISRDSSKNTLYLQMNSLR AEDTAVYYCARDR TIFGVVLEYLGQGTLVTVSSASTKGPSVFPLAPSSK STSGGT AALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVN HKPSNTKVDKKEPKSCDKTHTCPPCP APELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYITLPPSRREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVVFSCSVMH EALHNHYTQKLSL SPGK</p>
			<p>SEQ ID NO: 380</p> <p>GAAATTGTGTTGACGCAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGAAAGAGCCACCCCTCTCCT GCAGGGCCAGTCAGATTTTACCAGCACCTACT TAGCCTGGTACACAGCAAGAACTGGCCAGGCTC CCAGGCTCCTCATCTATGTGTGATCCAGCAAGGG CCACTGGCATCCAGACAGGTTTCAGTGGCAGTG GGTCTGGGACAGACTTCACTCTCAACCATCAGCA GATTGGAGCCTGAAGATTTTGCAGTGTAATTACT</p>
IPS:359567	2A11.002	NA	<p>SEQ ID NO: 537</p> <p>CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCAAGTTTCAGTAGCTATGGC ATGCACTGGTCCGCCAGGCTCCAGGCAAGGGA CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAATACTATGAAGACGCCGTGAAGGGC CGATTACCATCTCCAGAGACAAATCCAAAGAAC ACGCTGTTTCTGCAAGTGAACAGCCTGAGAGCC</p>

		<p>GTCAGCAGTATGGTAGCTCACCTCGCTTCGGCC AAGGACACGACTGGAGATTAAACGAACGGTG GCTGCACCATCTGTCTTCATCTTCCCGCCATCTG ATGAGCAGTTGAAATCTGGAACCTGCCTCTGTTG TGTGCTGTGCTGAATAACTTCTATCCAGAGAGG CCAAAGTACAGTGAAGGTGGATAACGCCCTCC AATCGGGTAACCTCCAGGAGAGTGTCACAGAGC AGGACAGCAAGGACAGCACCTACAGCCTCAGC AGCACCTGACGCTGAGCAAGCAGACTACGAG AAACACAAAGTCTACGCTGCGAAGTCAACCCAT CAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTC AACAGGGGAGAGTGT</p>	<p>GAGGACACGGCTGTGTATTACTGTGCGAGAGGG ATTACGATTTTGGTCATGGGTTTGAATATTGGG GCCAGGAACCTGGTCAACCTCTCCTCAGCCT CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC CCTCTCCAAGAGCACCTCTGGGGGACAGCGG CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCTGTGGAACCTCAGGCGCC TGACCAGCGGCTGCACACCTTCCCCGGCTGTCC TACAGTCTCAGGACTCTACTCTCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAGCCAG CAACACCAAGGTGGACAAAGAAATTGAGCCCA AATCTGTGACAAACTCACACATGCCACCGT GCCCAGCACCTGAACCTCTGGGGGACCGTCAG TCTTCTCTTCCCCCACAACCCAAAGGACACCT CATGATCTCCCGGACCCCTGAGGTCACATGCGT GGTGTGACGTGAGCCACGAAGACCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGAGGT GCATAATGCCAAGACAAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTACGCGTCC TCACCGTCTGCCACGAGGACTGGCTGAATGGCA AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC TCCCAGCCCCATCGAGAAACCATCTCCAAG CCAAAGGCGAGCCCCGAGAACCCACAGGTGTAC ACCTGCCCCATCCC'GGGAGGAGATGACCAAG AACAGGTCAGCCTGACCTGCCTGGTCAAAGGC TTCTATCCAGCGACATCGCCGTGGAGTGGGAG AGCAATGGGCGAGCGGAGAACACTACAAGAC CACGCTCCCTGTGTGGACTCCGACGGCTCCTTC TTCTCTATAGCAAGCTCACCGTGGACAAAGC AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACAG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
	AA	<p>SEQ ID NO: 1951 EIVLTQSPGTLSPGERATLSCRASQIFTSTYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDF</p>	<p>SEQ ID NO: 2108 QVQLVESGGGVVQPRSLRLSCAASGFSFSSYGM HWVRQAPGKGLEWVAVIWYDASNKYYEDAVKG</p>

			TLTISRLEPEDFAVYYCQYQYGSSPRFGQGRLEIKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNFFYPREA KVQWKVDNALQSGNSQESVTEQDSKSDSTYSLSST LTLKADYEEKHKVYACEVTHQGLSSPVTKSFNRG EC		RFTISRDN SKNTLFLQVNSLRAEDTAVYYCARGITI FGHGEYWGQGLTVTVSSASTKGPSVFPLAPSSKS TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPS VFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVVFSCSVMHEALHNHYTQKSLSLSP GK
			SEQ ID NO: 381		SEQ ID NO: 538
			GAAATTGTGTGACGCAGTCTCCAGGCACCCCTG TCCTTTGCTCCAGGGGAAAGAGCCACCCCTCTCCT GCAGGGCCAGTCAGATTTTTACCAGCACCTACT TAGCCTGGTACCGACGAGAAACCTGGCCAGGCTC CCAGGCTCCTCATCTATGGTGATCCAGCAGGG CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG GGTCTGGGACAGACTTCACTCTCACCATCAGCA GATTGGAGCCTGAAGATTTTGCAGTGATTAAT GTCAGCAGTATGTTAGTCACTCACCTCGCTTCGGCC AAGGGACACGACTGGAGATTAAACGAACGGTG GCTGCACCATCTGTCTTCATCTTCCCGCCATCTG ATGAGCAGTTGAAATCTGGAACTGCCCTCTGTTG TGTGCCCTGCTGAATAACTTCTATCCCAAGAGAG CCAAAGTACAGTGGAAAGGTGGATAACGCCCTCC AATCGGGTAACCTCCAGGAGAGTGTCAAGAGC AGGACAGCAAGGACAGCACCTACAGCCTCAGC AGCACCCCTGACGCTGAGCAAAAGCAGACTACGAG AAACACAAAGTCTACGCTGCGAAGTCAACCCAT CAGGGCCTGAGCTCGCCCGTCACAAAAGAGCTTC AACAGGGGAGAGTGT		CAGGTGCAGCTGGTGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGAATTCAGTTTCAGTAGCTATGGC ATGCACTGGTCCGCCAGGCTCCAGGCAAGGGA CTGGAGTGGTGGCAGTTATATGGTATGATGGA AGTAATAATACTATGAAGACTCCGTGAAGGGC CGATTCAACCATCTCCAGAGACAATCCAAAGAAC ACGCTGTTTCTGCAAGTGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGGG ATTACGATTTTGGTCAATGGGTTTGAATATTGGG GCCAGGGAACCTGGTCAACCGTCTCCTCAAGCCT CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC CCTCCTCCAAGAGCACCTCTGGGGGACACAGCGG CCCTGGGCTGCCGTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCTGTGGAACCTCAGGCGGCC TGACCAGCGGCTGCACACCTTCCCGGCTGTCC TACAGTCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGGACCCCA GACCTACATCTGCAACGTGAATCACAAGCCCAAG CAACACCAAGGTGGACAAGAAAGTTGAGGCCA AATCTTGTGACAAACTCACACATGCCCCACCGT GCCCAGCACCTGAACCTCTGGGGGACCGGTCAAG TCTTCTCTTCCCCCCCCAAAAACCAAGGACACCT
IPS:335965	2A11.003	NA			

		<div>SEQ ID NO: 1952</div> <div>EIVLTQSPGTLSPGERATLSCRASQIFTSTYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGTDF TLTISRLEPEDFAVYYCQQYGSSPRFGQGRLEIKR TVAAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSYSTYLSST LTLKADYEEKHKVYACEVTHQGLSSPVTKSFNRG EC</div>
	AA	<div>SEQ ID NO: 2109</div> <div>QVQLVESGGGVVQPGRSLRLSCAASGFSFSYGM HWVRQAPGKGLEWVAWIWDGSNKYYEDSVKVG RFTISRDNKNTLFLQVNSLRAEDTAVYYCARGITI FGHGFYWGQGTLVTVSSASTKGPSVFPLAPSSKS TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLT VLHQDWLNGKEYCKVSNKALPAPIEKITISKAKG QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVVFSCSVMHEALHNHYTQKSLSLSP GK</div>

				SEQ ID NO: 382	SEQ ID NO: 539
IP:361158	2A11.004	NA		<p>GAAATTGTGTGACGCAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCT GCAGGGCCAGTCAGATTTTACCAGCACCTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCAGGCTCCTCATCTATGGTGATCCAGCAGGG CCACTGGCATCCAGACAGGTTCACTGAGGAGTG GGTCTGGGACAGACTTCACTCTCACCATCAGCA GATTGGAGCCTGAAGATTTTGCAGTGATTAAT GTCAGCAGTATGGTAGCTCACCTCGCTTCGGCC AAGGGACACGACTGGAGATTAAACGAACGGTG GCTGCACCATCTGTCTTCACTTCCCGCCATCTG ATGAGCAGTTGAAATCTGGAACTGCCCTCTGTTG TGTGCCCTGCTGAATACTTCTATCCCAGAGAGG CCAAAGTACAGTGAAGGTGGATAACGCCCTCC AATCGGGTAACCTCCAGGAGAGTGTCACAGAGC AGGACAGCAAGGACAGCACCTACAGCCTCAGC AGCACCCCTGACGCTGAGCAAGCAGACTACGAG AAACACAAAGTCTACGCCCTGCGAAGTCAACCCAT CAGGGCCTGAGCTCGCCCGTCAACAAAGAGCTTC AACAGGGGAGAGTGT</p>	<p>CAGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCAAGTTTCAGTAGCTATGGC ATGCACTGGTCCGCCAGGCTCCAGGCAAGGGA CTGGAGTGGTGGCAGTTATATGGTATGATGGA AGTAATAATACTATGAAGACGCCGTGAAGGGC CGATTCAACATCTCCAGAGACAAATCCAGAAGC ACGCTGTTCTGCAAGTGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTAATGTGCGAGAGGG ATTACGATTTTGGTCAATGGGTTTGAATATTGGG GCCAGGGAACCTGGTCAACCGTCTCCTCAGCCT CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC CCTCCTCCAAGAGCACTCTGCGGGGACAGCGG CCCTGGGCTGCCGTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCTGGAACCTCAGCGGCC TGACCAGCGGCTGCACACCTTCCCCGGCTGTCC TACAGTCTCAGGACTCTACTCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAGCCAG CAACCAAGGTGGACAAAGAAAGTTGAGCCCCA AATCTGTGACAAACCTCACACATGCCACCGT GCCAGCACCTGAACCTCCTGGGGGACCGTCAG TCTTCTCTTCCCCCAAAACCCAAGGACACCCCT CATGATCTCCCGGACCCCTGAGGTCAATGCGT GGTGGTGGACGTGAGCCACGAAGACCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGT GCATAATGCCAAGACAAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTGACGCTCC TCACCGTCTGCAACGAGGACTGGCTGAATGGCA AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC TCCCAGCCCCCATCGAGAAACCATCTCCAAAG CCAAAGGCGACCCCGAGAACCAAGGTGTAC ACCTGCCCCCATCCCCGGGAGGAGATGACCAAG AACAGGTGACGCTGACCTGCCTGGTCAAGGC TTCTATCCCAAGCAGACATCGCCGTGGAGTGGGAG</p>

			<p>AGCAATGGCAGCCGGAACAACACTACAAGAC CACGCCTCCCTGCTGGACTCCGACGGCTCCTTC TTCCTCTATAGCAAGCTCACCCTGGACAAGAGC AGTGGCAGCAGGGGAACGTCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACAG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA</p> <p>SEQ ID NO: 2110</p> <p>QVQLVESGGGVVQGRSLRLSCAASGFSFSSYGM HWVRQAPGKGLEWVAWIYDGSNKYYEDAVKG RFTISRDNSKNTFLQVNSLRAEDTAVYYCARGITI FGHGEYWGQGTLVTVSSASTKGPSVFPLAPSSKS TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKG QPREPVYTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKLSLSP GK</p>
			<p>SEQ ID NO: 1953</p> <p>EIVLTQSPGTLSLSPGERATLSCRASQIFTSTYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDF TLTISRLEPEDFAVYYCQQYGSSPRFGQGRLEIKR TVAAPSVFIIPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSYSTLSST LTLISKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC</p> <p>AA</p>
IPS:361165	2A11.005	NA	<p>SEQ ID NO: 383</p> <p>GAAATTGTGTTGACGCAAGTCTCCAGGCACCCCTG TCCTTTGTCTCCAGGGAAAGAGCCACCCCTCTCCT GCAGGGCCAGTCAGATTTTACAGCACCTACT TAGCCTGGTACACAGCAGAAACCTGGCCAGGCTC CCAGGCTCCTCATCTATGTTGCAATCCAGCAGGG CCACTGGCATCCAGACAGGTTCAAGTGGCAGTG GGTCTGGGACAGACTTCACTCTCAACCATCAGCA GATTGGAGCCTGAAGATTTTGCAAGTGTATTACT GTCAGCAGTATGGTAGCTCACCTCGCTTCGGCC AAGGGACACGACTGGAGATTAAACGAACGGTG GCTGCACCATCTGTCTTCACTTCCCGGCATCTG ATGAGCAGTTGAAATCTGGAACTGCCCTCTGTTG TGTGCCCTGCTGAATACTTCTATCCCAAGAGAGG CCAAAGTACAGTGGAAAGGTGGATAACGCCCTCC</p>

	<p>AATCGGGTA AGGACAGCA AGCACCC AAACACA CAGGGCT AACAGGG</p> <p>AGTGTGTCACAGAGC AGCCTACAGCCTCAGC AAAGCAGACTACGAG TCAAGTCAAGTCAAGC TCAAGTCAAGTCAAGC</p>	<p>SEQ ID NO: 1954</p> <p>EIVLTQSPGTLSPGERATLSCRASQIFTSTYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDF TLTISRLEPEDFAVYYCQQYGSSPRFGQGRLEIKR TVAAPSVFIIPPSDEQLKSGTASVVCLLNFFPREA KVQWKVDNALQSGNSQESVTEQDSKDSYSTYLSST LTLSKADYEEKHKVYACEVTHQGLSSPVTKSFNRG EC</p>
	<p>AACCGGTGACGGTGTCTGTGGA TGACCAGCGGGCTGCACACCTT TACAGTCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAGCCAG CAACACCAAGGTGGACAAGAAAGTTGAGCCCA AATCTTGTGACAAAACTCACACATGCCACCGT GCCCAGCACCTGAACTCCTGGGGGACCGTCAG TCTTCTCTTCCCCCAAAACCCAAAGGACACCCCT CATGATCTCCCGGACCCCTGAGGTACATGCGT GGTGTGGACGTGAGCCACGAAGACCCGTGAGGT CAAGTTCAACTGGTACGTGGACGGCTGGAGGT GCATAATGCCAAGACAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTACGCGTCC TCACCGTCTGCACCAAGGACTGGCTGAATGGCA AGGAGTACAAGTGCAAGGTCTCCAAACAAAGCCC TCCCAGCCCCATCGAGAAACCATCTCCAAAG CCAAAGGGCAGCCCCGAGAACCAACAGGTGTAC ACCTGCCCTCATCCGGGAGGAGATGACCAAG AACCAAGGTACGCTGACCTGCCTGGTCAAGGC TTCTATCCCAGCGACATCGCCGTGGAGTGGGAG AGCAATGGGCAGCCGAGAACAACTACAAGAC CACGCTCCCGTGTCTGGACTCCGACGGCTCCTTC TTCCTCTATAGCAAGCTCACCGTGGACAAGAGC AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACACG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA</p> <p>SEQ ID NO: 2111</p> <p>QVQLVESGGGVVQPGRLRLSCAASGFSFSSYGM HWVRQAPGKGLEWVAWIWYDASNKYIEDSVKQ RFTISRDNSKNTFLQVNSLRAEDTAVYYCARGITI FGHGFYWGQGTLLVTVSSASTKGPSVFPLAPSSKS TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK</p>	

				FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG QPREQVYTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVVFSCSVMHEALHNHYTQKSLSLSP GK		
			SEQ ID NO: 384	SEQ ID NO: 541		
			GAAATAGTGATGACGCAGTCTCCAGCCACCCCTG TCTGTGCTCCAGGGGAAAGAGCCACCCCTCTCC TGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTA GCCTGTACCAAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAAGCCACAGGGCC ACTGGTATCCCAGCCAGGTTCAAGTGGCAGTGGG TCTGGGACAGAGTTCACCTCACCATCAGCAGC CTGCAGTCTGAAGATTTTGCAAGTTATTACTGTC AGCAGTATAATAACTGGCCTCTCACTTTCGGCG GAGGGACCAAGGTGGAGATCAACGAAACGGTG GCTGCACCATCTGTCTTCATCTTCCCGCCATCTG ATGAGCAGTTGAAATCTGGAACTGCCTCTGTTG TGTGCCCTGCTGAATAACTTCTATCCCAGAGAGG CCAAAGTACAGTGGAAAGGTGGATAACGCCCTCC AATCGGGTAACCTCCCAGGAGAGTGTACAGAGC AGGACAGCAAGGACAGCACCTACAGCCTCAGC AGCACCCCTGACGCTGAGCAAAAGCAGACTACGAG AAACACAAAGTCTACGCCCTGCGAAGTCAACCCAT CAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTC AACAGGGGAGAGTGT	NA	2G10_LC1.003	!PS:361172
			CAGTGCAGCTGGTGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGATTCACTTCAAGTAACTATGGC ATGCACTGGTCCGCCAGGCTCCAGGCGAGGGG CTGGAGTGGTGCGAGCTATATGTTTGTATGCA AGTGATAAATACTATGCAAGACGCCGTGAAGGGC CGATTACCAATCTCCAGAGACAACCTCCAAGAAC ACGCTGATCTGCAAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGCGGATTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCTGGTCAACCGTCTCCTCAGCC TCCACCAAGGGCCCACTCGGTCTTCCCCCTGGCA CCCTCTCCAAGAGCACTCTGGGGGACACAGCG GCCCTGGCTGCCCTGGTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCC CTGACCAAGCGGTGCACACCTTCCCCGGCTGTC CTACAGTCTCAGGACTCTACTCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTACAAACCTCAACATGCCACCC GTGCCAGCACCTGAACCTCCTGGGGGACCGTCT AGTCTTCTCTTCCCCCAAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCAATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAAGGACTGGCTGAATGG			

			<p>SEQ ID NO: 1955</p> <p>EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAAATRAATGIPARFSGSGSGTE FTLTISLSQSEDFAVYQCQYNNWPLTFGGGKVE IKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKDSITYSL SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEK</p>	<p>SEQ ID NO: 1955</p> <p>CAAGGAGTACAAAGTGCAAGGTCTCCAAACAAGC CTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCAACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACAGGTGAGCCTGACCTGCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGAGAACAACTACAAG ACCAGCCTCCCGTCTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGTAAA</p>
AA			<p>SEQ ID NO: 2112</p> <p>QVQLVESGGGVVQPGRLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAIWFDAADKYADAVKVG RFTISRDNSKNTLYQMNSLRAEDTAVYYCARDQ AIFGVDPDYWGQGLVTVSSASTKGPSVFPLAPSS KSTSGGTAAALGCLVKDYFPEPTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKEPKSCDKTHTCTCPPEPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFNCSVMHEALHNHYTQKSLS LSPGK</p>	<p>SEQ ID NO: 2112</p> <p>QVQLVESGGGVVQPGRLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAIWFDAADKYADAVKVG RFTISRDNSKNTLYQMNSLRAEDTAVYYCARDQ AIFGVDPDYWGQGLVTVSSASTKGPSVFPLAPSS KSTSGGTAAALGCLVKDYFPEPTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKEPKSCDKTHTCTCPPEPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFNCSVMHEALHNHYTQKSLS LSPGK</p>
2G10_LC1.004	IPS:361178	NA	<p>SEQ ID NO: 385</p> <p>GAAATAGTGATGACGAGTCTCCAGCCACCCCTG TCTGTGTCTCCAGGGGAAAGAGCCACCCCTCTCC TGACGGGCCAGTCAGAGTGTAGCAGCAACTTA GCCTGTACCAAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACCAAGGCC ACTGGTATCCCAAGCAGGTTCAAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCAACCATCAGCAGC CTGCAGTCTGAAGATTTTGACAGTTTATTACTGTC</p>	<p>SEQ ID NO: 542</p> <p>CAGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCAACCTTCACTAATATGGC ATGCACTGGTCCGCCAGGCTCCAGCGAGGGG CTGGAGTGGTGGCAGCTATATGTTTGTATGCA AGTGATAAATACTATGACAGACTCCGTGAAGGC CGATTACCATCTCCAGAGACAACCTCCAAAGAAC ACGCTGATCTGCAAAATGAACAGCCTGAGAGCC</p>

		<p>AGCAGTATAA AACTGGCCTCTCACTTTCCGGCG GAGGGACCAAGGTGGAGATCAAACGAAACGGTG GCTGCACCATCTGTCTTCACTTCCCGCCATCTG ATGAGCAGTTGAAATCTGGAACCTGCCTCTGTTG TGTGCTGTGCTGAATAACTTCTATCCAGAGAGG CCAAAGTACAGTGAAGGTGGATAACGCCCTCC AATCGGGTAACCTCCAGGAGAGTGTCACAGAGC AGGACAGCAAGGACAGCACCTACAGCCTCAGC AGCACCTGACGCTGAGCAAGCAGACTACGAG AAACACAAAGTCTACGCCCTGCGAAGTCAACCCAT CAGGGCCTGAGCTCGCCCGTCAACAAAGAGCTTC AACAGGGGAGAGTGT</p>	<p>GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGCGATTTTGGAGTGGTCCCGACTACTGG GGCCAGGGAACCTGGTCAACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCGCTGGCA CCCTCTCCAAGAGCACCTCTGGGGGACAGCG GCCCCTGGCTGCCTGGTCAAGGACTACTTCCCC GAACCGGTACGGTGTCTGGGAACCTCAGGGGCC CTGACCAAGGGGTGCACACCTTCCCGGCTGTC CTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGGCTTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCCCACC GTGCCAGCACCTGAACCTCTGGGGGACCGTCT AGTCTTCTCTTCCCCCAAAACCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGGTGGGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACCAAGGTACGCTGACCTGCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
	AA	<p>SEQ ID NO: 1956 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAAATRAATGIPARFSGSGSGTE</p>	<p>SEQ ID NO: 2113 QVQLVESGGGVVQPRSLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAIWFDASDKYYADSVKGG</p>

			FTLTISSLQSEDAVYYCQQYNNWPLTFGGGKVE IKRTVAAPSVFIPPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEK	SEQ ID NO: 386	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWQGGLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCTPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
IPS:361185	2G10_LC1.005	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCCTG TCTGTGTCCTCAGGGGAAGAGCCACCCCTCTCC TGACGGGCCAGTCAGAGTGTAGCAGCAACTTA GCCTGTACCCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAAGCCACCAAGGCC ACTGGTATCCCAGCCAGGTTCAAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGCAGTCTGAAGATTTTGCAAGTTTATTACTGTC AGCAGTATAATACTGGCCTCTCACTTTCCGGCG GAGGGACCAAGGTGGAGATCAACGAAACGGTG GCTGCACCATCTGTCTTCACTTCCCGCCATCTG ATGAGCAGTTGAAATCTGGAACTGCCCTCTGTTG TGTGCCCTGCTGAATACTTCTATCCCAGAGAGG CCAAAGTACAGTGGAAAGGTGGATAACGCCCTCC AATCGGGTAACCTCCAGGAGAGTGTCACAGAGC AGGACAGCAAGGACAGCACCTACAGCCTCAGC AGCACCCCTGACGCTGAGCAAGCAGACTACGAG AAACACAAAGTCTACGCCCTGCGAAGTCAACCCAT CAGGGCCTGAGCTCGCCCGTCAACAAAGAGCTTC AACAGGGGAGAGTGT	SEQ ID NO: 543	CAGGTGACGTGGTGAGTCTGGGGGAGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCAACCTTCAAGTAACATATGGC ATGCACTGGTCCGCCAGGTCCAGCGGAGGGG CTGGAGTGGTGCGCAGCTATATGTTTGTATGGA AGTGATAATACTATGCAGACGCCGTGAAGGGC CGATTACCATCTCCAGAGACAACCTCCAAAGAAC ACGCTGATCTGCAAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGCGGATTTTGGAGTGGTCCCGGACTACTGG GGCCAGGGAACCTGGTCAACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCTCTGGGGGACAGCG GCCCTGGGCTGCCGTGGTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCTGTGGAACCTCAGGGGCC CTGACCAAGCGGTGCACACCTTCCCCGGCTGTC CTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACCTCACACATGCCACCC GTGCCAGCACCTGAACCTCTGGGGGACCGTCTC AGTCTCCTCTTCCCCCCCCAAACCCCAAGGACAC

			CCTCATGATCTCCGGACCCCTGAGGTACATG CGTGGTGGTGACGTGAGCCACGAAGACCC'TGA GGTCAAGT'TCAACTGGTACGTGGACGGCGTGGA GGTGCAATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTCAAGCGT CCTCACCGTCTCGACCAAGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCCATCGAGAAAACCATCTCCAA AGCCAAGGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCGGGAGAGATGACCA AGAACAGGTGAGCCTGACCTGCCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGGAACAACACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1957	SEQ ID NO: 2114	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAIIWFDGSDKYYADA VKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCTPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK LTVDKSRWQQGNVVFSCSVMHEALHNHYTQKSLS LSPGK
	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAAATRAATGIPARFSGSGGTE FTLTISLSQSEDFAVYYCQQYNWPLTFGGGKVE IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKDSYSTSL SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEK		AA

IP:361192	2G10_LC1.006	NA	SEQ ID NO: 387	SEQ ID NO: 544
			<p>GAAATAGTGATGACGCAGCTCCAGGCCACCCCTG TCTGTGCTCCAGGGGAAAGAGCCACCCCTCTCC TGACGGGCCAGTCAGAGTGTAGCAGCAACTTA GCCTGTACACAGCAAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAAGCCACAGGGCC ACTGGTATCCCAGCCAGGGTCAAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGCAGTCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTGGCCTCTCACTTTCCGGCG GAGGGACCAGGTGGAGATCAACGAAACGGTG GCTGCACCATCTGTCTTCACTTCCCGGCATCTG ATGAGCAGTTGAAATCTGGAACCTGCCCTCTGTTG TGTGCCCTGCTGAATACTTCTATCCCAGAGAGG CCAAAGTACAGTGAAGGTGGATAACGCCCTCC AATCGGGTAACCTCCAGGAGAGTGTCACAGAGC AGGACAGCAAGGACAGCACCTACAGCCTCAGC AGCACCCCTGACGCTGAGCAAGCAGACTACGAG AAACACAAAGTCTACGCCCTGCGAAGTCAACCCAT CAGGGCCTGAGCTCGCCCCGTACAAAGAGCTTC AACAGGGGAGAGTGT</p>	<p>CAGTGCAGCTGGTGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCAACCTTCACTAATATGGC ATGCACTGGTCCGCAAGCTCCAGGCGAGGGG CTGGAGTGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCAACATCTCCAGAGACAACCTCCAGAAC ACGCTGATCTGCAAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGCGATTTTGGAGTGGTCCCGACTACTGG GGCCAGGGAACCTGGTCAACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA CCCTCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGCTGCCCTGGTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCTGTGGAACCTCAGGGCC CTGACCAAGCGGTGCACACCTTCCCGGCTGTC CTACAGTCTCAGGACTCTACTCCTCAGCAGC GTGTGACCGTGGCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAAACCCAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGGTGGTGACGTGAGCCACGAAGACCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCCTGTGTGTCAGCGT CCTCACCGTCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGAAGGTCTCCACAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCCAGGTGT ACACCTGCCCATCCCGGAGGAGATGACCA AGAACCAAGTCAAGCTGACCTGCCTGCTCAAG GCTTCTATCCAGCGCATCGCCGTGGAGTGGG</p>

			<p>SEQ ID NO: 1958</p> <p>EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLIYGAAATRAATGIPARVSGSGSGTE FTLTISLSQSEDFAVYQCQYNWPLTFGGGKVE IKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKDSITYSL SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEK</p>	<p>SEQ ID NO: 1958</p> <p>AGGCAATGGCAGCCGGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
		AA	<p>SEQ ID NO: 545</p> <p>QVQLVESGGGVVQGRSLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAIWFDASDKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYCARDQ AIFGVVDPDYWGQGLVTVSSASTKGPSVFPLAPSS KSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHCTCPPELPG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEVESNGQPENNYKTTTPVLDSDGSEFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK</p>	<p>SEQ ID NO: 545</p> <p>CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCAACCTTCAGTAACATATGGC ATGCACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTACCACTCCAGAGACAACTCCAAGAAC ACGCTGTATCTGCAAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGCGGATTTTGGAGTGGTCCCGGACTACTGG GGCCAGGGAACCCCTGGTCAACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA CCCTCTCCAAAGACACCTCTGGGGGACACAGG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC</p>
IPS:359609	2G10_LC1.007	NA	<p>SEQ ID NO: 388</p> <p>GAAATAGTGATGACGCAGTCTCCAGCCACCCCTG TCTGTGTCTCCAGGGGAAGAGCCACCCCTCTCC TGCAGGGCCAGTCAGAGTGTAGCAGCAACTTA GCCTGTACCAAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACCAAGGCC ACTGGTATCCCAAGCAGGTTCAAGTGCAAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGGAGCCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTTCCCTCTCACTTTCGGCGG AGGGACCAAGGTGAGATCAAAAGAACCGGTGG CTGCACCATCTGTCTTCACTCTCCCGCCATCTGA TGAGCAGTTGAAAATCTGGAACTGCCTCTGTTGT GTGCTGTGTAATAACTTCTATCCCAAGAGAGGC CAAAAGTACAGTGGAAGGTGGATAACGCCCTCCA</p>	<p>SEQ ID NO: 388</p> <p>GAAATAGTGATGACGCAGTCTCCAGCCACCCCTG TCTGTGTCTCCAGGGGAAGAGCCACCCCTCTCC TGCAGGGCCAGTCAGAGTGTAGCAGCAACTTA GCCTGTACCAAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACCAAGGCC ACTGGTATCCCAAGCAGGTTCAAGTGCAAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGGAGCCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTTCCCTCTCACTTTCGGCGG AGGGACCAAGGTGAGATCAAAAGAACCGGTGG CTGCACCATCTGTCTTCACTCTCCCGCCATCTGA TGAGCAGTTGAAAATCTGGAACTGCCTCTGTTGT GTGCTGTGTAATAACTTCTATCCCAAGAGAGGC CAAAAGTACAGTGGAAGGTGGATAACGCCCTCCA</p>

ATCGGGTAACTCCAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCCTGACGCTGAGCAAGCAGACTACGAGA AACACAAGTCTACGCCCTGCGAAAGTCAACCCATC AGGCCCTGAGCTCGCCCGTCAACAAGAGCTTCA ACAGGGGAGAGTGT	SEQ ID NO: 1959 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAAATRAATGIPARFSGSGSGTE FTLTISSELEPEDFAVYYCQQYNFPLTFGGGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNFFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSYSTYSL STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEK
GAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCC CTGACCAGCGGCGTGACACACCTTCCCGGCTGTC CTACAGTCTCAGGACTCTACTCCTCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCACACC GTGCCAGCACCTGAACCTCTGGGGGACCCGTC AGTCTTCTCTTCCCCCAAAAACCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCAACATG CGTGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAAACTGGTACGTGGACGGCGTGA GGTGCAATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTCAAGCGT CCTCACCGTCTGCACCAAGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCATCGAGAAAACCATCTCCAA AGCCAAGGGCAGCCCCGAGAACCAACAGGTGT ACACCTGCCCCCATCCCGGGAGGAGATGACCA AGAACAGGTGAGCCTGACCTGCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAAGCCGGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAAGAAAGAGCCTCTCCCTGTCTCCGGGTAAA	SEQ ID NO: 2116 QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM HWVRQAPGKGLEWVAIWFDAADKYADAVKGV RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGTLLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCTPPCPAPPELLG GPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPE

				<p>VKFNWYVVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK</p>
				<p>SEQ ID NO: 389</p> <p>GAAATAGTGATACGCAGTCTCCAGCCACCCCTG TCTGTGTCCTCAGGGGAAGAGCCACCCCTCTCC TGACGGGCCAGTCAGAGTGTAGCAGCAACTTA GCCTGTACCCAGCAAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAAGCCACAGGGCC ACTGGTATCCCAGCCAGGTTCAAGTGCAAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGGAGCCTGAAGATTTTGCAAGTTATTACTGTC AGCAGTATAATAACTATCCTCTCACTTTCGGCGG AGGACCAAGGTGGAGATCAACGAAACGGTGG CTGCACCATCTGCTCTCATCTTCCCAGCATCTGA TGAGCAGTTGAAATCTGGAACTGCCCTCTGTTGT GTGCTGCTGAATAACTTCTATCCCAGAGAGGC CAAAAGTACAGTGAAGGTGGATAACGCCCTCCA ATCGGGTAACCTCCAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACTACAGCCTCAGCA GCACCTGACGCTGAGCAAGCAGACTACGAGA AACACAAAGTCTACGCCCTGCGAAGTCAACCATC AGGGCTGAGCTCGCCCGTCAACAAAGAGCTTCA ACAGGGGAGAGTGT</p>
				<p>SEQ ID NO: 546</p> <p>CAGGTGCAGCTGGTGGAGTCTGGGGGAGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCAACCTTCACTAATATGGC ATGCACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCAACATCTCCAGAGACAACCTCCAAAGAAC ACGCTGATCTGCAAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGCGATTTTGGAGTGGTCCCGGACTACTGG GGCAGGGAACCTGGTCAACCGTCTCCTCAGCC TCCACAAAGGCCCATCGGTCTTCCCCCTGGCA CCCTCTCCAAGAGCAACCTCTGGGGGCAACAGG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCC CTGACCAAGCGGTGCACACCTTCCCGGCTGTC CTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACACC GTGCCAGCACCTGAACCTCTGGGGGACCGTTC AGTCTTCTCTTCCCCCAAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGCGGTGGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTACGCGT CCTCACCGTCTTGCAACCAAGGACTGGCTGAATGG</p>

			<p>SEQ ID NO: 1960</p> <p>EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAAATRAATGIPARFSGSGSGTE FTLTISLSEPEDFAVYYCQQYNNYPLTFGGGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLS STLTLSKADYEKHKVYACEVTHQGLSPVTKSFN RGEK</p>	<p>SEQ ID NO: 1960</p> <p>CAAGGAGTACAAAGTGCAAGGTCTCCAAACAAGC CTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCAACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACAGGTCAAGCTGACCTGCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGAGAACAACTACAAG ACCACGCTCCCGTCTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
AA			<p>SEQ ID NO: 2117</p> <p>QVQLVESGGGVVQPGRLSLRSCAASGFTFSNYGM HWVRQAPGKGLEWVAIWFDASDKYYADAVKG RFTISRDNSKNTLYQMNSLR AEDTAVYYCARDQ AIFGVDPDYWGQGLTVTVSSASTKGPSVFPLAPSS KSTSGGT AALGCLVKDYFPEPTVSWNSGALTSG VHTFPAVLQSSGLYSLSVTVVPSSSLGTQTYICNV NHKPSNTKVDKKEPKSCDKTHTCTPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFNCSVMHEALHNHYTQKSLS LSPGK</p>	<p>SEQ ID NO: 2117</p> <p>QVQLVESGGGVVQPGRLSLRSCAASGFTFSNYGM HWVRQAPGKGLEWVAIWFDASDKYYADAVKG RFTISRDNSKNTLYQMNSLR AEDTAVYYCARDQ AIFGVDPDYWGQGLTVTVSSASTKGPSVFPLAPSS KSTSGGT AALGCLVKDYFPEPTVSWNSGALTSG VHTFPAVLQSSGLYSLSVTVVPSSSLGTQTYICNV NHKPSNTKVDKKEPKSCDKTHTCTPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFNCSVMHEALHNHYTQKSLS LSPGK</p>
2G10_LC1.009	IPS:361196	NA	<p>SEQ ID NO: 390</p> <p>GAAATAGTGATGACGCAGTCTCCAGCCACCCCTG TCTGTGTCTCCAGGGGAAGAGCCACCCCTCTCC TGACGGGCCAGTCAGAGTGTAGCAGCAACTTA GCCTGTGTAACAGCAAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAAGCCACCAAGGCC ACTGGTATCCCAAGCCAGGTTCAAGTGGCAAGTGGG TCTGGGACAGAGTTCACTCTCAACCATCAGCAGC CTGGAGCCTGAAGATTTTGACAGTTTATTACTGTC</p>	<p>SEQ ID NO: 547</p> <p>CAGTGCAGCTGGTGAGTCTGGGGAGGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCAACCTTCACTAATATGGC ATGCACTGGTCCGCCAGGCTCCAGCGAGGGG CTGGAGTGGTGCAAGCTATATGTTTGTATGCA AGTGATAAATACTATGCAAGCGCCGTGAAGGCC CGATTACCATCTCCAGAGACAACCTCCAAGAAC ACGCTGATCTTGCAAAATGAACAGCCTGAGAGCC</p>

		<p>AGCAGTATAA AACTGGCCTCTCACTTTCCGGCG GAGGGACCAAGGTGGAGATCAAACGAAACGGTG GCTGCACCATCTGTCTTCATCTTCCCGCCATCTG ATGAGCAGTTGAAATCTGGAACTGCCTCTGTTG TGTGCTGTGCTGAATAACTTCTATCCAGAGAGG CCAAAGTACAGTGAAGGTGGATAACGCCCTCC AATCGGGTAACCTCCAGGAGAGTGTCACAGAGC AGGACAGCAAGGACAGCACCTACAGCCTCAGC AGCACCTGACGCTGAGCAAAGCAGACTACGAG AAACACAAAGTCTACGCCTGCGAAGTCAACCCAT CAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTC AACAGGGGAGAGTGT</p>	<p>GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGCGATTTTGGAGTGGTCCCGACTACTGG GGCCAGGGAACCTGGTCAACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCGCTGGCA CCCTCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCCTGGCTGCCTGGTCAAGGACTACTTCCCC GAACCGGTACGGTGTCTGGGAACCTCAGGGGCC CTGACCAAGGGGTGCACACCTTCCCGGCTGTC CTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGGCTTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCAACAAGCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACCC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAAACCAAGGACAC CCTCATGATCTCCCGACCCCTGAGGTACATG CGTGGTGGGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTACCGT CCTCACCGTCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACCAAGGTACGCTGACCTGCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGACAACATAAAG ACCAAGCCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTA</p>
	AA	<p>SEQ ID NO: 1961</p> <p>EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAAATRAATGIPARFSGSGSGTE</p>	<p>SEQ ID NO: 2118</p> <p>QVQLVESGGGVVQPGRSRLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAIIWFDASDKYYADAVKVG</p>

			FTLTISLEPEDEAVYYCQQYNNWPLTFGGGKVE IKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEN	SEQ ID NO: 391	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCTPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
IPS:361202	2G10_LC1.010	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCCTG TCTGTGTCTCCAGGGAAAGAGCCACCCCTCTCC TGACGGGCCAGTCAGAGTGTAGCAGCAACTTA GCCTGTACCCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAAGCCACCAAGGCC ACTGGTATCCCAGCCAGGTTCAAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGGAGCCTGAAGATTTTGCAAGTTATTACTGTC AGCAGTATAATACTGGCCTCTCACTTTCCGGCG GAGGGACCAAGGTGGAGATCAACGAAACGGTG GCTGCACCATCTGTCTTCACTTCCCGCCATCTG ATGAGCAGTTGAAATCTGGAACTGCCCTCTGTTG TGTGCCCTGCTGAATACTTCTATCCCAGAGAGG CCAAAGTACAGTGGAAAGGTGGATAACGCCCTCC AATCGGGTAACCTCCAGGAGAGTGTCACAGAGC AGGACAGCAAGGACAGCACCTACAGCCTCAGC AGCACCCCTGACGCTGAGCAAGCAGACTACGAG AAACACAAAGTCTACGCCTGCGAAGTCAACCCAT CAGGGCCTGAGCTCGCCCGTCAACAAAGAGCTTC AACAGGGGAGAGTGT	SEQ ID NO: 548	CAGGTGACGTGGTGAGTCTGGGGGAGCGGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCAACCTTCAGTAACATAAGGC ATGCACTGGTCCGCCAGGTCCAGGCAAGGGG CTGGAGTGGTGCGAGCTATATGGTTTGTATGCA AGTGATAATACTATGACAGACGCCGTGAAGGGC CGATTACCATCTCCAGAGACAACTCCAAGAAC ACGCTGATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTGGAGTGGTCCCGGACTACTGG GGCCAGGGAACCTGGTCAACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCTCTGGGGGCAACAGG GCCCTGGGCTGCCGTGGTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCTGTGGAACCTCAGGGGCC CTGACCAAGCGGTGCACACCTTCCCGGCTGTC CTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAAGAAAGTTGAGCC CAAATCTTGTGACAAACCTCACACATGCCACCC GTGCCAGCACCTGAACCTCTGGGGGACCGTCTC AGTCTCCTCTTCCCCCCCCAAACCCCAAGGACAC

			CCTCATGATCTCCGGACCCCTGAGGTACATG CGTGGTGGTGACGTGAGCCACGAAGACCC'TGA GGTCAAGT'TCAACTGGTACGTGGACGGCGTGGA GGTGCAATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTCAAGCGT CCTCACCGTCTCGACCAAGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCCATCGAGAAAACCATCTCCAA AGCCAAGGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCGGGAGAGATGACCA AGAACAGGTACGCTGACCTGCCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGGAACAAC'TACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1962	SEQ ID NO: 2119	QVQLVESGGGVVQPGRLSLRSCAASGFTFSNYGM HWVRQAPGKGLEWVAIWFDAADKYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCTCPAPPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK LTVDKSRWQQGNVVFSCVMHEALHNHYTQKSLS LSPGK
	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAAATRAATGIPARFSGSGGTE FTLTISLEPEDFAVYYCQQYNNWPLTFGGGTKEVE IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKDSYSTSL SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEN		AA

IP:359644	18E3.002	NA	SEQ ID NO: 392	SEQ ID NO: 549
			<p>GAAATTGTGTGACGCAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCCGCTCCTCATCTATGGTGATCCAGCAGGG CCACTGGCATCCAGACAGGTTCACTGAGCAGTG GGTCTGGGACAGACTTCACTCTCACCATCAGCA GACTGGAGCCTGATGATTTTGCAGTGTATTACTG TCAGCAGTATGGTAGTTCACCGCTCACTTTCGGC GGAGGGACCAAGGTGGAGATCAACGAAACGGT GGCTGCACCATCTGTCTTCACTCTCCCGCCATCT GATGAGCAGTTGAATCTGGAACTGCCCTCTGTT GTGTCCCTGCTGAATACTTCTATCCAGAGAG GCCAAGTACAGTGGAAAGGTGGATAACGCCCTC CAATCGGGTAACTCCCAGGAGAGTGTACACAGAG CAGGACAGCAAGGACAGCACCTACAGCCTCAGC AGCACCTGACGCTGAGCAAGCAGACTACGAG AAACACAAGTCTACGCTGCGAAGTCAACCCAT CAGGGCCTGAGCTCGCCCGTCAACAAGAGCTTC AACAGGGGAGAGTGT</p>	<p>CAGTGCAAGTTCAGGAGTCTGGGCCCAGGACTG GTGAAGCCTTCAGAGACCCCTGTCCCTCACCTGC ACTGTCTCTGGTACTCCATCAGCAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCCCCCAGGGA AGGGCCTGGAGTGGATTGGGTACATCTATTACA GTGGGAGCACCTACTACAACCCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGCTCAAGA ACCAGTTCTCCCTGAAAGCTGAGCTCTGTGACTGC CGCGACACGGCCGTGTATTACTGTGCGAGAGA TCGTATTACGATTTTGGAGTGGTTATGGGGGGC GGTATGGAGCTGTGGGGCCAAAGGACCAACGGTC ACCGTCTCTCAGCTCCACCAAGGGCCCCATCG GTC'TTCCCCCTGGCACCCCTCCTCCAAGAGCACCT CTGGGGGCACAGCGGCCCTGGGCTGCCCTGGTCA AGGACTACTTCCCCGAAACCGGTGACGGTGTCTGT GGAAC'TCAGCGCCCTGACCAGCGGCGTGCACA CCTTCCCGGTGTCTCAGTCTCAGGACTCTA CTCCCTCAGCAGCGTGTGACCGTGCCTCCAG CAGCTTGGGACCCAGACCTACATCTGCAACGT GAATCACAAGCCCAAGCAACCAAGGTGGACA AGAAAGTTGAGCCCCAAATCTTGTGACAAAACTC ACACATGCCCCACCGTGCCCAAGCACCTGAACCTC TGGGGGACCGTCAAGTCTTCTTCCCCCCCCAAA ACCCAGGACACCCCTCATGATCTCCCGGACCCC TGAGGTCAATGCGTGGTGGTGACGTGAGCCA CGAAGACCTGAGGTCAAAGTTCAAAGTGGTACGT GGACGGCGTGGAGGTGCATAATGCCAAGACAA AGCCGTGTAGGAGCAGTACGGCAGCACGTACC GTTGTGTCAAGCTCTCACCGTCTTGCACCCAGG ACTGGCTGAATGGCAAGGAGTACAAGTGCAAG GTCTCCAACAAGCCCTCCCAAGGCCAGCCCCGA AAACCATCTCCAAGCCAAAGGCCAGGCCCGA GAACCAAGGTGTACACCTGCCCCCATCCCCGG GAGGAGATGACCAAGAACCAAGGTACGCTGAC CTGCCCTGGTCAAGGCTTCTATCCCAAGCGACAT</p>

			CGCCGTGGAGTGGGAGAGCAATGGGCAGCCGG AGAACAATAAGACACGCTCCCGTGGTGG ACTCCGACGGCTCTTCTTCCCTCTATAGCAAGCT CACCGTGGACAAGACGAGGTGGCAGCAGGGGA ACGTCTTCTCATGCTCCGTGATGCATGAGGCTCT GCACAACCACTACACGAGAGAGCCTCTCCCT GTCTCCGGGTAAA
		SEQ ID NO: 1963	SEQ ID NO: 2120
	AA	EIVLTQSPGTLSPGERATLSCRASQISYSYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGTDF TLTISRLEPDDFAVYYCQQYGSSPLTFGGGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLS TLTLTKADYEKHKVYACEVTHQGLSSLSPVTKSFNR GEC	QVQLQESGPGLVKPSETLSLTCTVSGDSISSGGYY WSWIRPPGKGLEWIGIYYSGSTYYNPSLKSRTV ISVDTSKNQFSLKLSVTAADTA VYYCARDRITIFG VVMGGMDVWVGQGTTVTVSSASTKGPSVFPPLAP SSKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLMISRTPETCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFLY SKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPGK
		SEQ ID NO: 393	SEQ ID NO: 550
	NA	GAAATTGTGTTGACGCAAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGAAAGAGCCACCCCTCTCCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACAGCAGAAACCTGGCCAGGCTC CCCGCTCCTCATCTATGGTGCAATCCAGCAGGG CCACTGGCATCCAGACAGGTTCAAGTGCGAGTG GGTCTGGGACAGACTTCACTCTCAACCATCAGCA GACAGGAGCCTGATGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGTTACCCGCTCACTTCGG CGGAGGGACCAAGGTGGAGATCAACGAAACGG TGGCTGCACCATCTGTCTTCACTCTCCCGCCATC TGATGAGCAGTTGAAATCTGGAACCTGCTCTGT TGTGTGCCTGCTGAATAACTTCTATCCACAGAGA	CAGGTGCAGTTGCAGGAGTCGGGCCAGGACTG GTGAAGCCTTCAGAGACCCCTGTCCCTCACCTGC ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCCCCAGGGA AGGCCCTGGAGTGGATTGGGTACATCTATTACA GTGGGAGCACCTACTACAACCCGTCCTCAAGA GTCGAGTTACCATATCAGTAGACACGCTCAAGA ACCAAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGACACGGCCGTGTATTACTGTGCGAGAGA TCGTATTACGATTTTGGAGTGGTTATGGGGGGC GGTATGGAGCTGTGGGGCCCAAGGACACACGGTC ACCGTCTCCTCAGCCTCCACCAAGGGGCCATCG GTCTTCCCCCTGGCACCCCTCCTCCAAAGAGCACCT

		<p>GGCCAAAGTACAGTGGAAGGTGGATAACGCCCT CCAATCGGGTAAC TCCAGGAGAGTGTACAGA GCAGGACAGCAAGGACAGCACCTACAGCCTCA GCAGCACCTTGACGCTGAGCAAGCAGACTACG AGAAACACAAAGTCTACGCTGCGAAGTCAACC ATCAGGGCCTGAGCTCGCCCGTCACAAAAGAGCT TCAACAGGGGAGAGTGT</p>	<p>CTGGGGGCACAGCGGCCCTGGGGCTGCCTGGTCA AGGACTACTTCCCCGAACCGGTGACGGTGTCTGT GGAATCAGCGGCCCTGACCAGCGGCGTGCACA CCTTCCGGCTGTCTACAGTCTCAGGACTCTA CTCCCTCAGCAGCGTGTGACCGTGCCCTCCAG CAGCTTGGGACCCAGACCTACATCTGCAACGT GAATCACAAGCCCAAGCAACCAAGGTGGACA AGAAAGTTGAGCCCAATCTTGTGACAAAATC ACACATGCCACCGTGCCAGCACCTGAACCTCC TGGGGGACCGTCAAGTCTCTTCTTCCCCCAAA ACCAAGGACACCTCATGATCTCCCGGACCCC TGAGGTACATGCGTGGTGGTGGACGTGAGCCA CGAAGACCTGAGGTCAAAGTTCAAAGTGTACGT GGACGGCTGGAGGTGCATAATGCCAAGACAA AGCCGTGAGGAGCAGTACGGCAGCACGTACC GTTGTGTCAGCGTCTCACCGTCTTGACCCAGG ACTGGCTGAATGGCAAGGAGTACAAGTGCAAG GTCTCCAACAAGCCCTCCAGCCCCCATCGAG AAAACCATCTCCAAGCCAAAGGCGAGCCCCGA GAACACAGGTGTACACCTTGCCCCCATCCCCG GAGGAGATGACCAGAACCAAGGTACGCTGAC CTGCTGGTCAAAGGCTTCTATCCAGCGACAT CGCCGTGGAGTGGGAGAGCAATGGGCAGCCGG AGAACAACTACAAGACACCGCTCCCGTGTGG ACTCCGACGGCTCTTCTTCTCTATAGCAAGCT CACCGTGGACAAGAGCAGGTGGCAGCAGGGGA ACGTCTTCTCATGCTCCGTGATGCATGAGGCTCT GCACAACCACTACACGCAAGAGAGCCTCTCCCT GTCTCCGGGTAAA</p>
AA	SEQ ID NO: 1964	<p>EIVLTQSPGTLSPGERATLSCRASQISYSYLA YQQKPGQAPRLLIYGASSRATGIPDRFSGSGTDF TLTSRQEPDDFAVYYCQQYGSSPLTFGGGTKVEI KRTVAAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSYSL</p>	<p>SEQ ID NO: 2121</p> <p>QVQLQESGPGLVKPSETLSLTCTVSGDSISGGYY WSWIRPPGKGLEWIGYIYSGSTYYPNPSLKSRT ISVDTSKNQFSLKLSVTAADTA VYCARDRITIFG VVMGGMDVWVGQGT TVTVSSASTKGPSVFP LAP SSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICN</p>

			STLTLKADYEKHKVYACEVTHQGLSSPVTKSFN RGE	VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPKPKDPTLMISRTPEVTCVVVDVSHED PEVKFNWYVVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFELY SKLTVDKSRWQQGNVFSQVMHEALHNHYTQKS LSLSPGK
			SEQ ID NO: 394	SEQ ID NO: 551
			GAAATTGTGTGACGCAGTCTCCAGGCACCCCTG TCCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACACAGCAAGAACCTGGCCAGGCTC CCCGCTCCTCATCTATGGTGATCCAGCAGGG CCACTGGCATCCAGACAGGTTCAAGTGGCAGTG GGTCTGGGACAGACTTCACTCTCAACCATCAGCA GACTGGAGCCTGATGATTTTGCAGTGTATTACTG TCAGCAGTATGTAGTTACCCGCTCACTTTCGGC GGAGGGACCAAGGTGGAGATCAACGAACGGT GGCTGCACCATCTGTCTTCACTTCCCGCCATCT GATGAGCAGTTGAAATCTGGAACTGCCCTCTGTT GTGTGCCTGCTGAATACTTCTATCCAGAGAG GCCAAGTACAGTGGAAAGGTGGATAACGCCCTC CAATCGGGTAACTCCCAGGAGAGTGTACACAGAG CAGGACAGCAAGGACAGCACCTACAGCCTCAGC AGCACCCCTGACGCTGAGCAAGCAGACTACGAG AAACACAAAGTCTACGCCTGCGAAGTCAACCCAT CAGGGCCTGAGCTCGCCCGTCAACAAAGAGCTTC AACAGGGGAGAGTGT	CAGTGCAGTTGCAGGAGTCTGGGCCCCAGGACTG GTGAAGCCTTACAGAGACCCTGTCCCTCACCTGC ACTGTCTCTGGTGAATCCATCAGCAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCCCCAGGGA AGGCCCTGGAGTGGATTGGTACATCTATTACA GTGGGAGCACCTACTACAACCCGCTCCCTCAAGA GTCGAGTTACCATATCAGTACAGACAGTCTAAGA ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGACACGGCCGTGTATTACTGTGCGAGAGA TCGTATTACGATTTTGGAGTGGTTATGGGGGGC GGTATGGAGCTCTGGGGCCAGGGACACAGGTC ACCGTCTCCTCAGCCTCCACCAAGGGCCCATCG GTCCTCCCTTGGCACCCTCCCTCCAAGAGCACCT CTGGGGGACAGCGGCCCTGGGCTGCCCTGGTCA AGGACTACTTCCCGCAACCGGTGACGGTGTCTGT GGAATCAGCGCCCTGACCAAGCGGCGTGCACA CCTTCCCGGCTGTCTACAGTCTCAGGACTCTA CTCCCTCAGCAGCGTGTGACCGTCCCTCCAG CAGCTTGGGACCCAGACCTACATCTGCAACGT GAATCACAAGCCCAAGCAACCAAGGTGGACA AGAAAGTTGAGCCCCAAATCTTGTGACAAAATC ACACATGCCCCACCGTGCCCAAGCACTGAACCTC TGGGGGACCGTCAAGTCTTCTTCCCTCCCAAA ACCAAGGACACCCCTCATGATCTCCCGGACCCC TGAGGTACATGCGTGGTGGTGGACGTGAGCCA CGAAGACCTGAGGTCAAGTTCAACTGGTACGT GGACGGCGTGGAGGTGCATATATGCCAAGACAA
IPS:359628	18E3.004	NA		

				<p>AGCCGTGTAGGAGCAGTACGGCAGCACGTACC GTTGTGTACGGCTCCTACCGTCTTGCACCCAGG ACTGGCTGAATGGCAAGGAGTACAAGTGCAAG GTCCTCAACAAGCCCTCCAGCCCCCATCGAG AAACCATCTCCAAGCCAAAGCCAAAGGCAGCCCCGA GAACCACAGGTGTACACCTTGCCCCCATCCCCG GAGGAGATGACCAAGAACCAAGGTACGCTGAC CTGCTGGTCAAGGCTTCTATCCACGCGACAT CGCCGTGGAGTGGGAGAGCAATGGGCAGCCGG AGAACAACTACAAGACCAACGCTCCCGTGTGG ACTCCGACGGCTCTTCTTCCCTCTATAGCAAGCT CACCGTGACAAGAGCAGGTGGCAGCAGGGGA ACGTCTTCTCATGCTCCGTGATGCATGAGGCTCT GCACAACCACTACACGACGAGAGAGCCTCTCCCT GTCTCCGGGTAAA</p>
				<p>SEQ ID NO: 1965</p> <p>SEQ ID NO: 2122</p>
	AA			<p>EIVLTQSPGTLSPGERATLSCRASQISISYSLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDF TLTISRLEPDDFAVYYCQQYGSSPLTFGGGTKEIK RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSYSTYSLSS TLTLTKADYEKHKVYACEVTHQGLSSLSPVTKSFNR GEC</p>
				<p>SEQ ID NO: 395</p> <p>SEQ ID NO: 552</p>
IPS:35963 7	18E3.005	NA		<p>GAAATTGTGTTGACGCAGTCTCCAGGCACCCCTG TCCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACACAGCAGAAACCTGGCCAGGCTC CCCGCTCCTCATCTATGTTGTCATCCAGCAGGG</p> <p>CAGTGCAAGTTGCAGGAGTCGGGCCAGGACTG GTGAAGCCTTCAGAGACCCCTGTCCCTCACCTGC ACTGTCTCTGGTGACTCCATCAGCAGTGTGGTT ACTACTGGAGCTGGATCCGCCAGCACCCAGGGA AGGGCCTGGAGTGGATTGGGTACATCTATTACA</p>

CCACTGGCATCCAGACAGGTTTCAGTGGCAGTG GGTCTGGGACAGACTTCACTCTCACCATCAGCA GACTGGAGCCTGATGATTTTGCAGTGATTAATG TCAGCAGTATGGTAGTTCACCGCTCACTTTCGGC GGAGGGACCAAGGTGGAGATCAACGAACGGT GGCTGCACCATCTGTCTTCACTTCCCGCCATCT GATGAGCAGTTGAATACTGGAACTGCCCTCTGTT GTGTCCCTGCTGAATAACTTCTATCCAGAGAG GCCAAGTACAGTGGAAAGGTGGATAACGCCCTC CAATCGGGTAACCTCCAGGAGAGTGTACACAGAG CAGGACAGCAAGGACAGCACCTACAGCCTCAGC AGCACCTGACGCTGAGCAAGCAGACTACGAG AAACACAAAGTCTACGCCTGCGAAGTCAACCCAT CAGGGCCTGAGCTCGCCCGTCAACAAAGAGCTTC AACAGGGGAGAGTGT	GTGGAGCACCTACTACAACCCGTCCCTCAAGA GTCGAGTTACCATATACGTAGACACGTCCTAAGA ACAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGACACGGCCGTGTATTACTGTGCGAGAGA TCGTATTACGATTTTGGAGTGGTTATGGGGGGC GGTATGGACGTCTGGGGCCAAAGGACCAACGGTC ACCGTCTCTCAGCCTCCACCAAGGGCCCATCG GTCTTCCCTTGGCACCTCCCTCCAAGAGCACCT CTGGGGGCACAGCGGCCCTGGGCTGCCCTGGTCA AGGACTACTTCCCGCAACCGGTGACGGTGTCTGT GGAATCAGGCGCCCTGACCAGCGGCGTGCACA CCTTCCCGGTGTCTACAGTCTCAGGACTCTA CTCCCTCAGCAGCGTGTGACCGTGCCCTCCAG CAGCTTGGGACCCAGACCTACATCTGCAACGT GAATCACAAGCCCAAGCAACCAAGGTGGACA AGAAAGTTGAGCCCAATCTTGTGACAAAATC ACATATGCCACCGTGCCCAAGCACCTGAACCTC TGGGGGACCGTCAAGTCTCTTCTTCCCTCCAAA ACCAAGGACACCTCATGATCTCCCGGACCCC TGAGGTACATGCGTGGTGGTGGACGTGAGCCA CGAAGACCTGAGGTCAAGTTCAACTGGTACGT GGACGGCGTGGAGGTGCATAATGCCAAGACAA AGCCGTGTAGGAGCAGTACGGCAGCACGTACC GTTGTGTACGCTCTCACCGTCTTGCACCAAG ACTGGCTGAATGGCAAGGAGTACAAGTGCAAG GTCTCCAACAAGCCCTCCAGCCCCCATCGAG AAACCATCTCCAAGCCAAAGGGCAGCCCCGA GAACCAAGGTGTACACCTTGCCCCCATCCCCG GAGGAGATGACCAGAACCAAGGTACGCTGAC CTGCTGGTCAAGGCTTCTATCCAGCGACAT CGCCGTGGAGTGGGAGAGCAATGGGCAGCCGG AGAACAACTACAAGACCAACGCTCCCGTGTGG ACTCCGACGGCTCTTCTTCTCTATAGCAAGCT CACCGTGGACAAGAGCAGGTGGCAGCAGGGGA ACGTCTCTCATGCTCCGTGATGCATGAGGCTCT
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			GCACAACCACTACACGCAGAGAGCCTCTCCCT GTCTCCGGGTAAA SEQ ID NO: 2123	
			QVQLQESGPGLVKPSETLSLTCTVSGDSISSGGYY WSWIRHPGKGLEWIGYIYSGSTYYPNPSLKSRVT ISVDTSKNQFSLKLSVTAADTA VYCARDRITIFG VVMGGMDVWVGQGT TVTVSSASTKGPSVFLAP SSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKD TLMISRTPETVTVVDVSHED PEVKFNWYVDGVEVHNATKTPCEEQYGSTYRCV SVLT V L H Q D W L N G K E Y K C K V S N K A L P A P I E K T I S K A K Q P R E P Q V Y T L P P S R E E M T K N Q V S L T C L V K G F Y P S D I A V E W E S N G Q P E N N Y K T T P P V L D S D G S F F L Y S K L T V D K S R W Q Q G N V F S C S V M H E A L H N H Y T Q K S L S L S P G K SEQ ID NO: 553	
			EIVLTQSPGTLSLSPGERATLSCRASQISISYSLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDF TLTISRLEPDDFAVYQCQYGSSPLTFGGGTKEIK RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSITYSLSS TLTL SKADY EKHKVYACEVTHQGLSSPVTKSFNR GEC AA	
			GAAATTGTGTGACGCAGTCTCCAGGCACCCCTG TCCTTTGTCTCCAGGGAAAGAGCCACCCCTCTCCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACACAGCAGAAACCTGGCCAGGCTC CCCGCTCCTCATCTATGGTGCA TCCAGCAGGG CCACTGGCATCCAGACAGGTTCAGTGCGAGTG GGTCTGGGACAGACTTCACTCTCAACCATCAGCA GACTGGAGCCTGATGATTTTGCA GTGTA T T A C T G TCAGCAGTATGGTAGTTCACCGCTCACTTTCGGC GGAGGGACCAAGGTGGAGATCAAACGAACGGT GGCTGCACCATCTGTCTTCACTTCCCGCCATCT GATGAGCAGTTGAAATCTGGAAC T G C T C T G T T GTGTGCTGCTGAATAACTTCTATCCAGAGAG GCCAAGTACAGTGGAAGGTGGATAACGCCCTC CAATCGGGTAAC T C C C A G G A G A G T G T C A C A G A G CAGGACAGCAAGGACAGCACCTACAGCCTCAGC AGCACCCCTGACGCTGAGCAAGCAGACTACGAG AAACACA AAGTCTACGCCTGCGAAGTCAACCCAT SEQ ID NO: 396	
IPS:361210	18E3.006	NA	CAGTGCAAGTTGCAGGAGTCGGGCCAGGACTG GTGAAGCCTTACAGACCCTGTCCCTCACCTGC ACTGTCTGTGACTCCATCAGCAGTGTGGTT ACTACTGGAGCTGGATCCGCCAGCACCCAGGGA AGGCCTGGAGTGGATTGGGTACATCTATTACA GTGGAGCACCTACTACAACCCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGCTAAGA ACCAAGTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGACACGGCCGTGTATTACTGTGCGAGAGA TCGTATTACGATTTTGGAGTGGTTATGGGGGGC GGTATGGAGCTGTGGGGCCAAGGACACACGGTC ACCGTCTCCTCAGCCTCCACCAAGGGCCCATCG GTCTTCCCTGGCACCCTCTCTCCAGAGCACCT CTGGGGCAACAGCGGCCCTGGGCTGCCTGGTCA AGGACTACTTCCCGCAACCGGTGACGGTGTGCT GGAAC T A G G C G C C T G A C C A G C G G C G T G C A C A CCTTCCCGGCTGTCTCTACAGTCTCAGGACTCTA CTCCCTCAGCAGCGTGTGTGACCGTGCCTCCAG	

		<p>CAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTC AACAGGGGAGAGTGT</p>	<p>CAGCTTGGGCAACCCAGACCTACATCTGCAACGT GAATCACAAGCCCAAGCAACACCAAGGTGGACA AGAAAGTTGAGCCCAATCTTGTGACAAATCTC ACATATGCCCACCGTGCCAGCACCTGAACCTCC TGGGGGACCGTCAAGTCTTCTTCTTCCCCCAAA ACCAAGGACACCCCTCATGATCTCCCGGACCCC TGAGGTACATGCGTGGTGGTGGACGTGAGCCA CGAAGACCTGAGGTCAAGTTCAACTGGTACGT GGACGGCTGGAGGTGCATAATGCCAAGACAA AGCCGTGAGGAGCAGTACGGCAGCACGTACC GTTGTGTCAGCTCCTACCGTCTTGCACCAAG ACTGGCTGAATGGCAAGGAGTACAAGTGCAAG GTCTCCAACAAGCCCTCCAGCCCCCATCGAG AAACCATCTCCAAGCCAAAGGCAGCCCCGA GAACACAGGTGTACACCTGCCCCCATCCCCG GAGGAGATGACCAAGAACCAAGGTACGCTGAC CTGCTGGTCAAGGCTTCTATCCAGCGACAT CGCCGTGGAGTGGAGAGCAATGGGCAGCCGG AGAACAACTACAAGACCAAGCCCTCCCGTGTGG ACTCCGACGGCTCTTCTTCTCTATAGCAAGCT CACCGTGACAAGAGCAGGTGGCAGCAGGGGA ACGCTTCTCATGCTCCGTGATGATGAGGCTCT GCACAACCACTACACGCAAGAGAGCCTCTCCCT GTCTCCGGGTAAA</p>
	AA	<p>EIVLTQSPGTLSPGERATLSCRASQISYSYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGTDF TLTSRLEPDDEFAVYYCQQYGSSPLTFGGGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLS TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC</p>	<p>SEQ ID NO: 1967</p> <p>SEQ ID NO: 2124</p> <p>QVQLQESGPGLVKPSQTLSTCTVSGDSISSGGYY WSWIRQHPGKGLEWIGYIYSGSTYYNPSLKSRT ISVDTSKNQFSLKLSVTAADTA VYCARDRITIFG VVMGGMDVWGQGT VTVSSASTKGPSVFP LAP SSKSTSGGT AALGCLVKDYFPEP VTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKD TLMISRTPETCVVDVSHED PEVKFNWYVDGVEVHN A KTKPCEEQYGSTYRCV SVLT V L HQDWLNGKEYKCKVSNKALPAPIEK TISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF</p>

				YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
				SEQ ID NO: 554
				CAGGTGACAGTTGCAGGAGTCGGGGCCAGGACTG GTGAAGCCTTCAGAGACCCCTGTCCCTCACCTGC ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCACCCAGGGA AGGGCTGGAGTGGATTGGGTACATCTATTACA GTGGGAGCACCTACTACAACCCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGCTCAAGA ACCAAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGACACGGCCGTGTATTACTGTGCGAGAGA TCGTATTACGATTTTGGAGTGGTTATGGGGGC GGTATGGAGCTCTGGGGCCAGGGACACAGGTC ACCGTCTCTCAGCCTCCACCAAGGGCCCATCG GTCCTCCCTGGCACCTCCCTCCAAAGAGCACCT CTGGGGCACAGCGGCCCTGGGCTGCCTGGTCA AGGACTACTTCCCGCAACGGTGACGGTGTCTGT GGAATCAGCGCCCTGACCAAGCGCGCTGCACA CCTTCCGGCTGTCTACAGTCTCAGGACTCTA CTCCCTCAGCAGCGTGGTGACCTGCCCCCAG CAGCTTGGGACCCAGACCTACATCTGCAACGT GAATCACAAGCCCAAGCAACCAAGGTGGACA AGAAAGTTGAGCCCAATCTTGTGACAAACTC ACATATGCCACCGTGCCCAAGCACTGAACCTC TGGGGGACCGTCAAGTCTCTCTTCCCCCCTAAA ACCAAGGACACCTCATGATCTCCCGGACCCC TGAGGTACATGCGTGGTGGTGACGTGAGCCA CGAAGACCTGAGTCAAGTTCAACTGGTACGT GGACGGCTGGAGGTGCATAATGCCAAGACAA AGCGGTGAGGAGCAGTACGGCAGCACGTACC GTTGTGTCAGCTCTCACCGTCTTGCACCCAGG ACTGGCTGAATGGCAAGGAGTACAAAGTGCAAG GTCTCCACCAAGCCCTCCCAAGCCCCCATCGAG AAACCATCTCCAAAGCCAAAGGGCAGCCCCGA
				SEQ ID NO: 397
				GAAATTGTGTGACGCAGTCTCCAGGCACCCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAGCAAAACCTGGCCAGGCTC CCCGCTCTCATCTATGGTGATCCAGCAGGG CCACTGGCATCCAGACAGGTTCAAGTGGCAGTG GGTCTGGGACAGACTTCACTCTCACCATCAGCA GACAGGACCTGATGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGTTACCCGCTCACTTTCGG CGAAGGACCAAGTGGAGATCAACGAACGG TGGCTGCACCATCTGTCTTCACTTCCCGCCATC TGATGAGCAGTTGAAATCTGGAACCTGCCTCTGT TGTGTGCCTGCTGAATAACTTCTATCCAGAGA GGCCAAAGTACAGTGGAAAGTGGATAACGCCCT CCAAATCGGGTAATCCCAAGGAGAGTGTACAGA GCAGGACAGCAAGGACAGCACCTACAGCCTCA GCAGCACCTGACGCTGAGCAAGCAGACTACG AGAAACACAAGTCTACGCTGCGAAGTCAACC ATCAGGGCCTGAGCTCGCCCGTCAACAAAGAGCT TCAACAAGGGAGAGTGT
			18E3.007	NA
			IPS:361214	

			<p>GAACCACAGGTGTACACCTGCCCCCATCCCCG GAGGAGATGACCAAGAACCAAGGTACGCTGAC CTGCTGGTCAAGGCTTCTATCCACGACAT CGCCGTGGAGTGGAGAGCAATGGGACGCCG AGAACAACTACAAGACACGCTCCCGTGTGG ACTCCGACGGCTCTTCTTCCCTCTATAGCAAGCT CACCGTGGACAAGACAGGTGGCAGCAGGGGA ACGTCTTCTCATGCTCCGTGATGCATGAGGCTCT GCACAACCACTACACGACAGAAAGACCTCTCCCT GTCTCCGGGTAA</p>
			<p>SEQ ID NO: 1968</p> <p>EIVLTQSPGTLSPGERATLSCRASQISYSYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGTDF TLTISRQEPDDFAVYYCQQYGSSPLTFGGGTKEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEN</p>
	AA		<p>SEQ ID NO: 2125</p> <p>QVQLQESGPGLVKPSETLSLTCTVSGDSISSGGYY WSWIRQHPGKGLEWIGYIYYSGSTYYPNPSLKSRVT ISVDTSKNQFSLKLSVTAADTA VYYCARDRITIFG VVMGGMDVWVGQGTTVTVSSASTKGPSVFPPLAP SSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTKISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK</p>
			<p>SEQ ID NO: 398</p> <p>GAAATTGTGTTGACGCAGTCTCCAGGCAACCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCTCTCTCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACACGACAGAACTGGCCAGGCTC CCCGCTCCTCATCTATGGTGCAATCCAGCAGGG CCACTGGCATCCAGACAGGTTCAAGTGCCAGTG GGTCTGGGACAGACTTCACTCTCAACCATCAGCA GACAGGAGCCTGATGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGTTACCCGCTCACTTCGG CGGAGGGACCAAGGTGGAGATCAACGAAACGG</p>
!PS:361218	18E3.008	NA	<p>SEQ ID NO: 555</p> <p>CAGTGCAGTTGCAGGAGTCGGGCCAGGACTG GTGAAGCCTTCACAGACCCTGTCCCTCACCTGC ACTGTCTCTGGTGACTCCATCAGCAGTGTGGTT ACTACTGGAGCTGGATCCGCCAGCCCCAGGGA AGGCCTGGAGTGGATTGGGTACATCTATTACA GTGGAGCACCTACTACAACCCGCTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGCTCAAGA ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGACACGGCCGTGTATTACTGTGCGAGAGA TCGTATTACGATTTTGGAGTGGTTATGGGGGC</p>

		<p>TGGCTGCACCATCTGTCTTCATCTTCCCGCCATC TGATGAGCAGTTGAAATCTGGAACCTGCCTCTGT TGTGTGCCTGCTGAATAACTTCTATCCACAGAGA GGCCAAAGTACAGTGAAGGTGGATAACGCCCT CCAAATCGGGTAACCTCCAGGAGAGTGTACACAGA GCAGGACAGCAAGGACAGCACCTACAGCCTCA GCAGCACCTTGACGCTGAGCAAGCAGACTACG AGAAACACAAAGTCTACGCTGCGAAGTCAACCC ATCAGGGCCTGAGCTCGGCCGTCACAAAAGAGCT TCAACAGGGGAGAGTGT</p>	<p>GGTATGGACGTCTGGGGCCAAAGGACCACGGTC ACCGTCTCTCAGCTCCACCAAGGGCCCATCG GTCCTCCCCCTGGCACCTCTCTCCAAAGACACCT CTGGGGCACAGCGGCCCTGGGCTGCCCTGGTCA AGGACTACTTCCCCGAACCGGTGACGGTGTCTGT GGAATCAGGCGCCCTGACCAGCGGCGTGCACA CCTTCCCGGTGTCTACAGTCTCAGGACTCTA CTCCCTCAGCAGCGTGTGACCGTGCCCTCCAG CAGCTTGGGACCCAGACCTACATCTGCAACGT GAATCACAAGCCCCAGCAACCAAGGTGGACA AGAAAGTTGAGCCCAATCTTGTGACAAAATC ACATATGCCACCGTGCCAGCACCTGAACCTC TGGGGGACCGTCAAGTCTCTTCCCCCCTCA ACCAAGGACACCTCATGATCTCCCGGACCCC TGAGGTACATGCGTGGTGGTGGACGTGAGCCA CGAAGACCTGAGGTCAAAGTTCAAAGTGTACGT GGACGGCGTGAGGTGCATAATGCCAAGACAA AGCGGTGAGGAGCAGTACGGCAGCACGTACC GTTGTGTCAGCTCTCACCGTCTTGACCCAGG ACTGGCTGAATGGCAAGGAGTACAAGTGCAAG GTCTCCAACAAGCCCTCCAGCCCCCATCGAG AAACCATCTCCAAGCCAAAGGCGAGCCCCGA GAACACAGGTGTACACCTTGCCCCCATCCCCG GAGGAGATGACCAGAACCAAGGTACGCTGAC CTGCTGGTCAAAGGCTTCTATCCAGCGACAT CGCCGTGGAGTGGGAGAGCAATGGGCAAGCCG AGAACAACTACAAGACACCGCTCCCGTGTGG ACTCCGACGGCTCTTCTTCTCTATAGCAAGCT CACCGTGACAAGAGCAGGTGGCAGCAGGGGA ACGTCTTCTCATGCTCCGTGATGCATGAGGCTCT GCACAACCACTACACGCAAGAGAGCCTCTCCCT GTCTCCCGGTAAA</p>
AA	SEQ ID NO: 1969	<p>EIVLTQSPGTLSPGERATLSCRASQISYSYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGTDF TLTISRQEPDDFAVYYCQQYGSPLTFGGGTKVEI</p>	<p>SEQ ID NO: 2126 QVQLQESGPGLVKPSQTLSTCTVSGDSISSGGYY WSWIRPPGKGLEWIGYIYSGSTYNPSTLKSRT ISVDTSKNQFSLKLSVTAADTAVVYCARDRTIFG</p>

			KRTVAAPSFIFFPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSYLSL STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGE	VVMGGMDVWVGQTTVTTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVVFSCVMHEALHNHYTQKS LSLSPGK
			SEQ ID NO: 399	SEQ ID NO: 556
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGCTCTGGCGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAAGAACTACATAGCTTGGTACCAGCAG CAACCAAGGACATCTCTCTAAGCTGCTCATTTACT GGGCATCTACCCGGGAATCCGGGTCCCTGACC GATTCAGTGGCAGCGGTCTGGGACAGATTTC CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAAAGGACCAAGGTGGA AATCAAACGAACGGTGGCTGCACCATCTGTCTT CATCTTCCCGCCATCTGATGAGCAGTTGAAATCT GGAACCTGCCCTCTGTTGTGTGCCTGCTGAATAACT TCTATCCCAGAGAGGCCAAAGTACAGTGGAAAG TGGATAACGCCCTCCAATCGGGTAACCTCCCAGG AGAGTGTCAAGAGCAGGACAGCAAGGACAGC ACCTACAGCCTCAGCAGCACCTTGACGCTGAGC AAAGCAGACTACGAGAAACACAAAGTCTACGC CTGCGAAGTCAACCCATCAGGGCCTGAGCTCGCC CGTCACAAAGAGCTTCAACAGGGGAGAGTGT	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATCCACTGGGTGCAGACAGGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATCAACCTGAAAGT GGTGGCACAGACTATTACAGAGGTTTCAAGGGC AGGTACCATGACCAGGGACACGTCCATCAGC ACAGCTACATGGAACCTGAACAGGCTGAGATCT GACGACACGGCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGCCAGGGAACCTGGTCAACCGTCT CCTCAGCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGACCTCTCTCCAAAGACACCTCTGGGGG CACAGCGCCTGGGTGCGCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTGTGGAACTC AGCGCCCTGACCAAGCGCGTGCACACCTTCCC GGCTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCAAACTTTGTGACAAAACTCACACATG CCCACCGTGGCCAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTG
IPS:361222	5C2.006	NA		

		ACATGCGTGGTGGACGTGAGCCACGAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGACGGC GTGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGC AGCTCCTCACCGTCTGCACCAAGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGCAGCCCCGAGAACACACA GGTGTACACCTGCCCTCCCATCCCGGAGGAGAT GACCAAGAACCAAGGTACGCTGACCTGCCTGGT CAAAGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGCAGCCGAGGAGAACAACT ACAAAGCCACGCTCCCGTGTGGACTCCGACG GCTCTTCTTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGAACGCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGAGAAAGCCCTCTCCCTGTCTCCGGG TAAA
	SEQ ID NO: 1970	SEQ ID NO: 2127
	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQPGHPKLLIYWASTRESGVPDFSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC	QVQLVQSGAEVKKPGASVKVSCKASGYFTGYI HWVRAQPGQGLEWMGWINPESGTDYISQRFQGR VTMTRDTSISTAYMELNRLRSDDTAVYICAREATI FGMVIVPFDYWGQGLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLMISRTPETCVVDVSHED PEVKFNWYVDGVEVHNATKTPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVVFSCSVMEALHNHYTQKS LSLSPGK
AA	SEQ ID NO: 400	SEQ ID NO: 557

IP:361229	5C2.007	NA	<p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAGAACTACATAGCTTGGTACCAGCAG CAACAGGACATCCTCCTAAGCTGCTCATTTACT GGCATCTACCCGGGAATCCGGGGTCCCTGACC GATTCAAGTGGCAGCGGGTCTGGGACAGATTCA CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAAGGACCAAGGTGGA AATCAACGAACGGTGGCTGCACCATCTGTCTT CATCTCCCGCCATCTGATGAGCAGTTGAAATCT GGAATGCCCTCTGTTGTGTGCCTGCTGAATAACT TCTATCCAGAGAGGCCAAAGTACAGTGGAAAG TGGATAACGCCCTCCAATCGGGTAACCTCCAGG AGAGTGTACAGAGCAGGACAGCAAGGACAGC ACCTACAGCCTCAGCAGCACCCTGACGCTGAGC AAAGCAGACTACGAGAAACACAAAGTCTACGC CTGCGAAGTCAACCATCAGGGCCTGAGCTCGCC CGTCACAAAGAGCTTCAACAGGGGAGAGTGT</p>
			<p>CAGTGCCCGCTGGTGCGAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAAGTCTCCTGC AAGGTTCTGGATACACCTTCAACCGGTACTAT ATCCACTGGTGCAGACGGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATCAACCTGAAAGT GGTGGCACAGACTATTACAGAGGTTTCAGGGC AGTTTCAACCATGACCAAGGACACGTCCATCAGC ACAGCCTACATGGAACCTGAACAGGCTGAGATCT GACGACACGGCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGTTATTGTACCGTTTG ACTACTGGGGCCAGGAAACCTGGTCAACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGG CACAGGGCCCTGGGTGCCAGGACCTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTGCGTGGAACTC AGCGCCCTGACCAAGCGGCTGCACACCTTCCC GGTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCAAATCTTGTGACAAACTCACACATG CCCACCGTGCCAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCCTCAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC CCTGAGGTCAAGTTCACCTGTAACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCAGTACCGTTGTGTC AGGTCTCTACCGTCTGCAACAGGACTGGCTG AATGGCAAGGAGTACAAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAAACACACA GGGTACACCTGCCCTCCCTCCCGGGAGGAGAT GACCAAGAACCAAGGTGAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGACGCCGAGAGAAACAAT</p>

			ACAAGACCACGCTCCCGTGCTGGACTCCGACG GCTCCTTCTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGAACGCTCTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGAGAAAGCCCTCTCCCTGTCTCCGGG TAAA
		SEQ ID NO: 1971	SEQ ID NO: 2128
	AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQHPKLLIYWASTRESGVPDFSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWINPESGGTDYVSRFQGR FTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGLVTDYFPEPVTVSWNSGALTS SKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
		SEQ ID NO: 401	SEQ ID NO: 558
	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGCGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAGAACTACATAGCTTGGTACCAGCAG CAACCAGGACATCTCTCTAAGCTGCTCATTTACT GGGCATCTACCCGGGAATCCGGGGTCCCTGACC GATTCAAGTGGCAGCGGTCTGGGACAGATTCA CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAAAGGACCAAGGTGGA AATCAAAACGAACGGTGGCTGCACCATCTGTCTT CATCTTCCCGCCATCTGATGAGCAGTTGAAATCT GGAACTGCCCTCTGTTGTGTGCTGCTGAATAACT TCTATCCCAGAGAGGCCAAAGTACAGTGGAAAGG	CAGGTGCAGCTGGTGCGAGTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATCCACTGGTGCGACAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATCAACCTTGACGCT GGTGGCACAGACTATTCACAGAGGTTTCAGGGC AGGTCAACATGACACAGGACACGTCATCAGC ACAGCCTACATGGAACCTGAACAGGCTGAGATCT GACGACACGGCGTGTTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGAAACCTGGTACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCTCTCTCCAAAGAGCACCTCTGGGGG CACAGCGGCCCTGGGCTGCCCTGGTCAAGGACTA
IPS:361236	5C2.008		

		<p>TGGATAACGCCCTCCAATCGGGTAACCTCCCAGG AGAGTGTACAGACGAGCAGGACAGCAAGGACAGC ACCTACAGCCTCAGCAGCACCCTGACGCTGAGC AAAGCAGACTACGAGAAACACAAAGTCTACGC CTGCGAAGTCAACCATCAGGGCCTGAGCTCGCC CGTCACAAAGAGCTTCAACAGGGGAGAGTGT</p>	<p>CTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTC AGCGCCCTGACACGCGGTGCACACCTTCCC GGTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGGTGGTACCGTGCCCTCCAGCAGCTTG GGCACCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAGAAAGT TGAGCCCAAATCTTGACAAACTCACACATG CCCACGTGCCAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGACGTGAGCCACGAAGAC CCTGAGGTCAAGTTCACTGGTACGTGGACGGC GTGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGC AGCTCTCACCCTCTGCACCAAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGCGAGCCCCGAGAACACACA GGTGTACACCTGCCCTCCATCCGGGAGGAGAT GACCAAGAACAGGTGACGCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGCGAGCCGAGAACAACT ACAAGACCAGCTTCCCGTGTGGACTCCGACG GCTCTTCTCTCTATAGCAAGCTCACCGTGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAAGAGAGCTCTCCCTGTCTCCGGG TAA</p>
	AA	<p>DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQPGHPKLLIYWASTRESGVPDFRSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC</p>	<p>SEQ ID NO: 1972</p> <p>SEQ ID NO: 2129</p> <p>QVQLVQSGAEVKKPGASVKVSKASGYTFTGYYI HWVRQAPGQGLEWMGWINPDAGGTDYSQRFQG RVMTTRDTSISTAYMELNRLRSDDTAVYYCAREA TIFGMVIVPFDYWGGQTLVTVSSASTKGPSVFPLA PSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL</p>

				<p>LGPSVFLFPPKPKDLMISRTPVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFEL YSKLTVDKSRWQQGNVFCFVSMHEALHNHYTQK SLSLSPGK</p>
				<p>SEQ ID NO: 402</p> <p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAGAACTACATAGCTTGGTACCAGCAG CAACAGGACATCCTCCTAAGCTGCTCATTTACT GGGCATCTACCCGGGAATCCGGGTCCCTGACC GATTCAGTGGCAGCGGTCTGGGACAGATTTC CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAGGGACCAAGGTGGA AATCAACGAACGGTGGCTGCACCATCTGTCTT CATCTCCCGCCATCTGATGAGCAGTTGAAATCT GGAACCTGCCCTCTGTTGTGTGCCTGCTGAATACT TCTATCCAGAGAGGCCAAAGTACAGTGGAAAG TGGATAACGCCCTCCAATCGGGTAACCTCCAGG AGAGTGTACAGAGCAGGACAGCAAGGACAGC ACCTACAGCCTCAGCAGCAGCCTGACGCTGAGC AAAGCAGACTACGAGAAACACAAAGTCTACGC CTGCGAAGTCAACCATCAGGGCCTGAGCTCGCC CGTCACAAAGAGCTTCAACAGGGGAGAGTGT</p>
				<p>SEQ ID NO: 559</p> <p>CAGTGCCGCTGGTGCGAGTCTGGGGCTGAGGTG AAGAAGCTGGGGCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATCCACTGGTGCGACAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATCAACCTTGACGCT GGTGGCACAGACTATTACACAGAGGTTTCAGGGC AGTTTACCATGACCAAGGACACGTCATCAGC ACAGCCTACATGGAACCTGAACAGGCTGAGATCT GACGACACGGCGTGTTATCTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGCCAGGAAACCTGGTCAACCGTCT CCTCAGCCTCCACCAAGGGCCATCGGTCTTCCC CCTGGACCCCTCCTCCAAGAGCACCTCTGGGGG CACAGCGCCCTGGGTGCCCTGGTCAAGGACTA CTTCCCAGAACCGGTGACGGTGTGCGTGGAACTC AGCGCCCTGACCAAGCGGCTGCACACCTTCCC GGCTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCCAAGCAACCAAGGTGGACAAGAAAGT TGAGCCCAATCTTGTGACAAACTCACACATG CCCACCGTGCCAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCCCTCTTCCCCCAAAACCCAA GACACCTCATGATCTCCCGGACCCCTGAGGTG ACATGCGTGGTGGACGTGAGCCACGAAAGAC CCTGAGGTCAAGTTCACCTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC</p>

			<p>AGGTCCTCACCGTCTCTGCACCAAGGACTGGCTG AATGGCAAGGAGTACAAAGTGCAAGGTCTCCAAC AAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAGCCAAAGGCAGCCCCGAGAACACACA GGGTACACCTGCCCTCCCATCCCGGAGGAGAT GACCAAGAACAGGTACGCTGACCTGCCTGGT CAAGGCTTCTATCCAGCGACATCGCCGTGGA GTGGAGAGCAATGGCAGCCGAGAACAACT ACAAGACCAGCTTCCCCTGCTGGACTCCGACG GCTCTTCTCTCTATAGCAAGCTACCCGTGGA CAAGAGCAGGTGGCAGCAGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGAGAAAGCCCTCTCCCCTGTCTCCGGG TAAA</p>
			<p>SEQ ID NO: 1973</p> <p>DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQPGHPKLLIYWASTRESGVPDFRSGS GSGTDFTLTISSLAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC</p>
	AA		<p>SEQ ID NO: 2130</p> <p>QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYI HWVRAQPGGLEWMGWINPDAGGTDYSQRFQG RFTMTRDTSISTAYMELNRLRSDDTAVYVCAREA TIFGMVVPFDYWGGQTLVTVSSASTKGPSVFPLA PSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFEL YSKLTVDKSRWQQGNVVFSCSVMHEALHNHYTQK SLSLSPGK</p>
			<p>SEQ ID NO: 403</p> <p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGCGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACACGACG CAACCAGGACATCTCTCTAAGCTGCTCATTTACT GGGCATCTACCCGGGAATCCGGGTCCCTGACC</p>
IPS:361240	5C2.010	NA	<p>SEQ ID NO: 560</p> <p>CAGTGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGCTCAGTGAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATCCACTGGGTGCGACAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATCAACCTTGACAGT GGTGGCACAGACTATTACACAGAGGTTTCAGGGC</p>

<p>GATTGAGTGGCAGCGGGTCTGGGACAGATTTCATCTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTTTACTGTCAACAATATTATAGTACTCCGTGGACGTTCCGGCCAAAGGACCAAGGTGGAATCAAACGAACGGTGGCTGCACCATCTGTCTTCATCTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCCCTCTGTTGTGTGCCTGCTGAATAACTCTATCCCAAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCCAATCGGGTAACCTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCAACCCATCAGGGCCTGAGCTCGCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT</p>	<p>AGGGTCACCATGACCAGGACACAGTCCATCAGCACAGCCTACATGGAACCTGAACAGGCTGAGATCTGACGACACGGCCGTGTATTACTGTGCGAGAGAGGCCACGATTTTGGAAATGGTTATTGTACCGTTTGACTACTGGGGCCAGGAACCCCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGCGGGCACAGGGCCCTGGGTGCCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCCCCTGACCAAGCGGTGCACACCTTCCCAGGTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAAGCCAGCAACCAAGGTGGACAAAGAAAGTTGAGCCCCAATCTTGTGACAAACTCACACATGCCCACCGTGCCCAGCACCTGAACCTCTGGGGACCGTCAGTCTTCCCTCTCCCCCAAACCCAAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGAGCGTGAGCCACGAAAGACCTGAGGTCAAGTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAGCCGTGTGAGGAGCAGTACGGCAGCACGTACCGTTGTGACAGTCTCACCCTCTGCACCAAGGACTGGCTGAATGGCAAGGATACAAGTGCAAGGTCTCCAACAAGCCCTCCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCCAGAGGTACACCTGCCCATCCCGGGAGGAGATGACCAAGAACAGGTACGCTGACCTGCCTGGTCAAGGCTTCTATCCAGCGACATCGCCGTGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCAGCCTCCCGTGTGGACTCCGACGGCTCTTCTCTATAGCAAGCTCACCCTGGAACAAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAAGAGCCCTCTCCCTGTCTCCGGGTAAA</p>
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		SEQ ID NO: 1974	<p>DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQPGHPPKLLIYWASTRESGVPDFRSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSIPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC</p> <p>AA</p>	SEQ ID NO: 2131	<p>QVQLVQSGAEVKKPGASVKVSKASGYTFTGYYI HWVRQAPGQGLEWMGWINDSGGTDYSQRFQGR VTMTRDTSISTAYMELNRLRSDDTAVYVCAREATI FGMVIPFDYWGGQTLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLISRTEPEVTGVVDVSHED PEVKFNWYVDGVEVHNATKPKCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGGSFFLY SKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPGK</p>
IPS:361247	5C2.011	NA	<p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCCTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTATCCAGCTCC AACATAAGAACTACATAGCTTGGTACCAGCAG CAACCAGGACATCCTCCTAAGCTGCTCATTTACT GGGCATCTACCCGGGAATCCGGGGTCCCTGACC GATTCAGTGGCAGCGGTCTGGGACAGATTCA CTCTCAACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAGGGACCAAGGTGGA AATCAACGAACGGTGGCTGCACCATCTGTCTT CATCTTCCCGCCATCTGATGAGCAGTTGAAATCT GGAACTGCCCTCTGTTGTGTGCTGCTGAATACT TCTATCCAGAGAGGCCAAAGTACAGTGGAAAG TGGATAACGCCCTCCAATCGGGTAACCTCCAGG AGAGTGTACAGAGCAGGACAGCAAGGACAGC ACCTACAGCCTCAGCAGCACCCTGACGCTGAGC AAAGCAGACTACGAGAAACACAAAGTCTACGC CTGCGAAGTCAACCATCAGGGCCTGAGCTCGCC CGTCACAAAGAGCTTCAACAGGGGAGAGTGT</p>	SEQ ID NO: 404	<p>CAGTGCAGCTGGTGCGAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAGTCTCCTGCG AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATCCACTGGTGCGACAGGCCCTGGACAAAGGG CTTGAGTGGATGGGTGGATCAACCTTGACAGT GGTGGCACAGACTATTACACAGAGGTTTCAGGGC AGGTTACCATGACCAAGGACACGTCATCAGC ACAGCCTACATGGAATGAACTGAACAGCTGAGATCT GACGACACGGCGGTGATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCTGGTACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGACCCCTCCTCCAAGAGCACCTCTGGGGG CACAGCGCCCTGGGTGCGTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTGCGTGGAACTC AGCGCCCTGACCAAGCGGGGTGCACACCTTCCC GGCTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCTGGTGACCGTGCCCTCCAGCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCACGCAACACCAAGGTGGACAAAGAAAGT</p>

		<p>TGAGCCCAAATCTTGTGACAAAACTCACACATG CCCACCGTGCCAGCACCTGAACCTCTGGGGG ACCGTAGTCTTCTCTTCCCCCAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGACGTGAGCCACGAAAGAC CCTGAGGTCAGTTCACTGGTACGTGGACGGC GTGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGT AGCTCTCACCGTCTTGCACCAAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGCAGCCCCGAGAAACACAC GGTGTACACCTGCCCTCCCATCCCGGAGGAGAT GACCAAGAACAGGTACGCTGACCTGCCTGGT CAAAGGCTTCTATCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGCAGCCGAGAACAACT ACAAGACCAGCTTCCCGTGTGGACTCCGACG GCTCTTCTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGAGAAAGAGCCTCTCCCTGTCTCCGGG TAAA</p>
	SEQ ID NO: 1975	SEQ ID NO: 2132
	<p>DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQPGHPPKLLIYWASTRESGVPDFRSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC</p>	<p>QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPQGQGLEWMGWINPDSGGTDYSQRFQGR FTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGGSFFLY</p>
	AA	

				SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
				SEQ ID NO: 405
				GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTATATCCAGCTCC AACATAAGAACTACATAGCTTGGTACCAGCAG CAACAGGACATCCTCCTAAGCTGCTCATTTACT GGGCATCTACCCGGGAATCCGGGGTCCCTGACC GATTCAAGTGGCAGCGGTCTGGGACAGATTTC CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAGGGACCAAGGTGGA AATCAACGAACGGTGGCTGCACCATCTGTCTT CATCTCCCGCCATCTGATGAGCAGTTGAAATCT GGAACCTGCCCTGTGTGTGCTGCTGAATAACT TCTATCCAGAGAGGCCAAAGTACAGTGGAAAG TGGATAACGCCCTCCAATCGGGTAACCTCCAGG AGAGTGTACAGAGCAGGACAGCAAGGACAGC ACCTACAGCCTCAGCAGCACCCTGACGCTGAGC AAAGCAGACTACGAGAAACACAAAGTCTACGC CTGCGAAGTCAACCATCAGGGCCTGAGCTCGCC CGTCACAAAGAGCTTCAACAGGGGAGAGTGT
			5C2.012	NA
			IP:361254	SEQ ID NO: 562
				CAGTGCCGCTGGTGCGAGTCTGGGGCTGAGGTG AAGAAGCTGGGCTCAGTGAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATCCACTGGTGCAGACGGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATCAACCTTGACAGT GGTGGCACAGACTATTACACAGAGGTTTCAGGGC AGGTCAACATGACACAGGACACGTCCATCAGC ACAGCTACATGGAACCTGAACAGGCTGAGATCT GACGACACGGCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGCGCAGGAAACCTGGTCAACCGTCT CCTCAGCTCCACCAAGGGCCATCGGTCTTCCC CCTGGACCCCTCCCTCCAAGAGCACTCTGGGGG CACAGGGCCCTGGCTGCCCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCTGTGGAACTC AGCGCCCTGACACAGCGGTGCACACCTTCCC GGTGTCTCAGTCTCAGGACTCTACTCCCTC AGCAGCTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCAATCTTGTGACAAACTCACACATG CCCACCGTGCCAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCCCTCTTCCCCCAAAACCCAA GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGTGGACGTGAGCCACGAAAGC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCAGTACCGTTGTGTC AGCTCTCACCCTCTGACCCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACCCACA GGTGTACACCCCTGCCCCCATCCCCGGGAGGAGAT

			<p>GACCAAGAACAGGTGACCTGACCTGCCTGGT CAAAGGCTTCTATCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGCAGCCGAGAACAACT ACAAAGACCAGCTTCCCGTGTGGACTCCGACG GCTCCTTCTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGAACGCTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGAGAAAGAGCCTCTCCCTGTCTCCGGG TAAA</p>
			<p>SEQ ID NO: 1976</p> <p>DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQPGHPPKLLIYWASTRESGVPDFRSGS GSGTDFTLTISSLAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC</p>
	AA		<p>SEQ ID NO: 2133</p> <p>QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRAQAPQGQGLEWMGWINPDSGTDYSQRFQGR VTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLMISRTPETCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTKISK AKQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPGK</p>
			<p>SEQ ID NO: 406</p> <p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGCGGAGAGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGTAACAGCAG CAACCAGGACATCTCTAAGCTGCTCATTTACT GGGCATCTACCCGGGAATCCGGGTCCCTGACC GATTCAAGTGGCAGCGGTCTGGGACAGATTCA CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGCCAAGGGACCAAGGTGGA AATCAACGAACGGTGGCTGCACCATCTGTCTT</p>
IPS:361261	5C2.013	NA	<p>SEQ ID NO: 563</p> <p>CAGTGCAGCTGGTGCGAGTCTGGGGCTGAGGTG AAGAAGCCTGGGCGCTCAGTGAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATCCACTGGTGCGACAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATCAACCTTGACGCT GGTGGCACAGACTATTACAGAGGTTTCAGGGC AGGTTACCATGACCAAGGACACGTCATCAGC ACAGCCTACATGGAACCTGAACAGGCTGAGATCT GACGACACGGCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGCCAGGGAACCTGGTACCGTCT</p>

		<p>CATCTTCCCGCCATCTGATGAGCAGTTGAAATCT GGAACCTGCCCTCTGTTGTGCTGCTGCTGAATAACT TCTATCCACAGAGAGGCCAAAGTACAGTGGAAAGG TGGATAACGCCCTCCAATCGGGTAACCTCCAGG AGAGTGTACAGAGCAGGACAGCAAGGACAGC ACCTACAGCCTCAGCAGCACCTTGACGCTGAGC AAAGCAGACTACGAGAAACACAAAGTCTACGC CTGCGAAGTCAACCATCAGGGCCTGAGCTCGCC CGTCACAAAGAGCTTCAACAGGGGAGAGTGT</p>	<p>CCTACGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCCTCCTCCAAAGAGCACCTCTGGGGG CACAGCGGCCCTGGGCTGCCCTGGTCAAGGACTA CTTCCCAGAACCGGTGACGGTGTCTGTGGAATC AGCGCCCTGACCAAGCGGGGTGCACACCTTCCC GGTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCAAATCTTGTGACAAACTCACACATG CCCACCGTGCCACAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCCTCAACCCAAAG GACACCTCATGATCTCCCCGACCCCTGAGGTC ACATGCGTGGTGGACGTGAGCCACGAAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCTCCTCACCGTCTTGACCCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAAACCACA GGTGTACACCTGCCCTCCCATCCCGGAGGAGAT GACCAAGAACCAAGGTACGCTGACCTGCCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGCAGCCGAGAGAACAACT ACAAAGCCACGCTTCCCGTGTGGACTCCGACG GCTCCTTCTCTCTATAGCAAGTCAACCGTGA CAAGAGCAGGTGGCAGCAGGGGAACGCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAAGAGAGCCTCTCCCCTGTCTCCGGG TAAA</p>
	SEQ ID NO: 1977	<p>DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQPGHPPKLLIYWASTRESGVPDFRSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL</p>	SEQ ID NO: 2134 <p>QVQLVQSGAEVKKPGASVKVSKKASGYFTGYI HWVVRQAPGQGLEWMGWINPDAGGTDYSQRFQ RFTMTRDTSISTAYMELNRLRSDDTAVYYCAREA TIFGMVIVPFDYWGQGTTLVTVSSASTKGPSVFPLA</p>
AA			

			<p>NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC</p>	<p>SEQ ID NO: 407</p> <p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGCGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAAGAACTACATAGCTTGGTACCAGCAG CAACCAAGGACATCCTCCTAAGCTGCTCATTTACT GGGCATCTACCCGGGAATCCGGGGTCCCTGACC GATTCAGTGGCAGCGGGTCTGGGACAGATTTC CTCTCACCATCAGCAGCCTGCAGGCTGAAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAGGGACCAAGGTGGA AATCAACGAAACGGTGGCTGCACCATCTGTCTT CATCTTCCCGCCATCTGATGAGCAGTTGAAATCT GGAACCTGCCCTCTGTTGTGTGCCTGCTGAATAACT TCTATCCCAGAGAGGCCAAAGTACAGTGGAAAG TGGATAACGCCCTCCAATCGGGTAACCTCCCAGG AGAGTGTCAAGAGCAGGACAGCAAGGACAGC ACCTACAGCCTCAGCAGCACCTTGACGCTGAGC AAAGCAGACTACGAGAAACACAAAGTCTACGC CTGCGAAGTCAACCCATCAGGGCCTGAGCTCGCC CGTCACAAAGAGCTTCAACAGGGGAGAGTGT</p>
			<p>SEQ ID NO: 564</p> <p>CAGGTGCCGCTGGTGCGAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATCCACTGGGTGCGACAGGCCCTGGACAAAGG CTTGAGTGATGGGTGGATCAACCTGACGCT GGTGGCACAGACTATTACAGAGGTTTCAAGGGC AGGTCAACATGACCAAGGACACGTCATCAGC ACAGCTACATGGAACAGGCTGAGATCT GACGACACGGCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCTGGTCAACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGACCTCTCTCCAAAGACACCTCTGGGGG CACAGCGCCCTGGGTGCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTC AGGCGCCTGACCAAGCGGCGTGCACACCTTCCC GGCTGTCTACAGTCTCAAGGACTCTACTCCCTC AGCAGCGTGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCCAAATCTTGTGACAAAACCTCACACATG CCCACCGTGGCCAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTG ACATGCGTGGTGGACGTGAGCCACGAAAGAC</p>	
IPS:361268	5C2.014	NA		

			<p>CCTGAGGTC AAGTTCACTGGTACGTGGACGGC GTGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCTCCTCACCGTCTGCACCAAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGCAGCCCCGAGAACACACA GGGTACACCTGCCCTCCCATCCCGGAGGAGAT GACCAAGAACAGGTACGCTGACCTGACCTGCCTGGT CAAGGCTTCTATCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGCAGCCGAGGAGAACAACT ACAAAGCCAGCTTCCCGTGTGGACTCCGACG GCTCTTCTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGAGAAAGCCCTCTCCCTGTCTCCGGG TAAA</p>
	SEQ ID NO: 1978	SEQ ID NO: 2135	<p>QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVVRQAPQGQGLEWMGWINPDAGGTDYSQRFQG RVMTTRDTSISTAYMELNRLRSDDTAVYYCAREAA TIFGMVIVPFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNKGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFEL YSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQK SLSLSPGK</p>
	<p>DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQQPGHPPKLLIYWASTRESGVPDFRFGS GSGTDFTLTISSLAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC</p>	AA	

	SEQ ID NO: 408	SEQ ID NO: 565
	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAAATAAGAACTACATAGCTTGGTACCAGCAG AAACCAAGGACAACCTCCTAAGCTGCTCATTTAC TGGGCACTCTACCCGGGAATCCGGGTCCCTGAC CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGAT GTGGCAGTTTTTTACTGTCAACAATATTATAGTA CTCCGTGGACGTTCCGGCCAAGGGACCAAGGTGG AAATCAAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAAATC TGGAACGTGCC'TCTGTTGTGTGCTGCTGAATAAC TTCTATCCCAAGAGAGGCCAAAGTACAGTGGAAAG GTGGATAACGCCCTCCAAATCGGGTAACTCCCAAG GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCCCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAGTCTACG CCTGCGAAGTCAACCCATCAGGGCCTGAGCTCGC CCGTCAACAAGAGCTTCAACAGGGGAGAGTGT	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATCCACTGGGTGCAGACAGGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATCAACCTGACGCT GGTGGCACAGACTATTACAGAGGTTTTCAGGGC AGGTCAACATGACCAAGGACACGTCCATCAGC ACAGCTACATGGAACCTGAACAGCCTGAGATCT GACGACACGGCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCAGGAAACCTGGTCAACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGACCCCTCCTCCAAAGAGCACCTCTGGGG CACAGCGCCCTGGGTGCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCTGGAACTC AGCGCCCTGACCAAGCGGTGACACACTTCCC GGTGTCTCTACAGTCTCTCAGGACTCTACTCCCTC AGCAGCTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCCAACAACCAAGGTGGACAAGAAAGT TGAGCCCAATCTTGTGACAAACTCACACATG CCCACCGTGCCAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTCT ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCGTCTCACCGTCTCTGCACCAAGGACTGGCTG AATGGCAAGGAGTACAAGTGAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAGCCAAGGGCAGCCCCGAGAACCCACA GGTGTACACCTTGCCCCCATCCCGGGAGGAGAT GACCAAGAACAGGTACGCTGACCTGCCTGGT CAAAGGCTTCTATCCCAAGCCACATCGCCGTGGA

			GTGGAGAGCAATGGGCAGCCGGAGAACAACT ACAAAGACCAGCCTCCCGTGGTGGACTCCGACG GCTCCTTCTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGAGAGAGCCCTCTCCCTGTCTCCGGG TAAA
		SEQ ID NO: 1979	SEQ ID NO: 2136
	AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQKPGQPPKLLIYWASTRESGVPDFRSGS GSGTDFTLTISSLAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWINPDAGGTDYSQRFQG RVMTTRDTSISTAYMELNSLRSDDTAVYCAREA TIFGMVIVPFDYWGGQTLVTVSSASTKGPSVFPLA PSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGPSVFLFPPKPKDITLMISRTPETCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI KAKGPQREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFEL YSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQK SLSLSPGK
		SEQ ID NO: 409	SEQ ID NO: 566
IPS:359678	SC2.016	NA	CAGTGCAGCTGGTGCACTCTGGGGCTGAGGTG AAGAAAGCCTGGGGCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATCCACTGGTGCGACAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATCAACCTTGAAAGT GGTGGCACAGACTATTCACAGAGGTTTCAGGGC AGGTCAACATGACAGGACAGGACATCCATCAGC ACAGCCTACATGGAACCTGAACAGCCTGAGATCT GACGACACGGCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCAGGGAACCTGGTACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGG

		<p>TTCTATCCAGAGAGGCCAAAAGTACAGTGGAAG GTGGATAACGCCCTCCAATCGGGTAACTCCCCAG GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCCCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCAACCCATCAGGGCCTGAGCTCGC CCGTCAACAAAGAGCTTCAACAGGGGAGAGTGT</p>	<p>CACAGCGGCCCTGGGCTGCCCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCTGTGGAATC AGCGCCCTGACCAAGCGGCTGCACACCTTCCC GGTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAGAAAGT TGAGCCCAAATCTTGTGACAAACTCACACATG CCCACCGTGCCAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGACGTGAGCCACGAAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGC AGCTCTCACCCTCTGCAACAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGCGAGCCCCGAGAACACACA GGTGTACACCTGCCCTCCATCCCGGAGGAGAT GACCAAGAACAGGTGACGCTGACCTGCCTGGT CAAAGGCTTCTATCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGCGAGCCGGAGACAACAT ACAAAGCCAGCTTCCCGTGTGGACTCCGACG GCTCTTCTCTCTATAGCAAGCTCACCGTGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAAGAGAGCCCTCTCCCTGTCTCCGGG TAAA</p>
	AA	<p>DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQKPGQPPKLLIYWASTRESGVPDFRSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK</p>	<p>SEQ ID NO: 2137 QVQLVQSGAEVKKPGASVKVSKKASGYTFTGYYI HWVRQAPGQGLEWMGWINPESGTDYSQRFQGR VTMTRDTSISTAYMELNSLRSDDTAVYYCAREATI FGMVIVPFDYWGQGTLTITVSSASTKGPSVFPLAPS SKSTSGGTAAAGCLVKDYFPEPVTVSWNSGALT GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN</p>

			DSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC	SEQ ID NO: 410 GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAGAACTACTTAGCTTGGTACCAACAG AAACCAAGGACAGCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAAGGCTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCAAGGTGG AAATCAACAGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAAGTTGAAATC TGGAAGTCCAGAGAGGGCCAAAGTACAGTGAATAC TTCTATCCAGAGAGGGCCAAAGTACAGTGAAG GTGGATAACGCCCTCCAAATCGGGTAACTCCCA GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCCTGACGCTGAG CAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCAACCATCAGGGCCTGAGCTCGC CCGTCAACAAAGAGCTTCAACAGGGGAGAGTGT
				SEQ ID NO: 567 CAGTGCCGCTGGTACAGTCTGGGGCTGAGGTG AAGAAGCTGGGGCTCAGTGAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATACACTGGTGCCTCAGGCCCTGGACAAGGG CTTGTGGATGGGGTGGATCAGCCCTAACAGT GGTGAACAAGCTATGCACAGAAATTTTCAGGAC AGGTCAACATGACAGGACACGTCATCAGC ACAGCCTATATGAGCTGAGCAGACTGAGATCT GACGACACGGCGTGTATTTCTGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGAAACCTGGTCAACGCTCT CCTCAGCCTCCACCAAGGGCCATCGGTCTTCCC CCTGGCACCTCCTCCAGAGCACCTCTGGGGG CACAGCGCCCTGGGCTGCCGTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCTGTGGAATC AGCGCCCTGACCAAGCGGCTGCACACCTTCCC GGCTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCGTGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCCCAGCAACCAAGGTGGACAAGAAAGT TGAGCCCCAATCTTGTGACAAACTCACACATG CCCCCGTGGCCAGCACCTGAACTCTGGGGG ACCGTCAGTCTTCCCTCTTCCCCCAAAACCCAA GACACCTCATGATCTCCCGGACCCCTGAGGTG ACATGCGTGTGGTGGACGTGAGCCACGAAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAGCCGTGT

IPS:361275

11C1.002

NA

				<p>GAGGAGAGTACGGCAGCACGTACCGTTGTGTC AGCTCCTCACCGTCTTGCACCAAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAGCCCTCCAGCCCCATCGAGAAACCATC TCCAAAGCCAAAGGCAGCCCCGAGAACACACA GGGTACACCTGCCCTCCCATCCGGGAGGAGAT GACCAAGAACAGGTACGCTGACCTGCCTGGT CAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGCAGCCGAGAACAACT ACAAAGCCAGCTTCCCTGCTGGACTCCGACG GCTCCTTCTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGAGAAAGAGCCTCTCCCCTGTCTCCGGG TAAA</p>
				<p>SEQ ID NO: 1981</p> <p>DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLA WYQQKPGQPPNLLIYWTSRESGVDRFSG SGSGTDFTLTINSLQAEDVA VYQCQQYYRTPTWF GQGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVC LLNFIYPREA KVQWKVDNALQSGNSQESVTEQDS KDSYSTLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC</p>
			AA	<p>SEQ ID NO: 2138</p> <p>QVPLVQSGAEVKKPGASVKVSKASGYTFTGYI HWVRA PQGLVWMGWISPNSETSYAQKFQDR VTMTRDTSISTAYMELSRLSDDTA VYFCAREATI FGMLIVPFDYWGGQTLVTVSSASTKGPSVFPLAPS SKSTSGGT AALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLISRTPETCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTKISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPGK</p>
				<p>SEQ ID NO: 411</p> <p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGCGAGAGGGCCACCAATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAGAACTACTTAGCTTGGTACCAACAG AAACCAAGACAGCCTCCTAACCTGCTCATTTAC</p>
IPS:36128	2	11C1.003	NA	<p>SEQ ID NO: 568</p> <p>CAGTGCCGCTGGTACAGTCTGGGGCTGAGGTG AAGAAGCCTGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATACACTGGTGCTCAGGCCCTGGACAAGGG CTTGTGTGGATGGGGTGGATCAGCCCTAACAGT</p>

TGGACTTCTACCCGAGAAATCCGGGGTCCCTGAC CGATTTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTACGAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCACAGGTGG AAATCAAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACTGCC'TCTGTTGTGTGCCTGCTGAATAAC TTCTATCCAGAGAGGCCAAAGTACAGTGGAG GTGGATAACGCCCTCCAAATCGGGTAACTCCAG GAGAGTGCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCAACCATCAGGGCCTGAGCTCGC CCGTCAACAAAGAGCTTCAACAGGGGAGAGTGT	GGTGACACAAAGCTATGCACAGAAAGTTTCAGGAC AGGTACACCATGACCAGGACACAGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGACTGAGATCT GACGACACGGCCGTGTATTCTGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGAAACCCCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGG CACAGGGCCCTGGGCTGCC'TGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCTGTGGAATC AGCGCCCTGACCAAGCGGCTGCACACCTTCCC GGTGTCTACAGTCTTCAGGACTCTACTCCCTC AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCAATCTTGTGACAAACTCACACATG CCCACCGTGCCAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGACGTGAGCCACGAAAGAC CCTGAGGTCAAGTTCACCTGTAAGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCAGTACCGTTGTGTC AGCTCTCACCCTCTGACCCAGGACTGGCTG AATGGCAAGGAGTACAAAGTGCAAGGTCTCCAA AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACACCA GGTGTACACCTGCCCTCCATCCCGGAGGAGAT GACCAAGAACAGGTGACGCTGACCTGCCTGGT CAAAGGCTTCTATCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGAACAACT ACAAGACCAGCCTCCCGTGTGGACTCCGACG GCTCTTCTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAAACCA
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			CTACACGAGAGAGCCCTCTCCCTGTCTCCGGG TAAA
		SEQ ID NO: 1982	SEQ ID NO: 2139
		DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLA WYQQKPGQPPNLLIYWTSTRESGVDRFSG SGSGTDFTLTINSLQAEDVA VYQCQQY YRTPWTF GQGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSYLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWV RQAPGQGLV WGMWISPNSGDTSYA QKFQDR VTMTRDTSISTAYMEL SRLSRDDTA VYFCAREATI FGMLIVPFDYWGQGLTVTVSSASTKGPSVFPLAPS SKSTSGGT AALGCL VKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKD TLMISRTPETVTVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPGK
	AA	SEQ ID NO: 412	SEQ ID NO: 569
		GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGCGGAGAGGGCCACCAATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAGAACTACTTAGCTTGGTACCAACAG AAACCAAGACAGCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGTCCCTGAC CGATTGAGTGCGAGCGGGTCTGGGACAGATTTC ACTCTACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTCCGGCCAGGGACCAAGGTGG AAATCAAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAATC TGGA ACTGCTCTGTGTGTGCTGCTGCTGAATAAC TTCTATCCAGAGAGGCCAAAGTACAGTGGAAG GTGGATAACGCCCTCCAAATCGGTAACCTCCAG GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCTGACGCTGAG CAAAAGCACTACGAGAAACACAAGTCTACG	CAGTGCCGCTGGTACAGTCTGGGGCTGAGGTG AAGAAGCTGGGCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACGGCTACTAT ATACACTGGTGCTCAGGCCCTGGACAAGGG CTTGTGTGGATGGGTGGATCAGCCCTAACAGT GGTGAAACAAGCTATGCACAGAA GTTTCAGGAC AGGTCAACATGACACAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGACTGAGATCT GACGACACGGCCGTGATTTCTGTGCGAGAGAG GCCACGATTTTGGAA TGCTTATTGTACCAATTG ACTACTGGGCCAGGAAACCTGGTCAACCGTCT CCTCAGCCTCCACCAAGGGCCATCGGTCTTCCC CCTGGACCTCTCTCCAAGAGCACCTCTGGGGG CACAGCGCCCTGGGTGCTGGTCAAGGACTA CTTCCCCGAACGGTGACGGTGTGCGGAACTC AGCGCCCTGACCAAGCGGTGTGACACCTTCCC GGCTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG
		11C1.004	
		IPS:361289	

		<p>CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC CCGTCAACAAGAGCTTCAACAGGGGAGAGTGT</p>	<p>GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGTGGACAAAGAAAGT TGAGCCCAATCTTGTGACAAACTCACACATG CCCACCGTGCCAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGGACGTGAGCCACGAAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTG AGCTCTCACCGTCTTGCACCAAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACACACA GGGTACACCTGCCCTCCCATCCCGGGAGGAGAT GACCAAGAACAGGTACGCTGACCTGCCTGGT CAAAGGCTTCTATCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGCAGCCGGAGAACAACT ACAAGACCAGCTTCCCGTGTGGACTCCGACG GCTCTTCTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAAGAGAGCCTCTCCCTGTCTCCGGG TAAA</p>
	AA	<p>SEQ ID NO: 1983</p> <p>DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPNNLLIYWTSTRDSGVPDFSG SGSGTDFTLTINSLQAEDVAVYCCQQYYRTPWTF GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYLSSTLTLSKADYEKHKVYACEVTHQQLSS PVTKSFNRGEC</p>	<p>SEQ ID NO: 2140</p> <p>QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYI HWV'RQAPGQGLVWMGWISPNSETSYAQKFQDR VTMTRDTSISTAYMELSRLSRDDTA VYFCAREATI FGMLIVPFDYWGQGLTVTVSSASTKGPSVFPLAPS SKSTSGGT AALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDPTLMISRTPETVTVVDVSHED PEVKFNWYVDGVEVHNATKTPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF</p>

				YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
				SEQ ID NO: 570
				CAGTGCCGCTGGTACAGTCTGGGGCTGAGGTG AAGAAGCTGGGGCTCAGTGAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGTACTAT ATACACTGGTGCCTAGGCCCTGGACAAGGG CTTGTGGATGGGGTGATCAGCCCTAACAGT GGTGAACAAGCTATGCACAGAAATTTTCAGGAC AGGTCAACATGACAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGACTGAGATCT GACGACACGGCGTGTATTTCTGTACGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCAATTG ACTACTGGGGCCAGGAAACCTGGTCAACCGTCT CCTCAGCCTCCACCAAGGGCCATCGGTCTTCCC CCTGGACCCCTCCCTCCAAGAGCACCTCTGGGGG CACAGGGCCCTGGCTGCCCTGGTCAAGGACTA CTTCCCGCAACCGGTGACGGTGTCTGGAACTC AGCGCCCTGACCAAGCGGTGACACACCTTCCC GGTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCTGGTGAACGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCCAACAACCAAGGTGGACAAGAAAGT TGAGCCCAATCTTGTGACAAACTCACACATG CCCACCGTGCCAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCCCTCTTCCCCCAAAACCCAA GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGACGTGAGCCACGAAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCAGTACCGTTGTGTG AGCTCTCACCCTCTGCACCAAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGGCAGCCCCCGAGAACACACA
				SEQ ID NO: 413
				GACATCGTATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAAGAACTACTTAGCTTGGTACCAACAG AAACCAAGACAGCTCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTACCATCAACAGCCTGCAAGGCTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTCCGGCCAGGGACCAAGGTGG AAATCAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAAGTTGAAATC TGGAACCTGCCCTGTGTGTGCTGCTGAATAAC TTCTATCCAGAGAGGCCAAAGTACAGTGGAAAG GTGGATAACGCCCTCCAAATCGGGTAACTCCAG GAGAGTGTACAGAGCAGGACAGCAAGGACAG CACCTACAGCTCAGCAGCACCTGACGCTGAG CAAAAGCAACTACGAGAAACACAAGTCTACG CCTGCGAAGTCAACCATCAGGGCTGAGCTCGC CCGTCAACAAGAGCTTCAACAGGGGAGAGTGT
				NA
				11C1.005
				IPS:359712

			GGGTACACCCCTGCCCATCCCGGAGGAGAT GACCAAGAACAGGTACGCTGACCTGCCTGGT CAAAGGCTTCTATCCAGCAGCATCGCCGTGGA GTGGGAGAGCAATGGCAGCCGGAGAACAACT ACAAAGACCAGCCTCCCGTGTGGACTCCGACG GCTCCTTCTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGAGAAAGCCCTCTCCCTGTCTCCCGG TAAA
		SEQ ID NO: 1984	SEQ ID NO: 2141
	AA	DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLA WYQQKPGQPNNLLIYWTSRESGVDRFSG SGSGTDFTLTINSLQAEDVA VYQCQQYYRTPTWTF GQGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSITYLSSTLTLSKADYEEKHKVYACEVTHQGLSS PVTKSFNRGEC	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYI HWVRQAPGQGLVWMGWISPNSETSYAQKFQDR VTMTRDTSISTAYMELSRLSDDTA VYFCTREATI FGMLIVPFDYWGGTLVTVSSASTKGPSVFPLAPS SKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTKISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPGK
		SEQ ID NO: 414	SEQ ID NO: 571
!PS:361293	11C1.006	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGCGGAGAGGGCCACCAATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAGAACTACTTAGCTTGGTACCAACAG AAACCAAGACAGCTCTCAACCTGCTCATTTAC TGGACTTCTACCCGAGAAATCCGGGTCCCTGAC CGATTCAAGTGCGAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTCCGGCCAAGGGACCAAGGTGG	CAGTGCCGCTGGTACAGTCTGGGGCTGAGGTG AAGAAGCCTGGGCTCAGTGAAGTCTCCTGCG AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATACACTGGTGCTCAGGCCCTGGACAAAGG CTTGTGTGGATGGGTGGATCAGCCCTAACAGT GGTGACACAAAGCTATGCACAGAAAGTTTCAGGAC AGGTCAACCATGACAGGACACGTCCTCAGCAGC ACAGCCTATATGGAGCTGAGCAGACTGAGATCT GACGACACGGCGGTGATTTCTGTACGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCAATTG

		<p>AAATCAAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACCTGCC'TCTGTGTGTGCTGCTGAATAAC TTCTATCCACAGAGAGGCCAAAGTACAGTGGAAG GTGGATAACGCCCTCCAAATCGGGTAACTCCACG GAGAGTGCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCAACCATCAGGGCCTGAGCTCGC CCGTCAACAAGAGCTTCAACAGGGGAGAGTGT</p>	<p>SEQ ID NO: 1985</p>
	AA	<p>ACTACTGGGGCCAGGAAACCCCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGG CACAGGGCCCTGGGCTGCC'TGGTCAAGGACTA CTTCCCAGAACCGGTGACGGTGTCTGTGGAATC AGGCGCCCTGACCAAGCGGGGTGCACACCTTCCC GGTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCGTGGTACCGTGGCTCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCAATCTTGTGACAAACTCACACATG CCCACCGTGCCACAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCCTAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGACGTGAGCCACGAAAGAC CCTGAGGTCAAGTTCACCTGTAACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCAGTACCGTTGTGTC AGCTCCTCACCGTCTTGCACCAAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACCCACA GGTGTACACCTGCCCTCCCATCCCGGAGGAGAT GACCAAGAACCAAGGTGACGCTGACCTGCCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGAGAACAACT ACAAAGCCAGCCTTCCCGTGTGGACTCCGACG GCTCTTCTTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAAGAAAGACCTCTTCCCCTGTCTCCGGG TAAA</p>	<p>SEQ ID NO: 2142</p> <p>QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYI HWV'RQAPGGQLVWMGWISPNSGDTSYAQKFQDR VTMTRDTSISTAYMELSLRLSRDDTAVYFCTREATI</p>

			<p>GGQTKVEIKRTVAAPSVFIFFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNREGC</p>	<p>FGMLIVPFDYWQQGTLTVTVSSASTKGSPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPETVTVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVVFSCSVMHEALHNHYTQKS LSLSPGK</p>
			<p>SEQ ID NO: 415</p> <p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAAGAACTACTTAGCTTGGTACCAACAG AAACCCAGGACAGCTCTCAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGGCTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCAAGGTGG AAATCAAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAAGTGCCTCTGTTGTGTGCTGCTGTAATAAC TTCTATCCCAAGAGAGGCCAAAGTACAGTGGGAAG GTGGATAACGCCCTCCAAATCGGGTAACCTCCAG GAGAGTGTACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCCCTGACGCTGAG CAAAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCAACCCATCAGGGCCTGAGCTCGC CCGTCAACAAAGAGCTTCAACAGGGGAGAGTGT</p>	<p>SEQ ID NO: 572</p> <p>CAGGTGCCGCTGGTACAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATACACTGGTGCCTAGGCCCTGGACAAAGG CTTGTGTGGATGGGTGGATCAGCCCTAACAGT GGTGAACAAGCTATGCACAGAAATTTTCAGGAC AGGTACCATGACCAAGGACACGTCATCAGC ACAGCCTATATGGAGCTGAGCAGACTGAGATCT GACGACACGGCGTGTATTTCTGTACGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGAAACCTGGTCAACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGACCTCTCTCCAAAGACACCTCTGGGGG CACAGCGCCCTGGCTGCCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTC AGGCGCCTGACCAAGCGCGGTGCACACCTTCCC GGCTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCGTGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCCAAATCTTGTGACAAAACCTCACACATG CCCACCGTGCCAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTG</p>
IPS:361297	11C1.007	NA		

		ACATGCGTGGTGGACGTGAGCCACGAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGACGGC GTGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGC AGCTCCTCACCGTCTGCACCAAGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACACACA GGTGTACACCTGCCCTCCCATCCCGGAGGAGAT GACCAAGAACAGGTACGCTGACCTGACCTGCTGGT CAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGCAGCCGAGGAGAACAACT ACAAAGCCACGCTCCCGTGTGGACTCCGACG GCTCCTTCTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGAGAAAGCCCTCTCCCTGTCTCCGGG TAAA
	SEQ ID NO: 1986	SEQ ID NO: 2143
	DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLA WYQQKPGQPPNLLIYWTSRDSGVPDFSG SGSGTDFTLTINSLQAEDVA VYCCQQY YRTPWTF GQGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVC LLNIFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWV RQAPGQGLVWMGWISPNSGETSYAQKFQDR VTMTRDTSISTAYMELSRLRSDDTAVYFCTREATI FGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGT AALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTK VDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNATKPCPEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNV FSCSV MHEALHNHYTQKS LSLSPGK
AA	SEQ ID NO: 416	SEQ ID NO: 573

PS:361301	11C1.008	NA	<div><div>GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTCTCTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAGAACTACTTAGCTTGGTACCAACAG AAACGAGACAGCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCAGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTACCATCAACAGCCCTGCAAGGCTGAAGAT GTGGCTGTTTATTACTGTACGCAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCAGGTGG AAATCAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACTGCC'TCTGTTGTGTGCCTGCTGAATAAC TTCTATCCAGAGAGGCCAAAGTACAGTGGAAG GTGGATAACGCCCTCCAAATCGGGTAAC'TCCCAG GAGAGTGCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCCCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCAACCATCAGGGCCTGAGCTCGC CCGTCAACAAAGAGCTTCAACAGGGGAGAGTGT</div></div>
			<div><div>CAGTGCCCGCTGGTACAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGTACTAT ATACACTGGTGCGTCAGGCCCTGGACAAGGG CTTGTGTGATGGGTGGATCAGCCCTAACAGT GGTGACACAAAGCTATGCACAGAAATTTTCAGGAC AGGTCAACCATGACCAGGGACACGTCCATCAGC ACAGCCTATATGGAGCTGACAGACTGAGATCT GACGACACGGCCGTGATTCTGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGAAACCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGG CACAGCGGCCCTGGGTGCC'TGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCTGTGGAACTC AGCGCCCTGACCAAGCGGTGCACACCTTCCC GGTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAGAAAGT TGAGCCCAAATCTTGTGACAAACTCACACATG CCCACCGTGCCCAAGCCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCCTAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCAGTACCGTTGTGTC AGCTCCTCACCGTCTTGCACCAAGGACTGGCTG AATGGCAAGGAGTACAAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACACACA GGGTACACCTGCCCTCCATCCCGGGAGGAGAT GACCAAGAACCAAGGTGAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGAGACAACACT</div></div>

			ACAAGACCACGCTCCCGTGCTGGACTCCGACG GCTCCTTCTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGAACGCTCTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACAGCAGAAAGCCCTCTCCCTGTCTCCGGG TAAA
		SEQ ID NO: 1987	SEQ ID NO: 2144
	AA	DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLA WYQQKPGQPPNLLIYWTSTRDSGVPDRFSG SGSGTDFTLTINSLQAEDVA VYQCQQY YRTPWTF GQGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSYLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC	QVPLVQSGAEVKKPGASVKVSKASGYTFTGYI HWVRQAPGQGLVWMGWISPNSGDTSYAQKFQDR VTMTRDTSISTAYMELSRRLSDDTA VYFCAREATI FGMLIVPFDYWGGTGLVTVSSASTKGPSVFPLAPS SKSTSGGT AALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTKISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
		SEQ ID NO: 417	SEQ ID NO: 574
IPS:359703	11C1.009	NA	CAGGTGCAGCTGGTACAGTCTGGGGCTGAGGTG AAGAAAGCTGGGGCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACGGCTACTAT ATACACTGGTGCGTCAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATCAGCCCTAACAGT GGTGAAACAAGCTATGCACAGAA GTTTCAGGAC AGGTACCATGACACAGGACACGTCCTCAGCAGC ACAGCCTATATGAGCTGAGCAGCCTGAGATCT GACGACACGGCGGTGATTTCTGTGCGAGAGAG GCCACGATTTTGGAA TGCTTATTTGACCATTTG ACTACTGGGCCAGGGAACCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCTCTCTCCAAGAGCACCTCTGGGGG CACAGCGGCCCTGGGCTGCCCTGGTCAAGGACTA

	<div>GTGGATAACGCCCTCCAAATCGGGTAACTCCCAG GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT</div>	<div>SEQ ID NO: 1988</div> <div>DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPKLLIYWTSRESGVPDFSG SGSGTDFLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC LLNFPYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC</div>
	<div>CTTCCCCGAACCGGTGACGGTGCTGCGAACTC AGCGCCCTGACCAGCGGCGTGACACACTTCCC GGTGCTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCGTGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCAAATCTTGACAAAACTCACACATG CCCACCGTGCCCAGCACCTGA ACTCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAA AACCC AAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGTGGTGACGTGAGCCACGAAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCGTCTCACCGTCTCTGCAACAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCATCGAGAAAACCATC TCCAAAGCCAAAGGCGAGCCCCGAGAACACACA GGGTACACCTGCCCTCCCATCCCGGAGGAGAT GACCAAGAACAGGTGACGCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAAGCCGAGAACAACT ACAAAGCCAGCCCTCCCGTGTGGACTCCGACG GCTCTTCTTCTCTATAGCAAGCTCACCGTGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAAGAGCCTCTCCCTGTCTCCGGG TAAA</div> <div>SEQ ID NO: 2145</div> <div>QVQLVQSGAEVKKPGASVKVSKASGYTFTGYVI HWVRQAPGQGLEWMGWISPNSETSYAQKFQDR VTMTRDTSISTAYMELSSLRDDTAVYFCAREATI FGMLIVPFDYWGQGTLLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCTPPCPAPELL</div>	

				GGPSVFLFPPKPKDTLMISRTPETVTCVVVDVSHED PEVKFNWYVVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK	
			SEQ ID NO: 418	SEQ ID NO: 575	
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAAGAACTACTTAGCTTGGTACC AACAG AAACCAAGGACAGCCTCCTAAOCTGCTCATTTAC TGGACTTCTACCCGAGAAATCCGGGGTCCCTGAC CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTTCGGCCAAGGGACCAAAGGTGG AAATCAAAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAAC TGCTCTGTTGTGTGCCTGCTGAATAAC TTCTATCCCAAGAGAGGCCAAAAGTACAGTGGAAAG GTGGATAACGCCCTCCAAATCGGGTAAC TCCACAG GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCCCTGACGCTGAG CAAAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCAACCCATCAGGGCCTGAGCTCGC CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	NA	CAGGTGCAGCTGGTACAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAGTCTCCTGCG AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATACACTGGTGCCTCAGGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATCAGCCCTAACAGT GGTGAACAAAGCTATGCACAGAAAGTTTCAGGAC AGGTCAACATGACCAAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGACTGAGATCT GACGACACGGCGTGTATTTCTGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGCCAGGGAACCTGGTCAACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCC CCTGGACCCCTCCTCCAAGAGCACCTCTGGGGG CACAGCGCCCTGGGTGCC TGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTGTCGTGGAAC TC AGCGCCCTGACCAAGCGGTGTGCACACCTTCCCC GGCTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCGTGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGC AACGTGAATCAC AAGCCCAAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCAATCTTGTGACAAA ACTCACACATG CCCACCGTGGCCAGCACCTGA ACTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCC AAG GACACCTCATGATCTCCCGGACCCCTGAGGTG ACATGCGTGGTGGACGTGAGCCACGAAAGAC CCTGAGGTCAAAGTTCAA ACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTGTC
	11C1.010				
IPS:361305					

				<p>AGGTCCTCACCGTCTCTGCACCAAGGACTGGCTG AATGGCAAGGAGTACAAAGTGCAAGGTCTCCAAC AAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGCGAGCCCCGAGAACACA GGGTACACCTGCCCTCCCATCCCGGAGGAGAT GACCAAGAACAGGTACGCTGACCTGACCTGGT CAAGGCTTCTATCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGAGCCGAGAACAACT ACAAAGACCAGCTTCCCGTGTGGACTCCGACG GCTCTTCTCTCTATAGCAAGCTACCCGTGGA CAAGAGCAGGTGGCAGCAGGGAACGTCTTCTC ATGCTCCGTGATGATGAGGCTCTGCACAACCA CTACACGAGAAAGCCCTCTCCCTGTCTCCGGG TAAA</p>
				<p>SEQ ID NO: 1989</p> <p>DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLA WYQQKPGQPPNLLIYWTSRESGVDRFSG SGSGTDFTLTINSLQAEDVA VYQCQQY YRTPWTF GQGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSYLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC</p>
			AA	<p>SEQ ID NO: 2146</p> <p>QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWISPNSETSYAQKFQDR VTMTRDTSISTAYMELSRRLSDDTAVYFCAREATI FGMLIVPFDYWGGQTLVTVSSASTKGPSVFPLAPS SKSTSGGT AALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLMISRTPETCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPGK</p>
				<p>SEQ ID NO: 419</p> <p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGCGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAGAACTACATAGCTTGGTACCAAGCAG AAACCAAGGACATCTCTCTAAGCTGCTCATTTACT GGGCATCTACCCGGGAATCCGGGTCCCTGAOC</p>
!PS:361312	13H12.002	NA		<p>SEQ ID NO: 576</p> <p>CAGTGCCGCTGGTGCAAGTCTGGGGCTGAGGTG AAGAAGCTGGGGCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATCCACTGGGTGCGACAGGCCCTGGACAAGGA CTTGAGTGGATGGGTGGATCAACCTTGAAAGT GGTGGCACAGACTATTACACAGAGGTTTCAGGGC</p>

<p>GATTGAGTGGCAGCGGGTCTGGGACAGATTTCATCTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTTTACTGTCAACAATATTATAGTACTCCGTGGACGTTCCGGCCAAAGGACCAAGGTGGAATCAAAACGAACGGTGGCTGCACCATCTGTCTTCATCTCCCGCCATCTGATGAGCAGTTGAAATCTGGAATGCTTGTGTGCTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAGTGGAAAGTGGATAACGCCCTCCATCGGGTAACCTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCAACCCATCAGGGCCTGAGCTCGCCGTACACAAAGAGCTTCAACAGGGGAGAGTGT</p>	<p>AGGGTCACCATGACCAGGACACAGTCCATCAGCACAGCCTACATGGAACCTGAGCAGGCTGAGATCTGACGACACGGCCGTGTATTACTGTGCGAGAGAGGCCACGATTTTGGAAATGGTTATTGTACCGTTTGACTACTGGGGCCAGGAACCCCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGCGGGCACAGCGCCCTGGCTGCCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGCGCCCTGACAGCGGGGTGCACACCTTCCCAGGTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGAGCACCCAGACCTACATCTGCAACGTGAATCACAAAGCCAGCAACCAAGGTGGACAAAGAAAGTTGAGCCCCAATCTTGTGACAAACTCACACATGCCCACCGTGCCCAGCACCTGAACCTCTGGGGACCGTCAGTCTTCCCTCTCCCCCAAACCCAAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGAGCGTGAGCCACGAAAGACCCTGAGGTCAAGTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGTGTGAGGAGCAGTACGGCAGCACGTACCGTTGTGTGAGTCTCACCCTCTGCACCAAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAAAGCCCTCCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGCGAGCCCCGAGAACACAGGTGTACCCCTGCCCATCCCGGGAGGAGATGACCAAGAACAGGTGAGCCTGACCTGCCTGGTCAAGGCTTCTATCCAGCGACATCGCCGTGAGTGGGAGAGCAATGGGCAAGCCGGAGAACAACTACAAGACCAGCCTCCCGTGTGGACTCCGACGCTCTTCTCTATAGCAAGCTCACCGTGAACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAAGAGCCCTCTCCCTGTCTCCGGGTAAA</p>
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		SEQ ID NO: 1990	<p>DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQKPGHPPKLLIYWASTRESGVPDFRSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSIPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC</p>	SEQ ID NO: 2147	<p>QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYI HWVRQAPGGGLEWMGWINPESGGTDYSQRFQGR VTMTRDTSISTAYMELSRRLSDDTAVYYCAREATI FGMVIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNATKPKCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK</p>
		AA		SEQ ID NO: 420	<p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCCTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAGAACTACATAGCTTGGTACCAGCAG AAACGAGGACATCTCTCTAAGCTGCTCATTTACT GGGCATCTACCCGGGAATCCGGGGTCCCTGACC GATTCAAGTGGCAGCGGTCTGGGACAGATTCA CTCTCAACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAGGGACCAAGGTGGA AATCAACGAACGGTGGCTGCACCATCTGTCTT CATCTTCCCGCCATCTGATGAGCAGTTGAAATCT GGAACTGCCCTCTGTTGTGTGCTGCTGAATACT TCTATCCAGAGAGGCCAAAGTACAGTGGAAAG TGGATAACGCCCTCCAATCGGGTAACCTCCAGG AGAGTGTACAGAGCAGGACAGCAAGGACAGC ACCTACAGCCTCAGCAGCACCTTGACGCTGAGC AAAGCAGACTACGAGAAACACAAAGTCTACGC CTGCGAAGTCAACCATCAGGGCCTGAGCTCGCC CGTCACAAAGAGCTTCAACAGGGGAGAGTGT</p>
IPS:359744	13H12.003	NA		SEQ ID NO: 577	<p>CAGTGCCGCTGGTGCGAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATCCACTGGTGCGACAGGCCCTGGACAAAGGA CTTGAGTGGATGGGTGGATCAACCTGAAAGT GGTGGCACAGACTATTACAGAGGTTTCAGGGC AGGTTACCATGACCAAGGACACGTCATCAGC ACAGCCTACATGGAATGAGCAGGCTGAGATCT GACGACACGGCGGTGTTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCTGGTACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGACCCCTCCTCCAAGAGCACCTCTGGGGG CACAGCGCCCTGGGTGCTGCTGGTCAAGGACTA CTTCCCGAAACCGGTGACGGTGTGCGTGGAACTC AGCGCCCTGACCAAGCGGCTGCACACCTTCCC GGTGTCTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCACGCAACACCAAGGTGGACAAAGAAAGT</p>

		TGAGCCCAAATCTTGTGACAAAACTCACACATG CCCACCGTGCCAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGTGGTGACGTGAGCCACGAAAGAC CCTGAGGTCAGTTCACTGGTACGTGGACGGC GTGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCTCTCACCGTCTTGCACCAAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGCAGCCCCGAGAAACACACA GGTGACACCTGCCCTCCCATCCCGGAGGAGAT GACCAAGAACAGGTACGCTGACCTGCCTGGT CAAAGGCTTCTATCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGCAGCCGAGAACAACT ACAAAGCCAGCTTCCCGTGTGGACTCCGACG GCTCTTCTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAAGAGGCTCTTCCCCTGTCTCCGGG TAAA
	SEQ ID NO: 1991	SEQ ID NO: 2148
	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQKPGHPPKLLIYWASTRESGVPDFRSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVVRQAPGQGLEWMGWINPESGTDYSQRFQGR FTMTRDTSISTAYMELSLRLRDDTA VYYCAREATI FGMVIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGT AALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDITLISRTPETVTVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGGSFFLY
		AA

				SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
				SEQ ID NO: 578
				CAGTGCCGCTGGTGCAAGTCTGGGGCTGAGGTG AAGAAGCTGGGGCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGTACTAT ATCCACTGGTGCGACAGGCCCTGGACAAGGA CTTGAGTGGATGGGTGGATCAACCTTGACAGT GGTGGCACAGACTATTACACAGAGGTTTTCAGGGC AGGTCAACATGACACAGGACACGTCCATCAGC ACAGCTACATGGAACCTGAGCAGGCTGAGATCT GACGACACGGCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGAAACCTGGTCAACCGTCT CCTCAGCTCCACCAAGGGCCATCGGTCTTCCC CCTGGACCCCTCCTCCAAGAGCACCTCTGGGGG CACAGGGCCCTGGCTGCCAGGCTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCTGGAACTC AGCGCCCTGACACAGCGGTGACACCTTCCC GGTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACCAAGGTGGACAAGAAAGT TGAGCCCAATCTTGTGACAAACTCACACATG CCCACCGTGCCAGCACCTGAACTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGACGTGAGCCACGAAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCAGTACCGTTGTGTC AGCTCTCAACCGTCTGACCCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACCCACA GGTGTACACCTGCCCTCCCATCCCCGGGAGGAGAT
				SEQ ID NO: 421
				GACATCGTATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTATATCCAGCTCC AACATAAGAACTACATAGCTTGGTACCAGCAG AAACAGGACATCTCCTAAGCTGCTCATTTACT GGGCATCTACCCGGGAATCCGGGTCCCTGACC GATTCAAGTGGCAGCGGTCTGGGACAGATTTC CTCTACCATCAGCAGCTGCAAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCCGGCCAGGGACCAAGGTGGA AATCAACGAACGGTGGCTGCACCATCTGTCTT CATCTTCCCGCCATCTGATGAGCAGTTGAAATCT GGAACCTGCCCTGTGTGTGCTGCTGAATAACT TCTATCCAGAGAGGCCAAAGTACAGTGGAAAG TGGATAACGCCCTCCAATCGGGTAACCTCCAGG AGAGTGTACAGAGCAGGACAGCAAGGACAGC ACCTACAGCTCAGCAGCAGCCCTGACGCTGAGC AAAGCAGACTACGAGAAACACAAAGTCTACGC CTGCGAAGTCAACCATCAGGGCCTGAGCTCGCC CGTCACAAAGAGCTTCAACAGGGGAGAGTGT
				NA
				13H12.004
				IPS:361319

			<p>GACCAAGAACCAAGGTGACCTGACCTGCCTGGT CAAAGGCTTCTATCCAGCGACATCGCCGTGGA GTGGAGAGCAATGGCAGCCGAGAACAACT ACAAAGACCAGCTTCCCGTGTGGACTCCGACG GCTCCTTCTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGAGAAAGAGCCTCTCCCTGTCTCCGGG TAAA</p>
			<p>SEQ ID NO: 1992</p> <p>DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQKPGHPPKLLIYWASTRESGVPDFRSGS GSGTDFTLTISSLAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC</p>
	AA		<p>SEQ ID NO: 2149</p> <p>QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRAQAPQGQGLEWMGWINPDGGTDYSQRFQGR VTMTRDTSISTAYMELSRLSDDTAVYYCAREATI FGMVIVPFDYWGQGLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDRLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTKISK AKQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSGGSFFLY SKLTVDKSRWQQGNVFSCSVMEALHNHYTQKS LSLSPGK</p>
			<p>SEQ ID NO: 579</p> <p>CAGGTGCAGTGGTGCGAGTCTGGGGCTGAGGTG AAGAAGCCTGGGCGCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATCCACTGGTGCGACAGGCCCTGGACAAGGA CTTGAGTGGATGGGTGGATCAACCTTGAAAGT GGTGGCACAGACTATTCACAGAGGTTTCAGGGC AGGTCAACATGACACAGGACACGTCCATCAGC ACAGCCTACATGGAACCTGAGCAGCCTGAGATCT GACGACACGGCGGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCTGGTACCGTCT</p>
IPS:359737	13H12.005	NA	<p>SEQ ID NO: 422</p> <p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGCGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG AAACGAGGACAACTCTCTAAGCTGCTCATTTAC TGGGCATCTACCCGGGAATCCGGGTCCCTGAC CGATTCAAGTGCGACGGGTCTGGGACAGATTTC ACTCTCAACCATCAGCAGCCTGCAAGGCTGAAGAT GTGGCAGTTTTTTACTGTCAACAATATTATAGTA CTCCGTGGACGTTCCGGCCAAAGGACCAAGGTGG AAATCAACGAACGGTGGCTGCACCATCTGTCT</p>

		<p>TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACCTGCCCTGTGTGCTGCTGCTGAATAAC TTCTATCCAGAGAGGCCAAAGTACAGTGGAAG GTGGATAACGCCCTCCAAATCGGGTAACTCCAG GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCAACCCATCAGGGCCTGAGCTCGC CCGTCAACAAAGAGCTTCAACAGGGGAGAGTGT</p>	<p>CCTACGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCCTCCTCCAAAGAGCACCTCTGGGGG CACAGCGGCCCTGGGCTGCCCTGGTCAAGGACTA CTTCCCAGAACCGGTGACGGTGTCTGTGGAATC AGCGCCCTGACCAAGCGGCTGCACACCTTCCC GGTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCGTGGTACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCAAATCTTGTGACAAACTCACACATG CCCACCGTGCCAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGACGTGAGCCACGAAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCTCTCACCCTGCTGCACCAAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACACACA GGGTACACCCCTGCCCATCCCGGAGGAGAT GACCAAGAACAGGTACGCTGACCTGACCTGCTGT CAAAGGCTTCTATCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGCAGCCGAGAGAACAACT ACAAAGCCAGCCCTCCCGTGTGGACTCCGACG GCTCTTCTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAAGAGCCCTCTCCCCTGTCTCCGGG TAAA</p>
	SEQ ID NO: 1993		SEQ ID NO: 2150
AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQKPGQPPKLLIYWASTRESGVPDFRSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL		<p>QVQLVQSGAEVKKPGASVKVSKKASGYFTGYI HWVROAPGGGLEWMGWINPESGTDYSQRFQGR VTMTRDTSISTAYMELSSLRDSDTAVYYCAREATI FGMVIVPFDYWGQGLVTVSSASTKGPSVFPLAPS</p>

			NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC	SEQ ID NO: 423 GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAAGAACTACATAGCTTGGTACCAGCAG AAACCAAGGACAACCTCCTAAGCTGCTCATTTAC TGGGCATCTACCCGGGAATCCGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCAACCATCAGCAGCCTGCAGGCTGAAGAT GTGGCAGTTTTTTACTGTCAACAATATTATAGTA CTCCGTGGACGTTCCGGCCAAGGGACCAAGGTGG AAATCAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACCTGCCCTCTGTTGTGTGCCTGCTGAATAAC TTCTATCCCAAGAGAGGCCAAAGTACAGTGGAAAG GTGGATAACGCCCTCCAAATCGGGTAACTCCCAAG GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCCCTGACGCTGAG CAAAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCAACCCATCAGGGCCTGAGCTCGC CCGTCAACAAAGAGCTTCAACAGGGGAGAGTGT
			SEQ ID NO: 580 CAGGTGCCGCTGGTGCGAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATCCACTGGGTGCGACAGGCCCTGGACAAGGA CTTGAGTGATGGGTGGATCAACCTGAAAGT GGTGGCACAGACTATTACAGAGGTTTCAAGGGC AGGTCAACATGACCAAGGACACGTCATCAGC ACAGCCTACATGGAACTGAGCAGGCTGAGATCT GACGACACGGCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGGTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCTGGTCAACCGTCT CCTCAGCCTCCACAAGGGCCCATCGGTCTTCCCC CCTGGACCCCTCTCTCCAAGAGCACCTCTGGGGG CACAGCGGCCCTGGGTGCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTC AGGCGCCCTGACCAAGCGGCGTGACACCTTCCCC GGCTGTCTCTACAGTCTCTCAGGACTCTACTCCCTC AGCAGCGTGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCCAAATCTTGTGACAAAACCTCACACATG CCCACCGTGCCAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTCT ACATGCGTGGTGGACGTGAGCCACGACCAAGAC	
IPS:361326	13H12.006	NA		

		<p>CCTGAGGTC AAGTTCACTGGTACGTGGACGGC GTGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCAGTACCGTTGTGTC AGCTCCTCACCGTCTGCACCAAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGCAGCCCCGAGAACACACA GGGTACACCTGCCCTCCCATCCCGGAGGAGAT GACCAAGAACAGGTACGCTGACCTGCCTGGT CAAGGCTTCTATCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGCAGCCGAGAACAACT ACAAAGCCAGCTCCCGTGTGGACTCCGACG GCTCTTCTCTCTATAGCAAGCTACCGTGGA CAAGAGCAGGTGGCAGCAGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGAGAAAGCCCTCTCCCTGTCTCCGGG TAAA</p>
	SEQ ID NO: 1994	SEQ ID NO: 2151
	<p>DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYIAWYQQKPGQPKLLIYWASTRESGVPDFRSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC</p>	<p>QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRAQPGQGLEWMGWINPESGTDYSQRFQGR VTMTRDTSISTAYMELSRLSDDTAVYYCAREATI FGMVIVPFDYWGQGLVTVSSASTKGPSVFPLAPS SKSTSGGT AALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNATKPCPEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVVFSCSVMEALHNHYTQKS LSLSPGK</p>
AA	SEQ ID NO: 424	SEQ ID NO: 581

IPS:361330	12H11.002	NA	<p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTCTCTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAATAAGAACTACTTAGCTTGGTACCAGCAG AAACCAGGACAGCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGTCCC TGAC CGATTCA GTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAAGGCTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACC AAGGTGG AAATCAAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACTGCC'TCTGTTGTGTGCCTGCTGAATAAC TTCTATCCAGAGAGGCCAAAGTACAGTGGAAG GTGGATAACGCCCTCC AATCGGGTA ACTCCCAG GAGAGTGCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAGTCTACG CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT</p>
			<p>CAGTGCCCGCTGGTGCA GTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAAGTCTCCTGC AAGGTTCTGGATACACCTTCAACCGGTACTAT ATACACTGGTGCGTCAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATAAGCCCTAACCAA GGTGAAACA AACTATGCACAGAA GTTTCAGGAC AGGTCAACCATGACAGGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT GACGACACGGCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGAAACCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGG CACAGCGGCCCTGGGTGCC TGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCTGTGGAAC TC AGCGCCCTGACCAAGCGGTGCACACCTTCCC GGTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACCAAGGTGGACAAAGAAAGT TGAGCCCCAATCTTGTGACAAACTCACACATG CCCACCGTGCCCAAGCCTGA ACTCTGGGGGG ACCGTCAGTCTTCTCTTCCCCCAA AACCC AAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC CCTGAGGTCAAGTTC AACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACA AAGCCGTGT GAGGAGCAGTACGGCAGCAGTACCGTTGTGTC AGCTCTCTACCGTCTTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAAACCACA GGGTACACCTGCCCTCCCATCCCGGGAGGAGAT GACCAAGAACCAAGGTCA GCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGAACAACT</p>

			ACAAGACCACGCCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGAGAAAGACCTCTCCCTGTCTCCGGG TAAA
		SEQ ID NO: 1995	SEQ ID NO: 2152
	AA	DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLA WYQQKPGQPNNLLIYWTSTRDSGVDRFSG SGSGTDFTLTINSLQAEDVA VYQCQQY YRTPWTF GQGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSITYLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYI HWVRQAPGGLEWMGWISPNQGETNYAQKFQD RVMTTRDTSISTAYMELSRLLSDDTA VYYCAREA TIFGMLIVPFDYWGQGLTVTVSSASTKGPSVFPLA PSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGPSVFLFPPKPKDITLMISRTPETCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNNGKEYKCKVSNKALPAPIEKTIS KAKGPQREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEVESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFNFSVMHEALHNHYTQK SLSLSPGK
		SEQ ID NO: 425	SEQ ID NO: 582
	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACAAATAAGAACTACTTAGCTTGGTACCGCAG AAACCAGGACAGCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAAGGCTGAAGAT GTGGCTGTTTATTACTGTACGAATATTATCGTA CTCCGTGGACGTTCCGCCAAGGGACCAAGGTGG AAATCAAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAATC TGGAAGTGCCTCTGTGTGTGCTGCTGCTGAATAAC TTCTATCCAGAGAGGCCAAAGTACAGTGAAG	CAGTGCCCGCTGGTGCGAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATACACTGGTGCGTCAAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATAAGCCCTAACCAA GGTGACACAACTATGCACAGAA GTTTCAGGAC AGGTCAACCATGACAGGACACGTCCTCATCAGC ACAGCCTATATGAGCTGAGCAGGCTGAGATCT GACGACACGGCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGAAACCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCCTCCTCCAAAGACACCTCTGGGGG CACAGCGGCCCTGGGCTGCCCTGGTCAAGGACTA

	<div>GTGGATAACGCCCTCCAAATCGGGTAACTCCCAG GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT</div>	<div>SEQ ID NO: 1996</div> <div>DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG SGSGTDFTLTINSLQAEDVAVYQCQQYYRTPTWTF GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC LLNFPYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC</div>
	<div>CTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTC AGCGCCCTGACCAGCGGCGTGACACACCTTCCC GGTGTCTACAGTCTCTCAGGACTCTACTCCCTC AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCAAATCTTGTGACAAAACTCACACATG CCCACCGTGCCCAGCACCTGA ACTCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAA AACCC AAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGTGGACGTGAGCCACGAAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCGTCTCACCCTCTCTGCAACAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCATCGAGAA AACCATC TCCAAAGCCAAAGGCAGCCCCGAGAACCCACA GGTGTACACCTGCCCTCCCATCCCGGAGGAGAT GACCAAGAACAGGTACGCTGACCTGCCTGGTGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCA GCCGGAGAACAACT ACAAAGCCAGCGCTCCCCTGCTGGACTCCGACG GCTCTTCTTCTCTATAGCAAGCTCACCGTGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAAGAGCCTCTCCCTGTCTCCGGG TAAA</div> <div>SEQ ID NO: 2153</div> <div>QVPLVQSGAEVKKPGASVKVSKASGYTFTGYVI HWVRQAPGQGLEWMGWISPNQGDNTNYAQKFQD RVMTTRDTSISTAYMEL SRLRSDDTAVYYCAREA TIFGMLIVPFDYWGQGLTVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVN HKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL</div>	

				<p>LGPSVFLFPPKPKDTLMISRTPVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFEL YSKLTVDKSRWQQGNVFSVSMHEALHNHYTQK SLSLSPGK</p>
				<p>SEQ ID NO: 426</p> <p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAGAACTACTTAGCTTGGTACCAGCAG AAACGAGACAGCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGTCCCTGAC CGATTGAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTCCGGCCAGGGACCAAGGTGG AAATCAACAGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACCTGCCCTCTGTTGTGTGCCTGCTGAATAAC TTCTATCCAGAGAGGGCCAAAGTACAGTGGAAAG GTGGATAACGCCCTCCAAATCGGGTAACTCCACAG GAGAGTGTACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCTGACGCTGAG CAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCAACCATCAGGGCCTGAGCTCGC CCGTCAACAAAGAGCTTCAACAGGGGAGAGTGT</p>
				<p>SEQ ID NO: 583</p> <p>CAGTGCCGCTGGTGCGAGTCTGGGGCTGAGGTG AAGAAGCTGGGGCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATACACTGGTGCGTCAAGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATAAGCCCTAACCAA GGTGAAACAACATAATGCACAGAAATTTTCAGGAC AGGTACCATGACACAGGACACGTCCATCAGC ACAGCCTATAATGAGCTGAGCAGGCTGAGATCT GACGACACGGCGTGATTAATGTACGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCAATTTG ACTACTGGGGCCAGGAAACCTGGTCAACCGTCT CCTCAGCCTCCACCAAGGGCCATCGGTCTTCCC CCTGGACCCCTCCTCCAAGAGCACCTCTGGGGG CACAGCGCCCTGGGTGCCCTGGTCAAGGACTA CTTCCCGCAACCGGTGACGGTGTGTCGAGAACTC AGCGCCCTGACCAAGCGGCTGCACACCTTCCC GGCTGTCTACAGTCTCAAGGACTCTACTCCCTC AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCACGTGAATCAC AAGCCCAAGCAACCAAGGTGGACAAAGAAAGT TGAGCCCAATCTTGTGACAAACTCACACATG CCCACCGTGGCCAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCCCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTG ACATGCGTGGTGGACGTGAGCCACGAAAGAC CCTGAGGTCAAGTTCACCTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC</p>

IPS:361344

12H11.004

NA

				<p>AGGTCCTCACCGTCTCTGCACCAAGGACTGGCTG AATGGCAAGGAGTACAAAGTGCAAGGTCTCCAAC AAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGCAGCCCCGAGAACACACA GGGTACACCTGCCCTCCCATCCCGGAGGAGAT GACCAAGAACAGGTACGCTGACCTGCCTGGT CAAGGCTTCTATCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGCAGCCGAGAACAACT ACAAAGACCAGCTTCCCCTGCTGGACTCCGACG GCTCCTTCTCTCTATAGCAAGCTACCCGTGGA CAAGAGCAGGTGGCAGCAGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGAGAAAGAGCCTCTCCCCTGTCTCCGGG TAAA</p>
				<p>SEQ ID NO: 1997</p> <p>DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLA WYQQKPGQPPNLLIYWTSRDSGVDRFSG SGSGTDFTLTINSLQAEDVA VYQCQQYYRTPTWTF GQGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSYLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC</p>
			AA	<p>SEQ ID NO: 2154</p> <p>QVPLVQSGAEVKKPGASVKVSKASGYTFTGYI HWVRQAPGQGLEWMGWISPNQGETNYAQKFQD RVMTTRDTSISTAYMELSRRLRSDDTAVYYCTREA TIFGMLIVPFDYWGQGLTVTVSSASTKGPSVFPLA PSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLEPPKPKDTLMISRTPETCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFEL YSKLTVDKSRWQQGNVVFSCSVMEALHNHYTQK SLSLSPGK</p>
			NA	<p>SEQ ID NO: 427</p> <p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGCGAGAGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAGAACTACTTAGCTTGGTACCAAGCAG AAACCAAGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCTGGGGTCCCTGAC</p>
	12H11.005	IPS:361351		

CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAAGGCTGAAGAT GTGGCTGTTTATTACTGTACGAATATTATCGTA CTCCGTGGACGTTCCGGCCAAGGACCACAGGTGG AAATCAAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACTGCC'TCTGTTGTGTGCCTGCTGAATAAC TTCTATCCACAGAGAGGCCAAAGTACAGTGGAG GTGGATAACGCCCTCCAATCGGTAAC'TCCCCAG GAGAGTGTACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCAACCCATCAGGGCCTGAGCTCGC CCGTCAACAAAGAGCTTCAACAGGGGAGAGTGT	AGGGTCACCATGACCAGGGACACAGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGAAACCCCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGG CACAGCGGCCCTGGGCTGCC'TGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCTGTGGAACTC AGCGCCCTGACCAAGCGGCTGCACACCTTCCC GGTGTCTACAGTCTTCAGGACTCTACTCCCTC AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCCAATCTTGTGACAAACTCACACATG CCCACCGTGCCACGACCTGA'ACTCCTGGGGG ACCGTCAGTCTTCCCTCTTCCCCCAA'AAACCAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGTGACGTGAGCCACGAAAGAC CCTGAGGTCAAGTTC'AACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCTCCTCACCGTCTTGCACCAAGGACTGGCTG AATGGCAAGGAGTACAAGTGC'AAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAAACACACA GGTGTACACCTGCCCTCCATCCCGGAGGAGAT GACCAAGAACAGGTGACGCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGAACAACT ACAAGACCAGCCTTCCCGTGTGGACTCCGACG GCTCCTTCTCTCTATAGCAAGTCAACCGTGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAAGAGCCCTCTCCCTGTCTCCGGG TAAA
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		SEQ ID NO: 1998	<p>DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWSTSTRDSGVPDRFSG SGSGTDFTLTINSLQAEDVAVYQCQQYYRTPWTF GQGTKVEIKRTVAAPSVFIIPPSDEQLKSGTASVVC LLNIFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSYLSSTLTLSKADYEKHKVYACEVTHQQLSS PVTKSFNRGEC</p>	SEQ ID NO: 2155	<p>QVPLVQSGAEVKKPGASVKVSKASGYTFTGYI HWVRQAPGGGLEWMGWISPNNGETNYAQKFQD RVTMTRDTSISTAYMELSRRLRSDDTAVYVCAREA TIFGMLIVPFDYWGQGLTVTVSSASTKGPSVFPLA PSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGPSPVFLPPKPKDITLMISRTPETCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGPQREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEVESNGQPENNYKTTTPPVLDSGGSFEL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK</p>
		SEQ ID NO: 428	<p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGCGAGAGGGCCACCAATCAAC TGCAAGTCCAGCCAGAGTGTITATCCAGCTCC AACATAAGAACTACTTAGCTTGGTACCAGCAG AAACGAGGACAGCTCCTAACTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGTCCCTGAC CGATTGAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTACCATCAACAGCCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCAAGGTGG AAATCAACGAAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACGTGCTCTGTGTGTGCTGCTGAATAAC TTCTATCCAGAGAGGCCAAAGTACAGTGGAAAG GTGGATAACGCCCTCCAAATCGGTAATCTCCAG GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCCCTGACGCTGAG CAAAAGCAGACTACGAGAAACACAAGTCTACG CCTGCGAAGTCAACCAATCAGGGCCTGAGCTCGC CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT</p>	SEQ ID NO: 585	<p>CAGTGCCGCTGGTGAGTCTGGGGCTGAGGTG AAGAAGCCTGGGCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACGGCTACTAT ATACACTGGTGCGTCAAGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATAAGCCCTAACAAAT GGTGACACAACTATGCACAGAAAGTTTCAGGAC AGGTCAACATGACACAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT GACGACACGGCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCAATTG ACTACTGGGCCAGGGAACCCCTGGTCAACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGACCCCTCCCTCCAAGAGCACCTCTGGGGG CACAGCGCCCTGGGTGCGTGGTCAAGGACTA CTTCCCGAAACCGGTGACGGTGTGCGTGGAACTC AGCGCCCTGACCAAGCGGCTGCACACCTTCCC GGTGTCTCTACAGTCTCAGGACTCTACTCCCTC AGCAGGTGGTGACCGTGCCCTCCAGCAGCCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCCAACAACCAAGGTGGACAAAGAAAGT</p>

		TGAGCCCAAATCTTGTGACAAAACTCACACATG CCCACCGTGCCAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGACGTGAGCCACGAAAGAC CCTGAGGTCAGTTCACTGGTACGTGGACGGC GTGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGT AGCTCTCACCGTCTTGCACCAAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGCAGCCCCGAGAAACACAC GGTGTACACCTGCCCTCCCATCCCGGAGGAGAT GACCAAGAACAGGTACGCTGACCTGCCTGGT CAAAGGCTTCTATCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGCAGCCGAGAACAACT ACAAAGACACGCTCCCGTGTGGACTCCGACG GCTCTTCTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGAGAAAGAGCCTCTCCCTGTCTCCGGG TAAA
	SEQ ID NO: 1999	SEQ ID NO: 2156
	DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLA WYQQKPGQPPNLLIYWTSRDSGVPDFSG SGSGTDFTLTINSLQAEDVA VYQCQQYYRTPTWTF GQGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYLSSTLTLSKADYEKHKVYACEVTHQQLSS PVTKSFNRGEC	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWISPNNGDTNYAQKFQD RV/TMTRDTSISTAYMELSRLSDDTAVYYCAREA TIFGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDITLMISRTPETCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
	AA	

				YSKLTVDKSRWQQGNVFCVSMHEALHNHYTQK SLSLSPGK
				SEQ ID NO: 586
				CAGTGCCGCTGGTGCAAGTCTGGGGCTGAGGTG AAGAAGCTGGGGCTCAGTGAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGTACTAT ATACACTGGTGCGTCAAGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATAAGCCCTAACCAA GGTGACACAACTATGCACAGAAATTTTCAGGAC AGGTCAACATGACAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGGTGAGATCT GACGACACGGCGGTGATTAATGTACGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCAATTG ACTACTGGGGCCAGGAAACCTGGTCAACCGTCT CCTCAGCCTCCACCAAGGGCCATCGGTCTTCCC CCTGGACCCCTCCCTCCAAGAGCACCTCTGGGG CACAGGGCCCTGGGTGCTGGTCAAGGACTA CTTCCCGCAACCGGTGACGGTGTGCGTGAAGTCT AGCGCCCTGACAGCGGTGACACACCTTCCC GGTGTCTACAGTCTCAAGGACTCTACTCCCTC AGCAGGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACCAAGGTGGACAAAGAAAGT TGAGCCCAATCTTGTGACAAACTCACACATG CCCACCGTGCCAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCCCTCTTCCCCCAAAACCCAA GACACCTCATGATCTCCCGGACCCCTGAGGTCT ACATGCGTGGTGGTGGACGTGAGCCACGAAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCAGTACCGTTGTGTC AGGTCTCTACCGTCTGACCCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACCCACA GGTGTACACCCCTGCCCCCATCCCCGGGAGGAGAT
				SEQ ID NO: 429
				GACATCGTGAATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTATATCCAGCTCC AACATAAGAACTACTTAGCTTGGTACCAGCAG AAACAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTACCATCAACAGCCTGCAAGGTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTCCGGCCAGGGACCAAGGTGG AAATCAACGAAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACCTGCCCTGTGTGTGCTGCTGCTGAATAAC TTCTATCCAGAGAGGCCCAAGTACAGTGGAAAG GTGGATAACGCCCTCCATCGGGTAACTCCAG GAGAGTGTACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCTGACGCTGAG CAAAAGCAGACTACGAGAAACACAAGTCTACG CCTGCGAAGTCAACCATCAGGGCCTGAGCTCGC CCGTCAACAAAGAGCTTCAACAGGGGAGAGTGT
				NA
				12H11.007
				IPS:361365

			<p>GACCAAGAACAGGTGAGCCTGACCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCAGCATCGCCGTGGA GTGGGAGAGCAATGGCAGCCGGAGAACAACT ACAAAGACCAGCCTCCCGTGTGGACTCCGACG GCTCCTTCTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGATGAGGCTCTGCACAACCA CTACACGAGAGAGCCTCTCCCTGTCTCCCGG TAAA</p>
			<p>SEQ ID NO: 2000</p> <p>DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLA WYQQKPGQPPNLLIYWTSRDSGVPDFSG SGSGTDFTLTINSLQAEDVA VYQCQQYYRTPTWTF GQGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSYLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC</p>
	AA		<p>SEQ ID NO: 2157</p> <p>QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYI HWVRQAPGQGLEWMGWISPNQGDNYAQKFQD RVMTTRDTSISTAYMELSRLSRDDTA VYCTREA TIFGMLIVPFDYWGQGLTVTVSSASTKGPSVFPLA PSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPEL LGPSVFLFPPKPKDTLMISRTPEVTCVVDVVSHE DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFEL YSKLTVDKSRWQQGNVVFSCSVMEALHNHYTQK SLSLSPGK</p>
			<p>SEQ ID NO: 430</p> <p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACATAAGAACTACTTAGCTTGGTACCAAGCAG AAACCAAGACAGCTCTCAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGTCCCTGAC CGATTCAAGTGCGAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCAAGGTGG AAATCAACGAACGGTGGCTGCACCATCTGTCT</p>
IPS:361372	12H11.008	NA	<p>SEQ ID NO: 587</p> <p>CAGTGCCGCTGGTGCAAGTCTGGGGCTGAGGTG AAGAAGCCTGGGCCTCAGTGAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATACACTGGTGCGTCAAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATAAGCCCTAACCAAT GGTGAAACAACTATGCACAGAA GTTTTCAGGAC AGGTCAACATGACACAGGACACGTCCATCAGC ACAGCCTATATGAGCTGAGCAGGCTGAGATCT GACGACACGGCGTGTATTACTGTACGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGCCAGGGAAACCCCTGGTACCGTCT</p>

		<p>TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAAC TGCTGTGTGCTGCTGCTGAATAAC TTCTATCCAGAGAGGCCAAAGTACAGTGGAAG GTGGATAACGCCCTCCAAATCGGGTAACTCCAG GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCAACCCATCAGGGCCTGAGCTCGC CCGTCAACAAAGAGCTTCAACAGGGGAGAGTGT</p>	<p>CCTACGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCCTCCTCCAAAGAGCACCTCTGGGGG CACAGCGGCCCTGGGCTGCCGTGGTCAAGGACTA CTTCCCAGAACCGGTGACGGTGTGCTGGAACCTC AGCGCCCTGACCAAGCGGCTGCACACCTTCCC GGTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCAAATCTTGACAAACTCACACATG CCCACCGTGCCAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGACGTGAGCCACGAAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCTCTCACCGTCTGCAACAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACACACA GGGTACACCCCTGCCCATCCCGGAGGAGAT GACCAAGAACAGGTGACGCTGACCTGCCCTGGT CAAAGGCTTCTATCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGCAGCCGAGAGAACAACT ACAAAGCCAGCTTCCCGTGTGGACTCCGACG GCTCTTCTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAAGAAAGCCCTCTCCCCTGTCTCCGGG TAAA</p>
	AA	<p>SEQ ID NO: 2001</p> <p>DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLA WYQQKPGQPPNLLIYWTSTRDSGVPDFSG SGSGTDFTLTINSLQAEDVA VYYCQQYYRTPTWTF GQGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVC</p>	<p>SEQ ID NO: 2158</p> <p>QVPLVQSGAEVKKPGASVKVSKASGYTFTGYI HWVRQAPGQGLEWMGWISPNNGETNYAQKFQD RVMTTRDTSISTAYMELSRLSRDDTAVYYCTREA TIFGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLA</p>

			LLNFPYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYKHKVYACEVTHQGLSS PVTKSFNRGEC	SEQ ID NO: 431	<p>PSSKSTSGGTAAAGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNHPKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLEFPPKPKDRLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAAKTKPCEEQYGSTYRC VSVLTVLHQDWLNQKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFEL YSKLTVDKSRWQQGNVVFSCVMHEALHNHYTQK SLSLSPGK</p>
				SEQ ID NO: 588	<p>CAGTGCCGCTGGTGCACTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATACACTGGTGCGTCAAGCCCTGGACAAGGG CTTGAGTGATGGGTGGATAGCCCTAACCAG GGTGAAACAACATATGCACAGAAATTTTCAGGAC AGGTCAACATGACAGGACACGTCATCAGC ACAGCCTATATGAGCTGAGCAGGCTGAGATCT GACGACACGGCGTGATTAATGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCAATTTG ACTACTGGGGCCAGGAAACCTGGTCAACCGTCT CCTCAGCCTCCACCAAGGGCCATCGGTCTTCCC CCTGGCACCTTCCCTCCAGAGCACCTCTGGGGG CACAGCGCCCTGGGTGCTGGTCAAGGACTA CTTCCCAGAACCGGTGACGGTGTGCGTGGAACTC AGCGCCCTGACCAAGCGGTGTGCACACCTTCCC GGTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCACGCTGAATCAC AAGCCCCAGCAACCAAGGTGGACAAAGAAAGT TGAGCCCCAATCTTGTGACAAACTCACACATG CCCACCGTGCCAGCACCTGAACTCTGGGGGG ACCGTCAGTCTTCCCTCTTCCCCCAAAACCCAG GACACCTCATGATCTCCCGGACCCCTGAGGTG ACATGCGTGGTGGTGACGTGAGCCACGAGAC</p>
				NA	<p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAGAACTACTTAGCTTGGTACCAGCAG AAACAGGACAGCTCTCAACCTGCTCATTTAC TGGACTTCTACCCGAGATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAAGGCTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTCCGGCCAGGGACCAAGGTGG AAATCAACAGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAAGTTGAAATC TGGAACCTGCCCTCTGTGTGTGCTGCTGAATAAC TTCTATCCAGAGAGGCCAAAGTACAGTGGAAAG GTGGATAACGCCCTCCAAATCGGGTAACTCCCAAG GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCTGACGCTGAG CAAAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCAACCATCAGGGCCTGAGCTCGC CCGTCAACAAAGAGCTTCAACAGGGGAGAGTGT</p>

			<p>CCTGAGGTC AAGTTCACTGGTACGTGGACGGC GTGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCTCCTCACCGTCTGCACCAAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACACACA GGTGTACACCTGCCCTCCCATCCCGGAGGAGAT GACCAAGAACAGGTACGCTGACCTGCCTGGT CAAGGCTTCTATCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGCAGCCGAGAACAACT ACAAAGCCAGCTTCCCTGCTGGACTCCGACG GCTCTTCTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGAGAAAGCCCTCTCCCTGTCTCCGGG TAAA</p>
		SEQ ID NO: 2002	SEQ ID NO: 2159
	AA	<p>DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLA WYQQKPGQPPNLLIYWTSTRESGVDRFSG SGSGTDFTLTINSLQAEDVA VYQCQQY YRTPWTF GQGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVC LLNFIYPREA KVQWKVDNALQSGNSQESVTEQDS KDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC</p>	<p>QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWISPNQGETNYAQKFQD RVMTTRDTSISTAYMEL SRLRSDDTAVYYCAREA TIFGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVN HKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLEPPPKPKDTLMISRTPEVTCVVVDVSH DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFEL YSKLTVDKSRWQQGNV FSCSVMEALHNHYTQK SLSLSPGK</p>
		SEQ ID NO: 432	SEQ ID NO: 589

IPs:361383	12H11.010	NA	<p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCCTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAGAACTACTTAGCTTGGTACCAGCAG AAACGAGACAGCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGAAATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTACCATCAACAGCCCTGAGGCTGAAGAT GTGGCTGTTTATTACTGTACGCAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCAGGTGG AAATCAAACGAAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACTGCC'TCTGTTGTGTGCCTGCTGAATAAC TTCTATCCAGAGAGGCCAAAGTACAGTGGAAG GTGGATAACGCCCTCCAAATCGGGTAACTCCAG GAGAGTGCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAGTCTACG CCTGCGAAGTCAACCATCAGGGCCTGAGCTCGC CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT</p>
			<p>CAGTGCCCGCTGGTGCGAGTCTGGGGCTGAGGTG AAGAAGCTGGGGCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGTACTAT ATACACTGGTGCGTCAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATAAGCCCTAACAA GGTGACACAACTATGCACAGAAATTTTCAGGAC AGGTCAACATGACAGGGGACACGTCCATCAGC ACAGCCTATATGAGCTGAGCAGGCTGAGATCT GACGACACGGCGGTGATTACTGTGCGAGAGAG GCCACGATTTTGGAATGCTTATTGTACCATTTG ACTAGTGGGCCAGGAAACCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCTTCTCCAGAGCACCTCTGGGGG CACAGCGGCCCTGGGTGCCAGGACCTCAAGGACTA CTTCCCGCAACCGGTGACGGTGTGCGTGGAACTC AGCGCCCTGACAGCGGGCTGCACACCTTCCC GGTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCAAATCTTGTGACAAACTCACACATG CCCACCGTGCCAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCAGTACCGTTGTGTC AGCTCCTCACCGTCTTGCACCAAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACACACA GGGTACACCTGCCCTCCATCCCGGGAGGAGAT GACCAAGAACAGGTGAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGACGCCGAGAACAACT</p>

			ACAAGACCACGCTCCCGTGCTGGACTCCGACG GCTCCTTCTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGAGAAAGCCCTCTCCCTGTCTCCGGG TAAA
		SEQ ID NO: 2003	SEQ ID NO: 2160
	AA	DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLA WYQQKPGQPNNLLIYWTSTRESGVDRFSG SGSGTDFTLTINSLQAEDVA VYQCQQY YRTPWTF GQGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSITYLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWISPNNGDNYAQKFQD RVMTTRDTSISTAYMELSRLSDDTA VYVCAREA TIFGMLIVPFDYWGQGLTVTVSSASTKGPSVFPLA PSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDITLMISRTPETCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFEL YSKLTVDKSRWQQGNVFSQSVMEALHNHYTQK SLSLSPGK
		SEQ ID NO: 433	SEQ ID NO: 590
	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGCGGAGAGGGCCACCAATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAGAACTACTTAGCTTGGTACCAGCAG AAACCAAGACAGCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGAAATCCGGGGTCCCTGAC CGATTGAGTGCGAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCCTGCAAGGCTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCAAGGTGG AAATCAAACGAAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAATC TGGAAC TGCTCTGTGTGTGCTGCTGCTGAATAAC TTCTATCCAGAGAGGCCAAAGTACAGTGGAAG	CAGTGCCGCTGGTGAGTCTGGGGCTGAGGTG AAGAAAGCTGGGCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATACACTGGTGCGTCAAGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATAGCCCTAACCAA GGTGACACAACTATGCACAGAA GTTTCAGGAC AGGTACCATGACACAGGACACGTCATCAGC ACAGCCTATATGAGCTGAGCAGGCTGAGATCT GACGACACGGCGGTGTTACTGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGCGCAGGAAACCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCTCTCTCCAAAGAGCACCTCTGGGGG CACAGCGGCCCTGGGCTGCCCTGGTCAAGGACTA

	<div>GTGGATAACGCCCTCCAAATCGGGTAACTCCCAG GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCAACCATCAGGGCCTGAGCTCGC CCGTCAACAAAGAGCTTCAACAGGGGAGAGTGT</div>	<div>SEQ ID NO: 2004</div> <div>DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPNLLIYWTSTRESGVPDFSG SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPTWTF GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC</div>
	<div>CTTCCCCGAACCGGTGACGGTGTCTGTGGAACTC AGCGCCCTGACCAAGCGGCTGCACACCTTCCC GGTGTCTCACAGTCTCTCAGGACTCTACTCCCTC AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAGAAAGT TGAGCCCAAATCTTGTGACAAAACCTCACACATG CCCACCGTGCCCAGCACCTGAACCTCCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGAGCTGAGCCACGAAAGAC CCTGAGGTCAAAGTTCAAATGGTGTACGTGGACGGC GTGAGGTGCATAATGCCAAGACAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCGTCTCACCGTCTCTGCACCAAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCATCGAGAAAACCATC TCCAAAGCCAAAGGCGAGCCCCGAGAACCA GGTGTACACCTGCCCTCCCATCCCGGAGGAGAT GACCAAGAACCAAGGTACGCTGACCTGCCTGGT CAAAGGCTTCTATCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAAGCCGGAGAACAACT ACAAGACCAGCCTCCCGTGTGGACTCCGACG GCTCCTTCTTCTCTATAGCAAGCTCACCGTGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAAGAGCCTCTCCCTGTCTCCGGG TAAA</div> <div>SEQ ID NO: 2161</div> <div>QVPLVQSGAEVKKPGASVKVSKASGYTFTGYVI HWVRQAPGQGLEWMGWISPNQGDITNYAQKFQD RVMTTRDTSISTAYMELSLRSLRSDDTAVYYCAREA TIFGMLIVPFDYWGQGLTVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL</div>	

				<p>LGPSVFLFPPKPKDLMISRTPVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL YSKLTVDKSRWQQGNVFSVSMHEALHNHYTQK SLSLSPGK</p>
				<p>SEQ ID NO: 434</p> <p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGCTCTGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAGAACTACTTAGCTTGGTACCAGCAG AAACGAGACAGCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTCCGGCCAGGGACCAGGTGG AAATCAACGAAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACCTGCCCTCTGTTGTGTGCCTGCTGAATAAC TTCTATCCAGAGAGGGCCAAAGTACAGTGGAAG GTGGATAACGCCCTCCAAATCGGGTAACTCCACG GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCCTGACGCTGAG CAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCAACCATCAGGGCCTGAGCTCGC CCGTCAACAAAGAGCTTCAACAGGGGAGAGTGT</p>
				<p>SEQ ID NO: 591</p> <p>CAGTGCCGCTGGTGCGAGTCTGGGGCTGAGGTG AAGAAGCTGGGGCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATACACTGGTGCGTCAAGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATAAGCCCTAACAT GGTGAAACAACATATGCACAGAAAGTTTCAGGAC AGGTCAACATGACACAGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT GACGACACGGCGTGTTACTGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGAAACCTGGTCAACCGTCT CCTCAGCCTCCACCAAGGGCCATCGGTCTTCCC CCTGGACCCCTCCTCCAAGAGCACCTCTGGGGG CACAGCGCCCTGGGTGCTGCTGGTCAAGGACTA CTTCCCGCAACCGGTGACGGTGTGCTGGAACTC AGCGCCCTGACCAAGCGGCTGCACACCTTCCC GGCTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCACGTGAATCAC AAGCCCAAGCAACCAAGGTGGACAAAGAAAGT TGAGCCCAATCTTGTGACAAACTCACACATG CCCACCGTGGCCAGCACCTGAACTCTGGGGG ACCGTCAGTCTTCCCTCTTCCCCCAAAACCCAA GACACCTCATGATCTCCCGGACCCCTGAGGTG ACATGCGTGGTGGACGTGAGCCACGAAAGAC CCTGAGGTCAAGTTCACCTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC</p>

IPS:361391

12H11.012

NA

			<p>AGGTCCTCACCGTCTCTGCACCAAGGACTGGCTG AATGGCAAGGAGTACAAAGTGCAAGGTCTCCAAC AAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGCAGCCCCGAGAACACACA GGGTACACCTGCCCTCCCATCCCGGAGGAGAT GACCAAGAACAGGTACGCTGACCTGCCTGGT CAAGGCTTCTATCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGCAGCCGAGAACAACT ACAAAGACCAGCTTCCCCTGCTGGACTCCGACG GCTCCTTCTCTCTATAGCAAGCTACCCGTGGA CAAGAGCAGGTGGCAGCAGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGAGAAAGCCCTCTCCCCTGTCTCCGGG TAAA</p>
			<p>SEQ ID NO: 2005</p> <p>DIVMTQSPDLSVSLGERATINCKSSQSVLSSNNK NYLA WYQQKPGQPPNLLIYWTSTRESGVDRFSG SGSGTDFTLTINSLQAEDVA VYQCQQY YRTPWTF GQGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSYLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC</p>
		AA	<p>SEQ ID NO: 2162</p> <p>QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYI HWVRQAPGQGLEWMGWISPNNGETNYAQKFQD RVMTTRDTSISTAYMELSRRLSDDTAVYYCAREA TIFGMLIVPFDYWGQGLTVTVSSASTKGPSVFPLA PSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLEPPKPKDTLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVVFSCSVMEALHNHYTQK SLSLSPGK</p>
		NA	<p>SEQ ID NO: 435</p> <p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGCGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAGAACTACTTAGCTTGGTACCAAGCAG AAACCAAGGACAGCTCTCTAAACTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC</p>
IPS:361395	12H11.013		<p>SEQ ID NO: 592</p> <p>CAGGTGACGTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCGGCTACTAT ATACACTGGTGCCTCAGGCCCTGGACAAGGG CTTGAGTGGATGGGTGGATAGCCCTAACCCAA GGTGAAACAACAACTATGCACAGAA GTTTCAGGAC</p>

CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAAGGCTGAAGAT GTGGCTGTTTATTACTGTACGAATATTATCGTA CTCCGTGGACGTTTCGGCCAAAGGACCACAGGTGG AAATCAAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACTGCC'TCTGTTGTGTGCCTGCTGAATAAC TTCTATCCACAGAGAGGCCAAAGTACAGTGGAG GTGGATAACGCCCTCCAATCGGGTAACTCCCCAG GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCAACCCATCAGGGCCTGAGCTCGC CCGTCAACAAAGAGCTTCAACAGGGGAGAGTGT	AGGGTCACCATGACCAGGGACACAGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGCCTGAGATCT GACGACACGGCCGTGATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGAAACCCCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGG CACAGGGCCCTGGGCTGCC'TGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCTGTGGAATC AGCGCCCTGACCAAGCGGCTGCACACCTTCCC GGTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCAGCAACACCAAGGTGGACAAAGAAAGT TGAGCCCAATCTTGTGACAAACTCACACATG CCCACCGTGCCACGACCTGA'ACTCCTGGGGG ACCGTCAGTCTTCCCTCTTCCCCCAA'AAACCAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGTGACGTGAGCCACGAAAGAC CCTGAGGTCAAGTTC'AACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCTCCTCACCGTCTTGCAACAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAAACACAA GGTGTACACCTGCCCTCCATCCCGGAGGAGAT GACCAAGAACAGGTGAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGAACAACT ACAAGACCAGCCTTCCCGTGTGGACTCCGACG GCTCCTTCTCTCTATAGCAAGCTCACCGTGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAAGAGCCCTCTCCCTGTCTCCGGG TAAA
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		SEQ ID NO: 2006	<p>DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYLAWYQQKPGQPPKLLIYWSTSTRDSGVPDFSG SGSGTDFTLTINSLQAEDVAVYQCQQYYRTPWTF GQGTKVEIKRTVAAPSVFIIPPSDEQLKSGTASVVC LLNIFYPREAKVQW/KVDNALQSGNSQESVTEQDS KDSTYLSSTLTLSKADYEKHKVYACEVTHQQLSS PVTKSFNRGEC</p>	SEQ ID NO: 2163	<p>QVQLVQSGAEVKKPGASVKVSKKASGYTFTGYYI HWVRQAPGGGLEWMGWISPNQGETNYAQKFQD RVTMTRDTSISTAYMELSSLRSDDTAVYYCAREA TIFGMLIVPDFYWGQGTLLVTVSSASTKGPSVFPLA PSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNHNKPSNTKVDKKVEPKSCDKTHTCPCPAPEL LGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGPQREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEVESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK</p>
		AA		SEQ ID NO: 436	<p>GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCCTGGCGGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTATCCAGCTCC AACATAAGAACTACTTAGCTTGGTACCAGCAG AAACCAAGACAGCTCTCTAACTGCTCATTTAC TGGACTTCTACCCGAGATCCGGGGTCCCTGAC CGATTCAAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAAGCAATATTATCGTA CTCCGTGGACGTTCCGGCCAAAGGACCAAGGTGG AAATCAACAGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACGTGCTCTGTGTGTGCTGCTGAATAAC TTCTATCCAGAGAGGCCAAAGTACAGTGGAAG GTGGATAACGCCCTCCAAATCGGTAACATCCCAAG GAGAGTGTCACAGACGAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCCTGACGCTGAG CAAAAGCAGACTACGAGAAACACAAGTCTACG CCTGCGAAGTCAACCAATCAGGGCCTGAGCTCGC CCGTCAACAAAGAGCTTCAACAGGGGAGAGTGT</p>
IPS:361402	12H11.014	NA		SEQ ID NO: 593	<p>CAGGTGCAGCTGGTGAGTCTGGGGCTGAGGTG AAGAAGCTGGGGCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACGGCTACTAT ATACACTGGTGCGTCAAGCCCTGGACAAAGG CTTGAGTGGATGGGTGGATAAGCCCTAACC GGTGAAACAACATAATGCACAGAAAGTTTCAGGAC AGGTCAACATGACACAGGACACGTCATCAGC ACAGCCTATAATGGAGCTGAGCAGCTGAGATCT GACGACACGGCGTGTATTACTGTGCGAGAGAG GCCACGATTTTGGAAATGCTTATTGTACCAATTG ACTACTGGGGCCAGGGAACCCCTGGTACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGACCCCTCCTCCAAGAGCACCTCTGGGGG CACAGCGCCCTGGGTGCGTGGTCAAGGACTA CTTCCCGCAACCGGTGACGGTGTGCGTGGAACTC AGCGCCCTGACCAAGCGGTGACACACCTTCCC GGCTGTCTACAGTCTCAGGACTCTACTCCCTC AGCAGCGTGGTGACCGTGCCCTCCACGACGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCCAACAACCAAGGTGGACAAAGAAAGT</p>

		TGAGCCCAAATCTTGTGACAAAACTCACACATG CCCACCGTGCCAGCACCTGAACCTCTGGGGG ACCGTCAGTCTTCTCTTCCCCCAAACCCAAAG GACACCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGACGTGAGCCACGAAGAC CCTGAGGTCAGTTCACTGGTACGTGGACGGC GTGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGT AGCTCTCACCGTCTTGCACCAAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAACCATC TCCAAAGCCAAAGGCAGCCCCGAGAAACACACA GGTGTACACCTGCCCTCCCATCCCGGAGGAGAT GACCAAGAACAGGTACGCTGACCTGCCTGGT CAAAGGCTTCTATCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGCAGCCGAGAACAACT ACAAAGCCAGCTTCCCGTGTGGACTCCGACG GCTCTTCTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAAGAGCCCTCTCCCTGTCTCCGGG TAAA
	SEQ ID NO: 2007	SEQ ID NO: 2164
	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNK NYLA WYQQKPGQPPKLLIYWTSSTRESGVDRFSG SGSGTDFTLTINSLQAEDVA VYQCQQY YRTPWTF GQGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYLSSTLTLSKADYEKHKVYACEVTHQQLSS PVTKSFNRGEC	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWISPNQGETNYAQKFQD RV/TMTRDTSISTAYMELSSLRSDDTAVYYCAREA TIFGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC NVNPKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPVFLFPPKPKDTLMISRTPEVTCVVVDVSH DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFL
	AA	

				YSKLTVDKSRWQQGNVFCVSMHEALHNHYTQK SLSLSPGK
				SEQ ID NO: 594
				CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCTGGGGCTCAGTGAAGTCTCCTGC AAGCTTCCGGATACACCTTCAACCGGCTACTAT ATGCATTGGTGCACAGGCCCTGGACAAGGG CTTGAGTGGATGGATGGATCAACCTTAACAGT GGTGGCACAACTATGCACAGAAATTTCAGGGC AGGTCAACATGACACAGGACACGTCCATCAGT ACAGCTACATGGAGCTGAGCAGGCTGAGGTCT GACGACACGGCGTGTATTACTGTGCGAGAGGG GGGATTACGTTTGGGGACTTATCGGCCTCAC TACTACTACGGTATGGACGTCTGGGGCCAAAGG ACCAGGTACCGTCTCCTCAGCCTCCACCAAG GGCCATCGGTCTTCCCCCTGGCACCTCTCCCA AGAGACCTCTGGGGGCACAGCGGCCCTGGGCT GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA CGGTGCTGTGGAACCTCAGGCGCCCTGACCAAGC GCGTGACACCTTCCCCGGCTGTCTACAGTCCCTC AGGACTTACTCCCTCAGCAGCGTGGTGACCGT GCCCCTCCAGCAGCTTGGGCACCCAGACCTACAT CTGCAACGTGAATCAAGCCACGCAACACCAA GGTGACACAGAAAGTTGAGCCCAATCTTGTGA CAAACTCACACATGCCCCACCGTGCCACGACC TGAACTCCTGGGGGACCGTCACTTCTCTTC CCCCAAAACCAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTACATGCGTGGTGGTGGAC GTGAGCCACGAAGACCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCC AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG CACGTACCGTTGTGTACGCGTCTCACCGTCCCTG CACCAGGACTGGTGAATGGCAAGGAGTACAA GTGCAAGGTCTCCACAAAGCCCTCCCAAGCCCC CATCGAGAAACCATCTCCAAAGCCAAAGGCA GCCCCGAGAACCAACAGGTGTACACCTGCCCC
				SEQ ID NO: 437
				CAGTCTGTGCTGACTAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGGTCAACCATCTCTTGT CTGGAAGTAGCTCCAACATCGGAAGTCAAACTG TAAACTGGTACCAAGCACTCCCAAGGAACGGCCC CCAAACTCCTCATCTATACATAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGTGATTATTCTGTG CAACATTCTGATGAAGCCTGAGTGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCTCAGGT AGCCCAAGGTGCCCCCTCGGTCACTCTGTTCCTC GCCCCTCTGAGGAGCTTCAAGCCCAACAAGGC CACACTGGTGTCTCATAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCTGGAAAGGCAGATAG CAGCCCCGTCAAGCGGGAGTGGAGACCAACAC ACCTTCCAAACAAGCAACAACAAGTACGGGC CAGCAGCTATCTGAGCCTGACGCTGAGCAGTG GAAGTCCACAGAAAGCTACAGTGCAGGTCTAC GCATGAAGGGAGCACCGTGGAGAGACAGTGG CCCCACAGATGTTCA
			NA	
		2C2.005.001		
		IPS:361406		

			<p>ATCCCGGAGGAGATGACCAAGAACACAGGTCA GCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA GCGACATCGCCGTGGAGTGGGAGAGCAATGGG CAGCCGAGAACAACTACAGACACGCTCTCC GTGCTGACTCCGACGGCTCTTCTTCTCTATA GCAAGCTCACCGTGGACAAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAAACCACTACACGCAAGAGAGC CTCTCCCTGTCTCCGGGTAAA</p> <p>SEQ ID NO: 2165</p>
			<p>QMQVVQSGAEVKKPGASVKVCKASGYTFTGY MHWVRQAPGQGLEWMGWNPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLSDDTA VYYCARG GDYVWGTYPHYYYGMDVWVGQGTITVTVSSAST KGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVVDGVEVHNAKTKPCE EQYGSTYRCVSLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LDSGSEFLYSKLTVDKSRWQQGNVVFSCSVMHEA LHNHYTQKLSLSLSPGK</p> <p>SEQ ID NO: 595</p>
	AA		<p>QSVLTQPPSASGTPGQRVTISCSGSSSNIGSQTVNW YQHLPGTAPKLLIYTNNQRPSGVPDFRFSGSKSGTS ASLAISGLQSEDEADYFCATFDESLSGPVFGGGTK LTVLGGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTTPSKQSNKYY AASSYLSLTPEQWKSHRYSYSCQVTHEGSTVEKTV APTECS</p> <p>SEQ ID NO: 2008</p>
	NA	2C2.005.002	<p>!PS:361412</p> <p>CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCGGCGCAGAGGTACCACTCTCTTGT CTGGAAGTAGCTCCAAACATCGGAAGTCAAACTG TAAACTGGTACCGACACCTCCCAGGAACGGCCC CCAAACTCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTCTGTG CAACATTTCGATGAAGCCTGCAAGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCTCAGGTC AGCCCCAAGGCTGCCCCCTCGGTCACTCTGTTC</p> <p>SEQ ID NO: 438</p>

		<p>GCCCTCCTCTGAGGAGCTTCAAGCCAAACAAGGC CACACTGGTGTCTCATAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCTGGAAGGCAGATAG CAGCCCCGTCAAGCGGGAGTGGAGACCACAC ACCTCCAAACAAGCAACAACAAGTACGCGGC CAGCAGCTATCTGAGCCTGACGCCCTGAGCAGTG GAACTCCACAGAAAGCTACAGCTGCCAGGTCAC GCATGAAGGAGCACCGTGGAGAAAGACAGTGG CCCCTACAGAAATGTTCA</p>	<p>SEQ ID NO: 2009</p>
	AA	<p>ACCACGGTCAACCGTCTCCTCAGCCTCCACCAAG GGCCCATCGTCTTCCCTCCCTGGCACCTCTCTCCA AGAGCACTCTGGGGGCACAGCGGCCCTGGGCT GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA CGGTGCTGTGAACCTCAGGGGCCCTGACCAAGC GCGTGACACCTTCCCGGTGTCTACAGTCTCTC AGGACTCTACTCCTCAGCAGCGTGGTGACCGT GCCCCCAGCAGCTTGGGCAACCCAGACCTACAT CTGCAACGTGAATCAAGCCCAAGCAACACCAA GGTGACAAAGAAAGTTGAGCCCAATCTTGTGA CAAACCTACACATGCCACCGTGCCAGCACCC TGAACTCCTGGGGGACCGTCAGTCTTCTCTTC CCCCCAAACCCAAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTACATGCGTGGTGGTGGAC GTGAGCCACGAAGACCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCC AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG CACGTACCGTTGTGTACGCTCTCACCGTCTCTG CACCAGGACTGGCTGAATGGCAAGGAGTACAA GTGCAAGGTCTCCAAACAAGCCCTCCCAGCCCC CATCGAGAAACCAATCTCCAAGCCAAAGGGCA GCCCCGAGAACCAAGGTGTACACCTGCCCTCC ATCCCGGAGGAGATGACCAAGAACCAAGGTCA GCCTGACCTGCCCTGGTCAAGGCTTCTATCCCA GCGACATCGCCGTGGAGTGGGAGAGCAATGGG CAGCCGAGAACAACTACAGACCAACGCTCCC GTGCTGGACTCCGACGGCTCTTCTTCTCTATA GCAAGCTCACCGTGGACAAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACCACTACACGCAAGAAAGC CTCTCCCTGTCTCCGGGTAAA</p>	<p>SEQ ID NO: 2166</p>
			<p>SEQ ID NO: 2166</p>
		<p>QSVLTQPPSASGTPGQRVTISCSGSSNIGSQTVNW YQHLPGTAPKLLIYTNNQRPSGVPDFRFSGSKSGTS ASLAISGLQSEDEADYFCAITFDESLOQPVFVGSGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD</p>	<p>QMQVVQSGAEVKKPGASVKVSKKASGYTFTGYY MHWVRAQAPGQGLEWMGWINPNSSGNTNYAQKFQ GRVTMTRDTSISTAYMELSRLLSDDTA VYYCARG GDYVWGTYPHYYYGMDVWVGQGTITVTVSSAST</p>

			FYPGAVTVAWKADSSPVKAGVETTTTPSKQSNKKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS		
		IPS:361418	2C2.005.003	NA	

		GTGAGCCACGAAGACCCCTGAGGTCAAGTTC AAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCC AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG CACGTACCGTTGTGTACGCGTCCACCGTCCCTG CACCAGGACTGGCTGAATGGCAAGGAGTACAA GTGCAAGGTCTCCAAACAAAGCCCTCCCAGCCCC CATCGAGAAACCATCTCCAAAGCCAAAGGGCA GCCCCGAGAACACAGGTGTACACCCTGCCCCC ATCCCGGAGGAGATGACCAAGAACACAGGTCA GCCTGACCTGCCCTGGTCAAGGCTTCTATCCCA GCGACATCGCCGTGGAGTGGGAGAGCAATGGG CAGCCGAGAACAACTACAAGACCACGCTCCC GTGCTGGACTCCGACGGCTCCTTCTTCTCTATA GCAAGCTACCGTGGACAAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAAACCACTACACGCAGAAAGAGC CTCTCCCTGTCTCCGGGTAAA SEQ ID NO: 2167
	SEQ ID NO: 2010 QSVLTQPPSASGTPGQRVITISCSGSSNIGSNYVNW YQHLPGTAPKLLIYTNNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDESLSGPVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGA VTVAWKADSSPVKAGVETTTTPSKQSNKYY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS	QMQVVQSGAEVKKPGASVKVSKASGYTFTGYY MHWVRQAPQGQGLEWMGWNPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLSDDTAVYYCARG GDYVWGTYPHYYYGMDVWVGQGTITVTVSSAST KGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPV VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDITLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTKSKAKGPQREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LSDSGSFELYSKLTVDKSRWQQGNVVFSCSVMHEA LHNHYTQKLSLSLSPGK SEQ ID NO: 597
	AA	SEQ ID NO: 440

IPs:361424	2C2.005.004	NA	<p>CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGGTCACCATCTCTTGT CTGGAAGTAGCTCCAAACATCGGAAGTAATTATG TAAACTGGTACCAGCACCTCCCAGGAACGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTCTGTG CAACATTTCGATGAAAGCCTGC AAGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCCTAGGTC AGCCCAAGGTGCCCCCTCGGTCACTCTGTTCCTC GCCCCTCCTGAGGAGCTTCAAGCCAAACAAGGC CACACTGGTGTGTCTCATAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCTGGAAAGGCAGATAG CAGCCCCGTC AAGCGGGAGTGGAGACCAACCAC ACCTTCCAAACAAGCAACAACAAGTACGGCGC CAGCAGCTATCTGAGCCTGACGCCCTGAGCAGTG GAAGTCCCACAGAAAGCTACAGTGCAGGTCTAC GCATGAAGGGAGCACCCGTGGAGAAAGACAGTGG CCCCACAGATGTTCA</p>	<p>CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAAGTCTCCTGC AAGCTTCCGGATACACCTTCAACCGGCTACTAT ATGCATTGGTGCAGACGGCCCTGGACAAGGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGGCACAACTATGCACAGAAATTTTCAGGGC AGGTCAACATGACAGGGACACGTCCATCAGT ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT GACGACACGGCGTGTATTACTGTGCGAGAGGG GGGGATTACGTTGGGGGACTTATCGGCCCTCAC TACTACTACGATGGACGTCTGGGGCCCAAGG ACCACGGTCAACGCTCTCCTCAGCCTCCACCAAG GGCCCATCGTCTTCCCCCTGGCACCCCTCCCTCCA AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA CGGTGCTGTGAACTCAGGGGCCCTGACCAAGC GCGTGCACACCTTCCCGGTGTCTACAGTCCCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT GCCCCCAGCAGCTTGGGCACCCAGACCTACAT CTGCAACGTGAATCAAGCCCAAGCAACACCAA GGTGGACAAGAAAGTTGAGCCCCAATCTTGTGA CAAACCTCACACATGCCCAACCGTGGCCAGCAC TGAACTCCTGGGGGACCGTCAGTCTTCTCTTC CCCCAAAACCAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTACATGCGTGGTGGTGGAC GTGAGCCACGAAGACCTGAGGTCAAGTTC AAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCC AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG CACGTACCGTTGTGTCAGCGTCTCACCGTCTG CACCAGGACTGGCTGAATGGCAAGGAGTACAA GTGCAAGGTCTCCAAACAAGCCCTCCCAGCCCC CATCGAGAAACCATCTCTCCAAGCCAAAGGGCA GCCCCGAGAACCAAGGTGTACACCTGCCCCC ATCCCGGAGGAGATGACCAAGAACCAAGGTCA GCCTGACCTGCCTGGTCAAGGCTTCTATCCCCA GCGACATCGCCGTGGAGTGGGAGAGCAATGGG</p>
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			<p>CAGCCGAGAACAACTACAAGACCACGCCTCCC GTGCTGACTCCGACGGCTCCTTCTTCTCTATA GCAAGCTCACCGTGGACAAAGAGCAGGTGGCAG CAGGGAAACGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACTACACGCAAGAGAGC CTCTCCCTGTCTCCGGTAAA</p> <p>SEQ ID NO: 2168</p> <p>QMQVVQSGAEVKKPGASVKVSKASGYTFTGYY MHWVRAQPGQGLEWGMWINPNSGGTNYAQKFQ GRVTMRDTSISTAYMELSRLSDDTA VYYCARG GDYVWGTYPHYYYGMDVWVGQGTTVTVSSAST KGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVVDGVEVHNAKTKPCE EQYGSTYRCVSLTVLHQDWLNGKEYKCKVSNK ALPAIEKTIKAKGQPREPQVYVTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LDSGSEFLYSKLTVDKSRWQQGNVVFSCSVMHEA LHNHYTQKLSLSLSPGK</p> <p>SEQ ID NO: 598</p> <p>CAGATGCAGGTGGTGCGAGTCTGGGGCTGAGGTG AAGAAGCTGGGGCTCAGTGAAAGTCTCCTGC AAGGCTCCGGATACACCTTCAACCGGCTACTAT ATGCATTGGTGCGACAGGCCCTGGACAAGGG CTTGAGTGGATGGGATGGATCAACCCTAACAGT GGTGGCACAACTATGCACAGAAATTTTCAGGGC AGGTCAACATGACAGGACACGTCATCAGT ACAGCTACATGAGCTGAGCAGGCTGAGGTCT GACGACACGGCGTGATTAATGTGCGAGAGGG GGGATTACGTTTGGGGGACTTATCGGCCTCAC TACTACTACGATGGACGTCTGGGGCCAAAGG ACCAAGGTCAACGTCTCCTCAGCCTCCACCAAG GGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCA AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT</p>
			<p>SEQ ID NO: 2011</p> <p>QSVLTQPPSASGTPGQRVTISCSGSSNIGSNYVNW YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDESLOGPVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTTPSKQSNKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS</p> <p>AA</p> <p>SEQ ID NO: 441</p> <p>CAGTCTGTGCTGACTCAGCCACCTCAGCGTCTG GGACCCCGGCGCAGAGGTACCACTCTTGT CTGGAAGTAGCTCCAAACATCGGAAGTCAAACTG TAAACTGGTACCAACACCTCCCAGGAACGGGCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGACCTCAGCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTCTGTG CAACATTGATGACAGCCTGAATGGTCCGGTAT TCGGCGGAGGACCAAGCTGACCGTCTAGGTC AGCCCCAAGCTGCCCCCTCGGTCACTCTGTTCCT GCCCTCCTCTGAGGAGCTTCAAGCCCAACAAGGC CACACTGGTGTGTCTCATAAAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCTGGAAGGCAGATAG</p>
		2C2.005.005	NA
		IPS:361430	

	<div>CAGCCCCGTCAAGCGGGAGTGGAGACCACCAC ACCCTCCAAACAAGCAACAACAAGTACGCGGC CAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG GAAGTCCACAGAAAGCTACAGCTGCCAGGTCAC GCATGAAGGGAGCACCGTGGAGAAAGACAGTGG CCCCTACAGAATGTTCA</div>	<div>SEQ ID NO: 2012</div> <div>QSVLTQPPSASGTPGQRVTISCSGSSNIGSQTVNW YQHLPGTAPKLLIYTNNQRPSPGVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDDSLNGPVFVGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTPSKQSNKYY AASSYLSLTPEQWKSHRSYSQCVTHEGSTVEKTV APTECS</div>
	<div>GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA CGGTGTCGTGAACTCAGGGCGCCCTGACCAGCG GCGTGCACACCTTCCCGGTGTCTACAGTCCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT GCCCTCCAGCAGCTTGGGCAACCCAGACCTACAT CTGCAACGTGAATCACAAGCCCAGCAACACCAA GGTGACAAGAAAGTTGAGCCCAAAATCTTGTGA CAAAACTCACACATGCCACACCGTGCCCAAGCAC TGAACCTCTGGGGGACCGTCAGTCTTCTCTCTTC CCCCAAAACCCAAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTACATGCGTGGTGGTGGAC GTGAGCCACGAAGACCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCC AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG CACGTACCGTTGTGTACGCGTCTCACCGTCTCTG CACCAGGACTGGCTGAATGGCAAGGAGTACAA GTGCAAGGTCTCCAACAAGCCCTCCCAGCCCC CATCGAGAAAACCATCTCCAAGCCAAGGGCA GCCCCGAGAACCAAGGTGTACACCTGCCCCC ATCCCGGAGGAGATGACCAAGAACCAAGGTCA GCCTGACCTGCCGTGGTCAAAGGCTTCTATCCCCA GCGACATCGCCGTGGAGTGGGAGAGCAATGGG CAGCCGGAGACAACACTACAAGACCACGCTCCC GTGCTGGACTCCGACGGCTCTTCTTCTCTATA GCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACCACTACACGCAGAAAGAGC CTCTCCCTGTCTCCGGGTAAA</div> <div>SEQ ID NO: 2169</div> <div>QMQVVQSGAEVKKPGASVKVSKASGYTFTGYY MHWVRQAPGQGLEWMGWNPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLSDDTAVYYCARG GDYVWGTYPHYYYGMDVWVGQGTITVTVSSAST KGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPS SSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTH</div>	

				<p>TCPPCPAPELLGGPSVFLFPPKPKD TLMISRTPEVT CVVVDVSHEDPEVKFNWYVVDGVEVHNATKPCPE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LDSGSEFLYSKLTVDKSRWQQGNVVFSCSVMHEA LHNHYTQKSLSLSPGK</p>
				<p>SEQ ID NO: 442</p> <p>CAGTCTGTGCTGACTAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGGTCACCATCTCTTGT CTGGAAGTAGCTCCAAACATCGGAAGTAATTATG TAAACTGGTACCAAGCAACCTCCCAAGGAACGGCCC CCAAACTCCTCATCTATACTATAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTCTGTG CAACATTTCGATGACAGCCTGAATGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCTCAGGTC AGCCCAAGGTGCCCCCTCGGTCACTCTGTTCCTC GCCCCTCTGAGGAGCTTCAAGCCCAACAAGGC CACACTGGTGTGTCTCATAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCCTGGAAAGGCAGATAG CAGCCCCGTCAAGCGGGAGTGGAAGCACCAACAC ACCTCCCAACAAGCAACAACAAGTACGCGGC CAGCAGCTATCTGAGCCTGACGCTGAGCAGTG GAAGTCCCAAGAAAGCTACAGCTGCCAGGTAC GCATGAAGGGAGCACCCGTGGAGAGACAGTGG CCCCACAGATGTTCA</p>
				<p>SEQ ID NO: 599</p> <p>CAGATGACAGTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCTGGGGCTCAGTGAAGTCTCCTGC AAGGCTTCGGATACACCTTCAACCGGCTACTAT ATGCAITGGGTGCACAGGCCCTGGACAAGGG CTTGAGTGGATGGGATGGATCAACCTTAACAGT GGTGGCACAACTATGCACAGAAAGTTTCAGGGC AGGTCAACATGACAGGACACGTCCATCAGT ACAGCCTACATGAGGCTGAGCAGGCTGAGGTCT GACGACACGGCGTGTATTACTGTGCGAGAGGG GGGATTACGTTTGGGGGACTTATCGGCCTCAC TACTACTACGATGACGCTCTGGGGCCAAAGG ACCAAGGTCAACGCTCTCCTCAGCCTCCACCAAG GGCCATCGGTCTCCCCCTGGCACCCCTCCCTCCA AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA CGGTGTCGTGGAACCTCAGCGGCCCTGACCAAGC GCGTGACACACCTTCCCCGGCTGTCTACAGTCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT GCCCCCAGCAGCTTGGGCACCCAGACCTACAT CTGCAACGTGAATCAAGGCCAGCAACACCAA GGTGGACAAGAAAGTTGAGCCCAATCTTGTGA CAAACCTCACATGCCACCCGTGCCAGCAC TGAACTCCTGGGGGACCGTCACTTCTCTCTC CCCCAAAACCAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTACATGCGTGGTGGTGGAC GTGAGCCACGAAGACCCCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCC AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG</p>

			<p> CACGTACCGTTGTGTCAGCGTCTCCACCGTCTCTG CACCAGGACTGGCTGAATGGCAAGGAGTACAA GTGCAAGGTCTCCAAACAAAGCCCTCCCAGCCCC CATCGAGAAACCATCTCCAAGCCAAAGGCA GCCCCGAGAACACAGGTGTACACCTGCCCCC ATCCCGGAGGAGATGACCAAGAACACAGGTCA GCCTGACCTGCCCTGGTCAAGGCTTCTATCCCA GCGACATCGCCGTGGAGTGGGAGAGCAATGGG CAGCCGAGAACAACTACAAGACCACGCTCCC GTGCTGACTCCGACGGCTCTTCTTCTCTATA GCAAGCTACCGTGGACAAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACTACTACACGAGAAAGAGC CTCTCCCTGTCTCCGGGTAA </p>
			<p> SEQ ID NO: 2013 QSVLTQPPSASGTPGQRVTISCSGSSNIGSNYVNW YQHLPGTAPKLLIYTNNQRPSGVPDFSGSKSGTS ASLAISGLQSEDEADYFCAIFDDSLNGPVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTTPSKQSNKYY AASSYLSLTPEQWKSHRYSYSCQVTHEGSTVEKTV APTECS </p>
	AA		<p> SEQ ID NO: 2170 QMQVVQSGAEVKKPGASVKVCKASGYTFTGYY MHWVRAQPGQGLEWGMWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLSDDTA VYYCARG GDYVWGTYPHYYYGMDVWVGQGTITVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LSDGGSFELYSKLTVDKSRWQQGNVVFSCVMHEA LHNHYTQKLSLSLSPGK </p>
			<p> SEQ ID NO: 443 CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGTCACCATCTCTTGT CTGGAAGTAGCTCCAACATCGGAAGTAATACTG TAAACTGGTACCGACACCTCCCAAGGAACGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA </p>
IPS:361442	2C2.005.007	NA	<p> SEQ ID NO: 600 CAGATGACGTTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCTGGGGCTCAGTGAAGTCTCCTGC AAGCTTCCGGATACACCTTCAACCGGCTACTAT ATGCATTGGGTGCGACAGGCCCTGGACAAAGG CTTGAGTGGATGGGATGGATCAACCCTAACAGT GGTGGCACAACTATGCACAGAAAGTTTCAGGGC </p>

GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGCTGATTATTCTGTG CAACATTCGATGAAAGCCTGAATGGTCCGGTAT TCGGCGGAGGGACCAGCTGACCGTCTCCTAGGTC AGCCCAAGGTGCCCCCTCGGTCACTCTGTTCCTC GCCCCTCTCTGAGGAGCTTCAAGCCAAACAAGGC CACACTGGTGTCTCATAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCTGGAAGGCAGATAG CAGCCCCGTCAAGCGGGAGTGGAGACCACCAC ACCCCTCCAAACAAGCAACAACAAGTACGCGGC CAGCAGCTATCTGAGCCTGACGCTGAGCAGTG GAACTCCACAGAAAGCTACAGCTGCCAGGTAC GCATGAAGGGAGCACCGTGGAGAAAGACAGTGG CCCCACAGATGTTCA	AGGGTCAACCATGACCAGGGACACGTCCATCAGT ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT GACGACACGGCGGTGATTACTGTGCGAGAGGG GGGGATTACGTTTGGGGGACTTATCGGCCCTCAC TACTACTACGGTATGGACGTCTGGGGCCCAAGG ACCACGGTCAACGCTCTCCCTCAGCCTCCACCAAG GGCCCATCGGTCTTCCCCCTGGCACCTCTCTCCA AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA CGGTGTCTGGAACCTCAGGGGCCCTGACCAAGCG GCGTGACACCTTCCCCGGGTGTCTACAGTCTCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT GCCCCCAGCAGCTTGGGCACCCAGACCTACAT CTGCAACGTGAATCAAGCCACAGCAACACCAA GGTGGACAAGAAAGTTGAGCCCCAATCTTGTGA CAAACCTCACATGCCCCACCGTGCCACGACC TGAACTCTGGGGGACCGTCAGTCTTCTCTCTC CCCCAAACCCAAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTACATGCGTGGTGGTGAC GTGAGCCACGAAGACCTGAGGTCAAGTTC AAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCC AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG CACGTACCGTTGTGTACGCTCTCACCGTCTCTG CACCAGGACTGGCTGAATGGCAAGGAGTACAA GTGCAAGGTCTCCAAACAAGCCCTCCCAGCCCC CATCGAAGAAACCATCTCCAAGCCAAAGGGCA GCCCCGAGAACACAGGTGTACCCCTGCCCCC ATCCCGGGAGGAGATGACCAAGAACAGGTCA GCCTGACCTGCCCTGGTCAAGGCTTCTATCCCCA GCGACATCGCCGTGGAGTGGGAGAGCAATGGG CAGCCGGAGAACAACTACAAGACCACGCTCCC GTGCTGGACTCCGACGGCTCTTCTTCTCTATA GCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACCACTACACGCAAGAGAGC CTCTCCCTGTCTCCGGGTAA
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		SEQ ID NO: 2014	<p>QSVLTQPPSASGTPGQRVITISCSGSSNIGSNTVNW YQHLPGTAPKLLIYTNNQRPSPVDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDESLNGPVFGGGK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTTPSKQSNKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS</p>	SEQ ID NO: 2171	<p>QMQVVQSGAEVKKPGASVKVSKASGYTFTGY MHWVVRQAPQGQGLEWGMWINPNSGGTNYAQKFQ GRVTMRDTSISTAYMELSRLSDDTA VYYCARG GDYVWGTYPHYYYGMDVWVGQGTTVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSLTVLHQDWLNGKEYKCKVSNK ALPAIEKTIKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LDSGDSFELYSKLTVDKSRWQQGNVVFSCVMHEA LHNHYTQKLSLSLSPGK</p>
		SEQ ID NO: 444	<p>CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCGGCGAGAGGTCACCATCTCTTGTT CTGGAAGTAGCTCCAAACATCGGAAGTAATACTG TAAACTGGTACAGCAACCTCCCAAGGAACGGGCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTCTGTG CAACATTCGATGACAGCCTGCAAGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCTAGGTC AGCCCAGGCTGCCCCCTCGGTCACTCTGTTCCT GCCCCTCTCTGAGGAGCTTCAAGCCCAACAAGGC CACACTGGTGTGTCTCATAAAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCTGGAAAGGCAGATAG CAGCCCCGTCAAGCGGGAGTGGAGACCAACAC ACCTCCAAACAAGCAACAACAAGTACGGGC CAGCAGCTATCTGAGCCTGACGCTGAGCAGTG GAAGTCCACAGAAAGCTACAGCTGCCAGGTAC GCATGAAGGGAGCACCGTGGAGAGACAGTGG CCCCACAGATGTTCA</p>	SEQ ID NO: 601	<p>CAGATCAGTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAGTCTCCTGC AAGGCTCCGGATACACCTTCAACCGGCTACTAT ATGATTGGTGCAGACGGCCCTGGACAAGGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGGCACAACTATGCACAGAAAGTTTCAGGGC AGGTCAACATGACACGGGACACGTCCATCAGT ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT GACGACACGGCGGTGATTACTGTGCGAGAGGG GGGATTACGTTTGGGGGACTTATCGGCCTCAC TACTACTACGATGGACGTCTGGGGCCAAAGG ACCAAGGTCAACGCTCTCCTCAGCCTCCACCAAG GGCCCATCGGTCTTCCCCCTGGCACCTCCTCCA AGAGCACCTCTGGGGCACAGCGGCCCTGGGT GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA CGGTGCTGTGAACCTCAGGCGCCCTGACCAAGC GCGTGACACCTTCCCCGGCTGTCTACAGTCTC AGGACTCTACTCCCTCAGCAGCGGTGGTACCGT GCCCCCAGCAGCTTGGGCACCCAGACCTACAT CTGCAACGTGAATCAACAAGCCACGCAACACCAA</p>

		GGTGACAAAGAAAGTTGAGCCCAATCTTGTGA CAAACCTACACATGCCACCGTGCCAGCACC TGAACCTCTGGGGGACCGTCAGTCTCCTCTC CCCCAAACCCAAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTCACATGCGTGGTGGTGAC GTGAGCCACGAAGACCCTGAGGTCAAGTTC AAC TGGTACGTGGACGGCGTGAGGAGCAGTACGGCAG AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG CACGTACCGTTGTGTCAGCGTCTCACCGTCTCTG CACCAGGACTGGCTGAATGGCAAGGAGTACAA GTGCAAGGTCTCCAAACAAAGCCCTCCCAGCCCC CATCGAGAAACCATCTCCAAGCCAAAGGCCA GCCCCGAGAACACAGGTGTACACCTGCCCCC ATCCCGGAGGAGATGACCAAGAACACAGGTCA GCCTGACCTGCCCTGGTCAAGGCTTCTATCCCCA GCGACATCGCCGTGGAGTGGGAGAGCAATGGG CAGCCGAGAACAACTACAAAGACCACGCTCCC GTGCTGGACTCCGACGGCTCTTCTTCTCTATA GCAAGCTCACCGTGAGCAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAAACCACTACACGCAGAAAGAGC CTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 2015	SEQ ID NO: 2172
	QSVLTQPPSASGTPGQQRVTISCSGSSNIGSNTVNW YQHLPGTAPKLLIYTNNQRPSGVPDFSGSKSGTS ASLAISGLQSEDEADYFCATFDDSLQGPVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTTPSKQSNK AASSYLSTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS	QMQVVQSGAEVKKPGASVKVSKASGYTFTGY MHWVRQAPGQGLEWMGWNPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLSDDTAVYYCARG GDYVWGTYPHYYYGMDVWGQGTITVTVSSAST KGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPPELLGGPSVFLFPPKPKDITLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTKSKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPV
	AA	

				<p>LDSDGSFELYSKLTVDKSRWQQGNVFCSCVMHEA LHNHYTQKSLSLSPGK</p>
				<p>SEQ ID NO: 445</p> <p>CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGGTCACCATCTCTTGT CTGGAAGTAGCTCCAACATCGGAAGTAATACTG TAAACTGGTACCAAGCAACCTCCCAAGGAACGGCCC CCAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTCTGTG CAACATTTCGATGACAGCCTGAGTGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCTCAGGTC AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTC GCCCCTCTGAGGAGCTTCAAGCCCAACAAGGC CACACTGGTGTGTCTCATAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCTGGGAAGGCAGATAG CAGCCCCGTCAAGCGGGAGTGGAGACCAACAC ACCTCCAAACAAGCAACAACAAGTACGGGGC CAGCAGCTATCTGAGCCTGACGCTGAGCAGTG GAAGTCCACAGAAAGCTACAGTGCCAGGTCA GCATGAAGGGAGCACCGTGGAGAGACAGTGG CCCCACAGATGTTCA</p>
				<p>SEQ ID NO: 602</p> <p>CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCTGGGGCTCAGTGAAGTCTCCTGC AAGGCTCCGGATACACCTTCAACCGGCTACTAT ATGCATTGGTGCAGACGGCCCTGGACAAGGG CTTGAGTGGATGGGATGGATCAACCTTAACAGT GGTGGCACAACTATGCACAGAAAGTTTCAGGGC AGGTCAACATGACACAGGACACGTCCATCAGT ACAGCCTACATGAGGTGAGCAGGCTGAGGTCT GACGACACGGCGTGTATTACTGTGCGAGAGGG GGGATTACGTTTGGGGACTTATCGGCCCTCAC TACTACTACGATGACGCTCTGGGGCCAAAGG ACCAGGTCAACGCTCTCCTCAGCCTCCACCAAG GGCCCATCGGTCTTCCCCCTGGCACCCCTCCCA AGAGACCTCTGGGGGCACAGCGGCCCTGGGCT GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA CGGTGCTGTGGAACCTCAGGGCCCTGACCAAGC GCGTGACACCTTCCCCGGCTGTCTACAGTCCCTC AGGACTTACTCCCTCAGCAGCGTGGTGACCGT GCCCCTCCAGCAGCTTGGGCACCCAGACCTACAT CTGCAACGTGAATCAAGGCCAGCAACACCAA GGTGGACAAGAAAGTTGAGCCCAATCTTGTGA CAAACCTCACATGCCCCACCGTGGCCAGCAC TGAACTCCTGGGGGACCGTCACTTCTCTTC CCCCAAAACCAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTACATGCGTGGTGGTGGAC GTGAGCCACGAAGACCCCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCC AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG CACGTACCGTGTGTGACGCTCTCACCGTCTG CACCAGGACTGGTGAATGGCAAGGAGTACAA GTGCAAGGTCTCCAACAAGCCCTCCCAAGCCCC CATCGAGAAACCATCTCCAAGGCCAAAGGGCA GCCCCGAGAACCAACAGGTGTACACCCCTGCC</p>

			<p>ATCCCGGAGGAGATGACCAAGAACACAGGTCA GCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA GCGACATCGCCGTGGAGTGGGAGAGCAATGGG CAGCCGAGAACAACTACAGACACGCTCTCC GTGCTGACTCCGACGGCTCTTCTTCTCTATA GCAAGCTACCGTGGACAAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACTACACGCAAGAGAGC CTCTCCCTGTCTCCGGGTAA</p> <p>SEQ ID NO: 2173</p>	
			<p>QMQVVQSGAEVKKPGASVKVCKASGYTFTGY MHWVRQAPGQGLEWMGWNPNSGGTNYAQKFQ GRVTMRDTSISTAYMELSRLSDDTAVYYCARG GDYVWGTYPHYYYGMDVWVGQGTITVTVSSAST KGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVVDGVEVHNAKTKPCE EQYGSTYRCVSLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTSKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LSDSGSFELYSKLTVDKSRWQQGNVVFSCVMHEA LHNHYTQKLSLSLSPGK</p> <p>SEQ ID NO: 603</p>	
	AA		<p>QSVLTQPPSASGTPGQRVTISCSGSSNIGSNTVNW YQHLPGTAPKLLIYTNNQRPSGVPDFRFSKSGTS ASLAISGLQSEDEADYFCATFDDSLSGPVFGGGTK LTVLGGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTTPSKQSNKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS</p> <p>SEQ ID NO: 446</p>	
	NA	2C2.005.010	<p>CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCCGGGCAGAGGTCACCACTCTTGT CTGGAAGTAGCTCCAAACATCGGAAGTAATACTG TAAACTGGTACCGACACCTCCCAGGAACGGCCC CCAAACTCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTCTGTG CAACATTTCGATGACAGCCTGAATGCTCCGGTAT TCGGGGGAGGGACCAAGCTGACCGTCTCAGGTC AGCCCCAAGGCTGCCCCCTCGGTCACTCTGTTC</p> <p>!PS:361460</p>	

	<p>GCCCTCCTCTGAGGAGCTTCAAGCCAAACAAGGC CACACTGGTGTCTCATAAAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCTGGAAGGCAGATAG CAGCCCCGTCAAGGCGGGAGTGGAGACCACCA ACCTCCAAACAAGCAACAACAAGTACGCGGC CAGCAGCTATCTGAGCCTGACGCCCTGAGCAGTG GAAGTCCACAGAAAGCTACAGCTGCCAGGTCAC GCATGAAGGAGCACCGTGGAGAAAGACAGTGG CCCCTACAGATGTTCA</p>	<p>SEQ ID NO: 2017</p> <p>QSVLTQPPSASGTPGQRVTISCSGSSNIGSNTVNW YQHLPGTAPKLLIYTNNQRPSGVPDFRFSKSGTS ASLAISGLQSEDEADYFCATFDDSLNAPVFGGGTK LTVLGOPKAAPSVTLFPPSSEELQANKATLVCLISD</p>	
	<p>ACCACGGTCAACGCTCTCCTCAGCCTCCACCAAG GGCCCATCGGTCTTCCCTTGGCACCCTCCTCTCCA AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA CGGTGCTGTGGAACCTCAGGGGCCCTGACCAAGC GCGTGACACCTTCCCGGCTGTCTACAGTCCCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT GCCCTCCAGCAGCTTGGGCAACCCAGACCTACAT CTGCAACGTGAATCACAGCCCAAGCAACACCAA GGTGACAAGAAAGTTGAGCCCAATCTTGTGA CAAAACTCACACATGCCACCGTGCCCAAGCACC TGAACTCCTGGGGGACCGTCAGTCTTCTCTCTTC CCCCAAACCCAAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTACATGCGTGGTGGTGGAC GTGAGCCACGAAGACCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCC AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG CACGTACCGTTGTGTCAAGCTCCTCACCGTCTCTG CACCAGGACTGGCTGAATGGCAAGGAGTACAA GTCAAGGTCTCCAACAAGCCCTCCCAGCCCC CATCGAGAAAACCATCTCCAAGCCAAAGGGCA GCCCGAGAACCAAGGTGTACACCTGCCCTCC ATCCCGGAGGAGATGACCAAGAACCAAGGTCA GCCTGACCTGCCCTGGTCAAGGCTTCTATCCCA GCGACATCGCCGTGGAGTGGGAGAGCAATGGG CAGCCGGAGAACAACTACAAGACCAACGCTCCC GTGCTGACTCCGACGGCTCCTTCTTCTCTATA GCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACCACTACACGCAGAGAAGC CTCTCCCTGTCTCCGGGTAAA</p>	<p>SEQ ID NO: 2174</p> <p>QMQVVQSGAEVKKPGASVKVSKASGYTFTGYY MHWVRAQAPQGQGLEWMGWNPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLSDDTAVYYCARG GDYVWGTYPHYYYGMDVWVGQGITTVTVSSAST</p>	AA

			FYPGAVTVAWKADSSPVKAGVETTTTPSKQSNKKY AASSYLSLTPEQWKSRSYSCQVTHEGSTVEKTV APTECS	KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAIEKTSKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LDSGGSFFLYSKLTVDKSRWQQGNVVFSCSVMHEA LHNHYTQKSLSLSPGK
			SEQ ID NO: 447 CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT CTGGAAGTAGCTCCAAACATCGGAAGTAATACTG TAAACTGGTACCAAGCACCTCCAGGAACGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTCTGTG CAACATTCTGATAGCAGCCTGAATGGTCCGGTAT TCGGCGGAGGACCAAGCTGACCGTCTCAGGTG AGCCCCAAGGCTGCCCTCGGTCACTCTGTTCCC GCCCTCCTCTGAGGAGCTTCAAGGCCAACAAAGGC CACACTGGTGTGTCTCATAAAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCTGGAAGGCAGATAG CAGCCCCGTCAAGGCGGGAGTGGAGACCAACCAC ACCCCTCCAAACAAGCAACAACAAGTACGCGGC CAGCAGCTATCTGAGCCTGACGCTGAGCAGTG GAAGTCCACAGAAAGCTACAGCTGCCAGGTCA GCATGAAGGAGCACCGTGGAGAAAGACAGTGG CCCCACAGAAATGTTCA	SEQ ID NO: 604 CAGATGCAGGTGGTGCACTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCGGATACACCTTCAACCGGCTACTAT ATGCATTGGTGCAGACAGGCCCTGGACAAGGG CTTGAGTGGATGGGATGGATCAACCTTAACAGT GGTGGCACAACTATGCACAGAAAGTTTCAGGGC AGGTCAACATGACCAAGGACACGTCCATCAGT ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT GACGACACGGCGTGTATTACTGTGCGAGAGGG GGGGATTACGTTTGGGGGACTTATCGGCCTCAC TACTACTACGGTATGGACGTCTGGGGCCAAAGG ACCACGGTCAACGCTCTCCTCAGCCTCCACCAAG GGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCA AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA CGGTGCTGTGGAACCTCAGGCGCCCTGACACGCG GCGTGACACACTTCCCGGCTGTCTACAGTCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT CTGCAACGTGAATCAAGCCAGCCAGCAACACCAA GGTGGACAAGAAAGTTGAGCCCCAAATCTTGTGA CAAAACTCACACATGCCACCGTGGCCAGCACCC TGAACTCCTGGGGGACCGTCAAGTCTTCTCTTC CCCCCAAAACCCAAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTCAATCGCTGGTGGTGGAC
IPS:361466	2C2.005.011	NA		

				GTGAGCCACGAAGACCCCTGAGGTCAAGTTC AAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCC AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG CACGTACCGTTGTGTACGCGTCTCACCGTCTCTG CACCAGGACTGGCTGAATGGCAAGGAGTACAA GTGCAAGGTCTCCAAACAAAGCCCTCCCAGCCCC CATCGAGAAACCATCTCCAAAGCCAAAGGGCA GCCCCGAGAACACAGGTGTACACCTGCCCTCC ATCCCGGAGGAGATGACCAAGACACAGGTCA GCCTGACCTGCCCTGGTCAAGGCTTCTATCCCCA GCGACATCGCCGTGGAGTGGGAGAGCAATGGG CAGCCGAGAACAACTACAAAGACACGCTCCCC GTGCTGGACTCCGACGGCTCTTCTTCTCTATA GCAAGCTACCGTGGACAAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAAACCACTACACGCAAGAGAGC CTCTCCCTGTCTCCGGTAAA
				SEQ ID NO: 2018
				SEQ ID NO: 2175
				QMQVVQSGAEVKKPGASVKVCKASGYTFTGYY MHWVRQAPQGQLEWGMWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLSDDTAVYYCARG GDYVWGTYPHYYYGMDVWVGQGTITVTVSSAST KGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSLTVLHQDWLNGKEYKCKVSNK ALPAIEKTIKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LDSGGSFELYSKLTVDKSRWQQGNVVFSCSVMHEA LHNHYTQKLSLSLSPGK
				SEQ ID NO: 605
				CAGATGCAGTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGCGCTCAGTGAAGGTCTCCTGC AAGGCTTCCGGATACACCTTTCACCGGCTACTAT
				SEQ ID NO: 448
				QSVLTQPPSASGTPGQRVITISCGSSNIGSNTVNW YQHLPGTAPKLLIYTNNQRPSGVPDFRFSKSGTS ASLAISGLQSEDEADYFCATFDSSLNGPVFVG GTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGA VTVAWKADSSPVKAGVETTTTPSKQSNKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS
			AA	SEQ ID NO: 2018
				SEQ ID NO: 448
			NA	CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCCGGGCAGAGGTCACCATCTCTTGT CTGGAAGTAGCTCCAAACATCGGAAGTAATTATG

TAAACTGGTACCAGCACCTCCAGGAACGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTCTGTG CAACATTTCGATAGCAGCCTGAATGCTCCGGTAT TCGGGGAGGGACCAGCTGACCGTCTCCTAGGTC AGCCCAAGGTGCCCCCTCGGTCACTCTGTTCCTC GCCCCTCTGAGGAGCTTCAAGCCAAACAAGGC CACACTGGTGTCTCATAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCTGGAAAGGCAGATAG CAGCCCCGTCAAGCGGGAGTGGAGACCACCAC ACCTTCCAAACAAGCAACAACAAGTACGGGGC CAGCAGCTATCTGAGCCTGACGCCCTGAGCAGTG GAACTCCACAGAAAGCTACAGCTGCCAGGTCAC GCATGAAGGGAGCACCGTGGAGAAAGACAGTGG CCCCACAGATGTTCA	ATGCATTGGGTGCGACAGGCCCCCTGGACAAAGG CTTGAGTGGATGGATGGATCAACCTTAACAGT GGTGGCACAACTATGCACAGAAAGTTTCAGGGC AGGTCAACCATGACAGGACAGGACGTCATCAGT ACAGCCTACATGAGGCTGAGCAGGCTGAGGTCT GACGACACGGCGGTGATTACTGTGCGAGAGGG GGGATTACGTTGGGGGACTTATCGGCCCTCAC TACTACTACGATATGGACGCTGCGGGCCCAAGG ACCACGGTCAACGCTCTCCCTCAGCCTCCACCAAG GGCCCATCGGTCTCCCCCTGGCACCTCCCTCCA AGACACCTCTGGGGGCACAGCGGCCCTGGGCT GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA CGGTGCTGTGAACTCAGGGGCCCTGACCAAGCG GCGTGACACACCTTCCCCGGGTGCTACAGTCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT GCCCCCAGCAGCTTGGGCACCCAGACCTACAT CTGCAACGTGAATCAAGCCACGCAACACCAA GGTGGACAAGAAAGTTGAGCCCAATCTTGTGA CAAACTCACACATGCCACCGTGGCCAGCAC TGAACTCTGGGGGACCGTCAGTCTTCTCTTC CCCCAAAACCAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTACATGCCGTGGTGGTGAC GTGAGCCACGAAGCCCTGAGGTCAAGTTC AAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCC AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG CACGTACCGTTGTGTCAGCGTCTCACCGTCTCTG CACCAGGACTGGCTGAATGGCAAGGAGTACAA GTGCAAGGTCTCCAAACAAAGCCCTCCAGCCCC CATCGAGAAACCATCTCCAAGCCAAAGGGCA GCCCCGAGAACCAAGGTGTACACCTGCCCCC ATCCCGGAGGAGATGACCAAGAACCAAGGTCA GCCTGACCTGCCGTGGTCAAGGCTTCTATCCCC GCGACATCGCCGTGGAGTGGGAGAGCAATGGG CAGCCGGAGAACAACTACAGACCAACGCTCCC GTGCTGGACTCCGACGGCTCTTCTTCTCTATA GCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
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			<p>SEQ ID NO: 2019</p> <p>QSVLTQPPSASGTPGQRVTISCSGSSNIGSNYVNW YQHLPGTAPKLLIYTNNQRPSPGVPDFRSGSKSGTS ASLAISGLQSEDEADYFCAITFDSSLNAPVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTTPSKQSNKYY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS</p>	<p>CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACCACTACACGCAGAAAGAGC CTCTCCCTGTCTCCGGGTAAA</p>
AA			<p>SEQ ID NO: 2176</p> <p>QMQVVQSGAEVKKPGASVKVSKASGYTFTGYY MHWVRQAPGQGLEWGMWINPNSGGTNYAQKFQ GRVTMRDTSISTAYMELSRLSDDTA VYYCARG GDYVWGTYPHYYYGMDVWVGQGITTVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSLTVLHQDWLNGKEYKCKVSNK ALPAIEKTSISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LDSGDSFELYSKLTVDKSRWQQGNVVFSCSVMHEA LHNHYTQKLSLSLSPGK</p>	<p>SEQ ID NO: 606</p> <p>CAGATGACAGTGGTGCGAGTCTGGGGCTGAGGTG AAGAAGCTGGGGCTCAGTGAAGTCTCCTGC AAGGCTCCGGATACACCTTCAACCGGCTACTAT ATGCATTGGTGCGACAGGCCCTGGACAAGGG CTTGAGTGGATGGGATGGATCAACCTAACAGT GGTGGCACAACTATGCACAGAACTTTCAGGGC AGGTCAACCATGACAGGACACGTCATCAGT ACAGCCTACATGGAGCTGAGCAGCCTGAGGTCT GACGACACGGCGGTGATTAAGTGTGCGAGAGGG GGGATTACGTTTTCGGGACTTATCGGCCCTCACT ACTACTACGGTATGGACGTCTGGGGCCAAAGGA CCACGGTCAACGTCTCCTCAGCCTCCACCAAGG GCCCATCGGTCTCCCGCTGGACCCCTCCTCCAA GAGCACCTCTGGGGGACAGCGGCCCTGGGTG CCTGTCAAGGACTACTTCCCCGAACCGGTGAC GGTGTCTGGAACCTCAGGCGCCCTGACACGCGG CGTGACACACTTCCCGGCTGTCTCTACAGTCTCA</p>
	IPS:361478	2C2.005.013	<p>SEQ ID NO: 449</p> <p>CAGTCTGTGCTGACTAGCCACCTCAGCGTCTG GGACCCCGGGCAGAGGTACCACTCTCTGT CTGGAAGTAGCTCCAAACATCGGAAGTAATTATG TAAACTGGTACCAAGCACCTCCCAGGAACGGCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTCTGTG CAACATTGATAGCAGCCTGAATGCTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCTAGGTC AGCCCAAGGTGCCCCCTCGGTCACTCTGTTCCT GCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGC CACACTGGTGTCTCATAAAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCTGGAAGGCAGATAG CAGCCCCGTCAAGCGGGGAGTGGAGACCAACAC ACCTTCCAAACAAGCAACAACAAGTACGCGGC CAGCAGCTATCTGAGCCTGACCGCTGAGCAGTG</p>	<p>SEQ ID NO: 449</p> <p>CAGTCTGTGCTGACTAGCCACCTCAGCGTCTG GGACCCCGGGCAGAGGTACCACTCTCTGT CTGGAAGTAGCTCCAAACATCGGAAGTAATTATG TAAACTGGTACCAAGCACCTCCCAGGAACGGCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTCTGTG CAACATTGATAGCAGCCTGAATGCTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCTAGGTC AGCCCAAGGTGCCCCCTCGGTCACTCTGTTCCT GCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGC CACACTGGTGTCTCATAAAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCTGGAAGGCAGATAG CAGCCCCGTCAAGCGGGGAGTGGAGACCAACAC ACCTTCCAAACAAGCAACAACAAGTACGCGGC CAGCAGCTATCTGAGCCTGACCGCTGAGCAGTG</p>
			NA	

		<p>GAAGTCCACAGAAAGCTACAGCTGCCAGGTAC GCATGAAGGAGCACCGTGGAGAAAGACAGTGG CCCCACAGAAATGTTCA</p>	<p>GGACTCTACTCCCTCAGCAGCGTGGTGACCGTG CCCTCCAGCAGCTTGGGCACCCAGACCTACATC TGCAACGTGAATCACAAGCCACGCAACACCAAG GTGGACAAAGAAAGTTGAGCCCCAAATCTTGTGAC AAACTCACACATGCCACCGTGCCAGCACCT GAACTCTGGGGGACCGTCAGTCTTCTCTTCC CCCCAAACCAAGACACCCCTCATGATCTCCC GGACCCCTGAGGTACATGCGTGGTGGTGGACG TGAGCCACGAAGACCCCTGAGGTCAAAGTTCAACT GGTACGTGGACGGCGTGGAGGTGCATAATGCCA AGACAAAGCCGTGTGAGGAGCAGTACGGCAGC ACGTACCGTTGTGTGACGCTCTCACCGTCTGTC ACGAGGACTGGCTGAATGGCAAGGAGTACAAGT GCAAGGCTCCCAACAAGCCCTCCAGCCCCCA TCGAGAAAACCATCTCCAAAGCCAAAGGCGAGC CCCGAGAACACAGGTGTACCCCTGCCCCCAT CCCGGAGGAGATGACCAAGAACCCAGGTGAGC CTGACCTGCTGGTCAAAGGCTTCTATCCCAGC GACATCGCGTGGAGTGGGAGAGCAATGGGCA GCGGAGAACAACTACAAAGACCACGCTCCCGT GCTGGACTCCGACGGCTCTTCTTCTCTATAGC AAGCTCACCGTGGACAAGACAGGTGGCAGCA GGGGAACGTCTTCTCATGCTCCGTGATGCATGA GGCTCTGCACAACCACTACACGCAGAAAGACCT CTCCCTGTCTCCGGGTA</p>
	AA	<p>QSVLTQPPSASGTPGQRTISCSSSNIIGSNYVNW YQHLPGTAPKLLIYTNNQRPSGVPDFSGSKSGTS ASLAISGLQSEDEADYFCATFDSSLNAPVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTTPSKQSNKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS</p>	<p>SEQ ID NO: 2177</p> <p>QMQVVQSGAEVKKPGASVKVSKASGYTFTGY MHWVVRQAPQGQGLEWMGWNPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSSLRSDDTAVVYCARG GDYVFGTYRPHYYYGMDVWVGQGTTVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSS SLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKA</p>

				LPAPIEKTISKAKGQPREPQVYVTLPPSREEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK
				SEQ ID NO: 450 CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGGTCACCATCTCTTGT CTGGAAGTAGCTCCAACATCGGAAGTCAAACTG TAAACTGGTACCAAGCAACCTCCCAAGGAACGGCCC CCAAACCTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTCTGTG CAACATTTCGATGAAGCCTGAGTGGTCCGGTAT TCGGGGAGGGACCAGCTGACCGTCTTAGGTC AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCTC GCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGC CACACTGGTGTGCTCATAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCTGGGAAGGCAGATAG CAGCCCCGTCAAGCGGGAGTGGAGACCAACCAC ACCCTCCAAACAAGCAACAACAAGTACGGGGC CAGCAGCTATCTGAGCCTGACGCTGAGCAGTG GAAGTCCACAGAAAGCTACAGTGCAGGTCTAC GCATGAAGGGAGCACCGTGGAGAGACAGTGG CCCCTACAGATGTTCA
				SEQ ID NO: 607 CAGATGAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAGTCTCCTGC AAGGCTCCGGATACACCTTCAACCGGCTACTAT ATGCATTGGTGCAGACGGCCCTGGACAAGGG CTTGAGTGGATGGGATGGATCAACCTTAACAGT GGTGGCACAACTATGCACAGAAAGTTTCAGGGC AGGTCAACCATGACCAAGGACACGTCCATCAGT ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT GACGACACGGCGTGTATTACTGTGCGAGAGGG GGGGATTACGTTTTCGGGACTTATCGGCCCTCACT ACTACTACGGTATGACGTCTGGGGCCCAAGGA CCACGGTCAACGCTCTCCTCAGCCTCCACCAAGG GCCCATCGGCTTCCCCCTGGCACCCCTCCTCCAA GAGCACCTCTGGGGGCACAGCGGCCCTGGGCTG CCTGTCAAGGACTACTTCCCCGAACCGGTGAC GGTGCTGTGAACCTCAGCGCCCTGACACAGCGG CGTGCAACCTTCCCCGGCTGTCTACAGTCTCA GGACTCTACTCCCTCAGCAGCGTGGTGACCGTG CCTCCAGCAGCTTGGGCACCCAGACCTACATC TGCAACGTGAATCACAAGCCCAAGCAACCCAAAG GTGGACAAGAAAGTTGAGCCCCAAATCTGTGAC AAACCTCACATGCCACCCGTGCCAGCACCT GAACCTCTGGGGGACCGTCAAGTCTTCTCTCC CCCCAAAACCAAGGACACCCCTCATGATCTCCC GGACCCCTGAGGTACATGCGTGGTGGTGGACG TGAGCCACGAAGACCCCTGAGGTCAAGTTCAACT GGTACGTGGACGGCGTGGAGGTGCATAATGCCA AGACAAAGCCGTGTGAGGAGCAGTACGGCAGC ACGTACCGTTGTGTGACGCTCCACCGTCTGC ACCAGGACTGGCTGAATGGCAAGGAGTACAAGT GCAAGGTCTCCCAACAAGGCCCTCCAGCCCCCA

			TCGAGAAAACCATCTCCAAAGCCAAAGGCAGC CCCGAGAACACAGGTGTACACCTGCCCCCAT CCCGGAGGAGATGACCAAGAACCCAGGTCAGC CTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC GACATCGCCGTGGAGTGGAGAGCAATGGGCA GCGGAGAACAACTACAAAGACCACGCCTCCCGT GCTGGACTCCGACGGCTCCTTCTTCCCTCTATAGC AAGCTCACCGTGGACAAGAGCAGGTGGCAGCA GGGGAACGTCTTCTCATGTCCGTGATGCATGA GGCTCTGCACAACCACTACACGCAGAAAGGCCT CTCCCTGTCTCCGGGTAA
		SEQ ID NO: 2021	SEQ ID NO: 2178
	AA	QSVLTQPPSASGTPGQRVITISCSGSSNIGSQTVNW YQHLPGTAPKLLIYTNNQRPSPGVPDFRSGSKSGTS ASLAISGLQSEDEADYFCATFDESLSGPVFGGGTK LTVLGGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGA VTVAWKADSSPVKAGVETTTTPSKQSNKKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS	QMQVVQSGAEVKKPGASVKVSKASGYTFTGY MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLSDDTA VYYCARG GDYVFGTYRPHYYYGMDVWVGQGTTVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS SLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTIKAKGQPREPQVYVTLPPSREEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVL DSDGSFFLYSKLTVDKSRWQQGNVVFSCSVMHEAL HNHYTQKLSLSLSPGK
		SEQ ID NO: 451	SEQ ID NO: 608
IPS:361845	18F2.013	NA	CAGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTTCAGTAACCTTTGGCA TGCACTGGTCCGCCAGGCCCAAGGCAAGGGGC TGGAGTGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGAGCCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAAACA CGCTGTATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATA

		<p>GGGACCAAAGTGGATATCAACGAACGGTGGCT GCACCATCTGTCTTTCATCTTCCCGCCATCTGATG AGCAGTTGAATCTGGAACCTGCCCTCTGTTGTGT GCCTGCTGAATACTTCTATCCCAAGAGAGGCCA AAGTACAGTGGAAAGGTGGATAACGCCCTCCAAAT CGGGTAAC'TCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCCGAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT</p>	<p>GGACGATCTTTGGAGTGGTCTTTGGGGGACTACT GGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCAG CTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGCTGCCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGC CCTGACCAAGCGGCTGCACACCTTCCC GGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAACCTCACACATGCCACCC GTGCCAGCACCTGAACCTCTGGGGGACCGTC AGTCTTCTCTTCCCCCAAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGTGGTGACGTGAGCCACGAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGA GGTGCAATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTACGCGT CCTCACCGTCTGCACCAAGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACCAAGGTGACCTGACCTGCCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAACTACAAG ACCAAGCTTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAAA</p>
	AA	<p>SEQ ID NO: 2022</p> <p>DIQMTQSPSSLSASIGDRVTITCRASQDLRLNYLGW YQQKPGKAPKRLIYGASSLSQGVPSRFSGSGSGTE FTLTISLQPEDFATYYCLQHNNYPFTFGQGTKVDI</p>	<p>SEQ ID NO: 2179</p> <p>QVQLVESGGGVVQPRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAWIWYDASNENYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR</p>

			<div>KRTVAAPSFIFFPPDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSYLSL STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGE</div>	<div>TIFGVVLGDYWGQGLTVTVSSASTKGSPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTEPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVVFSCVMHEALHNHYTQKS LSLSPGK</div>
			<div>SEQ ID NO: 452</div> <div>GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAGCCCCTA AGCGCTGATCTATGGTGCAATCCAGTTTGCAA GTGGGTCCCTTCAAGGTTTCAGCGGCAGTGGAT CTGGGACAGAAATTCATCTTCACAAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAGTGGATATCAAAACGAACGGTGGCT GCACCATCTGTCTTCACTTCCCGCCATCTGATG AGCAGTTGAATACTGGAACCTGCCCTCTGTTGTGT GCCTGCTGAATACTTCTATATCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT CGGGTAACCTCCAGGAGAGTGTACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCCTGCGAAGTCAACCCATCAGG GCCTGAGCTCGCCCGTCAAAAGAGCTTCAACA GGGGAGAGTGT</div>	<div>SEQ ID NO: 609</div> <div>CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGATTCACTTCACTTCACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCAACCATCTCCAGAGACAATTCACAAGAACA CGCTGATCTGCAAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATA GGACGATTTTGGAGTGTCTTGGGGGACTACT GGGGCCAGGAACCTGGTCAACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCTCTCTCCAAAGACACCTCTGGGGGCACAGC GGCCCTGGGCTGCCGTGTCAGAGACTACTTCCC CGAACCGGTGACGGTGTCTGTGGAACCTCAGGCG CCTGACAGCGGCTGCACACCTTCCCCGGCTGT CCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAACTTTGTGACAAAACTCACACATGCCACC GTGCCAGCACCTGAACCTCTGGGGGACCGTCT AGTCTTCTCTTCCCCCAAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACTG</div>
IPS:361851	6H1.009	NA		

		CGTGTGGTGACGTGAGCCACGAAAGACCCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCAATAATGCCAAGACAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGTGACCGT CCTCACCGTCTGCACCAAGACTGGCTGAATGG CAAGGAGTACAAAGTGCAAGGTCTCCAAACAAGC CCTCCAGCCCCCATCGAGAAACCATCTCCAA AGCCAAAGGCAAGCCCCGAGAACCCACAGGTGT ACACCTGCCCCCATCCCGGAGGAGATGACCA AGAACCAAGTCAAGCTGACCTGCCTGGTCAAAG GCTTCTATCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGCAGCCGAGAACAACTACAAG ACCACGCTCCCGTGTGGACTCCGACGGCTCC TTCTTCTCTATAGCAAGCTCACCCTGGACAAAG AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAAA SEQ ID NO: 2180
	SEQ ID NO: 2023	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLSQGVPSRFSGSGSGTEFT LTISLQPEDFATYYCLQHNNYPFTFGQGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLS TLTLTKADYEKHKVYACEVTHQGLSPVTKSFNR GEC
AA		QVQLVESGGGVVQPGRLSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDASNKYADAVKGG RFTISRDNKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLLGDYWGQGTLLVTVSSASTKGPSVFPLAPS SKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNATKPCPEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVVFSCSVMEALHNHYTQKS LSLSPGK SEQ ID NO: 610
	SEQ ID NO: 453	

IP:361855	2C2.005.015	NA	<p> CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTG GGACCCCGGGCAGAGGGTCACCATCTCTTGT CTGGAAGTAGCTCCAAACATCGGAAGTAATACTG TAAACTGGTACCAGCAACTCCCAGGAACGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTCTGTG CAACATTTCGATAGCAGCCTGAGTGGTCCGGTAT TCGGGGAGGGACCAGCTGACCGTCCTAGGTC AGCCCAAGGTGCCCCCTCGGTCACTCTGTTCCTC GCCCCTCCTGAGGAGCTTCAAGCCAAACAAGGC CACACTGGTGTCTCATAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCTGGAAAGGCAGATAG CAGCCCCGTCAGCGGGAGTGGAGACCACCAC ACCTCCAAACAAGCAACAACAAGTACGGGGC CAGCAGCTATCTGAGCCTGACGCCCTGAGCAGTG GAAGTCCACAGAAAGCTACAGTGCAGGTCTAC GCATGAAGGGAGCACCGTGGAGAAAGACAGTGG CCCCACAGAAATGTTCA </p>
			<p> CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAAGTCTCCTGC AAGCTTCCGGATACACCTTCAACCGGTACTAT ATGCATTGGTGCAGACGGCCCCCTGGACAAGGG CTTGAGTGGATGGATGGATCAACCTAACAGT GGTGGCACAACTATGCACAGAAATTTTCAGGGC AGGTCAACCATGACAGGGACACGTCCATCAGT ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT GACGACACGGCGTGTATTACTGTGCGAGAGGG GGGGATTACGTTGGGGGACTTATCGGCCCTCAC TACTACTACGATGGACGTCTGGGGCCCAAGG ACCACGGTCAACGCTCTCCTCAGCCTCCACCAAG GGCCCATCGTCTTCCCCCTGGCACCCCTCCCTCCA AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA CGGTGCTGTGAACTCAGGGGCCCTGACCAAGCG GCGTGCACACCTTCCCGGTGTCTACAGTCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT GCCCCCAGCAGCTTGGGCACCCAGACCTACAT CTGCAACGTGAATCAAGCCCAAGCAACACCAA GGTGGACAAGAAAGTTGAGCCCCAATCTTGTGA CAAACCTCACACATGCCCAACCGTGGCCAGCAC TGAACTCCTGGGGGACCGTCAGTCTTCTCTTC CCCCAAAACCAAGGACACCCCTCATGATCTCC CGGACCCCTGAGGTACATGCGTGGTGGTGAC GTGAGCCACGAAGACCTGAGGTCAAGTTCAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCC AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG CACGTACCGTTGTGTCAGCGTCTCACCGTCTG CACCAGGACTGGCTGAATGGCAAGGAGTACAA GTGCAAGGTCTCCAAACAAGCCCTCCAGCCCC CATCGAGAAACCATCTCTCCAAGCCAAAGGGCA GCCCCGAGAACCAAGGTGTACACCTGCCCCC ATCCCGGAGGAGATGACCAAGAACCAAGGTCA GCCTGACCTGCCTGGTCAAGGCTTCTATCCCCA GCGACATCGCCGTGGAGTGGGAGAGCAATGGG </p>

				<p>SEQ ID NO: 2024</p> <p>QSVLTQPPSASGTPGQRVITISCGSSNIGSNTVNW YQQLPGTAPKLLIYTNNQRPSPGVPDFSGSKSGTS ASLAISGLQSEDEADYFCATFDSSLGPFVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTTPSKQSNKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS</p>		<p>CAGCCGAGAACAACTACAAGACCACGCCTCCC GTGCTGACTCCGACGGCTCCTTCTTCTCTATA GCAAGCTCACCGTGGACAAAGAGCAGGTGGCAG CAGGGAAACGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAAACCACTACACGCAAGAGAGC CTCTCCCTGTCTCCGGGTAAA</p>
			AA	<p>SEQ ID NO: 2181</p> <p>QMQVVQSGAEVKKPGASVKVSKASGYTFTGYY MHWVVRQAPGQGLEWMGVNPNSSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLSDDTA VYYCARG GDYVWGTYPHYYYGMDVWVGQGITTVTVSSAST KGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVVDGVEVHNAKTKPCE EQYGSTYRCVSLTVLHQDWLNGKEYKCKVSNK ALPAIEKTIKAKGQPREPQVYVTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LSDGSFELYSKLTVDKSRWQQGNVVFSCSVMHEA LHNHYTQKLSLSLSPGK</p>		<p>SEQ ID NO: 611</p> <p>CAGTGCAGTTGGTGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT ACAGCGTCTGGATTCAACCTTCAGTAGCTATGGC ATACACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGGA AGTAATAAGTTCCATGCAGACTCCGTGAAGGGC CGATTACCACTCCAGAGACAAATCCAAAGAAC ACGCTGATCTGCAAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCTGAAGCTTTTGAATC TGGGGCCAAAGGACAAAGGTCAACGCTCTCTCA GCCTCCACCAAGGGCCCATCGGTCTTCCCCTG GCACCTCTCTCAAGAGCACCTCTGGGGGCACA GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC</p>
IPS:336067	5G12.006	NA		<p>SEQ ID NO: 454</p> <p>GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGGCAAGTCAGACCAATTAGCAGGTTTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTG AGCTCTGATCTATGTTGCAATCCAGTTTGCA AAG TGGGTCCCATCAAGATTCAAGTGGCAGTGGTTC TGGGACAGATTTCACCTCTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGATCAGTTTGGCCA GGGACCAAGCTGGAGATCACACGAACGGTGG CTGCACCATCTGTCTTCTATCTTCCCGCCATCTGA TGAGCAGTTGAAAATCTGGAACTGCCTCTGTTGT GTGCTGCTGAATAACTTCTATCCCAAGAGAGGC CAAAGTACAGTGGAAGGTGGATAACGCCCTCCA</p>		<p>SEQ ID NO: 2181</p> <p>QMQVVQSGAEVKKPGASVKVSKASGYTFTGYY MHWVVRQAPGQGLEWMGVNPNSSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLSDDTA VYYCARG GDYVWGTYPHYYYGMDVWVGQGITTVTVSSAST KGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVVDGVEVHNAKTKPCE EQYGSTYRCVSLTVLHQDWLNGKEYKCKVSNK ALPAIEKTIKAKGQPREPQVYVTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LSDGSFELYSKLTVDKSRWQQGNVVFSCSVMHEA LHNHYTQKLSLSLSPGK</p>

		<p>ATCGGGTAACTCCAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCCTGACGCTGAGCAAGCAGACTACGAGA AACACAAAGTCTACGCCCTGCGAAGTCACCCATC AGGCCCTGAGCTCGCCCGTCAACAAAGAGCTTCA ACAGGGGAGAGTGT</p>	<p>CCCGAACCCGGTGACGGTGTCTGTGGAACCTCAGGC GCCCTGACCAGCGCGTGCACACCTTCCCGGCT GTCCTACAGTCTCAGGACTCTACTCCCTCAGCA GCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA CCCAGACCTACATCTGCAACGTGAATCACAAGC CCAGCAACACCAAGGTGGACAAGAAAGTTGAG CCCAATCTTGTGACAAACTCACACATGCCCA CCGTGCCAGCACCTGAACCTCTGGGGGACCG TCAGTCTTCTCTTCCCCCAAAACCCAAAGACA CCCTCATGATCTCCCGGACCCCTGAGGTCACAT GCGTGGTGGTGAAGTGAAGCCACGAAGACCCTG AGGTCAAGTTCAACTGGTACGTGGACGGCGTGG AGTGCATAATGCCAAGACAAGCCGTGTGAGG AGCAGTACGGCAGCAGTACCCTGTGTGTACAGG TCCTCACCGTCTGCACCAAGGACTGGCTGAATG GCAAGGAGTACAAGTGAAGTCTTCCAACAAA GCCCTCCAGCCCCATCGAGAAAACCATCTCC AAAGCCAAAGGCAAGCCCGGAGAACACAGGT GTACACCTGCCCCATCCCGGAGGAGATGAC CAAGAACCAGGTACGCTGACCTGCCTGGTCAA AGGCTTCTATCCAGCGACATCGCCGTGGAGTG GGAGAGCAATGGGCAGCCGGAGAACACTACA AGACCACGCTCCCGTGTGCTGGACTCCGACGGCT CCTTCTTCTCTATAGCAAGCTCACCGTGGACAA GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATG CTCCGTGATGCATGAGGCTCTGCACAACCACTA CAGCAGAAAGACCTCTCCCTGTCTCCGGGTAA A</p>
	AA	<p>DIQLTQSPSSLASVGDVRVTITCRASQTISRFLNWX QQKPGKAPPELLIYVASSLQSGVPSRFSGSGTDF LTISSLQPEDFATYYCQOSYSTLISFGQGTGLEITRT VAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSYSTLSST LTLKADYEEKHKVYACEVTHQGLSSPVTKSFNRG EC</p>	<p>SEQ ID NO: 2182</p> <p>QVQLVESGGGVVQPRSLRLSCTASGFTFSYGIH WVRQAPGKGLEWVAWIYDGSNKFHADSVKGRF TISRDNKNTLYLQMNLSRAEDSAMYFCARGKVA GMPEAFEIWQQGTKVTVSSASTKGPSVFPLAPSSK STSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVN HKPSNTKVDKKEPKSCDKTHTCPPCPAPELGGP</p>

			SVFLFPPKPKDTLMISRTPVTCVVVDVSHEDPEV KFNWYVDGVEVHNATKPCEEQYGSTYRCVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVFSQSVMHREALHNHYTQKLSL SPGK
			SEQ ID NO: 612 CAAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAAGTTATGAT ATCAACTGGTGCACAGGCCACTGGACAAGGG CTTGAGTGGATGGGATGGATGAACCTAACAGT GGTAACACAGGCTATGCACAGAAAGTTCCAGGGC AGATCACCATGACAGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT CAGGACACGGCGTGTATTAATGTGCGAGAGGG GGTGATTACGTTTGGGGAGTTATCGTCCCTACT ACTACTACTAGGTATGGACGCTCTGGGGCCAAAG GGACCACGTCACCGTCTCCTCAGCCTCCACCA AGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTC CAAGAGCACCTCTGGGGGACAGCGGGCCCTGGG CTGCTGGTCAAGGACTACTTCCCCGAAACCGGT GACGGTGTGTGGAACCTCAGCGGCCCTGACCCAG CGCGTGCACACCTTCCCGGCTGTCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCAAGGCCAGCAACACC AAGGTGGACAAGAAAGTTGAGCCCAAAATCTTGT GACAAAACCTCACACATGCCCCACCGTGCCCAAGCA CCTGAACCTCTGGGGGACCGTCAGTCTTCTCTCT TCCCCCAAAACCAAGGACACCTCATGATCT CCCGGACCCCTGAGGTACATGCGTGGTGGTGG ACGTGAGCCACGAAGACCTGAGGTCAAGTTCA ACTGTAACGTGGACGGCGTGGAGGTGCATAATG CCAAGACAAGCCCGTGTGAGGAGCAGTACGGC
IPS:336169	17B11.002	NA	SEQ ID NO: 455 CAGTCTGTGTGACGCAGCCGCCCTCAGTGTCTG CGGCCCCAGGACAGAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCACATTGGAAATAATTATG TATCCTGGTATGAGCAGTTCCCAAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTACGCCACCTGGGCATCACCCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGTGTGT ATTCCGGCGGAGGACCAAACTGACCGTCTCAGG TCAGCCCCAAGGCTGCCCTCGGTCACTCTGTTC CCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAG GCCACACTGGTGTCTCATAGTGACTTCTACC CGGGAGCCGTGACAGTGGCCTGGAAGGCAGAT AGCAGCCCCGTCAAGCGGGGAGTGGAGACCCAC CACACCTCCAAACAAGCAACAACAAGTACGC GGCCAGCAGCTATCTGAGCCTGACGCTGAGCA GTGGAAGTCCCAAGAAAGCTACAGCTGCCAGGT CACGCATGAAGGAGCACCGTGGAGAAAGACAG TGGCCCCCTACAGAAATGTTCA

			<p>AGCACGTACCGTTGTGTACGCGTCTCCTCACCGTCC TGCACCAGGACTGGCTGAATGGCAAGGAGTACA AGTGCAAGGTCTCCACAAAGCCCTCCAGCCC CCATCGAGAAACCATCTCCAAGCCAAAGGGC AGCCCCGAGAACCACAGGTGTACACCCCTGCCCC CATCCCGGAGGAGATGACCAAGAACCAGGTC AGCTGACCTGCCTGGTCAAAGGCTTCTATCCC AGGACATCGCCGTGGAGTGGGAGAGCAATGG GCAGCCGGAGAAACAATAACAAGACCACGCCCTCC CGTGTGACTCCGACGGCTCCTTCTTCTCTAT AGCAAGCTCACCGTGGACAAGACAGGTGGCA GCAGGGGAACGTCTTCTCATGTCTCCGTGATGCA TGAGGCTCTGCACAACCACTACACGCAAGAAAG CCTCTCCCTGTCTCCGGGTAAA</p>
			<p>SEQ ID NO: 2026</p> <p>QSVLTQPPSVSAAPGQKVITISCSGSSNIGNNYVS WYEQFPGTAPKLLIYDNNKRPSPIDRFSKSGTS ATLGITGLQTGDEADYYCGTWDSSL SAVVFGGGT KLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLIS DFYPGA VTVAWKADSSPVKAGVETTTPSKQSNK YAASSYLSTPEQWKSHRSYSCQVTHEGSTVEKT VAPTECS</p>
	AA		<p>SEQ ID NO: 2183</p> <p>QMLVQSGAEVKKPGASVKVCKASGYTFTSYDI NWVRQATGQGLEWMGWMPNPSGNTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDTAVYYCARG GDYVWGSYRPYYYYGMDVWVGQGTITVTVSSAS TKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTP SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTSISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPV LSDSGSFELYSKLTVDKSRWQQGNVVFSCVMHEA LHNHYTQKLSLSPGK</p>
			<p>SEQ ID NO: 456</p> <p>GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGAGACAGAGTCACTATCACTT GCCGGGCAAGTCAGACCAATTAGCAGGTTTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCCCTG AGCTCCTGATCTATGTTGCAATCCAGTTTGCA AAG TGGGGTCCCATCAAGATTACAGTGGCAGTGGTTC</p>
!PS:361127	5G12.006.001	NA	<p>SEQ ID NO: 613</p> <p>CAGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGGCTCTGGATTCAACCTTCAGTAGCTATGGC ATACACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAGTTCCATGCAGACGCCCGTGAAGGGC</p>

TGGGACAGATTTCACTCTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGATCAGTTTGGCCA GGGACCAAGCTGGAGATCAACGAACGGTGG CTGCACCATCTGTCTTCACTTCCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCCTCTGTTGT GTGCTGTCTGAATAACTTCTATCCCAGAGAGGC CAAAGTACAGTGGAAAGGTGGATAACGCCCTCCA ATCGGGTAACCCCCAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCCTGACGCTGAGCAAGCAGACTACGAGA AACACAAAGTCTACGCCCTGCGAAGTCAACCCATC AGGCCCTGAGCTCGCCCCGTACAAAGAGCTTCA ACAGGGGAGAGTGT	CGATTCAACATCTCCAGAGACAATTCCAAGAAC ACGCTGATCTGCAAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCCTGAAGCTTTTGAATC TGGGGCCAAAGGACAAAGGTCAACCGTCTCTTCA GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTG GCACCTCTCTCAAGAGCACCTCTGGGGGCACA GCGGCCCTGGGCTGCCCTGGTCAAGGACTACTTC CCGAACCGGTGACGGTGTCTGTGGAACCTCAGGC GCCCTGACCAGCGGCGTGCACACCTTCCCCGGCT GTCTACAGTCTCTCAGGACTCTACTCCCTCAGCA GCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA CCCAGACCTACATCTGCAACGTGAATCACAAGC CCAGCAACACCAAGGTGGACAAGAAAGTTGAG CCCAATCTTGTGACAAACTCACACATGCCCA CCGTGCCAGCACCTGAACCTCTGGGGGACCG TCAGTCTTCTCTTCCCCCAAAACCAAGGACA CCCTCATGATCTCCCGACCCCTGAGGTCACAT GCGTGGTGGTGACGTGAGCCACGAAGACCCTG AGGTCAAGTTCAACTGGTACGTGGACGGCGTGG AGGTGCATAATGCCAAGACAAGCCGTGTGAGG AGCAGTACGGCAGCACGTACCGTTGTGTACGG TCCTCACCGTCTGCACCAGGACTGGCTGAATG GCAAGGAGTACAAGTGCAGGTCTCCAACAAA GCCCCTCCAGCCCCCATCGAGAAAACCATCTCC AAAGCCAAAGGGCAGCCCCCGAGAACACAGGT GTACACCTGCCCTCATCCGGGAGGAGATGAC CAAGAACCAGGTACGCTGACCTGCCCTGGTCAA AGGCTTCTATCCAGCGACATCGCCGTGGAGTG GGAGAGCAATGGGCAGCCGGAGAACACTACA AGACCACGCCCTCCGTGTGGACTCCGACGGCT CCTTCTTCTCTATAGCAAGCTCACCGTGGACAA GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATG CTCCGTGATGCATGAGGCTCTGCACAACCACTA CACGCAGAAAGACCCTCTCCCTGTCTCCGGGTAA
	A

		SEQ ID NO: 2027	DIQLTQSPSSLSASVGDRTTITCRASQTISRFLNWWY QQKPGKAPELLIYVASSLQSGVPSRFSGSGTDFDT LTISSLQPEDFATYYCQQSYSTLISFGQGTKLEIKRT VAAPSVFIFFPSDEQLKSGTASVVCLLNFFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSYSTYLSST LTLKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC	SEQ ID NO: 2184	QVQLVESGGGVVQGRSLRLSCAASGFTFSYGIH WVRQAPGKGLEWVAWIWYDASNKFHADAVKGR FTISRDNSKNTLYLQMNSLRAEDSAMFYFCARGKV AGMPEAFEIWWGQGTKVTVSSASTKGPSVFPLAPSS KSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCTPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK	
AA		SEQ ID NO: 457	GACATCCAGCTGACCCAGTCTCCATCCTCCTCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGGCAAGTCAGACCAATTAGCAGGTTTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTG AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG TGGGGTCCCATCAAGATTTCAGTGGCAGTGGTTC TGGGACAGATTTCACTCTCAACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCTGATCAGTTTGGCCA GGGACCAAGCTGGAGATCAACGAACGGTGG CTGCACCATCTGTCTTCACTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACCTGCCTCTGTTGT GTGCTGCTGAATAACTTCTATCCAGAGAGGC CAAAGTACAGTGGAAAGTGGATAACGCCCTCCA ATCGGGTAACCTCCAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCTTGACGCTGAGCAAAAGCAGACTACGAGA AACACAAAGTCTACGCTGCGAAGTCAACCATC AGGGCTGAGCTCGCCCGTCAACAAGAGCTTCA ACAGGGGAGAGTGT	NA	SEQ ID NO: 614	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGTCCTGAGACTCTCCTGT ACAGGCTCTGGAATCACCTTCAGTAGCTATGCG ATACACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGTTATGATGCA AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTAATCTGCAAAATGAACAGCCTGAGAGCC GAGGACTCGCTATGTAATCTCTGTGCGAGAGGA AAAGTGGTGGTATGCTGAAAGCTTTTGAAATC TGGGGCCAAGGACAAAGGTACCGTCTCTCTTCA GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTG GCACCTCTCTCAAGAGCACCTCTGGGGGCACA GCGGCCCTGGCTGCTTGGTCAAGGACTACTTTC CCCGAACCGGTGACGGTGTGCTGGAACCTCAGGC GCCCTGACCAAGCGGCTGCACACCTTCCCCGGCT GTCCTACAGTCTCAGGACTCTACTCCTCAGCA GCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA CCAGACCTACATCTGCAACGTGAATCACAAAGC CCAGCAACACCAAGGTGGACAAGAAAGTTGAG CCAGCAACACCAAGGTGGACAAGAAAGTTGAG
	IPS:361136	SG12.006.002				

			<p>CCCAATCTTGTGACAAAACTCACACATGCCCCA CCGTGCCAGCACCTGAACCTCTGGGGGACCG TCAGTCTTCTCTTCCCCCAAAACCAAGGACA CCCTCATGATCTCCCGGACCCCTGAGGTCACAT GCGTGGTGGAGCTGAGCCACGAAAGACCCTG AGTCAAGTTCAACTGGTACGTGGACGGCGTGG AGTGCATAATGCCAAGACAAGCCGTGTGAGG AGCAGTACGGCAGCACGTACCGTTGTGTACGG TCCTCACCGTCTGCACAGGACTGGCTGAATG GCAAGGAGTACAAGTCAAGTCTCCAACAAA GCCCCAGCCCCATCGAGAAACCATCTCC AAAGCCAAAGGCAGCCCCGAGAACACAGGT GTACACCTGCCCTATCCCGGAGGAGATGAC CAAGAACAGGTACAGCTGACCTGCCTGGTCAA AGGCTTCTATCCAGCGACATCGCCGTGGAGTG GGAGAGCAATGGGCAGCCGGAACAACATA AGACCAGCTCCCTGCTGGACTCCGACGGCT CCTTCTCTCTATAGCAAGCTCACCGTGGACAA GAGCAGGTGGCAGCAGGGAACGTCTTCTCATG CTCCGTGATGATGAGGCTCTGCACAACCACTA CAGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAA A</p>
	AA	<p>DIQLTQSPSSLASVGDRTTITCRASQTISRFLNWX QQKPGKAPPELLIYVASSLQSGVPSRFSGSGSTDF LTISSLQPEDFATYQCQSYSTLISFGQGTGLEIKRT VAAPSVFIPPSDEQLKSGTASVCLLNFFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSYSLST LTLKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC</p>	<p>SEQ ID NO: 2185</p> <p>QVQLVESGGGVVQGRSLRLSCTASGFTFSYGIH WVRQAPGKGLEWVAWIYDASNKFHADAVKGR FTISRDNSKNTLYLQMNSLRAEDSAMVFCARGKV AGMPEAFEIWGGQTKVTVSSASTKGPSVFPLAPSS KSTSGGTAAALGCLVKDYFPEPTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKEPKSCDKTHCTCPPEPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDSDGGSFFLYSK</p>

				LTVDKSRWQQGNVFSCSVMEALHNHYTQKSLS LSPGK
				SEQ ID NO: 615
				CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTACCTTCAGTAGCTATGGC ATACACTGGTCCCGCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC CGATTACCATCTCCAGAGACAAATCCAAAGAAC ACGCTGTATCTGCAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGTGGTATGCCTGAAGCTTTTGAATC TGGGGCCAAAGGACAAAGGTCAACCTCTCTTCA GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTG GCACCTCTCCAAAGAGCACCTCTGGGGGCACA GCGGCCCTGGGTGCTGGTCAAGGACTACTTC CCGGAACCGGTGACGGTGTCTGTGGAACCTCAGGC GCCCTGACCAGCGGCGTGACACCTTCCCGGCT GTCTACAGTCTCAGGACTCTACTCCCTCAGCA GCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA CCCAGACCTACATCTGCAACGTGAATCACAAGC CCAGCAACACCAAGGTGGACAAAGAAAGTTGAG CCCAATCTTGTGACAAAACTCACACATGCCCA CCGTGCCAGCACCTGAACCTCTGGGGGACCG TCAGTCTCTCTTCCCCCAAAACCAAGGACA CCCTCATGATCTCCCGGACCCCTGAGGTCACAT GCGTGGTGGTGGACGTGAGCCACGAAGACCCCTG AGGTCAAGTTCAACTGGTACGTGGACGGCGTGG AGGTGCATATATGCCAAGACAAAGCCGTGTGAGG AGCAGTACGGCAGCACGTACCGTTGTGTACGCG TCCTCACCGTCTGCACCCAGGACTGGCTGAATG GCAAGGAGTACAAGTGAAGGTCTCCCAACAAA GCCCTCCAGCCCCCATCGAGAAAACCATCTCC
				SEQ ID NO: 458
				GACATCCAGCTGACCCAGTCTCCATCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGGCAAGTCAGACCATAGCAGGTTTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTG AGCTCCTGATCTATGTTGCATCCAGTTTGCAAG TGGGTCCCATCAAGATTCAAGTGGCAGTGGTTC TGGGACAGATTTCACTCTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGATCAGTTTTTGCCA GGGACCAAGCTGGAGATCACACGAACGGTGG CTGCACCATCTGTCTTCACTTCCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCCTCTGTTGT GTGCTGTGTAATACTTCTATCCAGAGAGGC CAAAGTACAGTGAAGGTGGATAACGCCCTCCA ATCGGGTAACTCCAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCTGACGCTGAGCAAGCAGACTACGAGA AACACAAAGTCTACGCTGCGAAGTCAACCATC AGGGCCTGAGCTCGCCCCGTACAAAGAGCTTCA ACAGGGGAGAGTGT
			NA	
		5G12.006.003		
		IPS:361140		

			AAAGCCAAAGGGCAGCCCCGAGAACACAGGT GTACACCTGCCCCCATCCCGGAGAGATGAC CAAGAACCAGGTACGCTGACCTGCCTGGTCAA AGGCTTCTATCCAGCGACATCGCCGTGGAGTG GGAGAGCAATGGGCAGCCGGAACAACA AGACCACGCTCCCGTGTGGACTCCGACGGCT CCTTCTCCTCTATAGCAAGCTCACCGTGGACAA GAGCAGGTGGCAGCAGGGAAACGTCTTCTCATG CTCCGTGATGCATGAGGCTCTGCACAACCACTA CACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAA A
		SEQ ID NO: 2029	SEQ ID NO: 2186
	AA	DIQLTQSPSSLSASVGDVRVTITCRASQTISRFLNWY QQKPGKAPPELLIYVASSLQSGVPSRFSGSGTDFT LTISSLQPEDFATYYCQQSYSTLISFGQGTGLEITRT VAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSYSTLSST LTLISKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGIH WVRQAPGKGLEWVAWIYDASNKFHADAVKGR FTISRDNSKNTLYLQMNSLRAEDSAMFYFCARGKV AGMPEAFEIWGQGTKVTVSSASTKGPSVFPLAPSS KSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKEPKSCDKTHTCTPCPAPPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
		SEQ ID NO: 459	SEQ ID NO: 616
!PS:359919	5G12.006.004	GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGGCAAGTCAGACCAATTAGCAGGTTTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCCCTA AGCTCTGATCTATGTTGCAATCCAGTTTGCAAAG TGGGTCCCATCAAGATTTCAGTGGCAGTGGTTC TGGGACAGATTTCACCTCTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGATGATCAGTTTTTGCCA	CAGGTGCAGTTGGTGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCAACCTTCAGTAGCTATGGC ATACACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAGTTCCATGCAGACGCCGTGAAGGCG CGATTACCATCTCCAGAGACAATTCCAAGAAC ACGCTGATCTGCAAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGGAGAGGA

		<p>GGGACCAAGCTGGAGATCAACGAACGGTGG CTGCACCATCTGTCTTCACTTCCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCCTCTGTTGT GTGCTGTCTGAATAACTTCTATCCCAGAGAGGC CAAAGTACAGTGAAGGTGGATAACGCCCTCCA ATCGGTAACCTCCAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCTGACGCTGAGCAAGCAGACTACGAGA AACACAAAGTCTACGCCCTGCGAAGTCAACCATC AGGCCCTGAGCTCGCCCGTCAACAAAGAGCTTCA ACAGGGGAGAGTGT</p>	<p>AAAGTGGCTGGTATGCCTGAAGCTTTTGAATC TGGGCCAAGGACATTTGGTCACCGTCTCTTCA GCCTCCACCAAGGCCCATCGGTCTTCCCCCTG GCACCTCTCTCAAGAGCACCTCTGGGGGCACA GCGGCCCTGGGCTGCCCTGGTCAAGGACTACTTC CCGAACCGGTGACGGTGTCTGTGGAACCTCAGGC GCCCTGACCAAGCGCGTGCACACCTTCCCCGGCT GTCTACAGTCTCAGGACTCTACTCCCTCAGCA GCGTGTGACCGTGCCCTCCAGCAGCTTGGGCA CCCAGACCTACATCTGCAACGTGAATCACAAGC CCAGCAACACCAAGGTGGACAAGAAAGTTGAG CCCAATCTTGTGACAAACTCACACATGCCCCA CCGTGCCAGCACCTGAACCTCTGGGGGACCG TCAGTCTTCTCTTCCCCCAAAACCAAGGACA CCCTCATGATCTCCCGGACCCCTGAGGTCACAT GCGTGGTGGTGGACGTGAGCCACGAAGACCTG AGGTCAAGTTCAACTGGTACGTGGACGGCGTGG AGGTGCATAATGCCAAGACAAGCCGTGTGAGG AGCAGTACGGCAGCACGTACCGTTGTGTACGG TCCTCACCGTCTGCACCAAGGACTGGCTGAATG GCAAGGAGTACAAGTCAAGTCTCCCAACAAA GCCCCCCAGCCCCCATCGAGAAACCATCTCC AAAGCCAAAGGCGAGCCCCCGAGAACACAGGT GTACACCTGCCCCCATCCCCGGAGGAGATGAC CAAGAACCAGGTACGCTGACCTGCCCTGGTCAA AGGCTTCTATCCAGCGACATCGCCGTGGAGTG GGAGAGCAATGGGCGAGCCGGAACAACATA AGACCACGCTCCCGTGTGGACTCCGACGGCT CCTTCTTCTCTATAGCAAGCTCACCGTGGACAA GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATG CTCCGTGATGCATGAGGCTCTGCACAACCACTA CACGCAGAAAGACCTCTCCCTGTCTCCGGGTAA A</p>
	AA	<p>SEQ ID NO: 2030</p> <p>DIQLTQSPSSLSASVGDRTVTITCRASQTSRFLNWF QOKPGKAPKLLIYVASSLSQGVPSRFSGSGSGTDF</p>	<p>SEQ ID NO: 2187</p> <p>QVQLVESGGGVVQPRSLRLSCAASGFTFSYGIH WVRQAPGKGLEWVAWIYDASNKFHADAVKGR</p>

TLTISSLQPEDFATYYCQSYSTLISFGQGTKLEIKR TVAAPSVFIFPPSDEQLKSGTASVCLLNFFYPREA KVQWKVDNALQSGNSQESVTEQDSKSDSTYSLSST LTLKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC				SEQ ID NO: 460	<p>GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTG AGCTCTGATCTATGTTGCATCCAGTTTGCAAAG TGGGTCCCATCAAGATTCAAGTGGCAGTGGTTC TGGACAGATTTCACTCTCAACATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGATCAGTTTTGGCCA GGGACCAAGCTGGAGATCAACGAAACGCTGG CTGCACCATCTGTCTTCATCTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCCTCTGTTGT GTGCTGCTGAATAACTTCTATCCCAGAGAGGC CAAAGTACAGTGGAAAGGTGGATAACGCCCTCCA ATCGGTAACCTCCAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACTACAGCCTCAGCA GCACCTGACGCTGAGCAAGAGCAGACTACGAGA AACACAAAGTCTACGCCCTGCGAAGTCAACCCATC AGGGCTGAGCTCGCCCGTCAACAAAGAGCTTCA ACAGGGGAGAGTGT</p>
FTISRDNSKNTLYLQMNSLRAEDSAMFYFCARGKV AGMPEAFEIWGGQTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCTPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK				SEQ ID NO: 617	<p>CAGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCAACCTTCAGTAGCTATGGC ATACACTGGTCCCGAGGTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAGTTCCATGCAGACTCCCGTGAAGGC CGATTACCATCTCCAGAGACAATTCCAAGAAC ACGCTGATCTGCAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTAATCTGTGCGAGAGGA AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC TGGGGCCAAGGACAAGGTCAACCGTCTCTTCA GCCCTCACCAAGGCCCATCGGTCTTCCCCCTG GCACCTCTCCAAAGAGCACCTCTGGGGGCACA GCGGCCCTGGGCTGCTGGTCAAGGACTACTTC CCCGAACCGGTGACGGTGTGCTGGAACCTCAGGC GCCCTGACCAAGCGGTGCACACCTTCCCGGCT GTCTACAGTCTCAGGACTCTACTCCCTCAGCA GCGTGGTGACCGTGCCTCCAGCAGCTTGGGCA CCCAGACCTACATCTGCAACGTGAATCACAAAGC CCAGCAACACCAAGGTGGACAAGAAAGTTGAG CCCAATCTTGTGACAAACTCACACATGCCCA CCGTGCCAGCACCTGAACCTCCTGGGGGACCG TCAGTCTTCTCTTCCCCCAAAACCAAGGACA</p>

		CCCTCATGATCTCCCGGACCCCTGAGGTCACAT GCGTGGTGGTGGACGTGAGCCACGAAGACCCTG AGGTCAAGTTCAACTGGTACGTGGACGGCGTGG AGGTGCATATGCCAAGACAAAGCCGTGTGAGG AGCAGTACGGCAGCACGTACCGTTGTGTACGG TCCTCACCGTCTGCACCAAGACTGGCTGAATG GCAAGGAGTACAAGTGAAGTCTCCCAACAAA GCCCCTCCAGCCCCCATCGAGAAACCATCTCC AAAGCCAAAGGCAGCCCCCGAGAACACAGGT GTACACCTGCCCCCATCCCGGAGGAGATGAC CAAGAACCAGGTACGCTGACCTGCCTGGTCAA AGGCTTCTATCCAGCGACATCGCCGTGGAGTG GGAGAGCAATGGGCAGCCGGAGAACAACTACA AGACCACGCTCCCGTGTGGACTCCGACGGCT CCTTCTCCTCTATAGCAAGCTCACCGTGGACAA GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATG CTCCGTGATGATGAGGCTCTGCACAAACCACTA CACGCAGAAAGACCTCTCCCTGTCTCCGGGTAA A
	SEQ ID NO: 2031	SEQ ID NO: 2188
AA	DIQLTQSPSSLASVGDRTVTITCRASQTISRFLNWW QQKPGKAPELLIVASSLQSGVPSRFSGSGSGTDFT LTISSLQPEDFATYYCQQSYSTLISFGQGTGLEIKRT VAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSYSTLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYGIH WVRQAPGKGLEWVAWIYDASNKFHADSVKGRF TISRDNKNTLYLQMNSLRAEDSAMFYFCARGKVA GMPEAFEIWGQGTKVTVSSASTKGPSVFPLAPSSK STSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCDKTHTCPPCPAPPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVFCSCVMHEALHNHYTQKLSL SPGK
	SEQ ID NO: 461	SEQ ID NO: 618

IP:361151	5G12.006.006	NA	<p>GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTG AGCTCTGATCTATGTTGCATCCAGTTTGCAAAG TGGGTCCCATCAAGATTCAAGTGGCAGTGGTTC TGGACAGATTTCACCTCTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGATCAGTTTTGGCCA GGGACCAAGCTGGAGATCAACGAACGGTGG CTGCACCATCTGTCTTCATCTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCCTCTGTTGT GTGCTGTCTGAATACTTCTATCCCAGAGAGGC CAAAGTACAGTGAAGGTGGATAACGCCCTCCA ATCGGGTAACTCCAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCTGACGCTGAGCAAGCAGACTACGAGA AACACAAAGTCTACGCCCTGCGAAGTCAACCATC AGGCCCTGAGCTCGCCCCGTACAAAGAGCTTCA ACAGGGGAGAGTGT</p>	<p>CAGTGCAAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCAACCTTCAGTAGCTATGGC ATACACTGGTCCCGCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGGA AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC CGATTCAACATCTCCAGAGACAATTCCAAGAAC ACGCTGATCTGCAAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTAATCTGTGCGAGAGGA AAAGTGGTGGTATGCCGTGAAGCTTTTGAATC TGGGGCCAAAGGACAAAGGTCAACCGTCTTCA GCCTCCACCAAGGCCCATCGGTCTTCCCCCTG GCACCTCTCCAAAGACACCTCTGGGGGCACA GCGGCCCTGGGCTGCCGTGGTCAAGGACTACTTC CCGAAACCGGTGACGGTGCACACCTTCCCCGGCT GCCCTGACCAGCGGCGTGCACACCTTCCCCGGCT GTCTACAGTCTCAGGACTCTACTCCCTCAGCA GCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA CCCAGACCTACATCTGCAACGTGAATCACAAGC CCAGCAACACCAAGGTGGACAAGAAAGTTGAG CCCAATCTTGTGACAAACTCACACATGCCCA CCGTGCCAGCACCTGAACCTCTGGGGGACCG TCAGTCTCTCTTCCCCCAAAACCAAGGACA CCCTCATGATCTCCCGACCCCTGAGGTCACAT GCGTGGTGGTGGAGTGAACCCAGAACCCCTG AGGTCAAGTTCAACTGGTACGTGGACGGCGTGG AGGTGCATAATGCCAAGACAAGCCGTGTGAGG AGCAGTACGGCAGCACGTACCGTTGTGTACGG TCCTCACCGTCTGCACCGAGGACTGGCTGAATG GCAAGGAGTACAAGTGAAGTCTCCCAACAAA GCCCTCCAGCCCCCATCGAGAAAACCATCTCC AAAGCCAAAGGGCAGCCCCGAGAACACAGGT GTACACCTGCCCCCATCCCCGGGAGGAGATGAC CAAGAACCAGGTACGCTGACCTGCCTGGTCAA AGGCTTCTATCCAGCGACATCGCCCGTGGAGTG GGAGAGCAATGGGCAAGCCGGAGAACACTACA</p>
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			<p>AGACCACGCTCCCGTGCTGGACTCCGACGGCT CCTTCTCCTCTATAGCAAGCTCACCGTGGACAA GAGCAGGTGGCAGCAGGGAACGTCTTCTCATG CTCCGTGATGCATGAGGCTCTGCACAACCACTA CACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAA A</p>
			<p>SEQ ID NO: 2032</p> <p>DIQLTQSPSSLSASVGDRTVTITCRASQTSRFLNWW QQKPGKAPPELLIYVASSLQSGVPSRFSGSGTDFT LTISSLQPEDFATYYCQQSYSTLISFGQGTGLEIKRT VAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSYSTLSST LTLISKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC</p>
		AA	<p>SEQ ID NO: 2189</p> <p>QVQLVESGGGVVQGRSLRLSCAASGFTFSYGIH WVRQAPGKGLEWVAWIYDGSNKFHADAVKGR FTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKV AGMPEAFEIWGQGTKVTVSSASTKGPSVFPLAPSS KSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHITCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK</p>
			<p>SEQ ID NO: 462</p> <p>CAGTCTGTGTGACGCAGCCGCCCTCAGTGTCTG CGGCCCAAGACAGAGGTCACCACTCTCCTGCT CTGGAAGCAGCTCCAAACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTACGCCACCTGGGCATCACCGG ACTCCAGACTGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGTGTGGT ATTCGGCGGAGGACCAAACTGACCGTCTCCTAGG TCAGCCCAAGGCTGCCCTCGGTCACTCTGTTC CCGCCCTCCTCTGAGGAGCTTCAAGCCCAACAAG GCCACACTGGTGTCTCATAAAGTACTTCTACC CGGGAGCCGTGACAGTGGCCTGGAAAGGCAGAT</p>
IPS:361491	17B11.002.001	NA	<p>SEQ ID NO: 619</p> <p>CAATGCAGCTGGTGCGAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACAGTTATGAT ATCAACTGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGATGGATGAACCTAACAGT GGTGGCACAGGCTATGCACAGAAAGTTCCAGGGC AGAGTCAACATGACAGGACACCTCCATAAGC ACAGCCTACATGAGCTGAGCAGCCTGAGATCT CAGGACACGGCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGAGTTATCTGTCCTACT ACTACTACTAGGTATGACAGTCTGGGGCCAAAG GGACACGGTCACCGTCTCCTCAGCCTCCACCA AGGGCCCAATCGGTCTTCCCCCTGGCACCCCTCCTC CAAGAGCACCTCTGGGGGACACAGGGCCCTGGG</p>

	AGCAGCCCCGTCAAAGGCGGGAGTGGAGACCAC CACACCCCTCCAAACAAGCAACAACAAGTACGC GGCCAGCAGCTATCTGAGCCTGACGCCGTGAGCA GTGGAAGTCCACAGAAAGCTACAGCTGCCAGGT CACGCATGAAGGGAGCACCGTGGAGAAAGACAG TGGCCCCCTACAGAATGTTCA	SEQ ID NO: 2033 QSVLTQPPSVSAAPGQKVITISCSGSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLGITGLQTGDEADYYCGTWDSSLASVVFSGG TKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI SDFYPGAVTVAWKADSSPVKAGVETTTTPSKQSN KYAASSYLSTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS	AA
	CTGCCTGGTCAAGGACTACTTCCCCGAACCGGT GACGGTGTGTGGAACTCAGGCGCCCTGACCAG CGCGTGCACACCTTCCCCGGTGTCTCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCAACCAGACCTAC ATCTGCAACGTGAATCACAAAGCCCAAGCAACACC AAGTGGACAAGAAAGTTGAGCCCAAAATCTTGT GACAAAATCACAACATGCCACCGTGCCACAGCA CCTGAATCTCTGGGGGACCGTCAGTCTTCTCTCT TCCCCCAAAACCAAGGACACCCCTCATGATCT CCGGACCCCTGAGGTACATGCGTGGTGGTGG ACGTGAGCCACGAAGACCCCTGAGGTCAAAGTTCA ACTGTACGTGGACGGCGTGGAGGTGCATAATG CCAGACAAGCCGTGTGAGGAGCAGTACGGC AGCAGTACCGTTGTGTCAAGCGTCTCACCCTCC TGACCAAGGACTGGCTGAATGGCAAGGAGTACA AGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCC CCATCGAGAAACCATCTCCAAGCCAAAGGGC AGCCCCGAGAACCAAGGTGTACACCCTGCCCC CATCCCGGAGGAGATGACCAAGAACCAAGGTCT AGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC AGCGACATCGCCGTGGAGTGGGAGAGCAATGG GCAGCCGGAGAACACTACAAGACCACGCCCTCC CGTGTGGACTCCGACGGCTCCTTCTTCTCTAT AGCAAGCTCACCGTGGACAAGAGCAGGTGGCA GCAGGGGAACGTCTTCTCATGCTCCGTGATGCA TGAGGCTCTGCACAACCACTACACGCAGAAAGAG CCTCTCCCTGTCTCCGGGTAAA	SEQ ID NO: 2190 QMQLVQSGAEVKKPGASVKVSKASGYTFTSYDI NWVRQATGQGLEWMGWMPNPSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDQTAIVYFCARG GDYVWGSYRPIYYGYGMDVWVGQGTITVTVSSAS TKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH	

				<p>TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVVDGVEVHNATKPCPE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTSKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LDSGSEFLYSKLTVDKSRWQQGNVVFSCSVMHEA LHNHYTQKSLSLSPGK</p>
				<p>SEQ ID NO: 463</p> <p>CAGTCTGTGTGACGCAGCCGCCCTCAGTGTCTG CGGCCCCAGGACAGAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTACGCCACCTGGGCATCACCCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGTGTGT ATTCCGGCGGAGGACCAAACTGACCGTCTCAGG TCAGCCCCAAGGCTGCCCTCGGTCACTCTGTTC CCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAG GCCACACTGGTGTCTCATAGTGACTTCTACC CGGGAGCCGTGACAGTGGCTGGAAGGCAGAT AGCAGCCCCGTCAAGCGGGAGTGGAGACCCAC CACACCTCCAAACAAGCAACAACAAGTACGC GGCCAGCAGCTATCTGAGCCTGACGCTGAGCA GTGGAAGTCCACAGAAAGCTACAGCTGCCAGGT CACGCATGAAGGGAGCACCTGGAGAAAGACAG TGGCCCCCTACAGAAATGTTCA</p>
			NA	
		17B11.002.002		
		IPS:361499		
				<p>SEQ ID NO: 620</p> <p>CAATGCAGCTGGTGCACTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACAGTTATGAT ATCAACTGGTGCGACAGGCCACTGGACAAAGGG CTTGAGTGGATGGGATGGATGAACCTAACAGT GGTAACACAGGCTATGCACAGAAAGTTCCAGGGC AGAGTCACCATGACACAGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT CAGGACACGGCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGAGTTATCGTCCCTACT ACTACTACTAGGTATGGACGCTCTGGGGCCAAAG GGACCACGTCACCGTCTCCTCAGCCTCCACCA AGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTC CAAGAGCACCTCTGGGGGACAGCGGGCCCTGGG CTGCCGTGGTCAAGGACTACTTCCCCGAAACCGGT GACGGTGTGTGGAACCTCAGCGGCCCTGACCCAG CGCGGTGCACACCTTCCCGGCTGTCTCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCAAGGCCAGCAACACC AAGGTGGACAAAGAAAGTTGAGCCCAAAATCTGT GACAAAACCTCACACATGCCCCACCGTGCCCAAGCA CCTGAACCTCTGGGGGACCGTCAGTCTTCTCTCT TCCCCCAAAACCAAGGACACCCCTCATGATCT CCCGGACCCCTGAGGTACATGCGTGGTGGTGG ACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCA ACTGTAACGTGGACGGCGTGGAGGTGCATAATG CCAAGACAAAGCCGTGTGAGGAGCAGTACGGC</p>

			AGCACGTACCGTTGTGTGACGCTCCTCACCGTCC TGACACGAGACTGGCTGAATGGCAAGGAGTACA AGTGCAAGGTCTCCACAAAGCCCTCCAGCCC CCATCGAGAAACCATCTCCAAGCCAAAGGGC AGCCCCGAGAACACAGGTGTACACCTGCCCC CATCCCGGAGGAGATGACCAAGAACCAAGGTC AGCTGACCTGCCTGGTCAAAGGCTTCTATCCC AGGACATCGCCGTGGAGTGGGAGAGCAATGG GCAGCCGGAGAAACAATAACAAGACCACGCCTCC CGTGTGACTCCGACGGCTCCTTCTTCTCTAT AGCAAGCTCACCGTGGACAAGACAGGTGGCA GCAGGGGAACGTCTTCTCATGCTCCGTGATGCA TGAGGCTCTGCACAACCACTACACGCAAGAAAG CCTCTCCCTGTCTCCGGGTAAA
		SEQ ID NO: 2034	SEQ ID NO: 2191
	AA	QSVLTQPPSVSAAPGQKVITISCSGSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLGITGLQTGDEADYYCGTWDSSLASVVFSGG TKLTVLGGQPKAAPSVTLFPPSSEELQANKATLVCLI SDFYPGAVTVAWKADSSPVKAGVETTTTPSKQSN KYAASSYLSTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS	QMQLVQSGAEVKKPGASVKVCKASGYTFTSYDI NWVRQATGQGLEWMGWMPNPSGNTGYAQKFQ GRVTMRDTSISTAYMELSSLSQDIAVYVCARG GDYVWGSYRPPYYYYGMDVWVGQGTITVTVSSAS TKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTP SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LDSGGSFELYSKLTVDKSRWQQGNVVFSCVMHEA LHNHYTQKLSLSLSPGK
		SEQ ID NO: 464	SEQ ID NO: 621
	NA	CAGTCTGTGTGACGCAGCCGCCCTCAGTGTCTG CGGCCCAAGGACAGAGGTACCACTCTCCTGCT CTGGAAGCAGCTCCACATTGGAAATAATTATG TATCCTGGTATGAGCAGTTCACGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCTCTGACCGATTCTCTGGCTCCAA	CAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGCCCTCAGTGAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCAAGTTATGAT ATCAACTGGTGCAGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGATGGATGAACCCCTAACAGT GGTGGCACAGGCTATGCACAGAAAGTTCCAGGGC
		IPS:361503	17B11.002.00 3

GTCTGGCACGTCAGCCACCCTGGGCATCACCGG ACTCCAGACTGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGCTGTGGT ATTGCGCGGAGGGACCAAACTGACCGTCCTAGG TCAGCCCCAAGGCTGCCCCCTCGGTCACTCTGTTT CCGCCCTCCTCTGAGGAGCTTCAAGCCAAACAAG GCCACACTGGTGTCTCATAGTGACTTCTTACC CGGAGCCGTGACAGTGGCCTGGAAGGCAGAT AGCAGCCCCGTCAAGCGGGGAGTGGAGACCCAC CACACCCCTCCAAACAAGCAACAACAAGTACGC GGCCAGCAGCTATCTGAGCCTGACGCCGTGAGCA GTGGAAGTCCACAGAAAGCTACAGCTGCCAGGT CACGCATGAAGGGAGCACCGTGGAGAAAGACAG TGGCCCCCTACAGAAATGTTCA	AGAGTCACCATGACCAGGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCAAAG GGACCACGGTCACCGTCTCCTCAGCCTCCACCA AGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTC CAAGAGCACCTCTGGGGGACACAGGGCCCTGGG CTGCCCTGGTCAAGGACTACTTCCCCGAACCCGGT GACGGTGTGTGGAACTCAGGGCCCTGACCAG CGCGTGCACACCTTCCCCGGTGTCTCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCACAAGCCCCAGCAACACC AAGTGGACAAAGAAAGTTGAGCCCCAAATCTTGT GACAAACTCACACATGCCCACCGTGCCCCAGCA CCTGAACCTCTGGGGGACCGTCAGTCTTCTCTCT TCCCCCAAAACCAAGGACACCCCTCATGATCT CCCGGACCCCTGAGGTACATGCGTGGTGGTGG ACGTGAGCCACGAAGACCTGAGGTCAAAGTTCA ACTGTACGTGGACGGCGTGGAGGTGCATAATG CCAAGACAAGCCGTGTGAGGAGCAGTACGGC AGCACGTACCCTGTGTGTCAGCGTCTCACCGTCC TGCACCAGGACTGGCTGAATGGCAAGGAGTACA AGTGCAAGGTCTCCAAACAAGCCCTCCAGCCC CCATCGAGAAACCATCTCCAAGCCAAAGGGC AGCCCCGAGAACCACAGGTGTACACCTGCCCC CATCCCGGAGGAGATGACCAAGAACCAAGGTCT AGCTGACCTGCCTGGTCAAAGGCTTCTATCCC AGCGACATCGCCGTGGAGTGGGAGAGCAATGG GCAGCCGGAGAAACAATAAGAACACGCCCTCC CGTGTGACTCCGACGGCTCCTTCTTCTCTAT AGCAAGCTCACCGTGGACAAAGACAGGTGGCA GCAGGGGAACGTCTTCTCATGCTCCGTGATGCA TGAGGCTCTGCACAACCACTACACGCAAGAGAG CCTCTCCCTGTCTCCGGGTAAA
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		SEQ ID NO: 2035	QSVLTQPPSVSAAPGQKVITISCSGSSNIGNNYVS WYEQFPGTAPKLLIYDNNKRPSPGIPDRFSGSKSGTS ATLGITGLQTGDEADYYCGTWDSLSA VVFGGGT KLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLIS DFYPGAVTVAWKADSSPVKAGVETTTPSKQSNK YAASSYLSTPEQWKSHRSYSCQVTHEGSTVEKT VAPTECS	SEQ ID NO: 2192	QMLVQSGAEVKPGASVKVCKASGYTFTSYDI NWVRQATGQGLEWMGMWNPNSGGTGYAQKFQ GRVTMRDTSISTAYMELSSLSQDIAVYVCARG GDYVWGSYRPPYYYYGMDVWVGQGTITVTVSSAS TKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTP SSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTH TCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSLTVLHQDWLNGKEYKCKVSNK ALPAIEKTIKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LDSGSEFLYSKLTVDKSRWQQGNVVFSCSVMHEA LHNHYTQKSLSLSPGK
	AA			SEQ ID NO: 622	CAAATGCAGCTGGTGAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAAGTCTCCTGC AAGCTTCTGGATACACCTTCAACAGTTATGAT ATCAACTGGTGCACAGGCCCTGGACAAAGGG CTTGAGTGGATGGGATGGATGAACCTAACAGT GGTGGCACAGGCTATGCACAGAAAGTTCCAGGGC AGAGTCACCATGACACAGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT GACGACACGGCGGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGGAGTTATCGTCCCTACT ACTACTACTAGGTATGGACGCTCTGGGGCCAAAG GGACACGGTCACCGTCTCCTCAGCCTCCACCA AGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTC CAAGAGCACCTCTGGGGGACAGAGGGCCCTGGG CTGCTGGTCAAGGACTACTTCCCCGAACCCGGT GACGGTGTGTGGAACCTCAGCGGCCCTGACCCAG CGCGGTGCACACCTTCCCGGCTGTCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGGTGGTGACC GTGCCCTCCAGCAGCTTGGGACCCAGACCTAC ATCTGCAACGTGAATCACAAGCCCCAGCAACACC
		SEQ ID NO: 465	CAGTCTGTGTGACGCAGCGCCCTCAGTGTCTG CGGCCCAAGACAGAGGTACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAATAATTATG TATCCTGGTATCAGCAGCTCCAGGAACAGCCC CCAAACTCCTCAATTTATGACAATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTACGCCACCTGGCCATCACCGG ACTCCAGACTGGGACGAGGCCGATTATTACTG CGGAACATTCGAAAGCAGCCTGAGTGTGTGGT ATTCGGCGGAGGACCAAACTGACCGTCTCAGG TCAGCCCAAGGTGCCCCCTCGGTCACTCTGTTC CCGCCCTCCTCTGAGGAGCTTCAAGCCCAACAAG GCCACACTGGTGTCTCATAAGTGACTTCTACC CGGGAGCCGTGACAGTGGCTGGAAGGCAGAT AGCAGCCCCGTCAAGCGGGGAGTGGAGACCAC CACACCTCCAACAAGCAACAACAAGTACGC GGCCAGCAGCTATCTGAGCCTGACGCTGAGCA GTGGAAGTCCACAGAAAGCTACAGCTGCCAGGT CACGCATGAAGGAGCACCGTGGAGAAAGACAG TGGCCCCCTACAGAAATGTTCA	SEQ ID NO: 465	
		17B11.002.004	IPS:361507	NA	

			<p>AAGTGGACAAAGAAAGTTGAGCCCAAAATCTTGT GACAAAATCACAATGCCCCACCGTGCCCAAGCA CCTGAATCCTGGGGGACCGTCAGTCTTCTCT TCCCCCAAAACCAAGGACACCTCATGATCT CCCGACCCCTGAGTCAATGAGGTCAGGTCAGTTCA ACGTGAGCCACGAAGACCTGAGGTCAGGTCAGTCA ACTGTACGTGAGCGGCGTGAGGTCAGGTCAGTCA CCAAGACAAGCCGTGTGAGGTCAGGTCAGGTCAGGTC AGCACGTACCGTTGTGTCAGGTCAGGTCAGGTCAGGTC TGACCCAGGACTGGTGAATGGCAAGGAGTACA AGTGCAAGGTCTCCAAAGGTCAGGTCAGGTCAGGTC CCATCGAGAAACCATCTCCAAAGGTCAGGTCAGGTC AGCCCGAGAACACAGGTCAGGTCAGGTCAGGTCAGGTC CATCCCGGAGGAGTGAACCAAGACCAAGGTCAGGTC AGCTGACCTGCCTGGTCAAGGTCAGGTCAGGTCAGGTC AGGACATCGCCGTGGAGTGGGAGGTCAGGTCAGGTC GCAGCCGGAGAACAACTACAAAGACCAAGGTCAGGTC CGTGTGACTCCGACGGCTCTCTCTCTCTCTCTCTCT AGCAAGCTCACCGTGGACAAAGACCAAGGTCAGGTC GCAGGGGAACGTCTCTCTCTCTCTCTCTCTCTCTCTCT TGAGGCTCTGCACAAACCACTACACGCAAGAAAGAG CCTCTCCCTGTCTCCGGGTA</p>
	SEQ ID NO: 2036	SEQ ID NO: 2193	<p>QSVLTQPPSVSAAPGQKVITISCSGSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSPGIPDRFSGSKSGT SATLAITGLQTGDEADYYCGTFESSLSAVVFGGGT KLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLIS DFYPGA VTVAWKADSSPVKAGVETTTTPSKQSNK YAASSYLSTPEQWKSRSYSCQVTHEGSTVEKT VAPTECS</p>
	AA		<p>QMLVQSGAEVKPGASVKVSKASGYTFTSYDI NWVRQAPQGQLEWMGMWNPNSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDDTAVVYCARG GDYVWGSYRPYYYYGMDVWVGQGTITVTVSSAS TKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTP SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPPELLGGPSVFLFPPKPKDITLMSRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTPPV</p>

					LDSDGSFFLYSKLTVDKSRWQQGNVFSVMHEA LHNHYTQKSLSLSPGK
					SEQ ID NO: 623
					CAAATGCAGCTGGTGACAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAAGTTATGAT ATCAACTGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGATGGATGAACCTAACAGT GGTGGCACAGGCTATGCACAGAAAGTTCCAGGGC AGAGTCACCATGACCAGGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCAAG GGACCACGGTACCGTCTCTCCTCAGCCTCCACCA AGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTC CAAGAGCACCTCTGGGGGCACAGCGGCCCTGGG CTGCCTGGTCAAGGACTACTTCCCCGAACCGGT GACGGTGTCTGGAACCTCAGGCGCCCTGACCAG CGCGTGCACACCTTCCCCGGCTGTCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCACAAAGCCAGCAACACC AAGGTGGACAAGAAAGTTGAGCCCCAAATCTTGT GACAAAAC'TCACACATGCCACCCGTGCCAGCA CCTGAAC'TCCTGGGGGACCGTCAGTCTTCTCT TCCCCCAAAAACCAAGGACACCCCTCATGATCT CCCGGACCCCTGAGGTCAATGCGTGGTGGTGG ACGTGAGCCACGAAGACCC'TGAGGTCAAGTTCA ACTGTTACGTGACGGCGTGGAGGTGCATAATG CCAAGACAAAAGCCGTGTGAGGAGCAGTACGGC AGCACGTACCGTTGTGTCAAGCGTCTCACCGTCC TGCAACAGGACTGGCTGAATGGCAAGGAGTACA AGTGCAAGGTCTCCAACAAAAGCCCTCCAGCCCC CCATCGAGAAAACCATCTCCAAGCCAAAGGGC AGCCCCGAGAACCAACAGGTGTACACCCCTGCCCC
					SEQ ID NO: 466
					CAGTCTGTGTTGACGACGCCGCCCTCAGTGTCTG CGGCCCCAGGACAGAAAGGTCAACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCAGGAACAGCCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTACGCCACCTGGCCATCACCCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGTGTGT ATTCTGGCGGAGGGACCAAACTGACCGTCTTAGG TCAGCCCCAAGGTGCCCTCGGTCACTCTGTTC CCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAG GCCACACTGGTGTCTCAT AAGTGACTTCTACC CGGGAGCCGTGACAGTGGCCTGGAAGGCAGAT AGCAGCCCCGTCAAGCGGGAGTGGAGACCAC CACACCC'TCCAAACAAGCAACAACAAGTACGC GGCCAGCAGCTATCTGAGCCTGACGCCTGAGCA GTGGAAGTCCCACAGAAGCTACAGCTGCCAGGT CACGCATGAAGGGAGCACCGTGGAGAAGACAG TGCCCCCTACAGAATGTTCA
					NA
					17B11.002.005
					IP:361514

			<p>CATCCCGGAGGAGATGACCAAGAACCAGGTC AGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC AGGACATCGCCGTGGAGTGGGAGAGCAATGG GCAGCCGGAGAAACAATAACAAGACCACGCCTCC CGTGTGACTCCGACGGCTCCTTCTTCTCTAT AGCAAGCTCACCGTGGACAAGACAGGTGGCA GCAGGGGAACGTCTTCTCATGCTCCGTGATGCA TGAGGCTCTGCACAACCACTACACGCAAGAGAG CCTCTCCCTGTCTCCGGGTAAA</p> <p>SEQ ID NO: 2194</p>	<p>CATCCCGGAGGAGATGACCAAGAACCAGGTC AGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC AGGACATCGCCGTGGAGTGGGAGAGCAATGG GCAGCCGGAGAAACAATAACAAGACCACGCCTCC CGTGTGACTCCGACGGCTCCTTCTTCTCTAT AGCAAGCTCACCGTGGACAAGACAGGTGGCA GCAGGGGAACGTCTTCTCATGCTCCGTGATGCA TGAGGCTCTGCACAACCACTACACGCAAGAGAG CCTCTCCCTGTCTCCGGGTAAA</p> <p>SEQ ID NO: 2194</p>
		AA	<p>QSVLTQPPSVSAAPGQKVITISCSGSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSPGIPDRFSGSKSGT SATLAITGLQTGDEADYYCGTWDSSLASVVFSGG TKLTVLGQPKAAPSVTLFPPSSSEELQANKATLVCLI SDFYPGAVTVAWKADSSPVKAGVETTTTPSKQSN KYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS</p> <p>SEQ ID NO: 2037</p>	<p>QSVLTQPPSVSAAPGQKVITISCSGSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSPGIPDRFSGSKSGT SATLAITGLQTGDEADYYCGTWDSSLASVVFSGG TKLTVLGQPKAAPSVTLFPPSSSEELQANKATLVCLI SDFYPGAVTVAWKADSSPVKAGVETTTTPSKQSN KYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS</p> <p>SEQ ID NO: 2037</p>
		NA	<p>CAGTCTGTGTGACGCAGCCGCCCTCAGTGTCTG CGGCCCAAGGACAGAGGTACCACTCTCCTGCT CTGGAAGCAGCTCCACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTACGCCACCTGGCCATCACCCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGTGTGGT ATTCGGCGGAGGGACCAAACTGACCGTCTCCTAGG TCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTC</p> <p>SEQ ID NO: 467</p>	<p>CAGTCTGTGTGACGCAGCCGCCCTCAGTGTCTG CGGCCCAAGGACAGAGGTACCACTCTCCTGCT CTGGAAGCAGCTCCACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTACGCCACCTGGCCATCACCCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGTGTGGT ATTCGGCGGAGGGACCAAACTGACCGTCTCCTAGG TCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTC</p> <p>SEQ ID NO: 467</p>
IPS:360582	17B11.002.006		<p>CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGCCCTCAGTGAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACAGTTATGAT ATCAACTGGTGCAGACAGGCCCTGGACAAAGGG CTTGAGTGGATGGGATGGATGAACCTAACAGT GGTAACACAGGCTATGCACAGAAAGTTCCAGGGC AGAGTCAACATGACACAGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGCTCTGGGGCCAAAG</p> <p>SEQ ID NO: 624</p>	<p>CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGCCCTCAGTGAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACAGTTATGAT ATCAACTGGTGCAGACAGGCCCTGGACAAAGGG CTTGAGTGGATGGGATGGATGAACCTAACAGT GGTAACACAGGCTATGCACAGAAAGTTCCAGGGC AGAGTCAACATGACACAGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGCTCTGGGGCCAAAG</p> <p>SEQ ID NO: 624</p>

		<p>CCGCCCTCCTGTAGGAGCTTCAAGCCAACAAG GCCACACTGGTGTCTCATAGTGACTTCTACC CGGAGCCGTGACAGTGGCTGGAAGGCAGAT AGCAGCCCGTCAAGCGGGAGTGGAGACCCAC CACACCTCCAACAAGCAACAACAAGTACGC GGCAGCAGCTATCTGAGCCTGACGCTGAGCA GTGGAAGTCCACAGAAGCTACAGCTGCCAGGT CACGCATGAAGGAGCACCGTGGAGAAGACAG TGGCCCTACAGAAATGTTCA</p>	<p>SEQ ID NO: 2038</p>
		<p>GGACCACGGTCACCGTCTCCTCAGCCTCCACCA AGGGCCATCGGTCTTCCCCCTGGCACCCCTCCTC CAAGAGCACCTCTGGGGGACAGCGGGCCCTGGG CTGCTGGTCAAGGACTACTTCCCCGAACCCGGT GACGGTGTGTGGAACCTCAGGCGCCCTGACCAAG CGCGTGCACACCTTCCCCGGTGTCTCTACAGTCC TCAGGACTCTACTCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGACCCAGACCTAC ATCTGCAACGTGAATCACAAGCCCAAGCAACACC AAGTGGACAAGAAAGTTGAGCCCAATCTTGT GACAAACTCACACATGCCACCGTGCCCCAGCA CCTGAACCTCTGGGGGACCGTCAGTCTTCTCT TCCCCCAAAACCAAGGACACCCCTCATGATCT CCCGGACCCCTGAGGTACATGCGTGGTGGTGG ACGTGAGCCACGAAGACCTGAGGTCAAAGTTCA ACTGTACGTGGACGGCGTGGAGGTGCATAATG CCAAGACAAGCCGTGTGAGGAGCAGTACGGC AGCAGTACCGTTGTGTCAGCGTCTCACCCTCC TGACCCAGGACTGGCTGAATGGCAAGGAGTACA AGTGCAAGGTCTCCACAAAGCCCTCCCAGCCC CCATCGAGAACAACCATCTCCAAGCCAAAGGGC AGCCCCGAGAACCACAGGTGTACACCCTGCCCC CATCCCGGAGGAGATGACCAAGAACCAAGGTC AGCTGACCTGCCTGGTCAAAGGCTTCTATCCC AGCAGATCGCCGTGGAGTGGGAGAGCAATGG GCAGCCGGAGAACAACTACAAGACCAAGCCCTCC CGTGTGACTCCGACGGCTCCTTCTTCTCTAT AGCAAGCTCACCGTGGACAAAGCAGGTGGCA GCAGGGGAACGTCTTCTCATGCTCCGTGATGCA TGAGGCTCTGCACAACCACTACACGCAAGAGAG CCTCTCCCTGTCTCCGGGTAAA</p>	<p>SEQ ID NO: 2195</p>
	AA	<p>QSVLTQPPSVSAAPGQKVITISCSGSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLAITGLQTGDEADYYCGTWDSSL SAVVFGGG TKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLLI</p>	<p>SEQ ID NO: 2038</p>
		<p>QMLVQSGAEVKKPGASVKVSKASGYTFTSYDI NWVRAAPGQGLEWMGMWNPNSGNTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDDTAVVYCARG GDYVWGSYRPYYYYGMDVWVGQGTITVTVSSAS</p>	<p>SEQ ID NO: 2195</p>

			SDFYPGAVTVAWKADSSPVKAGVETTTTPSKQSN KYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS	TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSQVHTFPAVLQSSGLYSLSSVVTVP SSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTH TCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSLTVLHQDWLNGKEYKCKVSNK ALPAIEKTIKAKGPQREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LDSGSEFLYSKLTVDKSRWQQGNVVFSCSVMHEA LHNHYTQKSLSLSPGK
			SEQ ID NO: 468	SEQ ID NO: 625
			CAGTCTGTGTGACGCAGCGCCCTCAGTGTCTG CGGCCCAAGGACAGAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCAGCTCAGCCACCCTGGGCATCACCGG ACTCCAGACTGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGTGTGT ATTCGGCGGAGGGACCAAACTGACCGTCTCAGG TCAGCCCAAGGCTGCCCTCGGTCACTCTGTTC CCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAG GCCACACTGGTGTCTCATAGTGACTTCTACC CGGAGCCGTGACAGTGGCTGGAAGGCAGAT AGCAGCCCGTCAAGCGGGAGTGGAGACCCAC CACACCTCCAACAAGCAACAACAAGTACGC GGCCAGCAGCTATCTGAGCCTGACGCTGAGCA GTGGAAGTCCCAAGAAAGCTACAGCTGCCAGGT CACGCATGAAGGAGCACCGTGGAGAAGACAG TGGCCCTACAGAAATGTTCA	CAATGCAGCTGGTGAGTCTGGGGCTGAGGTG AAGAAGCTGGGGCTCAGTGAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACAGTTATGAT ATCAACTGGTGCGACAGGCCACTGGACAAAGGG CTTGAGTGGATGGGATGGATGAACCTAACAGT GGTGGCACAGGCTATGCACAGAAAGTTCCAGGGC AGAGTCAACATGACAGGACACCTCCATAAGC ACAGCTACATGAGGCTGAGCAGCCTGAGATCT CAGGACACGGCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTTCGGGAGTTATCGTCCCTACT ACTACTACTAGGATGGACGCTGGGGCCAAAG GGACACGTCACCGTCTCCTCAGCCTCCACCA AGGGCCCATCGGTCTCCCGCTGGCACCCCTCCTC CAAGAGCACCTCTGGGGGACAGCGGGCCCTGGG CTGCTGGTCAAGGACTACTTCCCGCAACCGGT GACGGTGTGTGGAACCTCAGCGGCCCTGACCCAG CGCGTGCACACCTTCCCGGTGTCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCAAGGCCAGCAACACC AAGGTGGACAAAGAAAGTTGAGCCCAATCTGT GACAAAACCTCACACATGCCCCACCGTGCCCAAGCA CCTGAACCTCTGGGGGACCGTCAGTCTTCTCTCT TCCCCCAAAACCAAGGACACCCCTCATGATCT CCCGGACCCCTGAGGTCAATGCGTGTGTGTGG
IPS:361518	17B11.002.007	NA		

		<p>ACGTGAGCCACGAAGACCCCTGAGGTCAAAGTTCA ACTGGTACGTGGACGGCGTGGAGGTGCATAATG CCAAAGACAAGCCGTGTGAGGAGCAGTACGGC AGCAGTACCGTTGTGTCAGCGTCTCACCCTCC TGACCCAGGACTGGCTGAATGGCAAGGAGTACA AGTGCAAGGTCTCCAAAGCCCTCCAGGCC CCATCGAGAAACCATCTCCAAAGCCAAAGGGC AGCCCCGAGAACACAGGTGTACACCCCTGCCCC CATCCCGGAGGAGATGACCAAGAACCAAGGTC AGCTGACCTGCCTGGTCAAGGCTTCTATCCC AGCAGATCGCCGTGGAGTGGGAGAGCAATGG GCAGCCGGAGAACTACAAAGACACGCCCTCC CGTGTGACTCCGACGGCTCCTTCTTCTCTAT AGCAAGCTCACCGTGGACAAGAGCAGGTGGCA GCAGGGGAACGTCTTCTCATGCTCCGTGATGCA TGAGGCTCTGCACAACCACTACACGCAGAAAGAG CCTCTCCCTGCTCCGGGTAAA</p>
	SEQ ID NO: 2039	SEQ ID NO: 2196
AA	<p>QSVLTQPPSVSAAPGQKVITISCSGSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLGITGLQTGDEADYYCGTWDSSLASVVFSGG TKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI SDFYPGAVTVAWKADSSPVKAGVETTTTPSKQSN KYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS</p>	<p>QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQATQGLEWMGWMPNPSGGTGYAQKFKQ GRVTMTRDTSISTAYMELSSLRSDQTAIVYCARG GDYVFGSYRPYYYYGMDVWGQGTITVVSAST KGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTSISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LDSGGSFELYSKLTVDKSRWQQGNVVFSCSVMHEA LHNHYTQKSLSLSPGK</p>
	SEQ ID NO: 469	SEQ ID NO: 626

PS:360570	17B11.002.008	NA	<p>CAGTCTGTGTGACGCAGCCGCCCTCAGTGTCTG CGCCCCCAGACAGAAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTACGCCACCCTGGCCATCACCCGG ACTCCAGACTGGGACGAGGCCGATTATTACTG CGGAACATTTCGAAAGCAGCCTGAGTGTGTGGT ATTGCGCGGAGGGACCAAACTGACCGTCTCCTAGG TCAGCCCCAAGGCTGCCCCCTCGGTCACTCTGTTC CCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAG GCCACACTGGTGTCTCATAGTGACTTCTTACC CGGAGCCGTGACAGTGGCCTGGAAGGCAGAT AGCAGCCCCGTCAAGCGGGAGTGGAGACCCAC CACACCCCTCCAAACAAGCAACAACAAGTACGC GGCCAGCAGCTATCTGAGCCTGACGCTGAGCA GTGGAAGTCCACAGAAGCTACAGCTGCCAGGT CACGCATGAAGGGAGCACCGGTGGAGAAGACAG TGGCCCCCTACAGAAATGTTCA</p>
			<p>CAAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAAGTCTCCTGC AAGGCTTCTGGATACACCTTCAACCAAGTTATGAT ATCAACTGGTGCACAGGCCCTTGACAAAGGG CTTGAGTGGATGGATGGATGAACCTAACAGT GGTGGCACAGGCTATGCACAGAAAGTTCCAGGGC AGAGTCACCATGACCAGGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTTCGGGAGTTATCGTCCCCTACT ACTACTACTACGATATGGACGTCTGGGGCCAAAG GGACCACGGTCACCGTCTCTCTCAGCCTCCACCA AGGGCCCATCGGTCTTCCCCCTTGGCACCCCTCCTC CAAGAGCACCTCTGGGGGACAGCGGCCCTGGG CTGCTGGTCAAGGACTACTTCCCCGAACCCGGT GACGGTGTGTGGAACCTCAGGCGCCCTGACCAG CGCGTGCACACCTTCCCCGGTGTCTCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCACAAGCCCAAGCAACACC AAGTGGACAAAGAAAGTTGAGCCCAATCTTGT GACAAACTCACACATGCCCACCGTGCCCCAGCA CCTGAACCTCTGGGGGACCGTCAGTCTTCTCTCT TCCCCCAAAACCCAAGGACACCCCTCATGATCT CCCGGACCCCTGAGGTACATGCGTGGTGGTGG ACGTGAGCCACGAAGACCTGAGGTCAAAGTTCA ACTGTAAGTGGACGGCGTGGAGGTGCATAATG CCAAGACAAGCCGTGTGAGGAGCAGTACGGC AGCACGTACCGTGTGTGACGCTCTCACCCGTCC TGCACCAAGGACTGGCTGAATGGCAAGGAGTACA AGTGCAAGGTCTCCAAAGCCCTCCAGGCC CCATCGAGAAACCATCTCCAAGCCAAAGGGC AGCCCCGAGAACCACAGGTGTACACCTGCCCC CATCCCGGAGGAGATGACCAAGAACCAAGGT AGCCTGACCTGCCTGGTCAAGGCTTCTATCCC AGCGACATCGCCCGTGGAGTGGGAGAGCAATGG</p>

			GCAGCCGGAGAACTACAAGACCACGCCTCC CGTGTGGACTCCGACGGCTCCTTCTTCTCTAT AGCAAGCTCACCGTGGACAAGACGAGGTGGCA GCAGGGGAACGTCTTCTCATGCTCCGTGATGCA TGAGGCTCTGCACAACCACTACACGCAGAAAGAG CCTCTCCCTGTCTCCGGGTAAA
		SEQ ID NO: 2040	SEQ ID NO: 2197
	AA	QSVLTQPPSVSAAPGQKVITISCSGSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSPGIDRFSGSKSGT SATLAITGLQTGDEADYYCGTFESSLSA VVFGGGT KLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLIS DFYPGA VTVAWKADSSPVKAGVETTTPSKQSNK YAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKT VAPTECS	QMLVQSGAEVKKPGASVKVCKASGYTFTSYDI NWVRQAPGGLEWMGMNPNSSGGTGYAQKFQ GRVTMRDTSISTAYMELSSLRSDDTAVYYCARG GDYVFGSYRPYYYYGMDVWVGQGTIVTVSSAST KGPSVFPLAPSSKSTSGGTAAAGCLVKDYFPEPV VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSLTVLHQDWLNGKEYKCKVSNK ALPAIEKTIKAKGQPREPQVYVTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LDSGSEFLYSKLTVDKSRWQQGNVVFSCSVMHEA LHNHYTQKLSLSLSPGK
		SEQ ID NO: 470	SEQ ID NO: 627
IPS:362051	SG12.005.001	NA	CAGTGCAGTTGGTGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTCACTAGCTATGGC ATACACTGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGTGGCAGTTATATGGTATGATGCA AGTAATAAGTTCCATGCAGAGCCCGTGAAAGGC CGATTACCACTCCAGAGACAATTCCAAGAAC ACGCTGTATCTGCAAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGGAGAGGA AAAGTGGCTGGTATGCCTGAAGCTTTTGAATC TGGGGCCAAAGGACATTTGGTCACTCTCTTCA GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTG GCACCTCTCTCAAGAGACCTCTGGGGGCACA GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC

	<p>ATCGGGTAACTCCCAGGAGAGTGTACAGAGCA GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCCTGACGCTGAGCAAGCAGACTACGAGA AACACAAGTCTACGCCCTGCGAAAGTCACCCATC AGGGCCTGAGCTCGCCCGTCAACAAGAGCTTCA ACAGGGGAGAGTGT</p>	<p>SEQ ID NO: 2041</p>	
AA	<p>DIQLTQSPSSLASVGDVRVTITCRASQTISRFLNWI QQKPGKAPKLLIYVASSLQSGVPSRFSGSGTDF TLTISSLQPEDFATYYCQQSYSTLLSFGQGTKLEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNFPYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSYSTYLSLS TLTLTKADYEEKHKVYACEVTHQGLSSPVTKSFNR GEC</p>	<p>SEQ ID NO: 2198</p>	<p>QVQLVESGGGVVQPRSLRLSCAASGFTFSYGIH WVRQAPGKGLEWVAWIYDASNKFHADAVKGR FTISRDNSKNTLYLQMNSLR AEDSAM YFCARGKV AGMPEAFEIWGGQTLVTVSSASTKGPSVFLAPSS KSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHHTCPPCPAPELLG</p>

				GPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPE VKFNWYVVDGVEVHNATKPCCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLS LSPGK
			SEQ ID NO: 471	SEQ ID NO: 628

[0253] 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. In one embodiment the antibody or fragment thereof comprises a heavy chain variable region comprising a sequence selected from the group consisting of SEQ ID NOs: 158-314. 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. 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 comprising SEQ ID NO: 18 and a heavy chain variable region comprising SEQ ID NO: 175; a light chain variable region comprising SEQ ID NO: 19 and a heavy chain

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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.

[0254] 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. In one embodiment the antibody or fragment thereof comprises a heavy chain variable region encoded by a polynucleotide selected from the group consisting of SEQ ID NOs: 1728-1884. 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. 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 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

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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.

[0255] 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.

[0256] 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).

[0257] 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.

[0258] The various combinations of heavy chain variable regions may be combined with any of the various combinations of light chain variable regions.

[0259] 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.

[0260] 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.

[0261] 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.

[0262] 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.

[0263] In one embodiment the antibody or fragment thereof comprises a CDRL1, a CDRL2, a CDRL3, a CDRH1, a CDRH2, and a CDRH3. In one embodiment the antibody or fragment thereof comprises a CDRL1 comprising a sequence selected from the group consisting of SEQ ID NOs: 629-785. In one embodiment the antibody or fragment thereof comprises a CDRL2 comprising a sequence selected from the group consisting of SEQ ID NOs: 786-942. In one embodiment the antibody or fragment thereof comprises a CDRL3 comprising a sequence selected from the group consisting of SEQ ID NOs: 943-1099. In one embodiment the antibody or fragment thereof comprises a CDRH1 comprising a sequence selected from the group consisting of SEQ ID NOs: 1100-1256. In one embodiment the antibody or fragment thereof comprises a CDRH2 comprising a sequence selected from the group consisting of SEQ ID NOs: 1257-1413. In one embodiment the antibody or fragment thereof comprises a CDRH3 comprising a sequence selected from the group consisting of SEQ ID NOs: 1414-1570. 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 NO: 637, SEQ ID NO: 794, SEQ ID NO: 951, SEQ ID NO: 1108, SEQ ID NO: 1265, and SEQ ID NO: 1422; SEQ ID NO: 638, SEQ ID NO: 795, SEQ ID NO: 952, SEQ ID NO: 1109, SEQ ID NO: 1266, and SEQ ID NO: 1423; SEQ ID NO: 639, SEQ ID NO: 796, SEQ ID NO: 953, SEQ ID NO: 1110, SEQ ID NO: 1267, and SEQ ID NO: 1424; SEQ ID NO: 640, SEQ ID NO: 797, SEQ ID NO: 954, SEQ ID NO: 1111, SEQ ID NO: 1268, and SEQ ID NO: 1425; SEQ ID NO: 641, SEQ ID NO: 798, SEQ ID NO: 955, SEQ ID NO: 1112, SEQ ID NO: 1269, and SEQ ID

NO: 1426; SEQ ID NO: 642, SEQ ID NO: 799, SEQ ID NO: 956, SEQ ID NO: 1113, SEQ ID NO: 1270, and SEQ ID NO: 1427; SEQ ID NO: 643, SEQ ID NO: 800, SEQ ID NO: 957, SEQ ID NO: 1114, SEQ ID NO: 1271, and SEQ ID NO: 1428; SEQ ID NO: 644, SEQ ID NO: 801, SEQ ID NO: 958, SEQ ID NO: 1115, SEQ ID NO: 1272, and SEQ ID NO: 1429; SEQ ID NO: 645, SEQ ID NO: 802, SEQ ID NO: 959, SEQ ID NO: 1116, SEQ ID NO: 1273, and SEQ ID NO: 1430; SEQ ID NO: 646, SEQ ID NO: 803, SEQ ID NO: 960, SEQ ID NO: 1117, SEQ ID NO: 1274, and SEQ ID NO: 1431; SEQ ID NO: 647, SEQ ID NO: 804, SEQ ID NO: 961, SEQ ID NO: 1118, SEQ ID NO: 1275, and SEQ ID NO: 1432; SEQ ID NO: 648, SEQ ID NO: 805, SEQ ID NO: 962, SEQ ID NO: 1119, SEQ ID NO: 1276, and SEQ ID NO: 1433; SEQ ID NO: 649, SEQ ID NO: 806, SEQ ID NO: 963, SEQ ID NO: 1120, SEQ ID NO: 1277, and SEQ ID NO: 1434; SEQ ID NO: 650, SEQ ID NO: 807, SEQ ID NO: 964, SEQ ID NO: 1121, SEQ ID NO: 1278, and SEQ ID NO: 1435; SEQ ID NO: 651, SEQ ID NO: 808, SEQ ID NO: 965, SEQ ID NO: 1122, SEQ ID NO: 1279, and SEQ ID NO: 1436; SEQ ID NO: 652, SEQ ID NO: 809, SEQ ID NO: 966, SEQ ID NO: 1123, SEQ ID NO: 1280, and SEQ ID NO: 1437; SEQ ID NO: 653, SEQ ID NO: 810, SEQ ID NO: 967, SEQ ID NO: 1124, SEQ ID NO: 1281, and SEQ ID NO: 1438; SEQ ID NO: 654, SEQ ID NO: 811, SEQ ID NO: 968, SEQ ID NO: 1125, SEQ ID NO: 1282, and SEQ ID NO: 1439; SEQ ID NO: 655, SEQ ID NO: 812, SEQ ID NO: 969, SEQ ID NO: 1126, SEQ ID NO: 1283, and SEQ ID NO: 1440; SEQ ID NO: 656, SEQ ID NO: 813, SEQ ID NO: 970, SEQ ID NO: 1127, SEQ ID NO: 1284, and SEQ ID NO: 1441; SEQ ID NO: 657, SEQ ID NO: 814, SEQ ID NO: 971, SEQ ID NO: 1128, SEQ ID NO: 1285, and SEQ ID NO: 1442; SEQ ID NO: 658, SEQ ID NO: 815, SEQ ID NO: 972, SEQ ID NO: 1129, SEQ ID NO: 1286, and SEQ ID NO: 1443; SEQ ID NO: 659, SEQ ID NO: 816, SEQ ID NO: 973, SEQ ID NO: 1130, SEQ ID NO: 1287, and SEQ ID NO: 1444; SEQ ID NO: 660, SEQ ID NO: 817, SEQ ID NO: 974, SEQ ID NO: 1131, SEQ ID NO: 1288, and SEQ ID NO: 1445; SEQ ID NO: 661, SEQ ID NO: 818, SEQ ID NO: 975, SEQ ID NO: 1132, SEQ ID NO: 1289, and SEQ ID NO: 1446; SEQ ID NO: 662, SEQ ID NO: 819, SEQ ID NO: 976, SEQ ID NO: 1133, SEQ ID NO: 1290, and SEQ ID NO: 1447; SEQ ID NO: 663, SEQ ID NO: 820, SEQ ID NO: 977, SEQ ID NO: 1134, SEQ ID NO: 1291, and SEQ ID NO: 1448; SEQ ID NO: 664, SEQ ID NO: 821, SEQ ID NO: 978, SEQ ID NO: 1135, SEQ ID NO: 1292, and SEQ ID NO: 1449; SEQ ID NO: 665, SEQ ID NO: 822, SEQ ID NO: 979, SEQ ID NO: 1136, SEQ ID NO: 1293, and SEQ ID NO: 1450; SEQ ID NO: 666, SEQ ID NO: 823, SEQ ID NO: 980, SEQ ID NO: 1137, SEQ ID NO: 1294, and SEQ ID NO: 1451; SEQ ID NO: 667, SEQ ID NO: 824, SEQ ID NO: 981, SEQ ID NO: 1138, SEQ ID NO: 1295, and SEQ ID NO: 1452; SEQ ID

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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.

[0264] In one embodiment the antibody or fragment thereof comprises a CDRL1, a CDRL2, a CDRL3, a CDRH1, a CDRH2, and a CDRH3 encoded by a polynucleotide. In one embodiment the antibody or fragment thereof comprises a CDRL1 encoded by a polynucleotide sequence selected from the group consisting of SEQ ID NOs: 2199-2355. In one embodiment the antibody or fragment thereof comprises a CDRL2 encoded by a polynucleotide sequence selected from the group consisting of SEQ ID NOs: 2356-2512. In one embodiment the antibody or fragment thereof comprises a CDRL3 encoded by a polynucleotide sequence selected from the group consisting of SEQ ID NOs: 2513-2669. In one embodiment the antibody or fragment thereof comprises a CDRH1 encoded by a polynucleotide sequence selected from the group consisting of SEQ ID NOs: 2700-2826. In one embodiment the antibody or fragment thereof comprises a CDRH2 encoded by a polynucleotide sequence selected from the group consisting of SEQ ID NOs: 2827-2983. In one embodiment the antibody or fragment thereof comprises a CDRH3 encoded by a polynucleotide sequence selected from the group consisting of SEQ ID NOs: 2984-3140. 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, 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 NO: 2373, SEQ ID NO: 2530, SEQ ID NO: 2687, SEQ ID NO: 2844, and SEQ ID NO: 3001 ; SEQ ID NO: 2217, SEQ ID NO: 2374, SEQ ID NO: 2531, SEQ ID NO: 2688, SEQ ID NO: 2845, and SEQ ID NO: 3002 ; SEQ ID NO: 2218, SEQ ID NO: 2375, SEQ ID NO: 2532, SEQ ID NO: 2689, SEQ ID NO: 2846, and SEQ ID NO: 3003 ; SEQ ID NO: 2219, SEQ ID NO: 2376, SEQ ID NO: 2533, SEQ ID NO: 2690, SEQ ID NO: 2847, and SEQ ID NO: 3004 ; SEQ ID NO: 2220, SEQ ID NO: 2377, SEQ ID NO: 2534, SEQ ID NO: 2691, SEQ ID NO: 2848, and SEQ ID NO: 3005 ; SEQ ID NO: 2221, SEQ ID NO: 2378, SEQ ID NO: 2535, SEQ ID NO: 2692, SEQ ID NO: 2849, and SEQ ID NO: 3006 ; SEQ ID NO: 2222, SEQ ID NO: 2379, SEQ ID NO: 2536, SEQ ID NO: 2693, SEQ ID NO: 2850, and

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SEQ ID NO: 3058 ; SEQ ID NO: 2274, SEQ ID NO: 2431, SEQ ID NO: 2588, SEQ ID NO: 2745, SEQ ID NO: 2902, and SEQ ID NO: 3059 ; SEQ ID NO: 2275, SEQ ID NO: 2432, SEQ ID NO: 2589, SEQ ID NO: 2746, SEQ ID NO: 2903, and SEQ ID NO: 3060 ; SEQ ID NO: 2276, SEQ ID NO: 2433, SEQ ID NO: 2590, SEQ ID NO: 2747, SEQ ID NO: 2904, and SEQ ID NO: 3061 ; SEQ ID NO: 2277, SEQ ID NO: 2434, SEQ ID NO: 2591, SEQ ID NO: 2748, SEQ ID NO: 2905, and SEQ ID NO: 3062 ; SEQ ID NO: 2278, SEQ ID NO: 2435, SEQ ID NO: 2592, SEQ ID NO: 2749, SEQ ID NO: 2906, and SEQ ID NO: 3063 ; SEQ ID NO: 2279, SEQ ID NO: 2436, SEQ ID NO: 2593, SEQ ID NO: 2750, SEQ ID NO: 2907, and SEQ ID NO: 3064 ; SEQ ID NO: 2280, SEQ ID NO: 2437, SEQ ID NO: 2594, SEQ ID NO: 2751, SEQ ID NO: 2908, and SEQ ID NO: 3065 ; SEQ ID NO: 2281, SEQ ID NO: 2438, SEQ ID NO: 2595, SEQ ID NO: 2752, SEQ ID NO: 2909, and SEQ ID NO: 3066 ; SEQ ID NO: 2282, SEQ ID 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 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 ; 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: 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, 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 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 ; 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: 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, 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 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 ; 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: 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, 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 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 ; 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: 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, 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 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.

[0265] In another aspect, an antigen binding protein includes 1, 2, 3, 4, 5, or 6 variant forms of the CDRs listed in TABLES 4A and 4B, each having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% sequence identity to a CDR sequence listed in TABLES 4A and 4B. Some antigen binding proteins include 1, 2, 3, 4, 5, or 6 of the CDRs listed in TABLES 4A and 4B, each or collectively differing by no more than 1, 2, 3, 4 or 5 amino acids from the CDRs listed in this table.

[0266] In various other embodiments, the antigen binding protein is derived from such antibodies. For instance, in one aspect, the antigen binding protein comprises 1, 2, 3, 4, 5 or all 6 of the CDRs listed in one of the rows for any particular antibody listed in TABLES 4A and 4B. In another aspect, an antigen binding protein includes 1, 2, 3, 4, 5, or 6 variant forms of the CDRs listed in one of the rows for an antibody in TABLES 4A and 4B, each CDR having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% sequence identity to a CDR sequence listed in TABLES 4A and 4B. Some antigen binding proteins include 1, 2, 3, 4, 5, or 6 of the CDRs listed in one of the rows of TABLES 4A and 4B, each differing by no more than 1, 2, 3, 4 or 5 amino acids from the CDRs listed in these tables. In another aspect, the antigen binding protein comprises all 6 of the CDRs listed in a row of TABLES 4A and 4B and the total number of amino acid changes to the CDRs collectively is no more than 1, 2, 3, 4, or 5 amino acids.

[0267] 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. In one embodiment the antibody or fragment thereof comprises a heavy chain comprising a sequence selected from the group consisting of SEQ ID NOs: 472-628. 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. 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 and a heavy chain comprising SEQ ID NO: 494; a light chain comprising SEQ ID NO: 338 and a heavy chain comprising SEQ ID NO: 495; a light chain comprising SEQ ID NO: 339 and a heavy chain comprising SEQ ID NO: 496; a light chain comprising SEQ ID NO: 340 and a heavy chain comprising SEQ ID NO: 497; a light chain comprising SEQ ID NO: 341 and a heavy chain comprising SEQ ID NO: 498; a light chain comprising SEQ ID NO: 342 and a heavy chain comprising SEQ ID NO: 499; a light chain comprising SEQ ID NO: 343 and a heavy chain comprising SEQ ID NO: 500; a light chain comprising SEQ ID NO: 344 and a heavy chain comprising SEQ ID NO: 501; a light chain comprising SEQ ID NO: 345 and a heavy chain comprising SEQ ID NO: 502; a light chain comprising SEQ ID NO: 346 and a heavy chain comprising SEQ ID NO: 503; a light chain comprising SEQ ID NO: 347 and a heavy chain comprising SEQ ID NO: 504; a light chain comprising SEQ ID NO: 348 and a heavy

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

[0268] 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. In one embodiment the antibody or fragment thereof comprises a heavy chain encoded by a polynucleotide sequence selected from the group consisting of SEQ ID NOs: 2042-2198. 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. In one embodiment the antibody or fragment thereof comprises a combination of light chain variable region and a heavy chain variable region selected from the group consisting of a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 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

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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.

[0269] In some aspects, the invention comprises an antibody or fragment thereof that binds to GIPR, wherein the antibody or fragment thereof binds to GIPR within a location corresponding to residues 123-134 of SEQ ID NO: 3141. In one embodiment, the antibody or fragment thereof binds to GIPR within the discontinuous epitope of residues 29-30 and 123-134 of SEQ ID NO: 3141. In some embodiments, when the antibody or fragment thereof is bound to GIPR, the antibody or fragment thereof when bound to GIPR is positioned 8 angstroms or less from at least one residue of GIPR (SEQ ID NO: 3141) selected from the group consisting of G29, Q30, T31, A32, G33, E34, L35, Y36, Q37, R38, W39, E40, R43, F65, D66, M67, Y68, V69, W71, P85, Y87, L88, P89, W90, R101, L111, W112, R113, H115, T116, C118, E119, N120, E122, K123, N124, E125, A126, L128, D129, Q130, R131, L132, I133, and L134. In some embodiments, when the antibody or fragment thereof is bound to GIPR, the antibody or fragment thereof when bound to GIPR is positioned 8 angstroms or less from at least one residue of GIPR (SEQ ID NO: 3141) selected from the group consisting of G29, Q30, K123, N124, E125, A126, L128, D129, Q130, R131, L132, I133, and L134. In some embodiments, when the antibody or fragment thereof is bound to GIPR, the antibody or fragment thereof when bound to GIPR is positioned 8 angstroms or less from at least one residue of GIPR (SEQ ID NO: 3141) selected from the group consisting of K123, N124, E125, A126, L128, D129, Q130, R131, L132, I133, and L134. In some embodiments, when the antibody or fragment thereof is bound to GIPR, the antibody or fragment thereof when bound to GIPR is positioned 8 angstroms or less from at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, or 13 residues of GIPR (SEQ ID NO: 3141) selected from the group consisting of G29, Q30, K123, N124, E125, A126, L128, D129, Q130, R131, L132, I133, and L134. In some embodiments, when the antibody or fragment thereof is bound to GIPR, the antibody or fragment thereof when bound to GIPR is positioned 8 angstroms or less from at least 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 residues of GIPR (SEQ ID NO: 3141) selected from the group consisting of K123, N124, E125, A126, L128, D129, Q130, R131, L132, I133, and L134.

[0270] In some embodiments, when the antibody or fragment thereof is bound to GIPR, the antibody or fragment thereof when bound to GIPR is positioned 5 angstroms or less from at

least one residue of GIPR (SEQ ID NO: 3141) selected from the group consisting of Q30, T31, A32, G33, E34, L35, Y36, Q37, W39, D66, M67, Y68, Y87, L88, P89, W90, R101, R113, H115, E119, K123, E125, L128, D129, L132, and I133. In some embodiments, when the antibody or fragment thereof is bound to GIPR, the antibody or fragment thereof when bound to GIPR is positioned 5 angstroms or less from at least one residue of GIPR (SEQ ID NO: 3141) selected from the group consisting of Q30, T31, K123, E125, L128, D129, L132, and I133. In some embodiments, when the antibody or fragment thereof is bound to GIPR, the antibody or fragment thereof when bound to GIPR is positioned 5 angstroms or less from at least one residue of GIPR (SEQ ID NO: 3141) selected from the group consisting of K123, E125, L128, D129, L132, and I133. In some embodiments, when the antibody or fragment thereof is bound to GIPR, the antibody or fragment thereof when bound to GIPR is positioned 5 angstroms or less from at least 2, 3, 4, 5, 6, 7, or 8 residues of GIPR (SEQ ID NO: 3141) selected from the group consisting of Q30, T31, K123, E125, L128, D129, L132, and I133. In some embodiments, when the antibody or fragment thereof is bound to GIPR, the antibody or fragment thereof when bound to GIPR is positioned 5 angstroms or less from at least 2, 3, 4, 5, or 6 residues of GIPR (SEQ ID NO: 3141) selected from the group consisting of K123, E125, L128, D129, L132, and I133.

[0271] In some aspects, the invention comprises an antibody or fragment thereof that binds to GIPR, wherein the antibody or fragment thereof binds to GIPR within a location corresponding to residues 102-107 of SEQ ID NO: 3141. In one embodiment, the antibody or fragment thereof binds to GIPR within the discontinuous epitope of residues 60-63 and 102-107 of SEQ ID NO: 3141. In some embodiments, when the antibody or fragment thereof is bound to GIPR, the antibody or fragment thereof when bound to GIPR is positioned 8 angstroms or less from at least one residue of GIPR (SEQ ID NO: 3141) selected from the group consisting of Q30, T31, A32, G33, E34, L35, Y36, W39, E40, R43, Q47, A60, C61, N62, G63, S64, F65, D66, M67, Y68, V69, W71, N77, P85, Y87, L88, P89, W90, V99, L100, R101, Q102, C103, G104, S105, D106, G107, Q108, W109, G110, L111, W112, R113, D114, H115, T116, Q117, C118, E119, N120, and P121. In some embodiments, when the antibody or fragment thereof is bound to GIPR, the antibody or fragment thereof when bound to GIPR is positioned 8 angstroms or less from at least one residue of GIPR (SEQ ID NO: 3141) selected from the group consisting of Q30, A60, C61, N62, G63, N77, L100, Q102, C103, G104, S105, D106, G107, W109, and G110. In some embodiments, when the antibody or fragment thereof is bound to GIPR, the antibody or fragment thereof when bound to GIPR is positioned 8 angstroms or less from at least one residue of GIPR (SEQ ID NO:

3141) selected from the group consisting of A60, C61, N62, G63, Q102, C103, G104, S105, D106, and G107. In some embodiments, when the antibody or fragment thereof is bound to GIPR, the antibody or fragment thereof when bound to GIPR is positioned 8 angstroms or less from at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 residues of GIPR (SEQ ID NO: 3141) selected from the group consisting of Q30, A60, C61, N62, G63, N77, L100, Q102, C103, G104, S105, D106, G107, W109, and G110. In some embodiments, when the antibody or fragment thereof is bound to GIPR, the antibody or fragment thereof when bound to GIPR is positioned 8 angstroms or less from at least 2, 3, 4, 5, 6, 7, 8, 9, or 10 residues of GIPR (SEQ ID NO: 3141) selected from the group consisting of A60, C61, N62, G63, Q102, C103, G104, S105, D106, and G107.

[0272] In some embodiments, when the antibody or fragment thereof is bound to GIPR, the antibody or fragment thereof when bound to GIPR is positioned 5 angstroms or less from at least one residue of GIPR (SEQ ID NO: 3141) selected from the group consisting of T31, A32, L35, Y36, W39, N62, S64, F65, D66, M67, Y68, W71, Y87, L88, P89, W90, R101, G104, S105, D106, Q108, W109, G110, L111, W112, R113, D114, H115, T116, and E119. In some embodiments, when the antibody or fragment thereof is bound to GIPR, the antibody or fragment thereof when bound to GIPR is positioned 5 angstroms or less from at least one residue of GIPR (SEQ ID NO: 3141) selected from the group consisting of T31, N62, S64, W71, R101, G104, S105, D106, Q108, W109, G110, L111, W112, D114, and T116. In some embodiments, when the antibody or fragment thereof is bound to GIPR, the antibody or fragment thereof when bound to GIPR is positioned 5 angstroms or less from at least one residue of GIPR (SEQ ID NO: 3141) selected from the group consisting of R101, G104, S105, D106, Q108, W109, G110, L111, W112, D114, and T116. In some embodiments, when the antibody or fragment thereof is bound to GIPR, the antibody or fragment thereof when bound to GIPR is positioned 5 angstroms or less from at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 residues of GIPR (SEQ ID NO: 3141) selected from the group consisting of T31, N62, S64, W71, R101, G104, S105, D106, Q108, W109, G110, L111, W112, D114, and T116. In some embodiments, when the antibody or fragment thereof is bound to GIPR, the antibody or fragment thereof when bound to GIPR is positioned 5 angstroms or less from at least 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 residues of GIPR (SEQ ID NO: 3141) selected from the group consisting of R101, G104, S105, D106, Q108, W109, G110, L111, W112, D114, and T116.

[0273] In some embodiments, when the antibody or fragment thereof is bound to GIPR, the antibody or fragment thereof when bound to GIPR is positioned 8 angstroms or less from at

least one residue of GIPR (SEQ ID NO: 3141) selected from the group consisting of A32, G33, E34, L35, Y36, Q37, R38, W39, E40, R43, F65, D66, M67, Y68, P85, Y87, L88, P89, W90, L111, W112, R113, D114, H115, C118, E119, N120, and P121. In some embodiments, when the antibody or fragment thereof is bound to GIPR, the antibody or fragment thereof when bound to GIPR is positioned 5 angstroms or less from at least one residue of GIPR (SEQ ID NO: 3141) selected from the group consisting of A32, G33, E34, L35, Y36, Q37, W39, E40, R43, D66, M67, Y87, L88, P89, W90, L111, W112, H115, E119, and N120. In some embodiments, when the antibody or fragment thereof is bound to GIPR, the antibody or fragment thereof when bound to GIPR is positioned 5 angstroms or less from at least one residue of GIPR (SEQ ID NO: 3141) selected from the group consisting of E34, L111, W112, and N120.

[0274] In some aspects, the invention comprises an antibody or fragment thereof that binds to GIPR, wherein the antibody or fragment thereof binds to GIPR within a location corresponding to residues 102-107 of SEQ ID NO: 3141. In one embodiment, the antibody or fragment thereof binds to GIPR within the discontinuous epitope of residues 60-63 and 102-107 of SEQ ID NO: 3141. In some embodiments, when the antibody or fragment thereof is bound to GIPR, the antibody or fragment thereof when bound to GIPR is positioned 8 angstroms or less from at least one residue of GIPR (SEQ ID NO: 3141) selected from the group consisting of Q30, T31, A32, G33, E34, L35, Y36, Q37, R38, W39, E40, R43, F65, D66, M67, Y68, V69, W71, P85, Y87, L88, P89, W90, V99, R101, L111, R113, D114, H115, T116, C118, E119, and N120. In some embodiments, when the antibody or fragment thereof is bound to GIPR, the antibody or fragment thereof when bound to GIPR is positioned 8 angstroms or less from Q30 of GIPR (SEQ ID NO: 3141).

[0275] In some embodiments, when the antibody or fragment thereof is bound to GIPR, the antibody or fragment thereof when bound to GIPR is positioned 5 angstroms or less from at least one residue of GIPR (SEQ ID NO: 3141) selected from the group consisting of Q30, T31, A32, G33, L35, Y36, Q37, W39, E40, R43, D66, M67, Y68, Y87, L88, P89, W90, R113, H115, and E119. In some embodiments, when the antibody or fragment thereof is bound to GIPR, the antibody or fragment thereof when bound to GIPR is positioned 5 angstroms or less from at least one residue of GIPR (SEQ ID NO: 3141) selected from the group consisting of Q30 and T31. In some embodiments, when the antibody or fragment thereof is bound to GIPR, the antibody or fragment thereof when bound to GIPR is positioned 5 angstroms or less from both Q30 and T31 of GIPR (SEQ ID NO: 3141).

[0276] In some aspects, the invention comprises an antibody that binds to GIPR, wherein the antibody binds to GIPR and reduces the likelihood that GIPR binds to GIP.

[0277] In some aspects, the invention comprises an antibody or fragment thereof that binds to GIPR, wherein the antibody or fragment thereof binds to GIPR within a location corresponding to residues 28-108 of SEQ ID NO: 231 of the heavy chain of the antibody or fragment thereof. In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 8 angstroms or less from at least one residue of the heavy chain of the antibody or fragment thereof selected from the group consisting of T28, F29, S30, N31, Y32, G33, A50, I51, W52, F53, D54, A55, S56, D57, K58, Y59, Y60, A61, D62, V64, K65, G66, R67, F68, T69, I70, S71, R72, D73, N74, S75, Q82, N84, S85, R98, D99, Q100, A101, I102, F103, G104, V105, V106, and D108 corresponding to the heavy chain of SEQ ID NO: 231. In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 8 angstroms or less from at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, or 44 residues of the heavy chain of the antibody or fragment thereof selected from the group consisting of T28, F29, S30, N31, Y32, G33, A50, I51, W52, F53, D54, A55, S56, D57, K58, Y59, Y60, A61, D62, V64, K65, G66, R67, F68, T69, I70, S71, R72, D73, N74, S75, Q82, N84, S85, R98, D99, Q100, A101, I102, F103, G104, V105, V106, and D108 corresponding to the heavy chain of SEQ ID NO: 231.

[0278] In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 5 angstroms or less from at least one residue of the heavy chain of the antibody or fragment thereof selected from the group consisting of S30, N31, Y32, W52, F53, D54, A55, S56, D57, K58, Y59, Y60, K65, G66, R67, T69, I70, S71, N84, Q100, A101, I102, F103, and V105 corresponding to the heavy chain of SEQ ID NO: 231. In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 5 angstroms or less from at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, or 24 residues of the heavy chain of the antibody or fragment thereof selected from the group consisting of S30, N31, Y32, W52, F53, D54, A55, S56, D57, K58, Y59, Y60, K65, G66, R67, T69, I70, S71, N84, Q100, A101, I102, F103, and V105 corresponding to the heavy chain of SEQ ID NO: 231.

[0279] In some aspects, the invention comprises an antibody or fragment thereof that binds to GIPR, wherein the antibody or fragment thereof binds to GIPR within a location corresponding to residues 29-96 of SEQ ID NO: 74 of the light chain of the antibody or fragment thereof. In some embodiments, when the antibody or fragment thereof is bound to

GIPR, GIPR is positioned 8 angstroms or less from at least one residue of the light chain of the antibody or fragment thereof selected from the group consisting of V29, S30, S31, N32, L33, L46, Y49, G50, T53, Q90, Y91, N92, N93, W94, P95, and L96 corresponding to the light chain of SEQ ID NO: 74. In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 8 angstroms or less from at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16 residues of the light chain of the antibody or fragment thereof selected from the group consisting of V29, S30, S31, N32, L33, L46, Y49, G50, T53, Q90, Y91, N92, N93, W94, P95, and L96 corresponding to the light chain of SEQ ID NO: 74.

[0280] In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 5 angstroms or less from at least one residue of the light chain of the antibody or fragment thereof selected from the group consisting of S30, N32, Y49, Y91, N92, N93, W94, and L96 corresponding to the light chain of SEQ ID NO: 74. In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 5 angstroms or less from at least 2, 3, 4, 5, 6, 7, or 8 residues of the light chain of the antibody or fragment thereof selected from the group consisting of S30, N32, Y49, Y91, N92, N93, W94, and L96 corresponding to the light chain of SEQ ID NO: 74.

[0281] In some aspects, the invention comprises an antibody or fragment thereof that binds to GIPR, wherein the antibody or fragment thereof binds to GIPR within a location corresponding to residues 28-108 of SEQ ID NO: 231 of the heavy chain of the antibody or fragment thereof and within a location corresponding to residues 29-96 of SEQ ID NO: 74 of the light chain of the antibody or fragment thereof. In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 8 angstroms or less from at least one residue of the heavy chain of the antibody or fragment thereof selected from the group consisting of T28, F29, S30, N31, Y32, G33, A50, I51, W52, F53, D54, A55, S56, D57, K58, Y59, Y60, A61, D62, V64, K65, G66, R67, F68, T69, I70, S71, R72, D73, N74, S75, Q82, N84, S85, R98, D99, Q100, A101, I102, F103, G104, V105, V106, and D108 corresponding to the heavy chain of SEQ ID NO: 231; and 8 angstroms or less from at least one residue of the light chain of the antibody or fragment thereof selected from the group consisting of V29, S30, S31, N32, L33, L46, Y49, G50, T53, Q90, Y91, N92, N93, W94, P95, and L96 corresponding to the light chain of SEQ ID NO: 74. In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 8 angstroms or less from at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, or 44 residues of the heavy chain of the antibody or fragment thereof selected from the group consisting of T28, F29,

S30, N31, Y32, G33, A50, I51, W52, F53, D54, A55, S56, D57, K58, Y59, Y60, A61, D62, V64, K65, G66, R67, F68, T69, I70, S71, R72, D73, N74, S75, Q82, N84, S85, R98, D99, Q100, A101, I102, F103, G104, V105, V106, and D108 corresponding to the heavy chain of SEQ ID NO: 231; and 8 angstroms or less from at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16 residues of the light chain of the antibody or fragment thereof selected from the group consisting of V29, S30, S31, N32, L33, L46, Y49, G50, T53, Q90, Y91, N92, N93, W94, P95, and L96 corresponding to the light chain of SEQ ID NO: 74.

[0282] In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 5 angstroms or less from at least one residue of the heavy chain of the antibody or fragment thereof selected from the group consisting of S30, N31, Y32, W52, F53, D54, A55, S56, D57, K58, Y59, Y60, K65, G66, R67, T69, I70, S71, N84, Q100, A101, I102, F103, and V105 corresponding to the heavy chain of SEQ ID NO: 231; and 5 angstroms or less from at least one residue of the light chain of the antibody or fragment thereof selected from the group consisting of S30, N32, Y49, Y91, N92, N93, W94, and L96 corresponding to the light chain of SEQ ID NO: 74. In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 5 angstroms or less from at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, or 24 residues of the heavy chain of the antibody or fragment thereof selected from the group consisting of S30, N31, Y32, W52, F53, D54, A55, S56, D57, K58, Y59, Y60, K65, G66, R67, T69, I70, S71, N84, Q100, A101, I102, F103, and V105 corresponding to the heavy chain of SEQ ID NO: 231; and 5 angstroms or less from at least 2, 3, 4, 5, 6, 7, or 8 residues of the light chain of the antibody or fragment thereof selected from the group consisting of S30, N32, Y49, Y91, N92, N93, W94, and L96 corresponding to the light chain of SEQ ID NO: 74.

[0283] In some aspects, the invention comprises an antibody or fragment thereof that binds to GIPR, wherein the antibody or fragment thereof binds to GIPR within a location corresponding to residues 1-118 of SEQ ID NO: 294 of the heavy chain of the antibody or fragment thereof. In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 8 angstroms or less from at least one residue of the heavy chain of the antibody or fragment thereof selected from the group consisting of Q1, M2, S25, G26, Y27, T28, F29, T30, G31, Y32, N54, R98, G99, G100, D101, Y102, V103, F104, G105, T106, Y107, R108, P109, H110, Y111, Y112, Y113, G114, M115, D116, V117, and W118 corresponding to the heavy chain of SEQ ID NO: 294. In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 8 angstroms or less from

at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, or 32 residues of the heavy chain of the antibody or fragment thereof selected from the group consisting of Q1, M2, S25, G26, Y27, T28, F29, T30, G31, Y32, N54, R98, G99, G100, D101, Y102, V103, F104, G105, T106, Y107, R108, P109, H110, Y111, Y112, Y113, G114, M115, D116, V117, and W118 corresponding to the heavy chain of SEQ ID NO: 294.

[0284] In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 5 angstroms or less from at least one residue of the heavy chain of the antibody or fragment thereof selected from the group consisting of M2, G26, Y27, T28, Y32, R98, G100, D101, Y102, F104, G105, Y107, H110, Y111, Y112, Y113, and D116 corresponding to the heavy chain of SEQ ID NO: 294. In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 5 angstroms or less from at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 residues of the heavy chain of the antibody or fragment thereof selected from the group consisting of M2, G26, Y27, T28, Y32, R98, G100, D101, Y102, F104, G105, Y107, H110, Y111, Y112, Y113, and D116 corresponding to the heavy chain of SEQ ID NO: 294.

[0285] In some aspects, the invention comprises an antibody or fragment thereof that binds to GIPR, wherein the antibody or fragment thereof binds to GIPR within a location corresponding to residues 32-63 of SEQ ID NO: 137 of the light chain of the antibody or fragment thereof. In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 8 angstroms or less from at least one residue of the light chain of the antibody or fragment thereof selected from the group consisting of Q32, T33, N35, Y37, K46, L47, L48, I49, Y50, T51, N53, Q54, R55, P56, S57, G58, V59, P60, D61, R62, and F63 corresponding to the light chain of SEQ ID NO: 137. In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 8 angstroms or less from at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or 21 residues of the light chain of the antibody or fragment thereof selected from the group consisting of Q32, T33, N35, Y37, K46, L47, L48, I49, Y50, T51, N53, Q54, R55, P56, S57, G58, V59, P60, D61, R62, and F63 corresponding to the light chain of SEQ ID NO: 137.

[0286] In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 5 angstroms or less from at least one residue of the light chain of the antibody or fragment thereof selected from the group consisting of L47, Y50, Q54, R55, P56, S57, G58, V59, or D61 corresponding to the light chain of SEQ ID NO: 137. In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 5

angstroms or less from at least 2, 3, 4, 5, 6, 7, 8, or 9 residues of the light chain of the antibody or fragment thereof selected from the group consisting of L47, Y50, Q54, R55, P56, S57, G58, V59, or D61 corresponding to the light chain of SEQ ID NO: 137.

[0287] In some aspects, the invention comprises an antibody or fragment thereof that binds to GIPR, wherein the antibody or fragment thereof binds to GIPR within a location corresponding to residues 1-118 of SEQ ID NO: 294 of the heavy chain of the antibody or fragment thereof and within a location corresponding to residues 32-63 of SEQ ID NO: 137 of the light chain of the antibody or fragment thereof. In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 8 angstroms or less from at least one residue of the heavy chain of the antibody or fragment thereof selected from the group consisting of Q1, M2, S25, G26, Y27, T28, F29, T30, G31, Y32, N54, R98, G99, G100, D101, Y102, V103, F104, G105, T106, Y107, R108, P109, H110, Y111, Y112, Y113, G114, M115, D116, V117, and W118 corresponding to the heavy chain of SEQ ID NO: 294; and 8 angstroms or less from at least one residue of the light chain of the antibody or fragment thereof selected from the group consisting of Q32, T33, N35, Y37, K46, L47, L48, I49, Y50, T51, N53, Q54, R55, P56, S57, G58, V59, P60, D61, R62, and F63 corresponding to the light chain of SEQ ID NO: 137. In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 8 angstroms or less from at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, or 32 residues of the heavy chain of the antibody or fragment thereof selected from the group consisting of Q1, M2, S25, G26, Y27, T28, F29, T30, G31, Y32, N54, R98, G99, G100, D101, Y102, V103, F104, G105, T106, Y107, R108, P109, H110, Y111, Y112, Y113, G114, M115, D116, V117, and W118 corresponding to the heavy chain of SEQ ID NO: 294; and 8 angstroms or less from at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or 21 residues of the light chain of the antibody or fragment thereof selected from the group consisting of Q32, T33, N35, Y37, K46, L47, L48, I49, Y50, T51, N53, Q54, R55, P56, S57, G58, V59, P60, D61, R62, and F63 corresponding to the light chain of SEQ ID NO: 137.

[0288] In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 5 angstroms or less from at least one residue of the heavy chain of the antibody or fragment thereof selected from the group consisting of M2, G26, Y27, T28, Y32, R98, G100, D101, Y102, F104, G105, Y107, H110, Y111, Y112, Y113, and D116 corresponding to the heavy chain of SEQ ID NO: 294; and 5 angstroms or less from at least one residue of the light chain of the antibody or fragment thereof selected from the group consisting of L47, Y50, Q54, R55, P56, S57, G58, V59, or D61 corresponding to the light

chain of SEQ ID NO: 137. In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 5 angstroms or less from at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 residues of the heavy chain of the antibody or fragment thereof selected from the group consisting of M2, G26, Y27, T28, Y32, R98, G100, D101, Y102, F104, G105, Y107, H110, Y111, Y112, Y113, and D116 corresponding to the heavy chain of SEQ ID NO: 294; and 5 angstroms or less from at least 2, 3, 4, 5, 6, 7, 8, or 9 residues of the light chain of the antibody or fragment thereof selected from the group consisting of L47, Y50, Q54, R55, P56, S57, G58, V59, or D61 corresponding to the light chain of SEQ ID NO: 137.

[0289] In some aspects, the invention comprises an antibody or fragment thereof that binds to GIPR, wherein the antibody or fragment thereof binds to GIPR within a location corresponding to residues 26-110 of SEQ ID NO: 208 of the heavy chain of the antibody or fragment thereof. In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 8 angstroms or less from at least one residue of the heavy chain of the antibody or fragment thereof selected from the group consisting of G26, F27, T28, F29, S30, Y31, F32, W52, Y53, D54, S56, N57, Y59, N74, N77, R98, D99, G100, T101, I102, F103, G104, V105, L106, L107, D109, and Y110 corresponding to the heavy chain of SEQ ID NO: 208. In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 8 angstroms or less from at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, or 27 residues of the heavy chain of the antibody or fragment thereof selected from the group consisting of G26, F27, T28, F29, S30, Y31, F32, W52, Y53, D54, S56, N57, Y59, N74, N77, R98, D99, G100, T101, I102, F103, G104, V105, L106, L107, D109, and Y110 corresponding to the heavy chain of SEQ ID NO: 208.

[0290] In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 5 angstroms or less from at least one residue of the heavy chain of the antibody or fragment thereof selected from the group consisting of T28, Y31, F32, W52, Y53, R98, G100, T101, I102, F103, G104, V105, and L106 corresponding to the heavy chain of SEQ ID NO: 208. In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 5 angstroms or less from at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 residues of the heavy chain of the antibody or fragment thereof selected from the group consisting of T28, Y31, F32, W52, Y53, R98, G100, T101, I102, F103, G104, V105, and L106 corresponding to the heavy chain of SEQ ID NO: 208.

[0291] In some aspects, the invention comprises an antibody or fragment thereof that binds to GIPR, wherein the antibody or fragment thereof binds to GIPR within a location corresponding to residues 29-96 of SEQ ID NO: 51 of the light chain of the antibody or fragment thereof. In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 8 angstroms or less from at least one residue of the light chain of the antibody or fragment thereof selected from the group consisting of I29, R30, D31, Y32, L33, L46, I48, Y49, G50, A51, S52, S53, L54, Q55, S56, Q90, H91, N92, N93, Y94, and F96 corresponding to the light chain of SEQ ID NO: 51. In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 8 angstroms or less from at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or 21 residues of the light chain of the antibody or fragment thereof selected from the group consisting of I29, R30, D31, Y32, L33, L46, I48, Y49, G50, A51, S52, S53, L54, Q55, S56, Q90, H91, N92, N93, Y94, and F96 corresponding to the light chain of SEQ ID NO: 51.

[0292] In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 5 angstroms or less from at least one residue of the light chain of the antibody or fragment thereof selected from the group consisting of Y32, Y49, G50, S53, Q55, H91, N92, N93, and Y94 corresponding to the light chain of SEQ ID NO: 51. In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 5 angstroms or less from at least 2, 3, 4, 5, 6, 7, 8, or 9 residues of the light chain of the antibody or fragment thereof selected from the group consisting Y32, Y49, G50, S53, Q55, H91, N92, N93, and Y94 corresponding to the light chain of SEQ ID NO: 51.

[0293] In some aspects, the invention comprises an antibody or fragment thereof that binds to GIPR, wherein the antibody or fragment thereof binds to GIPR within a location corresponding to residues 26-110 of SEQ ID NO: 208 of the heavy chain of the antibody or fragment thereof and within a location corresponding to residues 29-96 of SEQ ID NO: 51 of the light chain of the antibody or fragment thereof. In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 8 angstroms or less from at least one residue of the heavy chain of the antibody or fragment thereof selected from the group consisting of G26, F27, T28, F29, S30, Y31, F32, W52, Y53, D54, S56, N57, Y59, N74, N77, R98, D99, G100, T101, I102, F103, G104, V105, L106, L107, D109, and Y110 corresponding to the heavy chain of SEQ ID NO: 208; and 8 angstroms or less from at least one residue of the light chain of the antibody or fragment thereof selected from the group consisting of I29, R30, D31, Y32, L33, L46, I48, Y49, G50, A51, S52, S53, L54, Q55, S56, Q90, H91, N92, N93, Y94, and F96 corresponding to the light chain of SEQ ID NO: 51. In

some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 8 angstroms or less from at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, or 27 residues of the heavy chain of the antibody or fragment thereof selected from the group consisting of G26, F27, T28, F29, S30, Y31, F32, W52, Y53, D54, S56, N57, Y59, N74, N77, R98, D99, G100, T101, I102, F103, G104, V105, L106, L107, D109, and Y110 corresponding to the heavy chain of SEQ ID NO: 208; and 8 angstroms or less from at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or 21 residues of the light chain of the antibody or fragment thereof selected from the group consisting of I29, R30, D31, Y32, L33, L46, I48, Y49, G50, A51, S52, S53, L54, Q55, S56, Q90, H91, N92, N93, Y94, and F96 corresponding to the light chain of SEQ ID NO: 51.

[0294] In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 5 angstroms or less from at least one residue of the heavy chain of the antibody or fragment thereof selected from the group consisting of T28, Y31, F32, W52, Y53, R98, G100, T101, I102, F103, G104, V105, and L106 corresponding to the heavy chain of SEQ ID NO: 208; and 5 angstroms or less from at least one residue of the light chain of the antibody or fragment thereof selected from the group consisting of Y32, Y49, G50, S53, Q55, H91, N92, N93, and Y94 corresponding to the light chain of SEQ ID NO: 51. In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 5 angstroms or less from at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 residues of the heavy chain of the antibody or fragment thereof selected from the group consisting of T28, Y31, F32, W52, Y53, R98, G100, T101, I102, F103, G104, V105, and L106 corresponding to the heavy chain of SEQ ID NO: 208; and 5 angstroms or less from at least 2, 3, 4, 5, 6, 7, 8, or 9 residues of the light chain of the antibody or fragment thereof selected from the group consisting Y32, Y49, G50, S53, Q55, H91, N92, N93, and Y94 corresponding to the light chain of SEQ ID NO: 51.

[0295] In some aspects, the invention comprises an antibody or fragment thereof that binds to GIPR, wherein the antibody or fragment thereof binds to GIPR within a location corresponding to residues 30-106 of SEQ ID NO: 171 of the heavy chain of the antibody or fragment thereof. In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 8 angstroms or less from at least one residue of the heavy chain of the antibody or fragment thereof selected from the group consisting of S30, S31, Y32, Y33, Y52, R97, D98, V99, A100, V101, A102, G103, F104, D105, and Y106 corresponding to the heavy chain of SEQ ID NO: 171. In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 8 angstroms or less from at least 2, 3, 4, 5, 6, 7,

8, 9, 10, 11, 12, 13, 14, or 15 residues of the heavy chain of the antibody or fragment thereof selected from the group consisting of S30, S31, Y32, Y33, Y52, R97, D98, V99, A100, V101, A102, G103, F104, D105, and Y106 corresponding to the heavy chain of SEQ ID NO: 171.

[0296] In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 5 angstroms or less from at least one residue of the heavy chain of the antibody or fragment thereof selected from the group consisting of S30, S31, Y32, Y52, R97, D98, V99, A100, V101, A102, and D105 corresponding to the heavy chain of SEQ ID NO: 171. In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 5 angstroms or less from at least 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 residues of the heavy chain of the antibody or fragment thereof selected from the group consisting of S30, S31, Y32, Y52, R97, D98, V99, A100, V101, A102, and D105 corresponding to the heavy chain of SEQ ID NO: 171.

[0297] In some aspects, the invention comprises an antibody or fragment thereof that binds to GIPR, wherein the antibody or fragment thereof binds to GIPR within a location corresponding to residues 27-94 of SEQ ID NO: 14 of the light chain of the antibody or fragment thereof. In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 8 angstroms or less from at least one residue of the light chain of the antibody or fragment thereof selected from the group consisting of Q27, G28, L29, I30, I31, W32, A34, L46, L47, I48, Y49, A50, A51, S52, S53, L54, Q55, S56, G57, S65, G66, S67, G68, F71, Q90, T91, N92, S93, and F94 corresponding to the light chain of SEQ ID NO: 14. In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 8 angstroms or less from at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, or 29 residues of the light chain of the antibody or fragment thereof selected from the group consisting of Q27, G28, L29, I30, I31, W32, A34, L46, L47, I48, Y49, A50, A51, S52, S53, L54, Q55, S56, G57, S65, G66, S67, G68, F71, Q90, T91, N92, S93, and F94 corresponding to the light chain of SEQ ID NO: 14.

[0298] In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 5 angstroms or less from at least one residue of the light chain of the antibody or fragment thereof selected from the group consisting of I30, I31, W32, L46, Y49, S52, S53, L54, Q55, S56, S67, T91, and N92 corresponding to the light chain of SEQ ID NO: 14. In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 5 angstroms or less from at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, or 13 residues of the light chain of the antibody or fragment thereof selected from the group consisting I30,

I31, W32, L46, Y49, S52, S53, L54, Q55, S56, S67, T91, and N92 corresponding to the light chain of SEQ ID NO: 14.

[0299] In some aspects, the invention comprises an antibody or fragment thereof that binds to GIPR, wherein the antibody or fragment thereof binds to GIPR within a location corresponding to residues 30-106 of SEQ ID NO: 171 of the heavy chain of the antibody or fragment thereof and corresponding to residues 27-94 of SEQ ID NO: 14 of the light chain of the antibody or fragment thereof. In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 8 angstroms or less from at least one residue of the heavy chain of the antibody or fragment thereof selected from the group consisting of S30, S31, Y32, Y33, Y52, R97, D98, V99, A100, V101, A102, G103, F104, D105, and Y106 corresponding to the heavy chain of SEQ ID NO: 171; and 8 angstroms or less from at least one residue of the light chain of the antibody or fragment thereof selected from the group consisting of Q27, G28, L29, I30, I31, W32, A34, L46, L47, I48, Y49, A50, A51, S52, S53, L54, Q55, S56, G57, S65, G66, S67, G68, F71, Q90, T91, N92, S93, and F94 corresponding to the light chain of SEQ ID NO: 14. In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 8 angstroms or less from at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 residues of the heavy chain of the antibody or fragment thereof selected from the group consisting of S30, S31, Y32, Y33, Y52, R97, D98, V99, A100, V101, A102, G103, F104, D105, and Y106 corresponding to the heavy chain of SEQ ID NO: 171; and 8 angstroms or less from at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, or 29 residues of the light chain of the antibody or fragment thereof selected from the group consisting of Q27, G28, L29, I30, I31, W32, A34, L46, L47, I48, Y49, A50, A51, S52, S53, L54, Q55, S56, G57, S65, G66, S67, G68, F71, Q90, T91, N92, S93, and F94 corresponding to the light chain of SEQ ID NO: 14.

[0300] In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 5 angstroms or less from at least one residue of the heavy chain of the antibody or fragment thereof selected from the group consisting of S30, S31, Y32, Y52, R97, D98, V99, A100, V101, A102, and D105 corresponding to the heavy chain of SEQ ID NO: 171; and 5 angstroms or less from at least one residue of the light chain of the antibody or fragment thereof selected from the group consisting of I30, I31, W32, L46, Y49, S52, S53, L54, Q55, S56, S67, T91, and N92 corresponding to the light chain of SEQ ID NO: 14. In some embodiments, when the antibody or fragment thereof is bound to GIPR, GIPR is positioned 5 angstroms or less from at least 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 residues of the heavy chain of the antibody or fragment thereof selected from the group consisting of S30,

S31, Y32, Y52, R97, D98, V99, A100, V101, A102, and D105 corresponding to the heavy chain of SEQ ID NO: 171; and 5 angstroms or less from at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, or 13 residues of the light chain of the antibody or fragment thereof selected from the group consisting I30, I31, W32, L46, Y49, S52, S53, L54, Q55, S56, S67, T91, and N92 corresponding to the light chain of SEQ ID NO: 14.

[0301] 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.

[0302] In another embodiment, the antigen binding protein consists of a just a light or a heavy chain polypeptide as set forth in TABLE 5.

[0303] 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.

[0304] 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.

[0305] 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:

[0306] all 6 of the CDRs listed for any antibody listed in TABLES 4A and 4B;

[0307] a VH and a VL listed for any antibody listed in TABLE 3; or

[0308] two light chains and two heavy chains as specified for any antibody listed in TABLE 5.

[0309] The antigen binding proteins that are provided include monoclonal antibodies that bind to GIPR. Monoclonal antibodies may be produced using any technique known in the art, e.g., by immortalizing spleen cells harvested from the transgenic animal after completion of the immunization schedule. The spleen cells can be immortalized using any technique known in the art, e.g., by fusing them with myeloma cells to produce hybridomas. Myeloma cells for use in hybridoma-producing fusion procedures preferably are non-antibody-producing, have high fusion efficiency, and enzyme deficiencies that render them incapable of growing in certain selective media which support the growth of only the desired fused cells (hybridomas). Examples of suitable cell lines for use in mouse fusions include Sp-20, P3-X63/Ag8, P3-X63-Ag8.653, NS1/1.Ag 4 1, Sp210-Ag14, FO, NSO/U, MPC-11, MPC11-X45-GTG 1.7 and S194/5XXO Bul; examples of cell lines used in rat fusions include R210.RCY3, Y3-Ag 1.2.3, IR983F and 4B210. Other cell lines useful for cell fusions are U-266, GM1500-GRG2, LICR-LON-HMy2 and UC729-6.

[0310] In some instances, a hybridoma cell line is produced by immunizing an animal (e.g., a transgenic animal having human immunoglobulin sequences) with a GIPR immunogen; harvesting spleen cells from the immunized animal; fusing the harvested spleen cells to a myeloma cell line, thereby generating hybridoma cells; establishing hybridoma cell lines

from the hybridoma cells, and identifying a hybridoma cell line that produces an antibody that binds a GIPR polypeptide. Such hybridoma cell lines, and anti-GIPR monoclonal antibodies produced by them, are aspects of the present application.

[0311] 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.

[0312] Chimeric and humanized antibodies based upon the foregoing sequences are also provided. Monoclonal antibodies for use as therapeutic agents may be modified in various ways prior to use. One example is a chimeric antibody, which is an antibody composed of protein segments from different antibodies that are covalently joined to produce functional immunoglobulin light or heavy chains or immunologically functional portions thereof. Generally, a portion of the heavy chain and/or light chain is identical with or homologous to a corresponding sequence in antibodies derived from a particular species or belonging to a particular antibody class or subclass, while the remainder of the chain(s) is/are identical with or homologous to a corresponding sequence in antibodies derived from another species or belonging to another antibody class or subclass. For methods relating to chimeric antibodies, *see*, for example, United States Patent No. 4,816,567; and Morrison *et al.*, 1985, *Proc. Natl. Acad. Sci. USA* 81:6851-6855, which are hereby incorporated by reference. CDR grafting is described, for example, in United States Patent No. 6,180,370, No. 5,693,762, No. 5,693,761, No. 5,585,089, and No. 5,530,101.

[0313] 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.

[0314] 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).

[0315] 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.

[0316] In certain embodiments, constant regions from species other than human can be used along with the human variable region(s) to produce hybrid antibodies.

[0317] 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.

[0318] 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.

[0319] 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.

[0320] 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.

[0321] 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).

[0322] 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.

[0323] 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.

[0324] Naturally-occurring amino acids may be divided into classes based on common side chain properties:

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

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

[0327] 3) acidic: Asp, Glu;

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

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

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

[0331] 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.

[0332] 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.

[0333] In making such changes, according to certain embodiments, the hydropathic index of amino acids may be considered. The hydropathic profile of a protein is calculated by assigning each amino acid a numerical value ("hydropathy index") and then repetitively averaging these values along the peptide chain. Each amino acid has been assigned a hydropathic index on the basis of its hydrophobicity and charge characteristics. They are: isoleucine (+4.5); valine (+4.2); leucine (+3.8); phenylalanine (+2.8); cysteine/cystine (+2.5); methionine (+1.9); alanine (+1.8); glycine (-0.4); threonine (-0.7); serine (-0.8); tryptophan (-0.9); tyrosine (-1.3); proline (-1.6); histidine (-3.2); glutamate (-3.5); glutamine (-3.5); aspartate (-3.5); asparagine (-3.5); lysine (-3.9); and arginine (-4.5).

[0334] The importance of the hydropathic profile in conferring interactive biological function on a protein is understood in the art (*see, e.g., Kyte et al., 1982, J. Mol. Biol.* 157:105-131). It is known that certain amino acids may be substituted for other amino acids having a similar hydropathic index or score and still retain a similar biological activity. In making changes based upon the hydropathic index, in certain embodiments, the substitution of amino acids whose hydropathic indices are within ± 2 is included. In some aspects, those which are within ± 1 are included, and in other aspects, those within ± 0.5 are included.

[0335] It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity, particularly where the biologically functional protein or peptide thereby created is intended for use in immunological embodiments, as in the present case. In certain embodiments, the greatest local average hydrophilicity of a protein, as governed by the hydrophilicity of its adjacent amino acids, correlates with its immunogenicity and antigen-binding or immunogenicity, that is, with a biological property of the protein.

[0336] 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±1); alanine (-0.5); histidine (-0.5); cysteine (-1.0); methionine (-1.3); valine (-1.5); leucine (-1.8); isoleucine (-1.8); tyrosine (-2.3); phenylalanine (-2.5) and tryptophan (-3.4). In making changes based upon similar hydrophilicity values, in certain embodiments, the substitution of amino acids whose hydrophilicity values are within ± 2 is included, in other embodiments, those which are within ± 1 are included, and in still other embodiments, those within ± 0.5 are included. In some instances, one may also identify epitopes from primary amino acid sequences on the basis of hydrophilicity. These regions are also referred to as “epitopic core regions.”

[0337] 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

[0338] 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.

[0339] 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.

[0340] 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.

[0341] A number of scientific publications have been devoted to the prediction of secondary structure. See, Moulton, 1996, *Curr. Op. in Biotech.* 7:422-427; Chou *et al.*, 1974, *Biochem.* 13:222-245; Chou *et al.*, 1974, *Biochemistry* 113:211-222; Chou *et al.*, 1978, *Adv. Enzymol. Relat. Areas Mol. Biol.* 47:45-148; Chou *et al.*, 1979, *Ann. Rev. Biochem.* 47:251-276; and Chou *et al.*, 1979, *Biophys. J.* 26:367-384. Moreover, computer programs are currently available to assist with predicting secondary structure. One method of predicting secondary structure is based upon homology modeling. For example, two polypeptides or proteins that have a sequence identity of greater than 30%, or similarity greater than 40% can

have similar structural topologies. The recent growth of the protein structural database (PDB) has provided enhanced predictability of secondary structure, including the potential number of folds within a polypeptide's or protein's structure. *See, Holm et al.*, 1999, *Nucl. Acid. Res.* 27:244-247. It has been suggested (Brenner *et al.*, 1997, *Curr. Op. Struct. Biol.* 7:369-376) that there are a limited number of folds in a given polypeptide or protein and that once a critical number of structures have been resolved, structural prediction will become dramatically more accurate.

[0342] 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*).

[0343] 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.

[0344] 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.

[0345] 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).

[0346] 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.

[0347] 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.

[0348] 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).

[0349] 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.

[0350] 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.

[0351] 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.

[0352] 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” fluore, or proteinaceous fluore.

[0353] 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.

[0354] 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).

[0355] 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.

[0356] 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.

[0357] 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.

[0358] 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.

[0359] 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.

[0360] 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.

[0361] 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.

[0362] Probes based on the sequence of a nucleic acid can be used to detect the nucleic acid or similar nucleic acids, for example, transcripts encoding a polypeptide. The probe can comprise a label group, *e.g.*, a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used to identify a cell that expresses the polypeptide.

[0363] Another aspect provides vectors comprising a nucleic acid encoding a polypeptide or a portion thereof (*e.g.*, a fragment containing one or more CDRs or one or more variable region domains). Examples of vectors include, but are not limited to, plasmids, viral vectors, non-episomal mammalian vectors and expression vectors, for example, recombinant expression vectors. The recombinant expression vectors can comprise a nucleic acid in a form suitable for expression of the nucleic acid in a host cell. The recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operably linked to the nucleic acid sequence to be expressed. Regulatory sequences include those that direct constitutive expression of a nucleotide sequence in many types of host cells (*e.g.*, SV40 early gene enhancer, Rous sarcoma virus promoter and cytomegalovirus promoter), those that direct expression of the nucleotide sequence only in certain host cells (*e.g.*, tissue-specific regulatory sequences, *see*, Voss *et al.*, 1986, *Trends Biochem. Sci.* 11:287, Maniatis *et al.*, 1987, *Science* 236:1237, incorporated by reference herein in their entireties), and those that direct inducible expression of a nucleotide sequence in response to particular treatment or condition (*e.g.*, the metallothionin promoter in mammalian cells and the tet-responsive and/or streptomycin responsive promoter in both prokaryotic and eukaryotic systems (*see, id.*). It will be appreciated by those skilled in

the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein.

[0364] Another aspect provides host cells into which a recombinant expression vector has been introduced. A host cell can be any prokaryotic cell (for example, *E. coli*) or eukaryotic cell (for example, yeast, insect, or mammalian cells (*e.g.*, CHO cells)). Vector DNA can be introduced into prokaryotic or eukaryotic cells *via* conventional transformation or transfection techniques. For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, for resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die), among other methods.

[0365] 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.

[0366] 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).

[0367] 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.

[0368] Recombinant expression constructs typically comprise a nucleic acid molecule encoding a polypeptide comprising one or more of the following: one or more CDRs provided herein; a light chain constant region; a light chain variable region; a heavy chain constant region (*e.g.*, C_H1, C_H2 and/or C_H3); and/or another scaffold portion of a GIPR antigen binding protein. These nucleic acid sequences are inserted into an appropriate expression vector using standard ligation techniques. In one embodiment, the heavy or light chain constant region is appended to the C-terminus of the anti-GIPR specific heavy or light chain variable region and is ligated into an expression vector. The vector is typically selected to be functional in the particular host cell employed (*i.e.*, the vector is compatible with the host cell machinery, permitting amplification and/or expression of the gene can occur). In some embodiments, vectors are used that employ protein-fragment complementation assays using protein reporters, such as dihydrofolate reductase (*see*, for example, U.S. Pat. No. 6,270,964, which is hereby incorporated by reference). Suitable expression vectors can be purchased, for example, from Invitrogen Life Technologies or BD Biosciences (formerly "Clontech"). Other useful vectors for cloning and expressing the antibodies and fragments include those described in Bianchi and McGrew, 2003, *Biotech. Biotechnol. Bioeng.* 84:439-44, which is hereby incorporated by reference. Additional suitable expression vectors are discussed, for example, in *Methods Enzymol.*, vol. 185 (D. V. Goeddel, ed.), 1990, New York: Academic Press.

[0369] 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.

[0370] 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.

[0371] Flanking sequences may be homologous (*i.e.*, from the same species and/or strain as the host cell), heterologous (*i.e.*, from a species other than the host cell species or strain), hybrid (*i.e.*, a combination of flanking sequences from more than one source), synthetic or native. As such, the source of a flanking sequence may be any prokaryotic or eukaryotic organism, any vertebrate or invertebrate organism, or any plant, provided that the flanking sequence is functional in, and can be activated by, the host cell machinery.

[0372] Flanking sequences useful in the vectors may be obtained by any of several methods well known in the art. Typically, flanking sequences useful herein will have been previously identified by mapping and/or by restriction endonuclease digestion and can thus be isolated from the proper tissue source using the appropriate restriction endonucleases. In some cases, the full nucleotide sequence of a flanking sequence may be known. Here, the flanking sequence may be synthesized using the methods described herein for nucleic acid synthesis or cloning.

[0373] Whether all or only a portion of the flanking sequence is known, it may be obtained using polymerase chain reaction (PCR) and/or by screening a genomic library with a suitable probe such as an oligonucleotide and/or flanking sequence fragment from the same or another species. Where the flanking sequence is not known, a fragment of DNA containing a flanking sequence may be isolated from a larger piece of DNA that may contain, for example, a coding sequence or even another gene or genes. Isolation may be accomplished by restriction endonuclease digestion to produce the proper DNA fragment followed by isolation using agarose gel purification, Qiagen[®] column chromatography (Chatsworth, CA), or other

methods known to the skilled artisan. The selection of suitable enzymes to accomplish this purpose will be readily apparent to one of ordinary skill in the art.

[0374] An origin of replication is typically a part of those prokaryotic expression vectors purchased commercially, and the origin aids in the amplification of the vector in a host cell. If the vector of choice does not contain an origin of replication site, one may be chemically synthesized based on a known sequence, and ligated into the vector. For example, the origin of replication from the plasmid pBR322 (New England Biolabs, Beverly, MA) is suitable for most gram-negative bacteria, and various viral origins (*e.g.*, SV40, polyoma, adenovirus, vesicular stomatitis virus (VSV), or papillomaviruses such as HPV or BPV) are useful for cloning vectors in mammalian cells. Generally, the origin of replication component is not needed for mammalian expression vectors (for example, the SV40 origin is often used only because it also contains the virus early promoter).

[0375] 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.

[0376] 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.

[0377] 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.

[0378] 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.

[0379] 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.

[0380] 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.

[0381] 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.

[0382] 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.

[0383] In one embodiment the leader sequence comprises SEQ ID NO: 3157 (MDMRVPAQLL GLLLLWLRGA RC) which is encoded by SEQ ID NO: 3158 (atggacatga gagtgccctgc acagctgctg ggccctgctgc tgctgtggct 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 ctcaactcagg gcacagggtc ctgggcc).

[0384] 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.

[0385] 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*.

[0386] 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.

[0387] 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.

[0388] 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.

[0389] In one aspect, a GIPR binding protein is administered for chronic treatment. In another aspect, the binding proteins are administered for acute therapy.

[0390] 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.

[0391] In certain embodiments, the pharmaceutical composition may contain formulation materials for modifying, maintaining or preserving, for example, the pH, osmolarity, viscosity, clarity, color, isotonicity, odor, sterility, stability, rate of dissolution or release, adsorption or penetration of the composition. In such embodiments, suitable formulation materials include, but are not limited to, amino acids (such as glycine, glutamine, asparagine, arginine or lysine); antimicrobials; antioxidants (such as ascorbic acid, sodium sulfite or sodium hydrogen-sulfite); buffers (such as borate, bicarbonate, Tris-HCl, citrates, phosphates or other organic acids); bulking agents (such as mannitol or glycine); chelating agents (such as ethylenediamine tetraacetic acid (EDTA)); complexing agents (such as caffeine, polyvinylpyrrolidone, beta-cyclodextrin or hydroxypropyl-beta-cyclodextrin); fillers; monosaccharides; disaccharides; and other carbohydrates (such as glucose, mannose or dextrans); proteins (such as serum albumin, gelatin or immunoglobulins); coloring, flavoring and diluting agents; emulsifying agents; hydrophilic polymers (such as polyvinylpyrrolidone); low molecular weight polypeptides; salt-forming counterions (such as sodium); preservatives (such as benzalkonium chloride, benzoic acid, salicylic acid, thimerosal, phenethyl alcohol, methylparaben, propylparaben, chlorhexidine, sorbic acid or hydrogen peroxide); solvents (such as glycerin, propylene glycol or polyethylene glycol); sugar alcohols (such as mannitol or sorbitol); suspending agents; surfactants or wetting agents (such as pluronics, PEG, sorbitan esters, polysorbates such as polysorbate 20, polysorbate, triton, tromethamine, lecithin, cholesterol, tyloxapal); stability enhancing agents (such as sucrose or sorbitol); tonicity enhancing agents (such as alkali metal halides, preferably sodium or potassium chloride, mannitol sorbitol); delivery vehicles; diluents; excipients and/or pharmaceutical adjuvants. REMINGTON'S PHARMACEUTICAL SCIENCES, 18"

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.

[0392] 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.

[0393] The pharmaceutical compositions can be selected for parenteral delivery. Alternatively, the compositions may be selected for inhalation or for delivery through the digestive tract, such as orally. Preparation of such pharmaceutically acceptable compositions is within the skill of the art.

[0394] The formulation components are present preferably in concentrations that are acceptable to the site of administration. In certain embodiments, buffers are used to maintain the composition at physiological pH or at a slightly lower pH, typically within a pH range of from about 5 to about 8.

[0395] When parenteral administration is contemplated, the therapeutic compositions may be provided in the form of a pyrogen-free, parenterally acceptable aqueous solution comprising the desired human GIPR antigen binding protein in a pharmaceutically acceptable vehicle. A particularly suitable vehicle for parenteral injection is sterile distilled water in which the GIPR antigen binding protein is formulated as a sterile, isotonic solution, properly preserved. In certain embodiments, the preparation can involve the formulation of the desired molecule with an agent, such as injectable microspheres, bio-erodible particles, polymeric compounds (such as polylactic acid or polyglycolic acid), beads or liposomes, that may provide controlled or sustained release of the product which can be delivered *via* depot injection. In certain embodiments, hyaluronic acid may also be used, having the effect of promoting

sustained duration in the circulation. In certain embodiments, implantable drug delivery devices may be used to introduce the desired antigen binding protein.

[0396] Certain pharmaceutical compositions are formulated for inhalation. In some embodiments, GIPR antigen binding proteins are formulated as a dry, inhalable powder. In specific embodiments, GIPR antigen binding protein inhalation solutions may also be formulated with a propellant for aerosol delivery. In certain embodiments, solutions may be nebulized. Pulmonary administration and formulation methods therefore are further described in International Patent Application No. PCT/US94/001875, which is incorporated by reference and describes pulmonary delivery of chemically modified proteins. Some formulations can be administered orally. GIPR antigen binding proteins that are administered in this fashion can be formulated with or without carriers customarily used in the compounding of solid dosage forms such as tablets and capsules. In certain embodiments, a capsule may be designed to release the active portion of the formulation at the point in the gastrointestinal tract when bioavailability is maximized and pre-systemic degradation is minimized. Additional agents can be included to facilitate absorption of the GIPR antigen binding protein. Diluents, flavorings, low melting point waxes, vegetable oils, lubricants, suspending agents, tablet disintegrating agents, and binders may also be employed.

[0397] Some pharmaceutical compositions comprise an effective quantity of one or a plurality of GIPR antigen binding proteins in a mixture with non-toxic excipients that are suitable for the manufacture of tablets. By dissolving the tablets in sterile water, or another appropriate vehicle, solutions may be prepared in unit-dose form. Suitable excipients include, but are not limited to, inert diluents, such as calcium carbonate, sodium carbonate or bicarbonate, lactose, or calcium phosphate; or binding agents, such as starch, gelatin, or acacia; or lubricating agents such as magnesium stearate, stearic acid, or talc.

[0398] Additional pharmaceutical compositions will be evident to those skilled in the art, including formulations involving GIPR binding proteins in sustained- or controlled-delivery formulations. Techniques for formulating a variety of other sustained- or controlled-delivery means, such as liposome carriers, bio-erodible microparticles or porous beads and depot injections, are also known to those skilled in the art. *See*, for example, International Patent Application No. PCT/US93/00829, which is incorporated by reference and describes controlled release of porous polymeric microparticles for delivery of pharmaceutical compositions. Sustained-release preparations may include semipermeable polymer matrices in the form of shaped articles, *e.g.*, films, or microcapsules. Sustained release matrices may include polyesters, hydrogels, polylactides (as disclosed in U.S. Patent No. 3,773,919 and

European Patent Application Publication No. EP 058481, each of which is incorporated by reference), copolymers of L-glutamic acid and gamma ethyl-L-glutamate (Sidman *et al.*, 1983, *Biopolymers* 2:547-556), poly (2-hydroxyethyl-inethacrylate) (Langer *et al.*, 1981, *J. Biomed. Mater. Res.* 15:167-277 and Langer, 1982, *Chem. Tech.* 12:98-105), ethylene vinyl acetate (Langer *et al.*, 1981, *supra*) or poly-D(-)-3-hydroxybutyric acid (European Patent Application Publication No. EP 133,988). Sustained release compositions may also include liposomes that can be prepared by any of several methods known in the art. *See, e.g.*, Eppstein *et al.*, 1985, *Proc. Natl. Acad. Sci. U.S.A.* 82:3688-3692; European Patent Application Publication Nos. EP 036,676; EP 088,046 and EP 143,949, incorporated by reference.

[0399] Pharmaceutical compositions used for *in vivo* administration are typically provided as sterile preparations. Sterilization can be accomplished by filtration through sterile filtration membranes. When the composition is lyophilized, sterilization using this method may be conducted either prior to or following lyophilization and reconstitution. Compositions for parenteral administration can be stored in lyophilized form or in a solution. Parenteral compositions generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

[0400] In certain formulations, an antigen binding protein has a concentration of at least 10 mg/mL, 20 mg/mL, 30 mg/mL, 40 mg/mL, 50 mg/mL, 60 mg/mL, 70 mg/mL, 80 mg/mL, 90 mg/mL, 100 mg/mL or 150 mg/mL. In one embodiment, a pharmaceutical composition comprises the antigen binding protein, a buffer and polysorbate. In other embodiments, the pharmaceutical composition comprises an antigen binding protein, a buffer, sucrose and polysorbate. An example of a pharmaceutical composition is one containing 50-100 mg/mL of antigen binding protein, 5-20 mM sodium acetate, 5-10% w/v sucrose, and 0.002-0.008% w/v polysorbate. Certain, compositions, for instance, contain 65-75 mg/mL of an antigen binding protein in 9-11 mM sodium acetate buffer, 8-10% w/v sucrose, and 0.005-0.006% w/v polysorbate. The pH of certain such formulations is in the range of 4.5-6. Other formulations have a pH of 5.0-5.5 (e.g., pH of 5.0, 5.2 or 5.4).

[0401] Once the pharmaceutical composition has been formulated, it may be stored in sterile vials as a solution, suspension, gel, emulsion, solid, crystal, or as a dehydrated or lyophilized powder. Such formulations may be stored either in a ready-to-use form or in a form (e.g., lyophilized) that is reconstituted prior to administration. Kits for producing a single-dose administration unit are also provided. Certain kits contain a first container having a dried

protein and a second container having an aqueous formulation. In certain embodiments, kits containing single and multi-chambered pre-filled syringes (*e.g.*, liquid syringes and lyosyringes) are provided. The therapeutically effective amount of a GIPR antigen binding protein-containing pharmaceutical composition to be employed will depend, for example, upon the therapeutic context and objectives. One skilled in the art will appreciate that the appropriate dosage levels for treatment will vary depending, in part, upon the molecule delivered, the indication for which the GIPR antigen binding protein is being used, the route of administration, and the size (body weight, body surface or organ size) and/or condition (the age and general health) of the patient. In certain embodiments, the clinician may titer the dosage and modify the route of administration to obtain the optimal therapeutic effect.

[0402] 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.

[0403] 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.

[0404] 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.

[0405] 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.

[0406] 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.

[0407] 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.

[0408] 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.

[0409] . 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.

[0410] 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.

[0411] 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

analog, and exendin agonists for use in the methods described herein may optionally be amidated, and may also be in an acid form, pharmaceutically acceptable salt form, or any other physiologically active form of the molecule.

[0412] In one embodiment, the molar ratio of a GLP-1 receptor agonist to a GIPR antagonist is from about 1:1 to 1:110, 1:1 to 1:100, 1:1 to 1:75, 1:1 to 1:50, 1:1 to 1:25, 1:1 to 1:10, 1:1 to 1:5, and 1:1. In one embodiment, the molar ratio of a GIPR antagonist to a GLP-1 receptor agonist is from about 1:1 to 1:110, 1:1 to 1:100, 1:1 to 1:75, 1:1 to 1:50, 1:1 to 1:25, 1:1 to 1:10, and 1:1 to 1:5.

[0413] In one embodiment, the GLP-1 receptor agonist is used in combination with the GIPR antagonist at therapeutically effective molar ratios of between about 1:1.5 to 1:150, preferably 1:2 to 1:50.

[0414] In one embodiment, the GLP-1 receptor agonist and the GIPR antagonist are present in doses that are at least about 1.1 to 1.4, 1.5, 2, 3, 4, 5, 6, 7, 8, 9, or 10 fold lower than the doses of each compound alone required to treat a condition and/or disease.

[0415] In one embodiment, the GLP-1 receptor agonist is GLP-1(7-37) or a GLP-1(7-37) analog.

[0416] In one embodiment, the GLP-1 receptor agonist is selected from the group consisting of exenatide, liraglutide, lixisenatide, albiglutide, dulaglutide, semaglutide, and taspoglutide.

[0417] In one aspect the present invention is directed to a method of treatment comprising administering to a subject a therapeutically effective amount of at least one GLP-1 receptor agonist in combination with administration of at least one GIPR antagonist which upon administration to a subject with symptoms of a metabolic disorder provides sustained beneficial effects.

[0418] 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.

[0419] 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.

[0420] In one embodiment, the therapeutically effective amounts of the GLP-1 receptor agonist and the GIPR antagonist are administered to the subject sequentially.

[0421] In one embodiment, the therapeutically effective amounts of a GLP-1 receptor agonist and a GIPR antagonist are synergistically effective amounts.

[0422] Exendin-4 (HGEGTFTSDLKSKQMEEEAVRLFIEWLKNGGPSSGAPPPS-NH₂ (SEQ ID NO: 3163)) is a peptide found in the saliva of the Gila monster, *Heloderma suspectum*;

and exendin-3 (HSDGTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGAPPPS-NH₂ (SEQ ID NO: 3164)) is a peptide found in the saliva of the beaded lizard, *Heloderma horridum*.

Exendins have some amino acid sequence similarity to some members of the glucagon-like peptide (GLP) family. For example, exendin-4 has about 53% sequence identity with glucagon-like peptide-1 (GLP-1)(7-37) (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 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).

[0423] Synthetic exendin-4, also known as exenatide, is commercially available as BYETTA® (Amylin Pharmaceuticals, Inc. and Eli Lilly and Company). A once weekly formulation of exenatide is described in WO 2005/102293, the disclosure of which is incorporated by reference herein.

[0424] “Exendin analog” refers to peptides which elicit a biological activity of an exendin reference peptide, preferably having a potency equal to or better than the exendin reference peptide (e.g., exendin-4), or within five orders of magnitude (plus or minus) of potency compared to the exendin reference peptide, when evaluated by art-known measures such as receptor binding and/or competition studies as described, e.g., by Hargrove et al., *Regulatory Peptides*, 141:113-119 (2007), the disclosure of which is incorporated by reference herein. Preferably, the exendin analogs will bind in such assays with an affinity of less than 1 μ M, and more preferably with an affinity of less than 3 nM, less than 1 nM, or less than 0.1 nM. The term “exendin analog” may also be referred to as “exendin agonist”. In a preferred embodiment, the exendin analog is an exendin-4 analog.

[0425] 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.

[0426] 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-carboxy-undecanoyl-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 extendins and exendin analogs may optionally be amidated.

[0427] 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).

[0428] Other extendins 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.

[0429] “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.

[0430] 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.

[0431] 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:

AESKYGPPPCPPAPX_{a16}X_{a17}X_{a18}GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQ
EDPEVQFNWYVDGVEVHNAKTKPREEQFX_{a80}STYRVVSVLTVLHQDWLNGKEYK
CKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHN
HYTQKSLSLSLGX_{a230}; wherein X_{a16} is P or E; X_{a17} is F, V or A; X_{a18} is L, E or A;

X_{a80} is N or A; and X_{a230} 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 (-GGGS-)_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:

HGEGTFTSDVSSYLEEQAAKEFIAWLVKGGGGGGGSGGGGSGGGGSAESKYGPPCP
PCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEV
HNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKG
QPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVL
DSDGSFFLYSR LTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG (SEQ ID
NO: 3205).

[0432] In another embodiment, the GLP-1(7-37) or GLP-1(7-37) analog may be covalently linked (directly or through a linking group) to one or two polyethylene glycol molecules. For example, a GLP-1(7-37) analog may comprise the amino acid sequence: HX_{a8}EGTFTSDVS
SYLEX_{a22}QAAKEFIAWLX_{a33}KGGPSSGAPPPC₄₅C₄₆-Z, wherein X_{a8} is: D-Ala, G, V,
L, I, S or T; X_{a22} is G, E, D or K; X_{a33} 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
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.

[0433] 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).

[0434] 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.

[0435] Table 7. Examples of GLP-1 Agonist Sequences

SEQ ID NO:	Sequence	Description
3163	HGEGTFTSDLSKQMEEEEAVRLFIEWLKN GGPSSGAPPPS	Exendin-4
3164	HSDGTFTSDLSKQMEEEEAVRLFIEWLKN GGPSSGAPPPS	Exendin-3
3165	HGEGTFTSDLSKQLEEEEAVRLFIEWLKN GGPSSGAPPPS	Leu ¹⁴ -exendin-4
3166	HGEGTFTSDLSKQLEEEEAVRLFIEFLKN 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	HGEGTFTSDLSKQLEEEEAVRLFIEWLKN GG	Leu ¹⁴ -exendin-4(1-30)
3170	HGEGTFTSDLSKQLEEEEAVRLFIEFLKN 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	HGEGTFTSDLSKQLEEEEAVRLFIEWLKN	Leu ¹⁴ -exendin-4(1-28)
3174	HGEGTFTSDLSKQLEEEEAVRLFIEFLKN	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)EEEEAVRLFIEWLKQGGPSSGAPPPS	octylGly ¹⁴ ,Gln ²⁸ -exendin-4
3179	HGEGTFTSDLSKQLEEEEAVRLFIEWLKQGGPSS(octylG)APPPS	Leu ¹⁴ ,Gln ²⁸ ,octylGly ³⁴ -exendin-4

3180	HGEFTFTSDLSKQLEEEAVRLFIEWLKQ GGPSKEIIS	Phe ⁴ ,Leu ¹⁴ ,Gln ²⁸ ,Lys ³³ ,Glu ³⁴ , Ile ^{35,36} ,Ser ³⁷ -exendin-4(1-37)
3181	HGEFTFTSDLSKQLEEKAAKEFIEWLKQ GGPSSGAPPPS	Phe ⁴ ,Leu ¹⁴ ,Lys ^{17,20} ,Ala ¹⁹ ,Glu ²¹ ,Gln ²⁸ -exendin-4
3182	HGEFTFTSDLVKILEAEAVRKFIIEFLKN GGPSSGAPPPS	Val ¹¹ ,Ile ¹³ ,Leu ¹⁴ ,Ala ¹⁶ ,Lys ²¹ ,Phe ²⁵ -exendin-4
3183	HGEFTFTSDLSKQMEEEAVRLFIEWLKN GGPSSGAPPPSK	exendin-4-Lys ⁴⁰
3184	HAEGTFTSDVSSYLEGQAAKEFIAWLK GRG	GLP-1(7-37)
3185	HAEGTFTSDVSSYLEGQAAKEFIAWLK GR	GLP-1(7-36)-NH ₂
3186	H(Aib)EGTFTSDVSSYLEGQAAREFIA FLVR(Aib)R	Aib ^{8,35} ,Arg ^{26,34} ,Phe ³¹ -GLP-1(7- 36))
3187	HXaa ₈ EGTFTSDVSSYLEXaa ₂₂ Xaa ₂₃ AAK EFI Xaa ₃₀ WLXaa ₃₃ Xaa ₃₄ GXaa ₃₆ Xaa ₃₇ wherein Xaa ₈ is A, V, or G Xaa ₂₂ is G, K, or E Xaa ₂₃ is Q or K Xaa ₃₀ is A or E Xaa ₃₃ is V or K Xaa ₃₄ is K, N, or R Xaa ₃₆ is R or G and Xaa ₃₇ is G, H, P, or absent	HXaa ₈ EGTFTSDVSSYLEXaa ₂₂ X aa ₂₃ AAKEFIXaa ₃₀ WLXaa ₃₃ Xaa ₃₄ G Xaa ₃₆ Xaa ₃₇ wherein Xaa ₈ is A, V, or G Xaa ₂₂ is G, K, or E Xaa ₂₃ is Q or K Xaa ₃₀ is A or E Xaa ₃₃ is V or K Xaa ₃₄ is K, N, or R Xaa ₃₆ is R or G and Xaa ₃₇ is G, H, P, or absent
3188	HAEGTFTSDVSSYLEGQAAKEFIAWLVR GRG	Arg ³⁴ -GLP-1(7-37)
3189	HAEGTFTSDVSSYLEGQAAKEFIEWLVK GRG	Glu ³⁰ -GLP-1(7-37)
3190	HAEGTFTSDVSSYLEKQAAKEFIAWLK GRG	Lys ²² -GLP-1(7-37)
3191	HGEFTFTSDVSSYLEEQAAKEFIAWLK GGG	Gly ^{8,36} ,Glu ²² -GLP-1(7-37)
3192	HVEGTFTSDVSSYLEEQAAKEFIAWLK GGG	Val ⁸ ,Glu ²² ,Gly ³⁶ -GLP-1(7-37)
3193	HGEFTFTSDVSSYLEEQAAKEFIAWLK GGG	Gly ^{8,36} ,Glu ²² ,Lys ³³ ,Asn ³⁴ -GLP- 1(7-37)
3194	HVEGTFTSDVSSYLEEQAAKEFIAWLK GGG	Val ⁸ ,Glu ²² ,Lys ³³ ,Asn ³⁴ ,Gly ³⁶ - GLP-1(7-37)
3195	HGEFTFTSDVSSYLEEQAAKEFIAWLK GGP	Gly ^{8,36} ,Glu ²² ,Pro ³⁷ -GLP-1(7-37)
3196	HVEGTFTSDVSSYLEEQAAKEFIAWLK GGP	Val ⁸ ,Glu ²² ,Gly ³⁶ ,Pro ³⁷ -GLP-1(7- 37)
3197	HGEFTFTSDVSSYLEEQAAKEFIAWLK GGP	Gly ^{8,36} ,Glu ²² ,Lys ³³ ,Asn ³⁴ ,Pro ³⁷ - GLP-1(7-37)
3198	HVEGTFTSDVSSYLEEQAAKEFIAWLK GGP	Val ⁸ ,Glu ²² ,Lys ³³ ,Asn ³⁴ ,Gly ³⁶ ,Pro ³⁷ -GLP-1(7-37)
3199	HGEFTFTSDVSSYLEEQAAKEFIAWLK GG	Gly ^{8,36} ,Glu ²² -GLP-1(7-36)
3200	HVEGTFTSDVSSYLEEQAAKEFIAWLK GG	Val ⁸ ,Glu ²² ,Gly ³⁶ -GLP-1(7-36)

3201	HVEGTFTSDVSSYLEEQAAKEFIAWLVN GG	Val ⁸ , Glu ²² , Asn ³⁴ , Gly ³⁶ -GLP-1(7-36)
3202	HGEGTFTSDVSSYLEEQAAKEFIAWLVN GG	Gly ^{8,36} , Glu ²² , Asn ³⁴ -GLP-1(7-36)
3203	AESKYGPPPCPPCPAPXaa ₁₆ Xaa ₁₇ Xaa ₁₈ G GPSVFLFPPKPKDTLMISRTPVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKTKPR EEQFXaa ₃₀ STYRVVSVLTVLHQDWLNGK EYKCKVSNKGLPSSIEKTISKAKGQPRE PQVYITLPPSQEEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTTPVLDSD 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 ₃₀ is N or A and Xaa ₂₃₀ is K or absent	Fc portion of an immunoglobulin
3204	(-GGGGS-) _x where x is 1, 2, 3, 4, 5 or 6	Linker
3205	HGEGTFTSDVSSYLEEQAAKEFIAWLK GGGGGGSGGGSGGGGSAESKYGPPCP PCPAPEAAGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSQEDPEVQFNWYVDGVE VHNAKTKPREEQFNSTYRVVSVLTVLHQ DWLNGKEYKCKVSNKGLPSSIEKTISKA KGQPREPQVYITLPPSQEEMTKNQVSLTCL LVKGFYPSDIAVEWESNGQPENNYKTTTP PVLDSGGSFFLYSR 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 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 .	GLP analog
3207	HVEGTFTSDVSSYLEEQAAKEFIAWLIK GGPSSGAPPPC ₄₅ C ₄₆ -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	GLP analog

	is attached to C ₄₅ and one polyethylene glycol moiety is attached to C ₄₆	
3208	HGEGTFTSDLSKQMEEEEAVKLFIEWLKN GGPSSGAPPPS	[N ^ε -(17-carboxyheptadecanoic acid)Lys ²⁰]exendin-4-NH ₂
3209	HGEGTFTSDLSKQMEEEEAVRLFIEWLKN GGPKSGAPPPS	[N ^ε -(17-carboxyheptadecanoyl)Lys ³²]exendin-4-NH ₂
3210	GEGTFTSDLSKQMEEEEAVKLFIEWLKN GPSSGAPPPS	[desamino-His ¹ ,N ^ε -(17-carboxyheptadecanoyl)Lys ²⁰]exendin-4-NH ₂
3211	HGEGTFTSDLSRQNorLeEEEAVRLFIEWL WLRNGGPKSGAPPPS	[Arg ^{12,27} ,NLe ¹⁴ ,N ^ε -(17-carboxyheptadecanoyl)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]exendin-4-NH ₂
3215	HGEGTFTSDLSKQMEEEEAVKLFIEWLKN GGPSSGAPPPS	[N ^ε -(11-carboxy-undecanoylamino)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	AEGTFTSDVSSYLEGQAAREFIAWLKGRG	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	AEGTFTSDVSSYLEGQAAREFIAWLKGRG	desamino-His ⁷ ,Arg ²⁶ ,Lys ³⁴ (N ^ε -octanoyl)-GLP-1(7-37)
3224	HAEGTFTSDVSSYLEGQAAREFIAWLVRGRGK	Arg ^{26,34} ,Lys ³⁸ (N ^ε -(ω-carboxypentadecanoyl))-GLP-1(7-38)
3225	HAEGTFTSDVSSYLEGQAAREFIAWLVRGRGK	Arg ^{26,34} ,Lys ³⁶ (N ^ε -(γ-Glu(N-α-hexadecanoyl)))-GLP-1(7-36) (core peptide disclosed as SEQ ID NO: 3225)

[0436] AEEA refers to [2-(2-amino)ethoxy]acetic acid

[0437] EDA refers to ethylenediamine.

[0438] MPA refers to maleimidopropionic acid.

[0439] 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.

[0440] Pharmaceutical compositions containing the GLP-1 receptor agonist compounds described herein may be provided for peripheral administration, such as parenteral (e.g., subcutaneous, intravenous, intramuscular), a continuous infusion (e.g., intravenous drip, intravenous bolus, intravenous infusion), topical, nasal, or oral administration. Suitable pharmaceutically acceptable carriers and their formulation are described in standard formulation treatises, such as Remington's Pharmaceutical Sciences by Martin; and Wang et al., *Journal of Parenteral Science and Technology*, Technical Report No. 10, Supp. 42:2S (1988). The GLP-1 receptor agonist compounds described herein can be provided in parenteral compositions for injection or infusion. They can, for example, be suspended in water; an inert oil, such as a vegetable oil (e.g., sesame, peanut, olive oil, and the like); or other pharmaceutically acceptable carrier. In one embodiment, the compounds are suspended in an aqueous carrier, for example, in an isotonic buffer solution at a pH of about 3.0 to 8.0, or about 3.0 to 5.0. The compositions may be sterilized by conventional sterilization techniques or may be sterile filtered. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions, such as pH buffering agents.

[0441] 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.

[0442] 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.

[0443] 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.

[0444] 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.

[0445] The therapeutically effective amount of the GLP-1 receptor agonist compounds described herein for use in the methods described herein will typically be from about 0.01 µg to about 5 mg; about 0.1 µg to about 2.5 mg; about 1 µg to about 1 mg; about 1 µg to about 50 µg; or about 1 µg to about 25 µg. Alternatively, the therapeutically effective amount of the GLP-1 receptor agonist compounds may be from about 0.001 µg to about 100 µg based on the weight of a 70 kg patient; or from about 0.01 µg to about 50 µg based on the weight of a

70 kg patient. These therapeutically effective doses may be administered once/day, twice/day, thrice/day, once/week, biweekly, or once/month, depending on the formulation. The exact dose to be administered is determined, for example, by the formulation, such as an immediate release formulation or an extended release formulation. For transdermal, nasal or oral dosage forms, the dosage may be increased from about 5-fold to about 10-fold.

[0446] In certain embodiments the GLP-1 receptor agonist will be administered concurrently with the GIPR antigen binding protein. In one embodiment the GLP-1 receptor agonist will be administered after the GIPR antigen binding protein. In one embodiment the GLP-1 receptor agonist will be administered before the GIPR antigen binding protein. In certain embodiments the subject or patient will already be being treated with a GLP-1 receptor agonist before being subjected to further treatment with a GIPR antigen binding protein.

[0447] 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.

[0448] The antigen binding proteins of the described can be used for diagnostic purposes to detect, diagnose, or monitor diseases and/or conditions associated with GIPR. The disclosed antigen binding proteins provide a means for the detection of the presence of GIPR in a sample using classical immunohistological methods known to those of skill in the art (*e.g.*, Tijssen, 1993, *Practice and Theory of Enzyme Immunoassays*, Vol 15 (Eds R.H. Burdon and P.H. van Knippenberg, Elsevier, Amsterdam); Zola, 1987, *Monoclonal Antibodies: A Manual of Techniques*, pp. 147-158 (CRC Press, Inc.); Jalkanen *et al.*, 1985, *J. Cell. Biol.* 101:976-985; Jalkanen *et al.*, 1987, *J. Cell Biol.* 105:3087-3096). The detection of GIPR can be performed *in vivo* or *in vitro*.

[0449] 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).

[0450] 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 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.

[0451] 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.

[0452] Another aspect of the disclosed provides for detecting the presence of a test molecule that competes for binding to GIPR with the antigen binding proteins provided. An example of one such assay would involve detecting the amount of free antigen binding protein in a solution containing an amount of GIPR in the presence or absence of the test molecule. An increase in the amount of free antigen binding protein (*i.e.*, the antigen binding protein not bound to GIPR) would indicate that the test molecule is capable of competing for GIPR binding with the antigen binding protein. In one embodiment, the antigen binding protein is labeled with a labeling group. Alternatively, the test molecule is labeled and the amount of free test molecule is monitored in the presence and absence of an antigen binding protein.

[0453] GIPR binding proteins can be used to treat, diagnose or ameliorate, a metabolic condition or disorder. In one embodiment, the metabolic disorder to be treated is diabetes, *e.g.*, type 2 diabetes. In another embodiment, the metabolic condition or disorder is obesity. In other embodiments the metabolic condition or disorder is dyslipidemia, elevated glucose levels, elevated insulin levels or diabetic nephropathy. For example, a metabolic condition or disorder that can be treated or ameliorated using a GIPR binding peptide includes a state in which a human subject has a fasting blood glucose level of 125 mg/dL or greater, for example 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190, 195, 200 or greater than 200 mg/dL. Blood glucose levels can be determined in the fed or fasted state, or at random. The metabolic condition or disorder can also comprise a condition in which a subject is at increased risk of developing a metabolic condition. For a human subject, such conditions include a fasting blood glucose level of 100 mg/dL. Conditions that can be treated using a pharmaceutical composition comprising a GIPR binding protein can also be found in the American Diabetes Association Standards of Medical Care in Diabetes Care-2011, American Diabetes Association, Diabetes Care Vol. 34, No. Supplement 1, S11-S61, 2010, incorporated herein by reference.

[0454] 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.

[0455] 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.

[0456] 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.

[0457] In one embodiment, a method of the instant disclosure comprises first measuring a baseline level of one or more metabolically-relevant compounds such as glucose, insulin, cholesterol, lipid in a subject. A pharmaceutical composition comprising a GIPR binding protein is then administered to the subject. After a desired period of time, the level of the one or more metabolically-relevant compounds (*e.g.*, blood glucose, insulin, cholesterol, lipid) in the subject is again measured. The two levels can then be compared in order to determine the relative change in the metabolically-relevant compound in the subject. Depending on the

outcome of that comparison another dose of the pharmaceutical composition comprising a GIPR binding protein can be administered to achieve a desired level of one or more metabolically-relevant compound.

[0458] It is noted that a pharmaceutical composition comprising a GIPR binding protein can be co-administered with another compound. The identity and properties of compound co-administered with the GIPR binding protein will depend on the nature of the condition to be treated or ameliorated. A non-limiting list of examples of compounds that can be administered in combination with a pharmaceutical composition comprising a GIPR binding protein include rosiglitazone, pioglitazone, repaglinide, nateglinide, metformin, exenatide, stagliptin, pramlintide, glipizide, glimepirideacarbose, and miglitol.

[0459] Also provided are kits for practicing the disclosed methods. Such kits can comprise a pharmaceutical composition such as those described herein, including nucleic acids encoding the peptides or proteins provided herein, vectors and cells comprising such nucleic acids, and pharmaceutical compositions comprising such nucleic acid-containing compounds, which can be provided in a sterile container. Optionally, instructions on how to employ the provided pharmaceutical composition in the treatment of a metabolic disorder can also be included or be made available to a patient or a medical service provider.

[0460] In one aspect, a kit comprises (a) a pharmaceutical composition comprising a therapeutically effective amount of a GIPR binding protein; and (b) one or more containers for the pharmaceutical composition. Such a kit can also comprise instructions for the use thereof; the instructions can be tailored to the precise metabolic disorder being treated. The instructions can describe the use and nature of the materials provided in the kit. In certain embodiments, kits include instructions for a patient to carry out administration to treat a metabolic disorder, such as elevated glucose levels, elevated insulin levels, obesity, type 2 diabetes, dyslipidemia or diabetic nephropathy.

[0461] Instructions can be printed on a substrate, such as paper or plastic, etc., and can be present in the kits as a package insert, in the labeling of the container of the kit or components thereof (e.g., associated with the packaging), etc. In other embodiments, the instructions are present as an electronic storage data file present on a suitable computer readable storage medium, e.g. CD-ROM, diskette, etc. In yet other embodiments, the actual instructions are not present in the kit, but means for obtaining the instructions from a remote source, such as over the internet, are provided. An example of this embodiment is a kit that includes a web address where the instructions can be viewed and/or from which the instructions can be downloaded.

[0462] Often it will be desirable that some or all components of a kit are packaged in suitable packaging to maintain sterility. The components of a kit can be packaged in a kit containment element to make a single, easily handled unit, where the kit containment element, e.g., box or analogous structure, may or may not be an airtight container, e.g., to further preserve the sterility of some or all of the components of the kit.

[0463] Example 1

[0464] Generation of anti-murine GIPR antibody. Immunizations were done in 129X BL/6 mice from Charles River by GeneGun with a pool of DNA (pTT5:E3K-muGIPR-E3K and pTT5:Mut1-mGIPR-Mut1) and CA-64. B-Cells were harvested from the mice with highest titers and fused with Sp2/0-Ag14 cells creating hybridomas. Antibodies were produced from hybridomas cultured in hyperflasks at 37C. Antibody was purified from cultured media by affinity chromatography (protein A FF, high salt/pH method) followed by a buffer exchange (UF/DF). N-terminal sequencing of variable domains was done using hybridomas. RNA was isolated from hybridoma lysate and converted to cDNA by TOPO-TA cloning of RACE PCR products. The light chain and heavy chain sequences were confirmed by LC/MS. The original isotype of the hybridoma antibodies were murine IgG2a. The subtype was changed to aglycosylated muIgG1 (N297 to G mutation) to be effector functionless. The recombinant sequence was cloned by GeneArt seamless cloning into pTT5 and pSLX240 for 293-6E mammalian transient and CHO S mammalian stable expression, respectively. Expression productions were done for 6 days in shake flasks at 36°C. Cultured media was harvested for purification. All protein lots were purified by affinity chromatography (Mab Select SuRe) followed by cation exchange (SP Sepharose HP) and finishing with a buffer exchange (UF/DF) into A5.2Su buffer. Protein analytics (size exclusion chromatography) showed all lots to contain >98% main peak with <1% high molecular weight species.

[0465] Example 2

[0466] Figure 1 provides an overview of the pharmacodynamics assay to test anti-murine GIPR antibodies. Seven week old male high fat diet (HFD)-induced obese C57BL/6 mice were purchased from Jackson Labs. After arrival, mice were continued on high fat diet with Research Diets D12492 (60 kcal % fat) (Research diet) for one to two weeks. Mice were randomized by body weight and were administrated intraperitoneally with testing GIPR antibody or vehicle (10 mM acetate, 150 mM NaCl, pH 5.0) the day before intraperitoneal glucose tolerance test (IPGTT). Mice were fasted for 7 hours and IPGTT was performed

immediately following exogenous GIP [D-Ala²]-GIP (50 nmol/kg, Phoenix Pharmaceuticals) given intraperitoneally. Blood samples were taken from tail nick at the times indicated. Glucose was measured using AlphaTrak blood glucose meter (Abbott). Blood insulin level was determined by using Insulin (mouse) ultra-sensitive EIA kit (ALPCO Diagnostics). Results are shown in Figure 2 and show that the anti-murine GIPR antibody 2.63.1 antagonizes GIP induced insulin secretion. 2.63.1 comprises a light chain with the following sequence:

[0467] MKLPVRLVL MFWIPASSSD VVMQTPLSL PVSLGDQASI SCRSSQSLVH
SNGDTYLHWY LQKPGQSPKL LIYKVSNRFS GVPDRFSGSG SGTDFTLKIS
RVEAADLGVY FCSQSTHVPP FTFGGGTKLE IKRADAAPTV SIFPPSSEQL
TSGGASVVCF LNNFYPKDIN VKWKIDGSER QNGVLNSWTD QDSKDSTYSM
SSTLTLTKE YERHNSYTCE ATHKTSTSPI VKSFNRNEC (SEQ ID NO: 3161)

[0468] And 2.63.1 comprises a heavy chain with the following sequence:

[0469] MGWSYIILFL VATATDVHSQ VQLQQPGAEL VKPGASVKLS CRASGYTFTS
NWMHWVKQRP RQGLEWIGEI NPSNGRSNYN EKFKTKATLT VDKSSSTAYM
QLSSLTSEDS AVYYCARFYY GTSWFAYWGQ GTLVAVSAAK TTPPSVYPLA
PGSAAQTNSM VTLGCLVKGY FPEPVTVTWN SGSLSSGVHT FPAVLQSDLY
TLSSSVTVPS STWPSETVTC NVAHPASSTK VDKKIVPRDC GCKPCICTVP
EVSSVFIFPP KPKDVLITL TPKVTCVVVD ISKDDPEVQF SWFVDDVEVH
TAQTQPREEQ FASTFRSVSE LPIMHQDWLN GKEFKCRVNS AAFPAPIEKT
ISKTKGRPKA PQVYTIPPPK EQMAKDKVSL TCMITDFFPE DITVEWQWNG
QPAENYKNTQ PIMDTDGSYF VYSKLVNPKS NWEAGNTFTC SVLHEGLHNH
HTEKSLSHSP GK (SEQ ID NO: 3162).

[0470] In one embodiment the present invention is directed to an anti-murine GIPR antibody comprising a light chain comprising SEQ ID NO: 3161 and a heavy chain comprising SEQ ID NO: 3162. In one embodiment the present invention is directed to an anti-murine GIPR antibody comprising a light chain variable region from SEQ ID NO: 3161 and a heavy chain variable region from SEQ ID NO: 3162. In one embodiment the present invention is directed to an anti-murine GIPR antibody comprising CDRL1, CDRL2, and CDRL3 from SEQ ID NO: 3161 and a CDRH1, CDRH2, and CDRH3 from SEQ ID NO: 3162.

[0471] Example 3

[0472] Figure 3 provides an overview of the study used to determine the effects of chronic treatment of diet induced obese (DIO) mice with the 2.63.1 antibody. 18 week old male C57BL/6 DIO mice fed Research Diets D12492 (60 kcal % fat) were randomized into

groups. Treatments were given twice a week intraperitoneally for 6 weeks. Blood glucose levels were measured from tail nick using a glucose meter (Abbott) after mice were fasted for 4 hours. Insulin levels were determined using mouse high range insulin ELISA (ALPCO Diagnostics). Triglyceride levels were measured using an Infinity triglyceride assay kit (Thermo Scientific). Total cholesterol was measured using an Infinity total cholesterol kit (Thermo Scientific). Body composition was determined using the minispec whole body composition analyzer (Bruker).

[0473] For intraperitoneal glucose tolerance test (IPGTT), mice were fasted for 4 hours. Glucose levels were measured and blood samples were taken from the tail vein before IPGTT was initiated. IPGTT was performed by intraperitoneal injection of glucose (1 g/kg body weight). Glucose levels were measured at 20, 40 and 60 minutes after glucose administration by using a glucose meter (Abbott). All data is presented in Figures 4-13. Figure 4. GIPR Antibody 2.63.1 Results In Reduced Body Weight Gain

[0474] Figure 5 shows that treatment with anti-murine GIPR antibody 2.63.1 results in lower fat mass. Figure 6 shows that treatment with anti-murine GIPR Antibody 2.63.1 results in lower epididymal white adipose tissue weights. Figure 7 shows that treatment with anti-murine GIPR antibody 2.63.1 results in lower fasting glucose levels. Figure 8 shows that treatment with anti-murine GIPR antibody 2.63.1 results in lower insulin levels. Figure 9 shows that treatment with anti-murine GIPR antibody 2.63.1 results in improved glucose tolerance. Figure 10 shows that treatment with anti-murine GIPR antibody 2.63.1 results in lower serum total cholesterol. Figure 11 shows that treatment with anti-murine GIPR antibody 2.63.1 results in a reduction in hepatocyte microvesicular change and corresponding lipid accumulation. Figure 12 shows that treatment with anti-murine GIPR antibody 2.63.1 results in reduced liver weight and triglyceride content. Figure 13 demonstrates reduced inflammation and reduced infiltrating macrophages cells surrounding adipocytes in epididymal white adipose tissue with anti-murine GIPR antibody 2.63.1 treatment.

[0475] At termination, liver and epididymal fat was isolated and weighed using a balance. One piece of each tissue was fixed in 10% buffered formalin for 24 hours. Tissues were sectioned and stained as indicated in Figures 11 and 13.

[0476] Example 4

[0477] Anti-GIPR Antibody Generation

[0478] Mouse Strains

[0479] Fully human antibodies to human GIPR were generated by immunizing XENOMOUSE® transgenic mice (U.S. Pat. Nos. 6,114,598; 6,162,963; 6,833,268; 7,049,426; 7,064,244, which are incorporated herein by references in their entirety; Green et al., 1994, *Nature Genetics* 7:13-21; Mendez et al., 1997, *Nature Genetics* 15:146-156; Green and Jakobovitis, 1998, *J. Ex. Med.* 188:483-495; Kellerman and Green, *Current Opinion in Biotechnology* 13, 593-597, 2002). Animals from the XMG2-K, XMG2-KL, XMG4-K and XMG4-KL XENOMOUSE® strains were used for all immunizations.

[0480] Immunizations

[0481] Multiple immunogens and routes of immunization were used to generate anti-human GIPR immune responses. For genetic immunizations, mice were immunized 12-14 times over 6-8 weeks using the Helios Gene Gun system according to the manufacturer's instructions (BioRad, Hercules, California). Briefly, expression vectors encoding wild type human or rhesus GIPR were coated onto gold beads (BioRad, Hercules, California) and delivered to the epidermis of a shaved mouse or rat abdomen. For soluble protein immunizations, mice were immunized with a human GIPR recombinant protein representing the complete N-terminal extracellular domain (1-139). Animals were immunized with recombinant protein mixed with Alum and CpG-ODN 10 times over 4-6 weeks using sub-cutaneous injections. The initial boost was comprised of 10µg while subsequent boosts contained 5-10µg. GIPR-specific serum titers were monitored by live-cell FACS analysis on an Accuri flow cytometer (BD Biosciences) using transiently transfected 293T or stably transfected CHO cells. Animals with the highest antigen-specific serum titers against human and rhesus GIPR were sacrificed and used for hybridoma generation (Kohler and Milstein, 1975).

[0482] Hybridoma Generation

[0483] Animals exhibiting suitable serum titers were identified and lymphocytes were obtained from spleen and/or draining lymphnodes. Pooled lymphocytes (from each immunization cohort) were dissociated from lymphoid tissue by grinding in a suitable medium (for example, Dulbecco's Modified Eagle Medium (DMEM); Invitrogen, Carlsbad, CA). B cells were selected and/or expanded using standard methods, and fused with a suitable fusion partner using techniques that were known in the art.

[0484] Example 5

[0485] Binding Analysis for GIPR Engineering Panel and covariance ("CV") Fixes using MASS-1

[0486] MASS-1, sensor chip SPR Affinity Sensor - High Capacity Amine and amine coupling kit were from Sierra Sensors (Greenville, RI). Surfactant P-20, 10 mM sodium acetate, pH 4.0, and 10 mM glycine pH1.5 were from Biacore, Inc. (Piscataway, NJ). Phosphate-buffered saline (PBS, 1X, no calcium chloride, no magnesium chloride) was from Gibco. Bovine serum albumin (BSA, fraction V, IgG free) was from Sigma. Goat-anti-huFc antibody was from Jackson ImmunoResearch Inc. (West Grove, PA).

[0487] Immobilization of goat-anti-huFc antibody to a sensor chip surface was performed according to manufacturer's instructions. Briefly, carboxyl groups on the sensor chip surfaces were activated by injecting 100 μ L of a mixture containing 75 mg/mL N-ethyl-N'-(dimethylaminopropyl) carbodiimide (EDC) and 1.9 mg/mL N-hydroxysuccinimide (NHS) at 12.5 μ L/min. Goat-anti-huFc antibody was diluted in 10 mM sodium acetate, pH 4.0 at 20 μ g/mL and injected over the activated chip surfaces (flow cells channel 1-8/A&B) at 12.5 μ L/min for 8 minutes. Excess reactive groups on the surfaces were deactivated by injecting 100 μ L of 1 M ethanolamine. Final immobilized level was $\sim$ 4000 - 5000 resonance units (RU).

[0488] Binding assays were carried out on the immobilized goat anti-huFc antibody surface by MASS-1. The experiment was performed at 25°C. The instrument running buffer was 0.005% P20/PBS. The goat anti-huFc capture antibody was covalently attached to the sensor chip surface via standard amine coupling to flow cells channel 1-8/A&B. The anti-huGIPR antibodies were diluted in sample buffer (0.1 mg/mL BSA, 0.005% P20, PBS) to 10 nM then captured to flow cells channel B. Channel A was as a blank reference surface without injection of anti-huGIPR antibody. The captured response range of channel B was $\sim$ 100 - 400 RU. Then 200 nM huGIPR ECD was injected over the goat anti-huFc antibody captured anti-huGIPR antibody surfaces at flow rate 25 μ L/min for 3 minutes. After a 6 minute dissociation, each surface was regenerated by injecting 10 mM Glycine, pH1.5 for 30 seconds. The sensorgrams were analyzed using MASS-1 software (AnalyserR2, version 0.1.6.5).

[0489] Each anti-huGIPR antibody sample was captured on a goat anti-huFc antibody coated MASS-1 sensor chip surface. 200 nM of huGIPR ECD was injected over captured sample surfaces. After a 6 minute dissociation, each surface was regenerated by injecting 10mM Glycine, pH1.5. The resulting sensorgrams showed huGIPR ECD binding with anti-huGIPR antibody 6H1 family. See Table 8 and Figure 15.

[0490] Table 8:

[0491] The table summarizes the dissociation rate constant (kd) for the 6H1 family samples.

Ab Name	iPS	Protein Lot	kd [1/s]
21-143_6H1.005	iPS:359879	PL-42048	9.1E-04
21-143_6H1.006	iPS:361069	PL-42049	1.9E-04
21-143_6H1.007	iPS:361073	PL-42050	7.6E-04
21-143_6H1.008	iPS:361077	PL-42051	4.9E-04
21-143_6H1.009	iPS:361853	PL-42052	7.0E-04
21-143_6H1	iPS:335940	PL-42053	8.3E-04
control 4B1.007	iPS:336119	PL-40272	1.4E-03

[0492] The sensorgrams were analyzed using MASS-1 software (AnalyserR2, version 0.1.6.5). The graph summarizes the calculated dissociation rate constant (1/s) for the tested samples binding with huGIPR ECD. Results are shown in Figure 14A-14Q and Figure 15.

[0493] Example 6

[0494] Description of Biological Assay used to Characterize Potency of Lead Panel

[0495] A cyclic AMP assay (no. 62AM4PEC CISBIO) was used to determine the potency of anti-GIPR antibodies. 293T cells were grown in suspension and transiently transfected with human GIPR using Lipofectamine 2000 (no. 11668027 Life Technologies). 24hrs after transfection, antibody was titrated from high to low concentration in black 384 well plates (no. 3712 Corning Life Sciences) with a final volume of 10 μ ls/well in assay buffer (DMEM no. D5671 Sigma supplemented with 15mM HEPES and 0.1% Bovine Serum Albumin). GIPR transfected cells were then added to the assay plate at 10,000 cells per well (10 μ ls/well) in the presence of 1:40 cAMP-d2 (CISBIO kit component). Assay plates were allowed to incubate for 30 minutes at 37°C, 5% CO₂. A working stock of Human GIP (no. 027-02 Phoenix Pharmaceuticals) at 175pM and 2.8mM IBMX was prepared in assay buffer and 10 μ ls/well of this solution was added to assay plates. Plates were then incubated at 37°C, 5% CO₂ for 30 minutes. Anti-cAMP-Eu3+-Cryptate (CISBIO kit component) was prepared at 1:40 in conjugate and lysis buffer (CISBIO kit component) and 15 μ ls/well of this solution was added to the assay plates and allowed to incubate for 1 hour at room temperature. Homogeneous time-resolved fluorescence was then collected on a Tecan Genios Pro multimode microplate reader using an excitation wavelength of 320 nM, a lag time of 150 μ s and an integration time of 50 μ s. Light emission was then detected at both 620 nM and 665 nM. Collected data was then reported as a FRET ratio of A665/A620 multiplied by a factor of

10000 as per CISBIO kit insert instructions. Percent inhibition of hGIP binding to transiently expressed GIPR was calculated by subtracting FRET ratio of cells plus hGIP (f1) from FRET ratio of cells plus antibody plus hGIP (f2) divided by FRET ratio of cells plus hGIP (f1) subtracted from FRET ratio of cells alone (f3) multiplied by 100: % Inhibition = $[(f2-f1) / (f3-f1)] \times 100$. IC60 values are shown in Figures 14Q-14Q and cAMP results are shown in Table 9.

[0496] Table 9

iPS	Construct	kd [1/s]	Hu GIPR cAMP Assay (Conc. mAb @ 60% Inhibition in nM)	Rhesus GIPR cAMP Assay (Conc. mAb @ 60% Inhibition in nM)
1	4H9.004			
iPS:336079	4H9.004	1.1E-03	0.12	0.43
iPS:359783	4H9.004.001	1.8E-03	0.51	0.43
iPS:360931	4H9.004.002	1.4E-03	0.75	0.76
iPS:360938	4H9.004.003	1.5E-03	0.59	0.50
iPS:360945	4H9.004.004	1.6E-03	0.81	0.44
iPS:360951	4H9.004.005	1.6E-03	0.27	0.65
iPS:359763	4H9.004.006	4.2E-03	1.15	0.35
2	4B1			
iPS:335916	4B1	1.7E-03	0.93	0.67
iPS:360957	4B1.010	3.8E-03	2.46	1.14
iPS:360964	4B1.011	1.2E-03	1.34	0.51
iPS:360970	4B1.012	3.0E-03	4.77	1.01
iPS:360976	4B1.013	3.4E-03	4.50	1.35
iPS:360980	4B1.014	2.8E-03	2.46	0.95
iPS:359787	4B1.015	5.6E-03	2.65	0.84
iPS:360984	4B1.016	3.1E-03	4.87	1.57
3	18F2			
iPS:335924	18F2	1.5E-03	0.72	0.80
iPS:360988	18F2.002	3.8E-03	3.59	2.23
iPS:360997	18F2.003	2.4E-03	6.69	2.01
iPS:361001	18F2.004	5.8E-03	7.04	2.72
iPS:361007	18F2.005	1.4E-03	1.62	1.13
iPS:361011	18F2.006	1.4E-03	1.59	0.52
iPS:361015	18F2.007	3.7E-03	2.72	1.94
iPS:361019	18F2.008	1.2E-03	4.89	1.76
iPS:361023	18F2.009	2.4E-03	2.23	1.28

iPS:361030	18F2.010	3.7E-03	5.73	1.75
iPS:360537	18F2.011	no binding	> [Ab] Tested	> [Ab] Tested
iPS:361037	18F2.012	2.8E-03	7.87	1.88
iPS:361847	18F2.013	2.8E-03	> [Ab] Tested	> [Ab] Tested
4	2F11			
iPS:335943	2F11	no binding	> [Ab] Tested	> [Ab] Tested
iPS:359942	2F11.002	6.0E-02	103.22	39.97
iPS:361041	2F11.003	9.8E-03	4.79	1.79
iPS:361045	2F11.004	5.3E-02	108.57	35.51
iPS:361051	2F11.005	3.6E-02	84.34	68.57
iPS:361057	2F11.006	1.1E-02	1.33	1.30
iPS:361061	2F11.007	1.2E-02	2.20	1.82
iPS:361065	2F11.008	3.0E-02	153.65	57.35
iPS:359951	2F11.009	3.6E-02	147.64	36.91
iPS:359958	2F11.010	4.3E-02	15.94	8.24
5	6H1			
iPS:335940	6H1	8.3E-04	0.21	
iPS:359867	6H1.002	7.6E-04	0.22	0.31
iPS:359871	6H1.003	3.7E-04	0.31	0.18
iPS:359875	6H1.004	1.2E-04	0.12	0.79
iPS:359879	6H1.005	9.1E-04	0.80	0.49
iPS:361069	6H1.006	1.9E-04	0.59	0.47
iPS:361073	6H1.007	7.6E-04	0.80	0.55
iPS:361077	6H1.008	4.9E-04	0.60	0.44
iPS:361853	6H1.009	7.0E-04	0.23	0.15
6	6A5			
iPS:336090	6A5.004	3.6E-04	0.60	0.76
iPS:361081	6A5.004.001	2.8E-03	0.27	0.90
iPS:361087	6A5.004.002	2.2E-03	0.15	0.88
iPS:361093	6A5.004.003	1.5E-03	0.42	0.78
iPS:361097	6A5.004.004	3.6E-03	0.76	0.97
iPS:361103	6A5.004.005	7.7E-04	0.28	0.62
iPS:361107	6A5.004.006	1.8E-03	0.28	0.77
iPS:361111	6A5.004.007	2.3E-03	0.39	0.61
iPS:361115	6A5.004.008	1.7E-03	0.53	0.82
iPS:361122	6A5.004.009	no binding	> [Ab] Tested	23.34
iPS:359898	6A5.004.010	4.6E-03	1.75	0.81
iPS:359892	6A5.004.011	2.7E-03	1.51	
7	5G12			
iPS:362053	5G12.005.001	8.2E-02	15.1	10.9
iPS:336069	5G12.006	7.3E-03	0.6	0.8
iPS:361129	5G12.006.001	8.1E-03	1.8	0.9

iPS:361138	5G12.006.002	8.1E-03	2.1	1.0
iPS:361142	5G12.006.003	6.2E-03	> [Ab] Tested	> [Ab] Tested
iPS:359921	5G12.006.004		no sample	no sample
iPS:361146	5G12.006.005	7.8E-03	26.1	5.3
iPS:361153	5G12.006.006	7.2E-03	1.0	0.9
8 2A11				
iPS:335959	2A11		no sample	no sample
iPS:359569	2A11.002	3.0E-03	> [Ab] Tested	> [Ab] Tested
iPS:335967	2A11.003	no binding	> [Ab] Tested	> [Ab] Tested
iPS:361160	2A11.004	no binding	> [Ab] Tested	> [Ab] Tested
iPS:361167	2A11.005	no binding	> [Ab] Tested	> [Ab] Tested
9 2G10_LC1				
iPS:336043	2G10_LC1	1.6E-03	0.80	0.67
iPS:361174	2G10_LC1.003	1.1E-03	0.57	0.85
iPS:361180	2G10_LC1.004	1.2E-03	0.31	0.58
iPS:361187	2G10_LC1.005	8.5E-04	0.72	0.43
iPS:361194	2G10_LC1.006	1.0E-03	1.04	0.52
iPS:359611	2G10_LC1.007	2.8E-02	68.24	16.31
iPS:359617	2G10_LC1.008	2.4E-02	11.93	4.00
iPS:361198	2G10_LC1.009	1.5E-03	2.78	0.71
iPS:361204	2G10_LC1.010	1.4E-03	1.83	0.86
10 17H11				
iPS:336101	17H11.004	1.0E-03	0.27	0.27
iPS:359623	17H11.004.001	9.3E-04	0.27	0.22
11 18E3				
iPS:336026	18E3	3.2E-03	0.31	0.25
iPS:359646	18E3.002	3.3E-03	0.45	0.16
iPS:361208	18E3.003	3.4E-03	0.29	0.12
iPS:359630	18E3.004	3.5E-03	0.31	0.06
iPS:359639	18E3.005	2.8E-03	0.29	0.10
iPS:361212	18E3.006	3.8E-03	0.06	0.12
iPS:361216	18E3.007	3.6E-03	0.07	0.24
iPS:361220	18E3.008	3.2E-03	0.25	0.37
12 5C2				
iPS:335972	5C2	2.4E-03	1.30	0.53
iPS:361224	5C2.006	3.2E-02	> [Ab] Tested	> [Ab] Tested
iPS:361231	5C2.007	2.9E-03	0.28	0.66
iPS:361238	5C2.008	3.0E-02	> [Ab] Tested	> [Ab] Tested
iPS:359687	5C2.009	2.3E-03	1.27	0.60
iPS:361242	5C2.010	2.6E-02	> [Ab] Tested	> [Ab] Tested
iPS:361249	5C2.011	2.6E-02	> [Ab] Tested	> [Ab] Tested
iPS:361256	5C2.012	2.7E-03	1.56	0.65
iPS:361263	5C2.013	1.5E-02	12.01	7.02
iPS:361270	5C2.014	2.5E-03	1.10	0.54
iPS:359671	5C2.015	2.8E-02	> [Ab] Tested	> [Ab] Tested

iPS:359680	5C2.016	2.9E-02	> [Ab] Tested	> [Ab] Tested
13	11C1			
iPS:335988	11C1	4.3E-03	1.24	0.65
iPS:361277	11C1.002	3.5E-03	0.40	0.39
iPS:361284	11C1.003	3.7E-03	0.73	0.48
iPS:361291	11C1.004	3.5E-03	0.29	0.33
iPS:359714	11C1.005	3.9E-03	0.43	0.42
iPS:361295	11C1.006	4.1E-03	0.48	0.51
iPS:361299	11C1.007	4.1E-03	0.25	0.40
iPS:361303	11C1.008	3.7E-03	0.15	0.43
iPS:359705	11C1.009	5.3E-02	> [Ab] Tested	> [Ab] Tested
iPS:361307	11C1.010	3.6E-02	> [Ab] Tested	> [Ab] Tested
14	13H12			
iPS:335980	13H12	1.5E-03	0.93	0.67
iPS:361314	13H12.002	1.1E-03	2.18	0.95
iPS:359746	13H12.003	2.0E-03	2.11	0.83
iPS:361321	13H12.004	1.8E-03	3.38	0.56
iPS:359739	13H12.005	2.7E-02	> [Ab] Tested	> [Ab] Tested
iPS:361328	13H12.006	6.3E-04	1.87	0.92
15	12H11			
iPS:335996	12H11	2.9E-03	3.17	0.79
iPS:361332	12H11.002	3.4E-03	1.01	0.45
iPS:361339	12H11.003	3.9E-03	0.71	0.60
iPS:361346	12H11.004		> [Ab] Tested	> [Ab] Tested
iPS:361353	12H11.005	3.8E-03	1.28	0.61
iPS:361360	12H11.006	3.6E-03	0.47	0.59
iPS:361367	12H11.007	3.0E-03	0.76	0.56
iPS:361374	12H11.008	2.1E-03	0.95	0.56
iPS:361381	12H11.009	2.4E-03	0.77	0.60
iPS:361385	12H11.010	2.6E-03	1.09	0.71
iPS:361389	12H11.011	3.3E-03	0.56	0.47
iPS:361393	12H11.012	1.3E-03	0.43	0.57
iPS:361397	12H11.013	3.7E-02	> [Ab] Tested	> [Ab] Tested
iPS:361404	12H11.014	3.6E-02	> [Ab] Tested	> [Ab] Tested
16	2C2			
iPS:336177	2C2.005	7.1E-04	0.89	0.61
iPS:361408	2C2.005.001	1.6E-03	0.73	0.96
iPS:361414	2C2.005.002	1.5E-03	0.94	0.95
iPS:361420	2C2.005.003	1.0E-03	0.86	1.23
iPS:361426	2C2.005.004	1.5E-03	0.97	1.26
iPS:361432	2C2.005.005	1.6E-03	0.07	0.85
iPS:361438	2C2.005.006	1.2E-03	0.69	0.97
iPS:361444	2C2.005.007	1.2E-03	0.62	0.76

iPS:361450	2C2.005.008	1.2E-03	0.78	0.65
iPS:361456	2C2.005.009	1.4E-03	0.82	0.68
iPS:361462	2C2.005.010	1.4E-03	0.76	0.58
iPS:361468	2C2.005.011	1.6E-03	0.75	0.49
iPS:361474	2C2.005.012	1.5E-03	0.69	0.50
iPS:361480	2C2.005.013	2.7E-03	1.33	1.23
iPS:361487	2C2.005.014	2.8E-03	2.23	1.14
iPS:361857	2C2.005.015	1.1E-03	3.07	0.83
17	17B11			
iPS:336171	17B11.002	3.1E-03	< 0.1nM	0.21
iPS:361493	17B11.002.001	2.8E-03	0.06	0.29
iPS:361501	17B11.002.002	3.0E-03	0.11	0.00
iPS:361505	17B11.002.003	2.1E-03	0.09	0.08
iPS:361509	17B11.002.004	2.6E-03	0.82	0.17
iPS:361516	17B11.002.005	3.2E-03	0.22	0.08
iPS:360584	17B11.002.006	3.6E-03	0.17	0.00
iPS:361520	17B11.002.007	1.4E-02	0.96	0.90
iPS:360572	17B11.002.008	1.9E-02	6.37	7.89

[0497] Example 7

[0498] Figure 16 provides an overview of the mouse pharmacodynamic assay to test anti-GIPR Antibodies. Male C57BL/6 DIO mice at 16 weeks old were purchased from Jackson laboratory. After arrival, mice were single housed and continued on high fat diet (60 kcal % fat, Research diet) for 2 weeks before pharmacological study. Four days before the start of treatments, 4 h fasting glucose and insulin were measured. Body weight was recorded twice a week during the week before the treatments start and the day of start. The mice were randomized into groups and received one of the following treatments: (1) vehicle (10 mM acetate, 150 mM NaCl, pH 5.0), (2) 0.008 mg/kg 5G12.006, (3) 0.04 mg/kg 5G12.006, (4) 0.2 mg/kg 5G12.006, (5) 1 mg/kg 5G12.006, (6) 5 mg/kg 5G12.006. All treatments were administrated once a week intraperitoneally for four weeks. Body weight was measured twice a week. Results are shown in Figure 17. Anti-GIPR antibody 5G12.006 binds to both murine and human GIPR.

[0499] Example 8

[0500] The study design is outlined in Figure 18. Male C57BL/6 Diet-Induced Obese mice (Jackson Lab), 18 weeks old at start (on high fat diet for 12 weeks) were randomized based on body weight. Mice were dosed each week for 4 weeks. Body weights were recorded twice

a week; not fasted glucose measured on day 18 and fasted insulin measured on day 29. Terminal blood collected for measurement of total cholesterol, and triglycerides. Intraperitoneal glucose tolerance test (IPGTT) was performed on day 25 with 4 hour fast with 1 g/kg of glucose. After 4 weeks, study was terminated following a 4 hour fast. Serum samples were collected and livers were weighed. Blood was collected from tail vein or cardiac puncture at termination. Serum samples were obtained by centrifugation of blood collection tubes at 10000rpm. Serum insulin levels were determined by using mouse high range insulin ELISA (ALPCO Diagnostics). The triglyceride levels were measured using an Infinity triglyceride assay kit (Thermo Scientific). Total cholesterol was measured using an Infinity total cholesterol kit (Thermo Scientific). At termination, liver and epididymal fat were isolated and weighed using a balance.

[0501] Figure 19 shows that GIPR Antibody 5G12.006 treatment results in reduced body weight gain. Figure 20 shows that GIPR Antibody 5G12.006 treatment results in improved glucose tolerance. Figure 21 shows that GIPR Antibody 5G12.006 treatment results in lower glucose and insulin levels. Figure 22 shows that GIPR Antibody 5G12.006 treatment results in lower liver weights. Figure 23 shows that GIPR Antibody 5G12.006 total cholesterol levels.

[0502] Example 9

[0503] Figure 24 provides an overview of the study used to determine the effects of chronic treatment of diet induced obese (DIO) mice with the mouse anti-mouse GIPR Ab (2.63.1) in combination with the GLP-1R agonist Liraglutide. Male C57BL/6 DIO mice were purchased from Jackson laboratory. Mice were single housed and continued on high fat diet (60 kcal % fat, Research Diets). Mice at 35 weeks old were randomized into groups and received one of the following treatments: A: vehicle (10 mM acetate, 9% sucrose, pH 5.2, and saline); B: 2.63.1 (30 mg/kg, twice a week); C: Liraglutide (0.3 mg/kg, once a day) and D: 2.63.1 (30 mg/kg, twice a week) and Liraglutide (0.3 mg/kg, once a day). All treatments were administrated intraperitoneally.

[0504] Blood samples were collected from tail vein or cardiac puncture at termination. Serum insulin levels were determined by using mouse high range insulin ELISA (ALPCO Diagnostics). Serum leptin levels were measured using mouse and rat leptin ELISA kit from BioVendor. The triglyceride levels were measured using an infinity triglyceride assay kit (Thermo Scientific). Total cholesterol was measured using an infinity total cholesterol kit

(Thermo Scientific). At termination, liver, epididymal fat and inguinal fat were isolated and weighed using a balance.

[0505] Body composition was determined using the minispec whole body composition analyzer (Bruker).

[0506] For the oral glucose tolerance test (OGTT), mice were fasted for 4 hours. Glucose levels were measured and blood samples were taken from the tail vein before the OGTT was initiated. A bolus of glucose (2g/kg) was given orally by a gavage needle. Glucose levels were measured at 15, 30 and 60 min after glucose administration using a glucose meter (Abbott).

[0507] Figures 25-34 show that treatment with anti-mouse GIPR (antibody 2.63.1) alone prevented weight gain, lowered glucose and insulin. In addition, there was dramatic weight loss from treatment of 2.63.1 in combination with Liraglutide. The effect is more than additive as the weight loss upon treatment with the combination was greater than the sum of the weight loss provided by each agent in isolation, indicating synergistic effect. The reduced body weight was predominantly loss of fat mass. The mice had improved glucose and insulin levels and improved glucose tolerance from Liraglutide alone and combination. The mice also had significantly lowered serum total cholesterol levels.

[0508] Example 10

[0509] Figure 35 provides an overview of the study used to determine the effects of chronic treatment of diet induced obese (DIO) mice with the mouse anti-mouse GIPR Ab (2.63.1) in combination with GLP-1R agonists Liraglutide, Dulaglutide or Exendin IV. Male C57BL/6 DIO mice were purchased from Jackson laboratory. Mice were singly housed and continued on high fat diet (60 kcal % fat, Research diet) after arrival. Mice at 37 weeks old were randomized into groups and received one of the following treatments: A: vehicle (10 mM acetate, 9% sucrose, pH 5.2 once a week, and saline once a day); B: 2.63.1 (25 mg/kg, once a week); C: DDulaglutide (1 mg/kg, twice a week); D: 2.63.1 (25 mg/kg, once a week) and DDulaglutide (1 mg/kg, twice a week); E: Liraglutide (0.3 mg/kg, once a day); F: 2.63.1 (25 mg/kg, once a week) and Liraglutide (0.3 mg/kg, once a day); G: Exendin IV (0.01 mg/kg, once a day); H: 2.63.1 (25 mg/kg, once a week) and Exendin IV (0.01 mg/kg, once a day). All treatments were administered intraperitoneally.

[0510] Blood samples were collected from tail vein or cardiac puncture at termination. Serum insulin levels were determined by using mouse high range insulin ELISA (ALPCO

Diagnostics). The triglyceride levels were measured using an infinity triglyceride assay kit (Thermo Scientific). Total cholesterol was measured using an infinity total cholesterol kit (Thermo Scientific).

[0511] Body composition was determined using the minispec whole body composition analyzer (Bruker).

[0512] For oral glucose tolerance test, mice were fasted for 4 h. Glucose levels were measured and blood samples were taken from the tail vein before the OGTT was initiated. A bolus of glucose (2 g/kg) was given orally by a gavage needle. Glucose levels were measured at 15, 30 and 60 min after glucose administration using a glucose meter (Abbott).

[0513] This study demonstrates that GIPR Ab 2.63.1 has synergistic effect on weight loss and fat mass loss with the GLP-1R agonists tested: Liraglutide, Dulaglutide, and Exendin IV (Figures 35-40).

[0514] Example 11

[0515] Figure 41 provides an overview of the study used to determine the effects of chronic treatment of diet induced obese (DIO) mice pre-treated with Liraglutide with the mouse anti-mouse GIPR Ab (2.63.1). C57BL/6 DIO male mice (17 week old) fed Research Diets D12492 (60% kcal fat) for 13 weeks were randomized into groups. During phase 1 (pre-treatment phase), animals were intraperitoneally dosed daily for 2 weeks with either 1) saline (0.9% sodium chloride), 2) Liraglutide (BACchem #H-6724-0005) at 0.05 mg/kg, 3) Liraglutide at 0.3 mg/kg, or 4) Liraglutide 0.3mg/kg in combination with a weekly dose of mouse anti-mouse GIPR Ab (2.63.1) in vehicle (10 mM acetate, 9% sucrose, pH 5.2) at 25 mg/kg; all other groups (1-3) received a weekly dose of vehicle. During phase 2 (experimental stage) mouse anti-mouse GIPR Ab (2.63.1) treatment was initiated in the animals pre-treated with Liraglutide. Blood glucose levels were measured from retro orbital sinus using a glucose meter (Abbott) after mice were fasted for 4 hours before phase 1, end of phase 1, and at the end of the experiment. Insulin levels were determined using mouse high range insulin ELISA (ALPCO Diagnostics). Food intake was averaged over 3 days at the beginning of phase 1, beginning of the phase 2, and end of the phase 2. At necropsy white adipose tissue (epididymis and inguinal) were collected along with terminal blood. Plasma was analyzed on the Olympus chemistry analyzer for liver enzymes, cholesterol, triglycerides, and NEFA. Plasma was analyzed in mouse metabolism multiplex assay (MMHMAG-44K – EMD Millipore) for mouse hormones. These data demonstrate that the weight loss effect of anti-GIPR can be observed in animals already receiving GLP-1R agonist therapy (Figures 42-47).

[0516] Example 12.

[0517] In order to validate the effects of a GIPR antagonistic Ab alone or in combination with GLP1R agonist, a non-human primate (NHP) model was utilized.

[0518] Naïve, male, spontaneously obese cynomolgus monkeys (*Macaca fascicularis*) were acclimated and trained to experimental procedures and were sorted into four final treatment groups of n=10 monkeys each:

[0519] Species: *Macaca fascicularis*

[0520] Body Weight: >7.0 kg

[0521] BMI Range: >41 kg/m²

[0522] Age range: 10-15 years

[0523] Source: KBI colony

[0524] Number and Sex: 40/male

[0525] Animals were dosed with vehicle, GIPR antagonistic Ab 2G10_LC1.006 ("2G10"), GLP1R agonist dulaglutide, or combination of 2G10_LC1.006 and dulaglutide (co-administration) following specific dosing regimen as shown in Figure 48.

[0526] Dulaglutide was introduced to pertinent groups in a dose loading fashion for 18 days prior to 2G10_LC1.006 treatment. Groups not receiving dulaglutide were treated with dulaglutide buffer during this time.

[0527] Main endpoints of study were body weight, food intake and post treatment OGTT. Clinical chemistry parameters were also analyzed (Figures 48-57). In naïve, spontaneously obese cynomolgus monkeys, weekly treatment with 2G10 for 5 weeks demonstrate a decrease in body weight and fasting triglycerides while also preventing an increase in fasting insulin as well as glucose and insulin AUC during OGTT. Body weight, insulin and triglyceride levels were further decreased in the group of animals treated with 2G10 and Dulaglutide in comparison to the group of animals treated with Dulaglutide only.

[0528] Example 13.

[0529] 2G10_LC1.006 mAb (hereafter and in figures known as "2G10") was expressed in 293-6E cells. The protein was purified by mAb SelectSure column and further purified on

size exclusion column. Purified mAb was cleaved with immobilized papain at 37 °C for 4 hour. The cleaved Fab and Fc were separated by mAb SelectSure column. Fab fragment was polished on size exchange column.

[0530] A Caspase 3 cleavage site was engineered in the hinge region for the following antibodies to allow efficient cleavage of Fc: 2C2.005.014 (hereafter and in figures known as “2C2”), 6H1.004 (hereafter and in figures known as “6H1”) and 17H11.004.001 (hereafter and in figures known as “17H11”). The antibodies are expressed in 293-6E cells and were purified by mAb Select Sure column. Purified mAb was cleaved with Caspase 3 at 4 °C overnight. The Fc, uncleaved mAb and Caspase 3 were removed by tandem His-Trap and mAb SelectSure column. The Fab fragment was polished on size exchange column.

[0531] Human GIPR ECD (amino acid 24-138) and a truncated version of human GIPR ECD (amino acid 24-123) were expressed in E.coli as inclusion bodies. The inclusion body was solubilized and refolded. Refolded human GIPR ECD were purified on size exclusion and MonoQ column, and polished on size exclusion column.

[0532] 1. Complex purification and crystallization

[0533] The following huGIPR-Fab complexes were formed by mixing Fab fragments and excess molar ratio of huGIPR:

[0534] 1). human GIPR ECD (24-138) with Fab 2G10,

[0535] 2). human GIPR ECD (24-138) with Fab 2C2,

[0536] 3). human GIPR ECD (24-138) with Fab 6H1,

[0537] 4). human GIPR ECD (24-123) with Fab 17H11.

[0538] The complexes were incubated on ice for 30 minutes and purified on Supderdex 75 16/600 column. Purified complexes were concentrated to 10-15 mg/ml and screened against commercial high throughput crystallization screens. Crystals were observed under following conditions for each complex:

[0539] huGIPR ECD (24-138) with Fab2G10: 10% PEG4000 and 20% isopropanol.

[0540] huGIPR ECD (24-138) with Fab2C2: 20-35% PEG4000, 0.2 M MgCl₂, 0.1 M Hepes or Tris pH 7.0-8.5,

[0541] huGIPR ECD (24-138) with Fab 6H1: : 20% PEG4000, 0.1 M Na Citrate, pH 5.5 18% isopropanol

[0542] huGIPR ECD (24-123) with Fab17H11: : 20% PEG4000, 18-20 % isopropanol, 0.1 M Na Citrate pH 5.5 or 0.1 M MES, pH 6.0

[0543] 2. Data collection and structure solution

[0544] The crystals were flash frozen in liquid nitrogen with either 25% glycerol supplemented to the well solution or oil as cryo-protectant. High-resolution datasets were collected at the Advanced Light Source, Lawrence Berkeley National Lab (Berkeley, CA) and Advanced Photon Source, Argonne National lab (Chicago, IL). The data was processed with XDS and scaled using AIMLESS in CCP4 program suite. The structure was solved by molecular replacement method with program PHASER using published huGIPR ECD domain structure (PDB code: 4HJ0) and the constant and variable domain of the Fab structure (Amgen internal data) as search model. Iterative structure refinement was carried out with REFMAC5 in CCP4 or Phenix.refine and model building is performed in COOT.

[0545] The interface analysis was carried out with program PISA, AREAMOL and NCONTACT in CCP4 package. The figures were prepared with Pymol.

[0546] 3. Results

[0547] A. Overall structure of huGIPR-Fab complexes

[0548] huGIPR-Fab 2G10 complex was crystallized and the structure solved at 1.9 Å resolution. There are two pairs of huGIPR-Fab 2G10 complexes in the asymmetric unit (Figure 57). Each complex consists of one huGIPR ECD molecule and one Fab 2G10 fragment. The huGIPR molecule adopts a typical $\alpha\beta\beta\alpha$ fold that is similar to other class B GPCR ECD domains, such as GCGR and GLP1R. The Fab 2G10 utilizes all six CDR loops of the heavy chain and light chain to interact with the huGIPR ECD domain (Figure 58A). The interface on huGIPR ECD includes $\alpha 1$, $\beta 1$ - $\beta 2$ loop, $\beta 3$ - $\beta 4$ loop, $\beta 4$ - αC loop and αC . Note that the αC segment is disordered in previously solved GIPR-GIP complex structure. The buried solvent accessible surface area on huGIPR is 1184 Å², of which 917 Å² is contributed by the 2G10 heavy chain and 267 Å² by the light chain.

[0549] The cocrystal structure of huGIPR-Fab 2C2 complex was solved at 2.3 Å resolution. There are two pairs of huGIPR-Fab 2C2 complexes in the asymmetric unit (Figure 59). Each complex consists of one huGIPR ECD molecule and one Fab 2C2 fragment. The Fab 2C2 utilizes CDR H1 and H3 of the heavy chain and CDR L2 of the light chain to interact with the huGIPR ECD domain (Figure 60A). The interface on the huGIPR ECD domain includes $\alpha 1$, $\beta 1$ - $\beta 2$ loop, $\beta 3$ - $\beta 4$ loop, and the long loop after $\beta 4$. The αC helix is disordered in the huGIPR-Fab 2C2 complex (Figure 60B). The total buried solvent accessible surface area between

huGIPR and Fab 2C2 is 1078 Å², of which 806 Å² is contributed by the 2C2 heavy chain and 272 Å² by the light chain.

[0550] The complex structure of huGIPR-Fab 6H1 was solved at 2.65 Å resolution. There is one pair of huGIPR-Fab 6H1 complex in the asymmetric unit (Figure 61). The Fab 6H1 utilizes all six CDR loops of the heavy chain and light chain to interact with the huGIPR ECD domain (Figure 62A). The interface on the huGIPR ECD domain includes α 1, β 1- β 2 loop, β 3- β 4 loop, and small part of the loop after β 4 (Figure 62B). The α C helix is disordered in the huGIPR-Fab 6H1 complex. The total buried solvent accessible surface area between huGIPR and Fab 6H1 is 784 Å², of which 505 Å² is contributed by the Fab 6H1 heavy chain and 279 Å² by the light chain.

[0551] The complex structure of huGIPR-Fab 17H11 was solved at 1.6 Å resolution. There is one pair of huGIPR-Fab 17H11 complex in the asymmetric unit (Figure 63). The Fab 17H11 utilizes all six CDR loops of the heavy chain and light chain to interact with the huGIPR ECD domain (Figure 64A). The interface on the huGIPR ECD domain includes α 1, β 1- β 2 loop, β 3- β 4 loop, and part of the loop after β 4. The total buried solvent accessible surface area between huGIPR and Fab 17H11 is 739 Å², of which 299 Å² is contributed by the Fab 17H11 heavy chain and 440 Å² by the light chain.

[0552] B. The interface analysis

[0553] Two different methods were used to define the interface residues. In the first method the interface residues were defined using solvent exposure difference. The solvent accessible surface area (ASA) was calculated for each residue in huGIPR ECD domain in the complex and compared to the solvent accessible surface area of the corresponding residue stripped from complex. All amino acids with different ASA are considered interface residues.

[0554] In the second method, interface residues were selected that have at least one atom within a predefined distance to its partner protein. Two shells were defined based on the distance.

[0555] 1) Core interaction shell includes all residues with distance shorter than 5.0 Å.

[0556] 2) Boundary shell includes all residues with distance longer than 5.0 Å, but shorter than 8.0 Å to the partner protein.

[0557] The complete list of amino acid residues for human GIPR ECD that interact with four Fabs are list in the following tables.

[0558] Table 10. GIPR ECD epitope residues in GIPR-Fab 2G10 complex defined by solvent exposure differences and distance cutoff method.

[0559] Table 11. GIPR ECD epitope residues in GIPR-Fab 2C2 complex defined by solvent exposure differences and distance cutoff method.

[0560] Table 12. GIPR ECD epitope residues in GIPR-Fab 6H1 complex defined by solvent exposure differences and distance cutoff method.

[0561] Table 13: GIPR ECD epitope residues in GIPR-Fab 17H11 complex defined by solvent exposure differences and distance cutoff method.

[0562] Important residues on the human GIPR ECD that form either hydrogen bond or salt bridge interactions with Fab are summarized in Table 14.

[0563] Using similar methods, we defined the paratope residues for each of the antibodies and summarized the results in the following tables.

[0564] Table 15: Fab 2G10 paratope residues defined by solvent exposure differences and distance cutoff method.

[0565] Table 16: Fab 2C2 paratope residues defined by solvent exposure differences and distance cutoff method.

[0566] Table 17: Fab 6H1 paratope residues defined by solvent exposure differences and distance cutoff method.

[0567] Table 18: Fab 17H11 paratope residues defined by solvent exposure differences and distance cutoff method.

[0568] The epitope of the Gipg013 antibody (Structural and Pharmacological Characterization of Novel Potent and Selective Monoclonal Antibody Antagonists of Glucose-dependent Insulinotropic Polypeptide Receptor. Ravn, *et al.* J Biol Chem. 2013 Jul 5;288(27):19760-72.) was analyzed from the published structure 4HJ0 using the same methods. The results are summarized in table 19.

[0569] Figure 65 highlights the epitope of the four antibodies (2G10, 2C2, 6H1 and 17H11) and the previously published antibody Gipg013 (PDB 4HJ0) on the human GIPR ECD domain surface.

[0570] The high-resolution crystal structure has allowed identification of the interface between huGIPR ECD and four antibodies. Using two different methods, the specific amino acid residues involved in the recognition were mapped. The spatial requirement and the nature of the interaction for every interface residue are elucidated.

Table 10: GIPR ECD epitope residues in GIPR-Fab 2G10 complex defined by solvent exposure differences and distance cutoff method.

GIPR residues within 5A of 2G10			GIPR residues with 8A of 2G10			GIPR residue identified by ASA difference	
30	GLN		29	GLY		30	GLN
31	THR		30	GLN		31	THR
32	ALA		31	THR		32	ALA
33	GLY		32	ALA		33	GLY
34	GLU		33	GLY		34	GLU
35	LEU		34	GLU		35	LEU
36	TYR		35	LEU		36	TYR
37	GLN		36	TYR		37	GLN
39	TRP		37	GLN		39	TRP
66	ASP		38	ARG		66	ASP
67	MET		39	TRP		67	MET
68	TYR		40	GLU		68	TYR
87	TYR		43	ARG		87	TYR
88	LEU		65	PHE		88	LEU
89	PRO		66	ASP		89	PRO
90	TRP		67	MET		90	TRP
101	ARG		68	TYR		101	ARG
113	ARG		69	VAL		113	ARG
115	HIS		71	TRP		115	HIS
119	GLU		85	PRO		119	GLU
123	LYS		87	TYR		120	ASN
125	GLU		88	LEU		123	LYS
128	LEU		89	PRO		125	GLU
129	ASP		90	TRP		128	LEU
132	ARG		101	ARG		129	ASP
133	LEU		111	LEU		132	ARG
			112	TRP		133	LEU
			113	ARG			
			115	HIS			
			116	THR			
			118	CYS			
			119	GLU			
			120	ASN			
			122	GLU			
			123	LYS			
			124	ASN			
			125	GLU			
			126	ALA			
			128	LEU			
			129	ASP			
			130	GLN			
			131	ALA			
			132	ARG			
			133	LEU			
			134	ILE			

Table 11: GIPR ECD epitope residues in GIPR-Fab 2C2 complex defined by solvent exposure differences and distance cutoff method.

GIPR residue within 5 A of 2C2			GIPR residue within 8 A of 2C2			GIPR residue identified by ASA difference	
31	THR		30	GLN		32	ALA
32	ALA		31	THR		35	LEU
35	LEU		32	ALA		36	TYR
36	TYR		33	GLY		39	TRP
39	TRP		34	GLU		62	ASN
62	ASN		35	LEU		64	SER
64	SER		36	TYR		65	PHE
65	PHE		39	TRP		66	ASP
66	ASP		40	GLU		67	MET
67	MET		43	ARG		68	TYR
68	TYR		47	GLN		87	TYR
71	TRP		60	ALA		88	LEU
87	TYR		61	CYS		89	PRO
88	LEU		62	ASN		90	TRP
89	PRO		63	GLY		101	ARG
90	TRP		64	SER		104	GLY
101	ARG		65	PHE		105	SER
104	GLY		66	ASP		106	ASP
105	SER		67	MET		108	GLN
106	ASP		68	TYR		109	TRP
108	GLN		69	VAL		110	GLY
109	TRP		71	TRP		111	LEU
110	GLY		77	ASN		112	TRP
111	LEU		85	PRO		113	ARG
112	TRP		87	TYR		114	ASP
113	ARG		88	LEU		115	HIS
114	ASP		89	PRO		116	THR
115	HIS		90	TRP		118	CYS
116	THR		99	VAL		119	GLU
119	GLU		100	LEU		120	ASN
			101	ARG			
			102	GLN			
			103	CYS			
			104	GLY			
			105	SER			
			106	ASP			
			107	GLY			
			108	GLN			
			109	TRP			
			110	GLY			
			111	LEU			
			112	TRP			
			113	ARG			
			114	ASP			
			115	HIS			
			116	THR			
			117	GLN			
			118	CYS			
			119	GLU			
			120	ASN			
			121	PRO			

Table 12: GIPR ECD epitope residues in GIPR-Fab 6H1 complex defined by solvent exposure differences and distance cutoff method.

GIPR residues within 5 Å of 6H1			GIPR residues within 8 Å of 6H1			GIPR residues identified by ASA difference	
32	ALA		32	ALA		32	ALA
33	GLY		33	GLY		33	GLY
34	GLU		34	GLU		34	GLU
36	TYR		35	LEU		35	LEU
37	GLN		36	TYR		36	TYR
40	GLU		37	GLN		37	GLN
43	ARG		38	ARG		39	TRP
35	LEU		39	TRP		40	GLU
39	TRP		40	GLU		43	ARG
66	ASP		43	ARG		66	ASP
67	MET		67	MET		67	MET
87	TYR		65	PHE		68	TYR
88	LEU		66	ASP		87	TYR
89	PRO		68	TYR		88	LEU
90	TRP		85	PRO		89	PRO
111	LEU		87	TYR		90	TRP
112	TRP		88	LEU		111	LEU
115	HIS		89	PRO		112	TRP
119	GLU		90	TRP		113	ARG
120	ASN		111	LEU		115	HIS
			112	TRP		118	CYS
			113	ARG		119	GLU
			114	ASP		120	ASN
			115	HIS			
			118	CYS			
			119	GLU			
			120	ASN			
			121	PRO			

Table 13: GIPR ECD epitope residues in GIPR-Fab 17H11 complex defined by solvent exposure differences and distance cutoff method.

GIPR residues within 5 Å of 17H11			GIPR residues within 8 Å of 17H11			GIPR residues identified by ASA difference	
30	GLN		30	GLN		30	GLN
31	THR		31	THR		31	THR
32	ALA		32	ALA		32	ALA
33	GLY		33	GLY		33	GLY
35	LEU		34	GLU		34	GLU
36	TYR		35	LEU		35	LEU
37	GLN		36	TYR		36	TYR
39	TRP		37	GLN		37	GLN
40	GLU		38	ARG		39	TRP
43	ARG		39	TRP		40	GLU
66	ASP		40	GLU		43	ARG
67	MET		43	ARG		66	ASP
68	TYR		65	PHE		67	MET
87	TYR		66	ASP		68	TYR
88	LEU		67	MET		87	TYR
89	PRO		68	TYR		88	LEU
90	TRP		69	VAL		89	PRO
113	ARG		71	TRP		90	TRP
115	HIS		85	PRO		111	LEU
119	GLU		87	TYR		112	TRP
			88	LEU		113	ARG
			89	PRO		114	ASP
			90	TRP		115	HIS
			99	VAL		116	THR
			101	ARG		119	GLU
			111	LEU		120	ASN
			113	ARG			
			114	ASP			
			115	HIS			
			116	THR			
			118	CYS			
			119	GLU			
			120	ASN			

Table 14: List of interface residue interactions**Interactions between Fab 2G10 heavy chain and huGIPR**

Hydrogen bond interactions

huGIPR	Dist.	2G10 HC
TYR 36 [OH]	2.8	GLN 100 [OE1]
ARG 113 [NH1]	3.1	ASN 31 [OD1]
ARG 113 [NH2]	3.1	SER 30 [O]
LYS 123 [NZ]	2.9	ASP 54 [O]
ARG 132 [NH2]	3.2	LYS 58 [O]

Salt Bridges

huGIPR	Dist.	2G10 HC
HIS 115 [NE2]	3.0	ASP 54 [OD2]
GLU 125 [OE1]	3.4	LYS 58 [NZ]
ASP 129 [OD1]	2.9	LYS 58 [NZ]
ASP 129 [OD2]	3.1	LYS 58 [NZ]

Interactions between Fab 2G10 light chain and huGIPR

Hydrogen Bonds

huGIPR	Dist.	2G10 LC
ALA 32 [N]	3.4	ASN 93 [OD1]
ALA 32 [N]	3.0	ASN 92 [O]
GLY 33 [N]	2.4	ASN 92 [O]
GLN 37 [OE1]	3.2	ASN 32 [ND2]

Interactions between Fab 2C2 heavy chain and huGIPR

Hydrogen Bonds

```

-----
huGIPR | Dist. | 2C2 HC
-----+-----+-----
ARG 113 [ O ] | 3.3 | TYR 32 [ OH ]
LEU 111 [ O ] | 3.5 | ARG 98 [ NH2 ]
ASP 66 [ OD2 ] | 2.7 | TYR 113 [ OH ]
ARG 113 [ NH2 ] | 2.6 | GLY 100 [ O ]
-----'-----'-----

```

Interactions between Fab 2C2 light chain and huGIPR

Hydrogen Bonds

```

-----
huGIPR | Dist. | 2C2 LC
-----+-----+-----
SER 57 [ OG ] | 3.1 | ASP 106 [ OD1 ]
GLY 58 [ N ] | 2.8 | ASP 106 [ OD2 ]
ARG 55 [ NE ] | 2.6 | GLN 108 [ OE1 ]
TYR 50 [ OH ] | 3.2 | ARG 101 [ NH2 ]
GLN 54 [ OE1 ] | 3.5 | ASN 62 [ ND2 ]
PRO 56 [ O ] | 3.0 | GLN 108 [ NE2 ]
VAL 59 [ O ] | 3.1 | :GLN 108 [ NE2 ]
-----'-----'-----

```


Interactions between Fab 6H1 heavy chain and huGIPR

Hydrogen Bonds

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-----
huGIPR | Dist. | 6H1 HC
-----+-----
LEU 111 [ O ] | 3.8 | TYR 31 [ OH ]

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Interactions between Fab 6H1 light chain and huGIPR

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huGIPR | Dist. | 6H1 LC
-----+-----
GLU 34 [ N ] | 3.6 | L:ASN 92 [ O ]

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Interactions between Fab 17H11 heavy chain and huGIPR

Hydrogen Bonds

```

-----
huGIPR | Dist. | 17H11 HC
-----+-----
GLN 37 [ NE2 ] | 3.3 | SER 31 [ O ]
ARG 43 [ NH2 ] | 3.8 | TYR 33 [ OH ]
GLU 40 [ OE2 ] | 3.0 | TYR 33 [ OH ]
-----'-----

```

Interactions between Fab 17H11 light chain and huGIPR

Hydrogen Bonds

```

-----
huGIPR | Dist. | 17H11 LC
-----+-----
ALA 32 [ N ] | 3.0 | GLN 55 [ OE1 ]
GLN 30 [ O ] | 3.9 | TYR 49 [ OH ]

```

Table 15: Fab 2G10 paratope residues defined by solvent exposure differences and distance cutoff method

2G10 Heavy Chain						2G10 Light Chain					
Distance cutoff 5 Å		Distance cutoff 8 Å		ASA difference		Distance cutoff 5 Å		Distance cutoff 8 Å		ASA difference	
number	residue	number	residue	number	residue	number	residue	number	residue	number	residue
30	SER	28	THR	30	SER	30	SER	29	VAL	30	SER
31	ASN	29	PHE	31	ASN	32	ASN	30	SER	31	SER
32	TYR	30	SER	32	TYR	49	TYR	31	SER	32	ASN
52	TRP	31	ASN	51	ILE	91	TYR	32	ASN	49	TYR
53	PHE	32	TYR	52	TRP	92	ASN	33	LEU	91	TYR
54	ASP	33	GLY	53	PHE	93	ASN	46	LEU	92	ASN
55	ALA	50	ALA	54	ASP	94	TRP	49	TYR	93	ASN
56	SER	51	ILE	55	ALA	96	LEU	50	GLY	94	TRP
57	ASP	52	TRP	56	SER			53	THR	96	LEU
58	LYS	53	PHE	57	ASP			90	GLN		
59	TYR	54	ASP	58	LYS			91	TYR		
60	TYR	55	ALA	59	TYR			92	ASN		
65	LYS	56	SER	60	TYR			93	ASN		
66	GLY	57	ASP	65	LYS			94	TRP		
67	ARG	58	LYS	66	GLY			95	PRO		
69	THR	59	TYR	67	ARG			96	LEU		
70	ILE	60	TYR	68	PHE						
71	SER	61	ALA	69	THR						
84	ASN	62	ASP	71	SER						
100	GLN	64	VAL	72	ARG						
101	ALA	65	LYS	84	ASN						
102	ILE	66	GLY	100	GLN						
103	PHE	67	ARG	101	ALA						
105	VAL	68	PHE	102	ILE						
		69	THR	103	PHE						
		70	ILE	105	VAL						
		71	SER	106	VAL						
		72	ARG								
		73	ASP								
		74	ASN								
		75	SER								
		82	GLN								
		84	ASN								
		85	SER								
		98	ARG								
		99	ASP								
		100	GLN								
		101	ALA								
		102	ILE								
		103	PHE								
		104	GLY								
		105	VAL								
		106	VAL								
		108	ASP								

Table 16: Fab 2C2 paratope residues defined by solvent exposure differences and distance cutoff method

2C2 Heavy Chain						2C2 Light Chain					
Distance cutoff 5A		Distance cutoff 8 A		ASA difference		Distance cutoff 5A		Distance cutoff 8 A		ASA difference	
number	residue	number	residue	number	residue	number	residue	number	residue	number	residue
2	MET	1	GLN	2	MET	47	LEU	32	GLN	47	LEU
26	GLY	2	MET	26	GLY	50	TYR	33	THR	50	TYR
27	TYR	25	SER	27	TYR	54	GLN	35	ASN	54	GLN
28	THR	26	GLY	28	THR	55	ARG	37	TYR	55	ARG
32	TYR	27	TYR	30	THR	56	PRO	46	LYS	56	PRO
98	ARG	28	THR	32	TYR	57	SER	47	LEU	57	SER
100	GLY	29	PHE	98	ARG	58	GLY	48	LEU	58	GLY
101	ASP	30	THR	100	GLY	59	VAL	49	ILE	59	VAL
102	TYR	31	GLY	101	ASP	61	ASP	50	TYR	61	ASP
104	PHE	32	TYR	102	TYR			51	THR		
105	GLY	54	ASN	104	PHE			53	ASN		
107	TYR	98	ARG	105	GLY			54	GLN		
110	HIS	99	GLY	107	TYR			55	ARG		
111	TYR	100	GLY	110	HIS			56	PRO		
112	TYR	101	ASP	111	TYR			57	SER		
113	TYR	102	TYR	112	TYR			58	GLY		
116	ASP	103	VAL	113	TYR			59	VAL		
		104	PHE	116	ASP			60	PRO		
		105	GLY					61	ASP		
		106	THR					62	ARG		
		107	TYR					63	PHE		
		108	ARG								
		109	PRO								
		110	HIS								
		111	TYR								
		112	TYR								
		113	TYR								
		114	GLY								
		115	MET								
		116	ASP								
		117	VAL								
		118	TRP								

Table 17: Fab 6H1 paratope residues defined by solvent exposure differences and distance cutoff method

6H1 Heavy Chain						6H1 Light Chain					
Distance cutoff 5A		Distance cutoff 8 A		ASA difference		Distance cutoff 5A		Distance cutoff 8 A		ASA difference	
number	residue	number	residue	number	residue	number	residue	number	residue	number	residue
28	THR	26	GLY	28	THR	32	TYR	29	ILE	32	TYR
31	TYR	27	PHE	30	SER	49	TYR	30	ARG	49	TYR
32	PHE	28	THR	31	TYR	50	GLY	31	ASP	50	GLY
52	TRP	29	PHE	32	PHE	53	SER	32	TYR	53	SER
53	TYR	30	SER	52	TRP	55	GLN	33	LEU	55	GLN
98	ARG	31	TYR	53	TYR	91	HIS	46	LEU	91	HIS
100	GLY	32	PHE	77	ASN	92	ASN	48	ILE	92	ASN
101	THR	52	TRP	98	ARG	93	ASN	49	TYR	93	ASN
102	ILE	53	TYR	100	GLY	94	TYR	50	GLY	94	TYR
103	PHE	54	ASP	101	THR			51	ALA	96	PHE
105	VAL	56	SER	102	ILE			52	SER		
106	LEU	57	ASN	103	PHE			53	SER		
		59	TYR	105	VAL			54	LEU		
		74	ASN	106	LEU			55	GLN		
		77	ASN	109	ASP			56	SER		
		98	ARG					90	GLN		
		99	ASP					91	HIS		
		100	GLY					92	ASN		
		101	THR					93	ASN		
		102	ILE					94	TYR		
		103	PHE					96	PHE		
		104	GLY								
		105	VAL								
		106	LEU								
		107	LEU								
		109	ASP								
		110	TYR								

Table 18: Fab 17H11 paratope residues defined by solvent exposure differences and distance cutoff method

17H11 Heavy Chain						17H11 Light Chain					
Distance cutoff 5A		Distance cutoff 8 A		ASA difference		Distance cutoff 5A		Distance cutoff 8 A		ASA difference	
number	residue	number	residue	number	residue	number	residue	number	residue	number	residue
31	SER	30	SER	31	SER	30	ILE	27	GLN	30	ILE
32	TYR	31	SER	32	TYR	31	ILE	28	GLY	31	ILE
33	TYR	32	TYR	33	TYR	32	TRP	29	LEU	32	TRP
52	TYR	33	TYR	52	TYR	46	LEU	30	ILE	46	LEU
97	ARG	52	TYR	97	ARG	49	TYR	31	ILE	49	TYR
98	ASP	97	ARG	98	ASP	52	SER	32	TRP	50	ALA
99	VAL	98	ASP	99	VAL	53	SER	34	ALA	52	SER
100	ALA	99	VAL	100	ALA	54	LEU	46	LEU	53	SER
101	VAL	100	ALA	101	VAL	55	GLN	47	LEU	54	LEU
102	ALA	101	VAL	102	ALA	56	SER	48	ILE	55	GLN
105	ASP	102	ALA	105	ASP	67	SER	49	TYR	56	SER
		103	GLY			91	THR	50	ALA	66	GLY
		104	PHE			92	ASN	51	ALA	67	SER
		105	ASP					52	SER	91	THR
		106	TYR					53	SER	92	ASN
								54	LEU		
								55	GLN		
								56	SER		
								57	GLY		
								65	SER		
								66	GLY		
								67	SER		
								68	GLY		
								71	PHE		
								90	GLN		
								91	THR		
								92	ASN		
								93	SER		
								94	PHE		

**Table 19 GIPR ECD epitope residues in GIPR-Fab Gipg013 complex (PDB 4HJ0)
defined by solvent exposure differences and distance cutoff method**

GIPR residues within 5 Å of Gipg013		GIPR residues within 8 Å of Gipg013		GIPR residues identified by ASA differences	
number	residue	number	residue	number	residue
32	ALA	31	THR	32	ALA
33	GLY	32	ALA	33	GLY
35	LEU	33	GLY	35	LEU
36	TYR	34	GLU	36	TYR
37	GLN	35	LEU	37	GLN
39	TRP	36	TYR	39	TRP
40	GLU	37	GLN	40	GLU
43	ARG	38	ARG	43	ARG
47	GLN	39	TRP	44	ARG
65	PHE	40	GLU	47	GLN
66	ASP	41	ARG	65	PHE
67	MET	43	ARG	66	ASP
68	TYR	44	ARG	67	MET
87	TYR	47	GLN	68	TYR
88	LEU	64	SER	87	TYR
89	PRO	65	PHE	88	LEU
90	TRP	66	ASP	89	PRO
113	ARG	67	MET	90	TRP
115	HIS	68	TYR	111	LEU
119	GLU	69	VAL	113	ARG
121	PRO	71	TRP	115	HIS
122	GLU	85	PRO	119	GLU
		87	TYR	121	PRO
		88	LEU	122	GLU
		89	PRO		
		90	TRP		
		91	HIS		
		99	VAL		
		101	ARG		
		108	GLN		
		111	LEU		
		112	TRP		
		113	ARG		
		114	ASP		
		115	HIS		
		116	THR		
		117	GLN		
		118	CYS		
		119	GLU		
		120	ASN		
		121	PRO		
		122	GLU		

[0571]

CLAIMS

What is claimed is:

1. An isolated antigen binding protein that specifically binds to a human gastric inhibitory peptide receptor (GIPR) polypeptide, wherein said antigen binding protein is an antibody or a fragment thereof, and wherein said antibody comprises a CDRL1, a CDRL2, a CDRL3, a CDRH1, a CDRH2, and a CDRH3, wherein said CDRL1 comprises SEQ ID NO: 702 ; said CDRL2 comprises SEQ ID NO: 859; said CDRL3 comprises SEQ ID NO: 1016; said CDRH1 comprises SEQ ID NO: 1173; said CDRH2 comprises SEQ ID NO: 1330; and said CDRH3 comprises SEQ ID NO: 1487.
2. The isolated antigen binding protein 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 isolated antigen binding protein of claim 1 or 2, wherein said antigen binding protein is a monoclonal antibody, a polyclonal antibody, a recombinant antibody, a human antibody, a humanized antibody, a chimeric antibody, a multispecific antibody, or an antibody fragment thereof.
4. The isolated antigen binding protein of claim 3, wherein said antibody fragment is a Fab fragment, a Fab' fragment, or a F(ab')₂ fragment.
5. The isolated antigen binding protein of claim 3, wherein said antigen binding protein is a human antibody.
6. The isolated antigen binding protein of claim 3, wherein said antigen binding protein is a monoclonal antibody.
7. The isolated antigen binding protein of claim 3, wherein said antigen binding protein is of the IgG1-, IgG2- IgG3- or IgG4-type.
8. The isolated antigen binding protein of claim 7, wherein said antigen binding protein is of the IgG1- or the IgG2-type.
9. The isolated antigen binding protein of any of claim 3, wherein said antigen binding protein is coupled to a labeling group.

10. The isolated antigen binding protein of one of claim 3, wherein said antigen binding protein inhibits binding of GIP to the extracellular portion of human GIPR.

11. The isolated antigen binding protein of claim 3, wherein said antigen binding protein is an antibody or a fragment thereof, and wherein said antibody or fragment thereof comprises a light chain variable region comprising SEQ ID NO: 74 and a heavy chain variable region comprising SEQ ID NO: 231.

12. The isolated antigen binding protein of claim 3, wherein said antigen binding protein is an antibody, and wherein said antibody comprises a light chain comprising SEQ ID NO:388 and a heavy chain comprising SEQ ID NO: 231.

13. The isolated antigen binding protein of claim 1, wherein said antibody comprises a CDRL1, a CDRL2, a CDRL3, a CDRH1, a CDRH2, and a CDRH3, wherein said CDRL1 consists of SEQ ID NO: 702; said CDRL2 consists of SEQ ID NO: 859; said CDRL3 consists of SEQ ID NO: 1016; said CDRH1 consists of SEQ ID NO: 1173; said CDRH2 consists of SEQ ID NO: 1330; and said CDRH3 consists of SEQ ID NO: 1487.

14. A pharmaceutical composition comprising at least one antibody or fragment thereof according to any one of claims 1, 11, 12, and 13, and pharmaceutically acceptable excipient.